Improving dry beans (*Phaseolus vulgaris* L.) of Middle American gene pool for canning and nutritional quality traits, and drought tolerance in Zimbabwe

By

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Thesis abstract

Among the different dry beans market classes, navy bean is a modern and specialised niche market-oriented product for domestic and foreign markets. Given the high navy bean import bill, increased prevalence of drought, and micronutrient malnutrition in Zimbabwe, the development of drought tolerant, high yielding and biofortified bean cultivars with superior canning quality offers a sustainable solution to the aforementioned challenges. Therefore, the objectives of this study were: (1) to identify farmers' perceived production and marketing constraints, preferred traits and cultivars of navy bean, and strategies used to mitigate drought and heat stress in the south east lowveld region of Zimbabwe, (2) to evaluate the adaptability and stability of navy bean genotypes for grain yield and nutritional quality traits (Fe and Zn) across multiple locations in Zimbabwe, (3) to investigate the impact of drought stress on agronomic, shoot, physiological, canning and nutritional quality traits of navy beans, and identify drought tolerant genotypes with superior canning and nutritional quality, (4) to determine combining ability effects and mode of gene action of grain yield and yield-attributing traits in navy bean under drought stressed and non-stressed environments and select best combiners for effective breeding, (5) to quantify genome-wide marker-trait association of agronomic and physiological traits in dry beans under non-stressed (NS) and drought stressed (DS) conditions and to identify candidate markers for marker-assisted selection (MAS).

A participatory rural appraisal (PRA) study conducted in four villages of the Lowveld region of Zimbabwe showed that the most important constraints to navy bean production were drought stress (79.5%), heat stress (56.5%), load shedding (50%), susceptibility to pod shattering (37.5%) and poor soil fertility (32.5%). Farmer-preferred traits included tolerance to drought and heat, early maturing varieties and disease resistance. Marketing constraints included non-payment for produce in hard currency, lack of diversity in terms of off-takers, high inflation, low grain producer price, and delayed payment. Suggested mitigation strategies were mulching (18%), ridges (12%), reduced acreage (11%), and cultivating to retain more soil moisture (11%) for drought stress, while irrigating at night (32%), and adjusting planting dates (29%) were used to manage heat stress. A study on the evaluation for adaptability and stability of 84 navy bean genotypes for grain yield (GYD), seed Fe and seed Zn across four locations over two seasons in Zimbabwe was done using additive main effects and multiplicative interaction (AMMI), AMMI stability value (ASV) and yield stability index (YSI). This resulted in the identification of six genotypes (G14, G49, G37, ICA BUNSIxSXB405/3C-1C-1C-8, NAE70 and CZ108-53) with high GYD, good GYD stability and desirable seed Fe and Zn

concentrations above breeding targets of 90 and 40 ppm, respectively. The vertex genotypes ZABRA16575-26F22, ICA BUNSIxSXB405/4C-1C-1C-8 and NAE13 combined specific adaptation and high GYD with desirable micronutrient density. Furthermore, the impact of drought stress on agronomic and shoot traits, canning and nutritional quality of navy beans was conducted on 110 navy bean genotypes in 2019 and 2020 at Save Valley Experiment Station, Zimbabwe under drought stressed (DS) and non-stressed (NS) field conditions. Across environments, the genotype effect on agronomic, shoot, physiological, canning and nutritional quality traits was significant ($p < 0.001$; $p < 0.05$). Broad-sense heritability estimates were high for all canning quality traits and moderate to high for most agronomic and nutritional quality traits. Under DS conditions, the predicted genotype values ($\hat{G}$) for seed micronutrient concentrations ranged from 72.3 (NAVY LINE-48) to 120 ppm (ZABRA16575-51F22) for Fe, 31.3 (NAVY LINE-46) to 60.8 (NAE70) for Zn, while washed drained weight (WDW) varied from 224.8 (Protea) to 310 (G24), and GYD ranged from 494 (SIRAJ) to 2619 kg/ha (ZABRA16573-78F22). Terminal drought stress reduced mean stomatal conductance (SC), leaf chlorophyll content (LCC), GYD, number of mature pods per plant, number of seeds per pod, number of seeds per plant and 100-seed weight by 80, 42, 28, 26, 3, 30 and 3%, respectively. Seed Fe concentration and leaf temperature (LT) increased by 1.4% and 34% in the DS environments, respectively, whereas seed Zn decreased by 0.9%. Terminal drought stress adversely impacted the canopy biomass, pod harvest index, hydration coefficient, WDW, uniformity, shape of seed and degree of splitting. The effect of DS was less severe on the degree of clumping and percent washed drained weight. ZABRA16575-86F22 had better mean ranks across four GYD based drought tolerance indices, canning and nutritional quality traits under DS compared to the standard checks. Combining ability analysis of 28 F_2 progenies generated from an 8 x 8 half-diallel mating design and evaluated under DS and NS conditions resulted in significant general and specific combining ability (GCA; SCA) effects ($p < 0.05$) under both DS and NS for most traits. This indicated the importance of both additive and non-additive gene effects in the expression of the traits. Parents with best GCA for most of the studied traits were CZ113-13, G97, NAVY LINE-60, and G550 under NS, and ZABRA16575-73F22, G37, G97 and G550 under DS. ZABRA16575-73F22 and NAVY LINE-60 were tolerant to DS with high values for drought tolerance index (DTI) and geometric mean productivity (GMP) and low values for percentage grain yield reduction (%GYR) and drought susceptibility index (DSI). There were significant ($p < 0.001$; $p < 0.05$) positive correlations for number of pods per plant (NPPP) and 100-seed weight (SW; g) with GYD under both DS and NS.

Using an andean and middle-american diversity panel (AMDP) comprising of 185 dry beans genotypes, genome-wide marker-trait association analysis of agronomic and physiological traits in dry beans under DS and NS conditions was conducted. Genotyping was done using 24,450 Diversity Arrays Technology (DArT) markers, while the following traits: days to 50% flowering (DFW), plant height (PH), days to physiological maturity (DPM), grain yield (GYD), 100-seed weight (SW), leaf temperature (LT), leaf chlorophyll content (LCC) and stomatal conductance (SC) were recorded. Principal component and association analysis were conducted using filtered 9370 DArTseq markers. Population structure analysis revealed two sub-populations, which correspond to the andean and middle-american gene pools. Markers explained 0.08 – 0.10, 0.22 – 0.23, 0.29 – 0.32, 0.43 – 0.44, 0.65 – 0.66 and 0.69 – 0.70 of the total phenotypic variability (R^2) for SC, LT, PH, GYD, SW and DFW, respectively under DS conditions. A total of 68 significant ($p < 10^{-03}$) marker-trait associations (MTAs) and 22 putative candidate genes were identified under contrasting water regimes. Most of the identified genes had known biological functions related to regulating drought stress response, growth and development under drought stress.

In conclusion, the identified farmer-preferred traits, marketing, and production constraints should be considered by the breeding programme in Zimbabwe during the development of improved cultivars. Stable genotypes identified to be drought tolerant and to possess desirable micronutrient density, superior canning and nutritional quality should be used as parents for crossing with other cultivars to improve micronutrient density, GYD and GYD stability and also recommended for deployment in their respective mega-environments. Good general and specific combiners with desirable values of drought tolerance indices and high significant positive effects under DS should be used further in breeding for drought stress tolerance. The identified markers should be validated for use in marker-assisted breeding for drought tolerance.

Declaration 1 - Plagiarism

I, Bruce Mutari, declare the following

1. The research reported in this thesis, except where otherwise indicated, is my original research.

2. This thesis has not been submitted for any degree or examination at any other University.

3. This thesis does not contain other persons' data, pictures, graphs or other information, unless specifically acknowledged as being sourced from other persons.

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Signed:

Bruce Mutari

As the candidate's supervisor, I agree to the submission of this Thesis

Prof. J. Sibiya (Supervisor)

Prof. E. Gasura (Co-supervisor)

Declaration 2 - Publications pertaining to this thesis

Five chapters have been published (Chapter 1, Chapter 2, Chapter 3, Chapter 4 and Chapter 5) in peer-reviewed journals, whilst one other chapter (Chapter 6) has been accepted for publication in PLoS ONE journal. Details of the manuscripts published are given below.

1. **Mutari, B**., J. Sibiya, E. Gasura, A. Kondwakwenda, K. Simango, and R. Chirwa. 2022. Canning quality improvement in navy beans: genetic, environmental and compositional factors. J. Crop Improv. 36:717-746. https://doi.org/ 10.1080/15427528.2021.1998940.
2. **Mutari, B**., J. Sibiya, N.E. Bogweh, K. Simango, and E. Gasura. 2021. Farmers' perceptions of navy bean (*Phaseolus vulgaris* L.) production constraints, preferred traits and farming systems and their implications on bean breeding: a case study from South East Lowveld region of Zimbabwe. J Ethnobiol Ethnomedicine 17:13. https://doi.org/10.1186/s13002-021-00442-3.
3. **Mutari, B**., J. Sibiya, E. Gasura, A. Kondwakwenda, P.M. Matova, et al. 2022. Genotype x environment interaction and stability analyses of grain yield and micronutrient (Fe and Zn) concentrations in navy bean (*Phaseolus vulgaris* L.) genotypes under varied production environments. Field Crops. Res. 286:108607. https://doi.org/10.1016/j.fcr.2022.108607.
4. **Mutari, B**., J. Sibiya, P.M. Matova, E. Gasura, and K. Simango. 2023. Drought stress impact on agronomic, shoot, physiological, canning and nutritional quality traits of navy beans (*Phaseolus vulgaris* L.) under field conditions in Zimbabwe. Field Crops. Res. 292:108826. https://doi.org/10.1016/j.fcr.2023.108826.
5. **Mutari, B**., J. Sibiya, E. Gasura, P.M. Matova, K. Simango, and A. Kondwakwenda. 2022. Genetic analysis of grain yield and yield-attributing traits in navy bean (*Phaseolus vulgaris* L.) under drought stress. Euphytica 218:1-20. https://doi.org/10.1007/s10681-022-03001-3.
6. **Mutari B**., J. Sibiya, A. Shayanowako, C. Chidzanga, P.M. Matova, and E. Gasura. 2023. Identification of genomic regions of dry bean (*Phaseolus vulgaris* L.) associated with agronomic and physiological traits under drought stressed and well-watered conditions using genome-wide association study. Accepted for publication in PLoS ONE Journal.

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Dedication

This thesis is dedicated to my father, the late Booker Mutari who never saw this adventure.

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Abbreviations and acronyms

%GYR	Percentage grain yield reduction
AAS	Atomic absorption spectrophotometer
ABC	Alliance of Bioversity International and International Center of Tropical Agriculture
AMDP	Andean middle-american diversity panel
AMMI	Additive main effects and multiplicative interaction
ASV	Additive main effects and multiplicative (AMMI) stability value
BLUPs	Best linear unbiased predictors
BMS	Breeding management system
CB	Canopy biomass
CLG	Degree of clumping
CBI	Crop Breeding Institute
CES	Chisumbanje experiment station
CRS	Chiredzi research station
DFW	Days to flowering
DII	Drought intensity index
DPM	Days to physiological maturity
DS	Drought stressed
DSF	Days to seed fill
DSI	Drought susceptibility index
DTI	Drought tolerance index
Fe	Iron
FGDs	Focus group discussions
$\hat{G}$	Predicted genotype value
$\hat{g}$	Predicted genotypic effect of genotype
GCA	General combining ability
GEI	Genotype by environment interaction
GGE	Genotype, genotype by environment
GMP	Geometric mean productivity
GT	Genotype by trait
GVTC	Gwebi variety testing center
GYD	Grain yield

UFY	Uniformity
HC	Hydration coefficient
HRS	Harare research station
ICP-AES	Inductively coupled plasma atomic emission spectrometry
IPCA	Interaction principal component axes
LCC	Leaf chlorophyll content
LT	Leaf temperature
MAS	Marker assisted selection
MET	Multi environment yield trials
MLM	Mixed linear model
MTA	Marker-trait association
NMPP	Number of mature pods per plant
NS	Non-stressed
NSP	Number of seeds per pod
NSPP	Number of seeds per plant
PCA	Principal component analysis
PH	Plant height
PHI	Pod harvest index
PIC	Polymorphic information content
PRA	Participatory rural appraisal
PWDW	Percent washed drained weight
REML	Restricted maximum likelihood
SC	Stomatal conductance
SCA	Specific combining ability
SPAD	Soil and plant analysis development
SPG	Degree of splitting
SSA	Sub-Saharan Africa
SVES	Save valley experiment station
SW	100 seed weight
WDW	Washed drained weight
XRF	X-ray fluorescence
YSI	Yield stability index
Zn	Zinc

Chapter 1 Introduction to thesis

Background

Dry beans (*Phaseolus vulgaris* L., 2*n* = 2x = 22) is an important food, nutritional and income security legume crop in Africa and Latin America (Assefa et al., 2013a). It is an inexpensive source of vegetable proteins, and important micronutrients [iron (iron) and zinc (Zn), and vitamins] and dietary fibre for millions in many African and Latin American countries (Khanal et al., 2014; Kamfwa et al., 2015). In SSA, the crop is mostly cultivated by smallholder farmers who primarily rely on dry beans for their household food, nutrition, and income security (Beebe et al., 2013). Dry beans are consumed in different forms, which include dry grain, canned beans, snap beans, bean porridge and pre-cooked beans.

The crop was subjected to two parallel domestication events on the American continent, resulting in two different primary gene pools, namely the andean and the middle-american (Sauer, 1993). The andean gene pool originated from the Andes mountains of South America. It consists of medium (25 - 40 g per 100 seeds) and large (≥ 40 g 100 per seeds) seeded genotypes (Singh et al., 1991). On the other hand, the middle-american gene pool is native to Central America and Mexico and comprises of small seeded genotypes (≤ 25 g per 100 seeds). Different market classes of dry beans exist, and these include sugars, pintos, small blacks, yellows, red kidneys, navy/small white beans, large whites, calimas, and small reds to name a few. Among the different dry beans market classes, navy bean (middle-american gene pool) is a modern and specialised niche market-oriented product for domestic and foreign markets, and therefore, offers farmers lucrative markets.

In countries such as Argentina, United States of America (USA), Canada and Ethiopia, navy beans are among the most important food and cash crops for export (Gebeyehu, 2017). These countries export the grain to lucrative markets in Eastern Europe, Middle East, North America, and Southern Africa. Navy beans constitute 10.9%, 10.4%, 9.4% and 2.4% of the market shares in Canada, USA, Argentina and Ethiopia, respectively (Gebeyehu, 2017). In South Africa, it is the most widely used dry beans market class for canning purposes, constituting 80% of dry beans that are processed into baked beans (De Lange and Labuschagne, 2001). Navy beans are preferred for canning purposes, particularly because; i) of preference for them in local, regional and global markets, and their superior canning (not prone to leaching) and culinary qualities (cook fast and highly palatable) (Assefa et al. 2013b; Cichy et al., 2015; Qureshi and Sadohara 2019); ii) they have lower levels of phytic acid and tannins compared to the darker coloured

market classes (Huma et al., 2008) and iii) they expand to the desired seed size after soaking in water due to their small seed size (≤ 25 g per 100 seeds) (Singh et al., 1991). In 2017, navy beans was grown on 25.9 million hectares (Gebeyehu, 2017). In Africa, the crop occupies an average production area of 239,000 ha, 122,000 ha and 68,000 ha, respectively in Eastern, Southern, and Western Africa (Farrow and Muthoni-Andriatsitohaina, 2020).

The bean canning industry in Zimbabwe has an annual requirement of 4000 tonnes of navy bean for canning purposes, and over 80% of the country's navy bean production is supplied to the bean canning industry (Mukweza, personal communication, May 2018[1]). On the other hand, the annual national requirement of the other dry beans market classes in Zimbabwe is 104 850 tonnes (Ministry of Lands, Agriculture, Fisheries, Water and Rural Resettlement, 2016). Significant navy bean production in Zimbabwe started in 1995 when canning companies imported the cultivar, Ex-Rico, which was locally called Michigan pea bean (Crop Breeding Institute, 2018). Before, 1995, farmers in the Lowveld region were producing navy beans mostly for subsistence since production quantities were insignificant to supply to the industry due to lack of improved cultivars. By the year 2000, the production of Michigan pea bean had been widespread in the Lowveld region of Zimbabwe as a result of contract farming by canning companies (Crop Breeding Institute, 2018). However, cultivar release and commercialization of navy bean in Zimbabwe started in 2018 (Protea –released in July 2018, Caledon and Camellia – both released in December 2019) (Crop Breeding Institute, 2018, 2019).

Problem statement

It is important to note that Participatory Rural Appraisal (PRA) studies for identifying farmers' perceived production and marketing constraints, drought and heat stress management strategies and preferred traits of navy bean cultivars have never been conducted in Zimbabwe. This is because, before the year 2018, the bean breeding efforts at Crop Breeding Institute (CBI) focused on improving other market classes other than navy beans such as the sugars, red kidneys and calimas. Even though Katungi et al. (2017) conducted a similar study in 2016, the sampled study Districts were not the main navy bean growing regions in Zimbabwe. According to Mukweza (personal communication, May, 2018[1]), the navy bean value chain in Zimbabwe is constrained by several factors ranging from biotic, abiotic to socio-economic, despite the lack of documented sources. Consequently, these constraints have significantly contributed to the decline in its production, productivity per unit area, and market supply in recent years

[1] Head Research and Development at Cairns Foods Limited in Zimbabwe (Dry Bean Canning Company)

(Mukweza, personal communication, May, 2018[1]). As a result of these constraints, national production meets only 40% of the local consumption requirements (Tsiko, 2018). Thus, the bean canning industry in Zimbabwe is obliged to import 60% of navy bean grain from countries such as Ethiopia, South Africa, China, Zambia, and Malawi resulting in increased production costs (Tsiko, 2018). Unfortunately, bean processors experience challenges with imported navy beans (especially the ones from Malawi), which are admixtures of cultivars with different canning qualities resulting in a canned product with poor quality (Mukweza personal communication, May 2018[1]; Philp Lahm personal communication, May 2018[2]). On monthly basis, canning companies such as Cairns Foods Limited and Africa Preserves Limited (formerly Selby) import 60 tonnes of navy bean grain, spending US$72 000 and US$24 000, respectively (Philp Lahm personal communication, May 2018[2]; Mukweza personal communication, May 2018[1]). Nationally, the dry beans canning industry imports more than 100 tonnes of navy bean grain per month worth around US$124 000 (Tsiko, 2018).

As reported by Katungi et al. (2017), terminal drought stress is the major abiotic constraint affecting dry beans production in Zimbabwe. Terminal drought stress, which impacts the reproductive stages of development (flower formation, full flowering, pod formation, and grain filling) has a negative effect on stomatal conductance, total chlorophyll content, number of days to physiological maturity, grain yield, grain quality and subsequently the market value of the bean grain (Beebe et al., 2010; Darkwa et al., 2016). Part of the smallholder farmers in Zimbabwe now cultivate navy beans under rain-fed conditions to reduce costs associated with the irrigated crop during the winter season (Crop Breeding Institute, 2018). Regrettably, all the regions in which the crop is produced during the main cropping season in summer frequently experience drought stress. Additionally, most of the smallholder farmers have no capacity to apply supplemental irrigation during periods of drought stress (Katungi et al., 2017). Furthermore, the rainfall pattern changes from season to season due to climate change, consequently exposing the crop to drought stress. In addition, no work has been conducted before in Zimbabwe related to breeding navy beans for water deficit environments. Consequently, all the navy bean cultivars that are being processed in Zimbabwe are not tolerant to drought stress (Mutari et al., 2021, 2022).

The lack of navy bean cultivars in Zimbabwe that are tolerant to drought stress prompted CBI to initiate a navy bean breeding program targeting the development of cultivars that are tolerant

[2] Manager at Africa Preserves Limited (Dry Bean Canning Company)

to terminal drought stress. However, the combining ability estimates of the navy bean germplasm at CBI that were introduced from the Alliance of Bioversity International and the International Center of Tropical Agriculture (ABC) are not known. Furthermore, literature on combining ability and gene action controlling drought stress tolerance, grain yield and yield attributing traits is scanty among navy bean lines in Zimbabwe and globally. Assefa et al. (2013a, 2017) identified navy bean genotypes that were tolerant to drought stress. Unfortunately, the combining ability estimates of the drought tolerant navy bean genotypes that were identified by Assefa et al. (2013a, 2017) were never determined, making it difficult for bean breeders to use these genotypes as donors in drought tolerance breeding programs. Therefore, the scarcity of information regarding the general combining ability (GCA) estimates of navy bean genotypes under drought stressed (DS) environments presents a challenge to the development of drought tolerant navy bean genotypes adapted to the drought stressed environments in Zimbabwe. Moreover, the available limited information on other dry beans market classes regarding the inheritance of grain yield and its attributing traits under DS and non-stressed (NS) conditions is contradictory (Senbetay et al., 2015; Winnyfred et al., 2015).

In addition to drought stress, micronutrient malnutrition or hidden hunger is an important challenge in Zimbabwe. Fe deficiency is common in children under the age of 5 years, estimated to be at 72% (World Health Organization, 2015). Furthermore, the prevalence of anemia is high in this group, estimated to be 31% (World Health Organization, 2015; Kairiza et al., 2020). Moreover, according to Kairiza et al. (2020), Fe deficiency is also high, among infants of 6 to 11 months old, estimated to be 81%. In 2018, 26% of children under the age of 5 years were stunted in Zimbabwe (ZimVAC, 2018). This is above the acceptable target of 20% which was set by the United Nations Children's Fund (UNICEF) (Kairiza et al., 2020). According to Bouis and Welch (2010) and Choukri et al. (2020), the immense uptake of staple food crops, mainly cereals with low dietary intake of Fe and Zn contributes to micronutrient malnutrition. Globally, various approaches, which include genetic biofortification, dietary diversification, nutrient supplementation, and food fortification have been practised in many countries for decades to alleviate the challenge of malnutrition (Bouis and Welch, 2010; Philipo et al., 2021). To reduce the prevalence of micronutrient malnutrition in Zimbabwe, the government launched the mandatory national food fortification strategy in 2015 (World Health Organization, 2015; Kairiza et al., 2020). However, the success of food fortification, dietary diversification and nutrient supplementation has had shortcomings in SSA including

Zimbabwe and, either in terms of reliability, cost-effectiveness, coverage, and sustainability (Talsma et al., 2017).

Therefore, most dry beans processing companies in Zimbabwe opt for biofortified navy bean grain for canning purposes (Mutari et al., 2022). Unfortunately, no biofortified navy bean cultivar has been released in Zimbabwe to date (Mutari et al., 2022). The review by Beebe (2020) indicated that most of the biofortified dry beans cultivars that have been released in Africa belong to other market classes other than navy beans. As a result, the mandatory food fortification policy in Zimbabwe coupled with the lack of micronutrient dense navy bean cultivars in the market has forced dry beans canning companies to process biofortified bean cultivars (NUA45 and Cherry) of other market classes other than navy beans, which were not developed for canning purposes (Crop Breeding Institute, 2018; Mutari et al., 2022). Regrettably, NUA45 is susceptible to splitting after thermal processing resulting in poor quality of the canned product (Figure 1.1; Crop Breeding Institute, 2018b; Mutari et al., 2022).

Figure 1.1 Undesirable canning quality of the micronutrient dense bean cultivar "NUA45". *Source*: Mutari et al., 2022.

Furthermore, the seed micronutrient concentrations of the elite navy bean genotypes at CBI are not known, hampering efforts to promote the widespread production and consumption of biofortified bean cultivars in Zimbabwe. Moreover, information on genotype by environment interactions (GEI) which may affect the expression of these micronutrients in elite navy bean genotypes at CBI is also not known. Contextually, there is no documented information

regarding the adaptability and stability of the elite navy bean genotypes across diverse multi-environments in Zimbabwe. On the other hand, some of the navy bean canning companies in Zimbabwe processing Protea have highlighted that the cultivar is sometimes prone to clumping during storage (Figure 1.2). As a result, the navy bean canning industry still imports the grain, a process which increases production costs and affects the profitability of a canning operation (Crop Breeding Institute, 2019). Farmers have also highlighted that Protea is a long duration cultivar, taking more than 110 days to reach physiological maturity (Crop Breeding Institute, 2019). Long duration cultivars require more irrigation cycles resulting in increased production costs. In Zimbabwe, the production of navy bean is done under diverse environmental conditions regarding weather conditions, soil structure, disease pressure, latitude, soil fertility, altitude, seasonal variation, temperature, planting times and rainfall (Katungi et al., 2017; Crop Breeding Institute, 2018).

Thus, genotypes are predisposed to the effect of genotype by environment interaction (GEI), thus reducing genetic progress and the association between genotypic and phenotypic values (Van Oosterom and Ceccarelli, 1993). As reported by Mutari et al. (2022), most scientists do not simultaneously study drought tolerance, canning and nutritional quality due to high phenotyping costs yet most of the farmers are in drought prone areas. According to Beebe et al. (2010), about 60% of cultivated dry beans globally are produced under the risk of either terminal or intermittent drought stress. Most studies have investigated the effects of GEI on canning quality (De Lange and Labuschagne, 2001; Khanal et al., 2014; Njau and Kimani, 2017; Amongi et al., 2021) and nutritional quality (Nchimbi-Msolla and Tryphone, 2010; Amongi et al., 2021) under stress free or yield potential conditions yet most of the farmers are in drought prone areas. As a result, limited information is available about the effects of drought stress on nutritional (Fe and Zn) and canning quality, and the available results are often inconclusive (Mutari et al., 2022). Amongi et al. (2021) phenotyped 578 dry beans genotypes for canning and nutritional quality under optimum environments in Uganda. However, Amongi et al. (2021), in their work, did not report important canning quality traits such as the seed shape, uniformity, washed drained weight (WDW), percent washed drained weight (PWDW), degree of clumping and splitting. Assefa et al. (2013a) identified high yielding navy bean breeding lines under drought stressed and optimal conditions. However, the canning and nutritional quality attributes of the superior breeding lines were not reported.

Figure 1.2 Demonstration of clumping in navy bean genotypes including Protea (CIM-NAV02-16-2-1). Source: Mutari et al., 2022

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Numerous genome wide association studies (GWAS) have been conducted in common bean to identify genomic regions associated with the following; drought tolerance (Briñez et al., 2017; Hoyos-Villegas et al., 2017; Valdisser et al., 2020), disease and insect pest resistance (Tock et al., 2017; Tigist et al., 2019; Nkhata et al., 2021), nutritional composition-related traits (Katuuramu et al., 2018), photosynthetic traits (Makunde, 2013; Dramadri et al., 2019), and agronomic traits (Kamfwa et al., 2015b; Moghaddam et al., 2016; Hoyos-Villegas et al., 2017; Dramadri et al., 2019). However, only a few GWAS have been carried out in common beans for drought resistance traits including physiological traits. Moreover, previous mapping studies (Tar'an et al., 2002; Beattie et al., 2003; Blair et al., 2006; Wright and Kelly, 2011; Checa and Blair, 2012; Mukeshimana et al., 2014; Hoyos-Villegas et al., 2017) conducted on agronomic and physiological traits used a small population size and a limited number of molecular markers. This resulted in quantitative trait loci (QTL) with low resolution or poor estimation of marker effects, making it difficult to make inferences on candidate genes correlated with the identified QTL.

Rationale of this study

The increasing market price of cooking fuels, electricity and fast growing urban population in Zimbabwe is driving an increased demand for processed and ready-made food products such as canned beans (Crop Breeding Institute, 2018). It is, therefore, important that the national navy bean production be increased to meet the required quantities and reduce the navy bean import bill. The best-bet navy bean cultivar must meet the preferences of farmers and the required canning quality standards of processors, micronutrient density and agronomic performance regardless of the production environment. Therefore, the participation of farmers in the initial breeding process in form of Participatory Rural Appraisal (PRA) will provide insight into navy bean trait preferences, production, and marketing constraints, so that they can be addressed during the breeding process. It is expected that navy bean farmers have gathered indigenous knowledge and experience over the years on production systems and how to manage or handle a number of biotic and abiotic stresses, socio-economic and marketing constraints. Thus, it is important to make use of this knowledge from the farmers during the development of new cultivars to improve the adoption rate of navy bean cultivars in Zimbabwe. Therefore, the PRA approach will result in comprehensive and focused breeding pipelines that are likely to result in genetic gains in farmer's fields. Furthermore, there is no documented participatory research on navy bean production status, biotic and abiotic stress management strategies, farmers' perceived production, and marketing constraints, and cultivar trait

preferences among the main navy bean growing regions in Zimbabwe. Moreover, the limited available information has not been documented, but is spread across different reports, which are not authentic as well as not available online.

There is a need to conduct studies on grain yield, canning quality and seed micronutrient stability and GEI in multi-location trials under diverse agro-ecologies and seasons for devising ideal breeding strategies to adopt, either wide or specific adaptation. Given the increasing demand for navy beans (Tsiko, 2018), increased prevalence of drought (Makunde, 2013) and micronutrient malnutrition (World Health Organization, 2015) in Zimbabwe, the development of genotypes which combine high grain yield stability with drought tolerance, superior canning and nutritional quality is a high-priority research area. This will contribute to increased productivity, production, and commercialization of navy beans in Zimbabwe. Furthermore, genetic biofortification is a cost-effective and reliable food-based strategy for reducing malnutrition and attaining nutrition security (Bouis and Welch, 2010; Philipo et al., 2021). Moreover, host plant resistance is a more effective, sustainable, environmentally friendly and labor-saving technology for managing drought stress in common beans compared to the multiple cultural practices such as soil mulching, ridging, and cultivating the soil to retain more moisture.

However, when improving crops for drought tolerance, information on the genetic control of traits of economic importance such as grain yield and the associated traits under DS conditions and the identification of good general and specific combiners are pre-requisites (Chiipanthenga et al., 2021). This information will help the navy bean improvement programme at CBI in selecting an effective breeding and selection strategy to follow when breeding for enhanced drought tolerance, grain yield and its components. On the other hand, the identification of genomic regions and diagnostic genetic markers associated with grain yield and its component traits under DS and non-stressed (NS) conditions will facilitate trait introgression and marker assisted selection (MAS). Thus, dissecting the genetic basis of polygenic traits of economic importance such as drought tolerance regarding genomic regions and/or genes involved and their effects through GWAS is important to improve genetic gains in breeding for enhanced grain yield in common beans under DS and NS conditions.

Aim

The overall goal of the study was to improve dry beans productivity, canning and nutritional quality under drought stressed environments through drought tolerance improvement to contribute to the national efforts to improve food, nutrition, and income security.

Specific objectives

The specific objectives of the study were:

(i) To identify farmers' perceived production and marketing constraints, preferred traits and cultivars of navy bean, and strategies used to mitigate drought and heat stress in the south east lowveld region of Zimbabwe.

(ii) To evaluate the adaptability and stability of navy bean genotypes for grain yield and nutritional quality traits (Fe and Zn) across multiple locations in Zimbabwe.

(iii) To investigate the impact of drought stress on agronomic, shoot, physiological, canning and nutritional quality traits of navy beans, and identify drought tolerant genotypes with superior canning and nutritional quality.

(iv) To determine combining ability effects and mode of gene action of grain yield and yield-attributing traits in navy bean under drought stressed and non-stressed environments and select best combiners for effective breeding.

(v) To quantify genome-wide marker-trait association of agronomic and physiological traits in dry beans under non-stressed and drought stressed conditions and to identify candidate markers for marker-assisted selection.

Research hypothesis

The current study was based on the following hypotheses:

(i) Participatory rural appraisal will facilitate the identification of farmers' perceived production and marketing constraints, drought and heat stress management strategies and preferred traits of navy bean in the South East Lowveld region of Zimbabwe.

(ii) Variability in adaptability and stability exists among navy bean genotypes with respect to grain yield and micronutrient (Fe and Zn) concentrations across multiple locations.

(iii) Agronomic, shoot, physiological, canning and nutritional quality traits significantly vary among navy bean genotypes under non-stressed and drought stressed environments.

(iv) The selected parents and their progenies exhibit good combining ability for grain yield and yield-attributing traits when evaluated under drought stressed and non-stressed conditions.

(v) Diversity Arrays Technology Sequencing (DArTseq) markers are significantly associated with agronomic and physiological traits in dry beans genotypes under non-stressed and drought stressed conditions.

Outline of the thesis

The thesis consists of eight distinct and interrelated research chapters with a journal paper format. Chapter 1 is a general introduction to the thesis and chapter 2 is written as a discrete review paper. Chapters 3-7 are written as discrete and stand-alone research papers (whether or not the chapter has already been published). The last chapter (8) presents general overview and implications of findings from the study. Some unavoidable overlap and repetition of references and information between chapters may exist since they have been written as independent journal research papers covering the ideal information. The Crop Science Society of America (CSSA) referencing system was used in all the chapters of this thesis.

Therefore, the outline of the thesis is as follows:

1. Chapter One: Introduction to thesis.
2. Chapter Two: Literature review.
3. Chapter Three: Farmers' perceptions of navy bean (*Phaseolus vulgaris* L.) production constraints, preferred traits, farming systems and their implications on bean breeding: A case study from south east lowveld region of Zimbabwe.
4. Chapter Four: Genotype x environment interaction and stability analyses of grain yield and micronutrient (Fe and Zn) concentrations in navy bean (*Phaseolus vulgaris* L.) genotypes under varied production environments.
5. Chapter Five: Drought stress impact on agronomic, physiological and shoot traits, canning, and nutritional quality of navy beans (*Phaseolus vulgaris* L.) under field conditions.
6. Chapter Six: Genetic analysis of grain yield and yield-attributing traits in navy bean (*Phaseolus vulgaris* L.) under drought and optimal environments.
7. Chapter Seven: Identification of genomic regions of dry beans (*Phaseolus vulgaris* L.) associated with agronomic and physiological traits under drought stressed and non-stressed conditions using genome-wide association study.
8. Chapter Eight: General overview and implications of the study.

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Chapter 2 [1]A review of the literature

2.1 Introduction

A successful dry beans (*Phaseolus vulgaris* L.) cultivar meant for canning purposes must not just perform well in farmers' fields but throughout the value chain (Mutari et al., 2021a). The best cultivar must, therefore, have desirable agronomic traits and also maintain the required level of canning and nutritional quality, regardless of the production environment (Mutari et al., 2021a). This review of literature gives an overview on breeding dry beans for enhanced drought tolerance, canning and nutritional quality. The origin of dry beans and its genetic diversity, dry beans production constraints, prevalence of micronutrient deficiency in sub-Saharan Africa (SSA), and possible interventions to alleviate the challenge of malnutrition are discussed. Drought stress, an important abiotic stress of dry beans causing significant grain yield losses in Zimbabwe is discussed. The management approaches of drought stress applicable to dry beans and the genetics of drought tolerance are discussed. Various canning quality parameters affecting the acceptability of a canned product are discussed. Breeding and screening strategies for drought stress tolerance, canning and nutritional quality are reviewed. In addition, the Participatory Rural Appraisal Approach (PRA) and the effect of genotype by environment interaction (GEI) on canning and nutritional quality traits are discussed.

2.2 Genetic diversity and origin of dry beans

Dry beans (*Phaseolus vulgaris* L., 2*n* = 2x = 22) belongs to the Fabaceae family, sub-family Papilonoideae, tribe Phaseoleae and sub-tribe Phaseolinae (Mercado-Ruaro and Delgado-Salinas, 2000). It is among the most important grain legume crops consumed globally with a relatively small diploid genome size of approximately 473 Mb (Schmutz et al., 2014). The domestication of dry beans on the American continent in two main centers of origin, andean and middle-american regions of America, resulted in two major diverse gene pools (Blair et al., 2006; Qureshi and Sadohara, 2019; Beebe, 2020). The andean and middle-american gene pools differ in their biochemical and morphological characteristics, such as phaseolin patterns, seed coat colour, growth habit, protein content, seed size, and agro-adaptation (Blair et al., 2006). As reported by Singh et al. (1991), the middle-american gene pool (from Central America) consists of all types of growth habits, and accessions that are small seeded (≤ 25 g

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per 100 seeds). In contrast, the andean gene pool (from South America) has plant growth habit types I, II and III, medium sized (≥ 25 ≤ 40 g per 100 seeds), and large-sized grains (≥ 40 g per 100 seeds). The type I growth habit is determinate bush and type II growth habit has an indeterminate upright short vine, narrow plant profile, with three to four branches. On the other hand, the type III growth habit has an indeterminate prostrate vine. According to Beebe et al. (2000), polymorphisms exist within the andean and middle-american gene pools as evidenced by genetic variability in adaptation range, growth habits, seed coat colour, seed size, and seed coat patterns. The middle-american gene pool comprises of four races namely middle-america (small seeded bush habits), Durango (prostrate bush types), Jalisco (climbing beans) (Singh et al., 1991) and Guatemala (Beebe et al., 2001, 2013).

The most common and widely cultivated type of dry beans is the race Mesoamerica which originated from Central America (Singh et al., 1991). According to Diaz and Blair (2006), genotypes from the race Mesoamerica are small seeded and are adapted to a wide range of production environments ranging from hot, humid to moderate. This race is also sub-divided into the following sub-races based on the type of seed and architecture of the plant; sub-race Mesoamerica 1 (type II growth habit, and small blacks) and sub-race Mesoamerica 2 (type III growth habit, and various seed coat colours – carioca, small whites and small reds) (Beebe et al., 2000). Race Durango which originated from dryland Mexico has the highest level of drought stress tolerance in dry beans (Beebe et al., 2013). Therefore, the race Durango is an important source of drought tolerance genes in most drought tolerance breeding programs globally (Teran and Singh, 2002). Genotypes from this race mature early, have high canopy biomass and grain yield potential under drought stressed environments (Makunde, 2013). The race Guatemala originated from Mexican state of Chiapas. Genotypes from this race are small seeded and have an intermediate climbing growth habit (Beebe et al., 2000). The andean gene pool comprises of three races namely Peru (originated from Argentina, Peru and Bolivia), Nueva Granada (originated from the northern Andes), and Chile (originated from Chile) (Singh et al., 1991).

2.3 Importance, trends in production and end-uses of dry beans

Dry beans is an important pulse crop in human diet, nutrition and cropping systems (Akibode and Maredia, 2011). In Sub-Saharan Africa (SSA) and Latin America, the crop is mainly consumed in form of immature seeds, mature grain, and young pods (Makunde, 2013). It is also an important income generating crop in many countries in SSA. Different market classes

of dry beans exist and these include navy bean (small whites), red kidney, sugars, small reds, large whites, yellows, small blacks, to name a few. Among the different market classes, navy beans, which fall under the middle-american gene pool are usually sold as canned or baked beans in many parts of the world (Uebarsax and Muhammad, 2012; Kelly and Cichy, 2012). In some other instances, navy beans are packaged in plastics and sold as raw-dry grains. Navy beans have important health and nutritional benefits for consumers as they are rich in protein, dietary fiber, minerals, and vitamins and very low in fat (Siddiq and Uebersax, 2012). The average seed compositional (proximate, minerals and vitamins) characteristics of navy beans are given in Table 2.1.

Table 2.1 Average seed compositional characteristics of navy beans (per 100g).

***Proximate*:**	**Quantity**
Water (g)	12.1
Energy (Kcal)	337.0
Protein (g)	22.3
Total lipid (fat) (g)	1.5
Carbohydrate (g)	60.8
Total dietary fiber (g)	24.4
Total Sugars (g)	3.9
***Minerals*:**	**Quantity**
Calcium (mg)	147.0
Iron (mg)	5.5
Magnesium (mg)	175.0
Phosphorous (mg)	407.0
Potassium (mg)	1185.0
Sodium (mg)	5.0
Zinc (mg)	3.7
***Vitamins*:**	**Quantity**
Thiamin (mg)	0.8
Riboflavin (mg)	0.2
Niacin (mg)	2.2
Vitamin B-6 (mg)	0.4
Folate[1] (µg)	364.0
Vitamin E[2] (mg)	0.0
Vitamin K[3] (µg)	2.5

[1] Dietary folate equiv, [2] As α-tocopherol, [3] As phylloquinone. *Source:* Adapted from US Agency for International Development (USAID) (2012) in Siddiq and Uebersax (2012).

In developing countries, navy beans are commonly consumed by high-income consumers as canned beans (Jackson et al., 2012). It is an important market class in Africa, particularly

because of preference for them in local markets and their superior canning and culinary qualities (Assefa et al., 2013a). The crop is in high demand in Kenya, South Africa, and Zimbabwe for industrial canning purposes either in tomato sauce, sweetened sauce or brine (Siddiq and Uebersax, 2012; Khanal et al., 2014). Production is on the increase in Burundi, Uganda, Rwanda and Tanzania (Farrow and Muthoni-Andriatsitohaina, 2020). According to De Lange and Labuschagne (2001), 80% of the raw materials (dry beans) used by the bean-canning industry in South Africa are navy beans. In Ethiopia, navy beans are mainly grown as a cash crop for export to Middle East, Southern Africa and Eastern Europe, generating foreign currency for the country (Teshome and Emire, 2012; Farrow and Muthoni-Andriatsitohaina, 2020).

The estimated production area of navy beans in Eastern-, Southern- and Western Africa is 239 000 ha, 122 000 ha and 68 000 ha, respectively (Farrow and Muthoni-Andriatsitohaina, 2020). This makes Africa the biggest producer and major exporter of navy beans for industrial processing into canned beans (Assefa et al., 2017). Ethiopia accounts for about 10% of the global supply of navy beans from Africa (Assefa et al., 2017). Thus, navy bean is increasingly becoming a commercial commodity for the lucrative export market and bean-canning industry, given the current trends of market globalization and urbanization (Katungi et al., 2009). In Zimbabwe, dry beans processors require around 4000 tonnes annually of navy bean grain for canning purposes, and over 80% of its total production is supplied to the bean canning industry (Mukweza, personal communication, May 2018[1]).

However, information on the estimated production area of navy beans including the average land area allocated to the production of the crop per household is not available (Crop Breeding Institute, 2018). The lack of documented information pauses a challenge during the development of new product profiles since it makes it difficult for a breeder to make comprehensive and informed decisions. This information is not available because the annual crop assessment surveys that are conducted by the government during the main cropping season (December – April) do not disaggregate the total bean area by market class. Moreover, the navy bean crop which is produced during the dry winter season is not subjected to crop assessment since it is grown during off-season. Similarly, Beebe et al. (2013) reported that information on the total area under dry beans globally is not well captured. They attributed this to the lack of capacity by government partners to conduct annual crop assessments in some nations.

[1] Head Research and Development at Cairns Foods Limited in Zimbabwe

2.4 Dry beans production constraints

Common beans are notably sensitive to climatic and environmental variations. Dry beans production constraints in Africa range from biotic (insect-pests and diseases), abiotic to socio-economic (Njoki, 2013; Katungi et al., 2017). The common insect-pests include, harvester termites [*Hodotermes mossambicus* (Hagen)], bean foliage beetles (*Otheca mutabilis* and *O. bennigseni*), cotton bollworm (*Helicoverpa armigera*), pod borer (*Maruca vitrata*), black bean aphid (*Aphis fabae*), bean storage bruchids (*Acanthoscelides obtectus* and *Zabrotes subfasciatus*), and bean fly (*Ophiomia phaseoli*, *O. spencerella*, and *O. centrosematis*) (Njoki, 2013). The major diseases include, angular leaf spot (*Pseudocercospora griseola*), bean common mosaic virus, bean rust (*Uromyces appendiculatus*), common bacterial blight (*Xanthomonas axonopodis pv. Phaseoli*), angular leaf spot (*Pseudocercospora griseola*), and anthracnose (*Colletotrichum lindemuthianum*) (Njoki, 2013). It is important to note that the incidence of black bean aphid, bean fly and harvester termites increases when there is drought stress (Sileshi et al., 2005; Ochilo and Nyamasyo, 2011). Maggots burrow through the stem causing the plant to wilt (Ambachew et al., 2015). This results in reduced plant stand. Termites attack all the growth stages of plants resulting in low grain yield (Nyagumbo et al., 2015). On the other hand, bean aphids suck sap from leaves and stems, reducing photosynthesis in the process (Tang and Feng, 2023). During the feeding process; aphids transmit the bean common mosaic necrosis virus which causes the bean common mosaic disease (Tang and Feng, 2023).

The major abiotic constraints in Africa include, heat stress, drought stress, and nutritional disorders such as salt (NaCl), aluminium (Al), nitrogen (N) and magnesium toxicities (Wortmann et al., 1998). Beebe et al. (2013), Hoyos-Villegas et al. (2017) and Valdisser et al. (2020) reiterated that drought stress is the most important grain yield-limiting abiotic factor of dry beans worldwide. In Southern Africa, drought is the most important abiotic stress that affect dry beans production, reducing bean grain yield by 50% or more (Wortmann et al., 1998). Wortmann et al. (1998) reported annual grain yield losses of up to 119 800 tonnes due to mid-season drought in Central and Southern Africa. Furthermore, smallholder farmers who produce most of the dry beans in SSA are located in marginal areas that frequently experience drought stress (Katungi et al., 2009). In Zimbabwe, drought stress is the major abiotic constraint affecting dry beans production due to high variability in the distribution and amount of precipitation during the growing season (Beebe et al., 2013). Regrettably, most of the smallholder farmers in Zimbabwe have no capacity to apply supplemental irrigation during periods of drought stress, resulting in significant grain yield losses (Katungi et al., 2017). In a

thorough search of the literature, I found that no work has been conducted before in Zimbabwe related to breeding navy beans for water deficit environments. Consequently, all the navy bean cultivars (Caledon, Protea, and Canpsula) that are currently being cultivated and processed in Zimbabwe were not bred for drought tolerance. Generally, progress in improving drought tolerance in navy beans worldwide has been limited compared to the other commercial classes of small seeded middle-american beans (Assefa et al., 2017). Therefore, it is imperative to develop navy bean genotypes that are tolerant to drought stress.

2.5 Iron and zinc deficiency status in Sub-Saharan Africa

Micronutrient deficiencies, particularly Fe and Zn are common in SSA (Beebe, 2020). The deficiency of Zn in human body causes impaired growth and cognition, resulting in stunting (reduced growth and development), and a weak human immune system (Philipo et al., 2021). It is estimated that 28% (approximately 2 million) of children under the age of 5 years in Southern Africa are stunted (Global Nutrition Report Stakeholder Group, 2017). On the other hand, Fe deficiency in human body causes anaemia. Regrettably, the SSA region has the highest prevalence of anaemia globally (Kassebaum, 2016; Beebe, 2020; Zegeye et al., 2021). An average of 190 million cases of anaemia are reported annually in SSA, and most of the cases have been reported in pre-school children (43%), followed by women of the reproductive age (29%) (Kassebaum, 2016). According to Zegeye et al. (2016), half of married women in SSA are affected by anaemia. The prevalence of anaemia is high in children under the age of 5 years, estimated to be 31% (World Health Organization, 2015; Kairiza et al., 2020). Moreover, according to Kairiza et al. (2020), Fe deficiency is also high, among infants of 6 to 11 months old, estimated to be 81%. In Zimbabwe, Fe deficiency is common in children under the age of 5 years, estimated to be at 72% (World Health Organization, 2015). Further, in 2018, 26% of children under the age of 5 years were stunted in Zimbabwe (ZimVAC, 2018). This is above the acceptable target of 20% which was set by the United Nations Children's Fund (UNICEF) (Kairiza et a., 2020).

2.5.1 Iron and zinc deficiency interventions

Various approaches, which include dietary diversification, nutrient supplementation (minerals and vitamins of pills, powder and syrup), and food fortification (adding essential micronutrients) have been practised in many countries for decades to alleviate the challenge of malnutrition (Kairiza et al., 2020). In SSA, several countries including Zimbabwe have mainstreamed the mandatory food fortification policies that aim to reduce and control the effect

of Fe and Zn deficiency (Kairiza et al., 2020; Philipo et al., 2021). However, a cost-effective and reliable compliment to food fortification is genetic biofortification (Philipo et al., 2021). Genetic biofortification is the development of micronutrient dense staple food crops either through molecular techniques or conventional plant breeding methods (Bouis and Welch, 2010). As a result, most dry beans-canning companies in Zimbabwe and SSA as a whole now advocate for micronutrient dense navy bean cultivars. This is probably because, the processing of genetically biofortified navy bean cultivars has low recurring costs on the part of the canning company compared to food fortification (Mutari et al., 2021a).

The most common navy bean cultivars that are currently being processed into canned beans in SSA come from Ethiopia (Mexican 142, Awash-1, Awash-2 and Awash Amelka), Malawi (UBR[92]25), South Africa (Teebus-RR 1, PAN 9141, Caledon, Lamberg, Helderbeg, OPS-KW 1, and Pan 123) and Zimbabwe (Caledon, Protea and Camellia) (Mutari et al., 2021a). In a thorough search of the literature, none of the aforementioned best-bet cultivars is biofortified. This is also supported by Glahn et al. (2020), who observed low seed Fe contents in Awash-2 (55 ppm), Awash Melka (64 – 65 ppm), Awash-1 (58 - 63 ppm) and Mexican 142 (59 ppm) against the bench mark of 90 ppm. Moreover, according to the review by Beebe (2020), most of the biofortified dry beans cultivars that have been released in Africa belong to other market classes other than navy beans. Therefore, the lack of biofortified navy bean cultivars has forced some of the bean processors in Zimbabwe to establish production lines for biofortified beans of other market classes (NUA45 and Cherry), which generally do not have good canning-quality attributes (Crop Breeding Institute, 2018). The cultivar NUA45 was not developed for canning purposes; thus, it has poor canning qualities (Figure 1.1 under Introduction to thesis). Therefore, it is imperative to identify navy bean breeding lines that combine drought stress tolerance with superior canning and nutritional quality traits (seed Fe and Zn concentrations). This can be a reliable and cost-effective strategy.

2.6 Drought stress

As reported by Katungi et al. (2010), 73% of common bean production in SSA occurs in environments which experience moderate to severe drought stress. It is predicted from various climate models that the duration and frequency of droughts are expected to increase in SSA (Kotir, 2011). Three major types of drought exist depending on the stage of bean development the stress occurs, and these include, early season, intermittent and terminal drought (Katungi et al., 2009). However, the intermittent and terminal droughts are the major types of droughts

which occur regularly in Africa and Latin America (Assefa et al., 2013a). Early season drought usually results from the delayed onset of rain in a cropping season (Makunde, 2013). In addition, early season drought might occur due to inadequate rain to support seed germination, seedling growth and development at the beginning of a cropping season. Intermittent drought is an episodic water deficit at varying intensities which occurs during the growing season. Thus, this type of drought is difficult to manage. This type of drought which is unpredictable is prevalent in East and Central Africa (Blair et al., 2010).

On the other hand, terminal drought occurs when the bean crop experiences soil water deficit during the reproductive phases of growth (flower formation, full flowering, pod formation, and grain filling). Terminal drought is prevalent in Southern Africa (Beebe et al., 2011). In Zimbabwe, the rainy season usually starts in November and ends in April. However, due to climate change, there has been a reduction in the duration of the rainy season in Southern Africa including Zimbabwe such that dry beans are prone to terminal drought stress (Beebe et al., 2011). This is because, dry beans are planted late in the cropping season (early February), and sometimes reach the reproductive stage of growth when the rains have gone.

2.6.1 Effects of drought stress on dry beans

Early season drought causes poor initial plant stand resulting in low grain yield. The symbiotic interaction of dry beans roots with rhizobia in the soil is also negatively affected by drought stress resulting in low grain yield and protein content (Dita et al., 2006). Terminal drought stress also reduces stomatal conductance, total chlorophyll content, leaf expansion, number of days to maturity, number of pods and seeds per plant, seed yield, seed size and harvest index (Teran and Singh, 2002; Beebe et al., 2008; Beebe et al., 2010; Darkwa et al., 2016). Asfaw et al. (2012), reported grain yield losses of up to 80% due to drought stress. However, the duration (early, intermittent and terminal), intensity, and type (severe and moderate) of drought stress, growth stages affected and cultivar genetics determine the level of reduction in grain yield (Beebe et al., 2010). Regarding navy beans, literature on the effects of drought stress on nutritional and canning-quality traits is scanty, as most of the studies have focused on other market classes as well as on the effect of drought stress on agronomic traits.

Literature search has shown that researchers do not simultaneously phenotype for drought tolerance, canning and nutritional quality yet most of the farmers are located in drought prone areas. As a result, limited information is available about the effects of drought stress on nutritional and canning quality in navy beans, and the available results are often inconclusive

(Assefa et al., 2013b; Warsame and Kimani, 2014; Assefa et al., 2017). Phenotyping for canning quality is considered laborious and expensive (Walters et al., 1997; Posa-Macalincag et al., 2002; Kelly and Cichy, 2012; Mendoza et al., 2014). Assefa et al. (2013a) identified high yielding navy bean breeding lines under drought stressed and non-stressed conditions. However, the canning and nutritional quality attributes of the superior breeding were not reported. Assefa et al. (2013b) evaluated eighty-one navy bean genotypes under drought stressed and non-stressed conditions at one location for two seasons. However, the canning quality of the genotypes, which had superior agronomic traits under drought stress, was not reported. On the other hand, Assefa et al. (2017) evaluated 36 navy bean genotypes for adaptation to drought stress at two locations for two seasons. However, only 24 genotypes were evaluated for canning quality. Amongi et al. (2021) phenotyped 578 dry beans genotypes for canning and nutritional quality under non-stressed environments. However, in their work, important canning quality traits such as the seed shape, uniformity, washed drained weight (WDW), percent washed drained weight (PWDW), degree of clumping and splitting were not reported.

In a thorough search of the literature, l found that reports on the effects of drought stress on seed Fe and Zn concentrations in dry beans in general are contradictory (Ghanbari et al., 2013; Pereira et al., 2014; Smith et al., 2019; Smith et al., 2022). Smith et al. (2019) reported that drought stress had no negative effect on the accumulation of Fe and Zn in dry beans seeds. Pereira et al. (2014) and Smith et al. (2022) found that drought stress increased seed Fe and Zn concentrations in dry beans. On the other hand, Ghanbari et al. (2013) reported a significant decrease in both seed Fe and Zn concentrations under drought stressed conditions. The specific mechanism on how drought stress increases seed Fe concentration is not entirely clear, and needs further investigation.

2.6.2 Management approaches of drought stress

The most common approaches of managing drought stress include cultural practices and host plant resistance.

2.6.2.1 Cultural practices

The effects of drought stress can be minimized through various cultural practices. Some of these include cloud seeding, soil mulching through the application of organic matter or residues from the previous crop to improve the water holding capacity of the soil, use of tied ridges, adjusting planting dates, water harvesting, and crop diversification to reduce risk (Mutari et al.,

2021b). As reported by Iqbal et al. (2020), the application of crop residues improves the water infiltration and retention capacity of the soil, and also reduces surface evaporation resulting in higher water use efficiency. The major disadvantage of soil mulching is that; it tends to attract harvester termites which reduce plant stand in dry beans by feeding on all plant parts (Nyagumbo et al., 2015). Nyagumbo et al. (2015) reported that the application of crop residues or organic mulches increases the activity of harvester termites as a result of the moist conditions in the underlying soil. Moreover, most of the best-bet cultural practices involve location specific considerations (Beebe et al., 2013). This suggests that the development of genotypes that are tolerant to drought stress must be a priority in dry beans breeding programs.

2.6.2.2 Host plant resistance

Host plant resistance is a more reliable, effective, sustainable, environmentally friendly and labor-saving technology for managing drought stress in dry beans compared to the multiple cultural practices such as soil mulching, ridging, and cultivating the soil to retain more moisture (Beebe et al., 2013). The drought resistance mechanisms used by plants to cope with drought stress include recovery, drought tolerance, drought avoidance and drought escape (Fang et al., 2015). Drought recovery is the ability of a plant to continue with growth and development after exposure to extreme drought stress. According to Hall and Patel (1985), long duration and indeterminate genotypes have the ability to recover from prolonged periods of drought stress. Drought escape is the ability of a plant to avoid drought stress by rapidly developing, reproducing and completing its full life-cycle before drought sets in or drought conditions become severe (Manavalan et al., 2009). Dry beans genotypes that exhibit this type of drought resistance mechanism usually belong to the short duration maturity group (early flowering and maturity). Genotypes which mature early are likely to escape from terminal drought stress due to early flowering time, shorter vegetative phase and grain filling period. However, a short vegetative phase and grain filling period has a penalty on plant biomass, grain yield, seed nutrient content and seed size (Assefa et al., 2013b; Darkwa et al., 2016).

Drought avoidance is the ability of a plant to maintain, sustain, and/or adjust important metabolic and physiological (stomatal regulation and deep root system development) processes when exposed to drought stress (Luo, 2010). Genotypes do this by minimizing water loss (dehydration avoidance and tolerance), reducing the rate of transpiration (leaf rolling and closing of stomata), and improving the efficiency of photosynthesis and water uptake from roots (fibrous and deep root system) (Luo, 2010). In addition, these genotypes are superior and

efficient in remobilizing photo-assimilates from vegetative parts to the pods, and from pod walls to the developing seeds when exposed to drought stress (Beebe et al., 2010). For example, the line G21212 of the middle-american gene pool produces high grain yields under water deficit environments due to its superiority and efficiency in remobilizing photosynthates from vegetative parts to the developing seeds. Drought tolerance is the ability of a plant to sustain dehydration via physiological processes such as osmotic adjustments and osmo-protectants (Luo, 2010).

2.7 Participatory rural appraisal in dry beans breeding

Participatory rural appraisal (PRA) relies on participation of the community (local people) and considers the value of stakeholders' knowledge, skill, experience, their needs, preferences, abilities, and innovation (Chandra, 2010). It has been widely used by researchers to identify production constraints of many crops (Mongi et al., 2016; Nduwumuremyi et al., 2016; Ngailo et al., 2016; Daudi et al., 2018; Abady et al., 2019). Morris and Bellon (2004) reported that the participation of farmers' in the initial breeding process provides insight into cultivar trait preferences, production and marketing constraints, so that they can be addressed during the breeding process and hence improve the adoption rate of newly released cultivars. Information from PRA helps the breeder to design product profiles and focussed breeding pipelines that result in genetic gains in farmers' fields and more income to the farmers (Danial et al., 2007). Mukankusi (2008) and Njoki (2013) successfully used information from PRA in the breeding process to develop dry beans genotypes with tolerance to fusarium wilt (yellows) (*Fusarium oxysporum* f. sp. *phaseoli*), bean stem maggot and angular leaf spot, respectively. Before the year 2018, dry beans breeding efforts at CBI, Zimbabwe focused on improving other market classes other than navy beans such as the sugars, red kidneys and calimas, thus there is no information on farmer's preferred traits, production and marketing constraints. Even though Katungi et al. (2017) conducted a similar study in 2016, the sampled study Districts were not the main navy bean growing regions in Zimbabwe. Consequently, this poses a challenge during the development of new product profiles as it makes it difficult for a breeder to make comprehensive and informed decisions.

2.8 Canning quality

The development of cultivars with improved canning-quality traits is usually considered a target secondary to grain yield because of high cost involved in phenotyping for canning-quality parameters and limited quantities of seed produced in early generations (Walters et al.,

1997; Posa-Macalincag et al., 2002; Kelly and Cichy, 2012; Mendoza et al., 2014). Thus, acceptable canning quality, rather than enhanced or superior quality, is the target in most navy bean-improvement programs. Nonetheless, physical characteristics, chemical composition, processing and cooking characteristics of the grains are the major determinants of canning quality (Hosfield, 1991).

A number of phenotypic quality parameters are used by bean breeders to predict the final canning quality of breeding materials. These are categorized as: i) traits that have an economic impact for the bean processor, such as hydration coefficient (HC) and can yield; ii) traits that affect the acceptability (visual appeal and palatability) of the processed bean by the consumer, such as degree of clumping, firmness and splits; and, iii) the composition traits such as protein, sucrose and raffinose, which are likely to have little effect on the acceptability of a processed bean cultivar since they can be corrected with changes in the brine or sauce mixture of a processed bean cultivar (Khanal et al., 2014). The primary measurements for evaluating dry beans-canning quality in a breeding program mainly comprise of washed drained weight (WDW), visual appearance and texture (Hosfield, 1991; Kelly and Cichy, 2012). Among the parameters that are economically important to the canning industry is the HC. It basically relates to the canning yield of a genotype to the processor, which is the number of cans that can be obtained from a given quantity of dry beans seed (Van Loggerenberg, 2004). Even though the optimum HC for the bean canning industry varies in different countries, the most commonly used HC value is 1.8 – 2.0 (Balasubramanian et al., 2000; Qureshi and Sadohara, 2019).

The visual appearance and color of canned beans are important parameters for both bean consumers and processors (Cichy et al., 2014). Therefore, after three weeks of storage, cans are opened and visual evaluation is done to assess the degree of clumping, degree of splits, seed size, colour retention, conformity of seed shape, extent of extruded starch and uniformity (Balasubramanian et al., 1999; Mendoza et al., 2017). These physical traits are often scored individually using either one of the following scales; 1-7 (Uebersax and Hosfield, 1985), 1-3 (Teshome and Emire, 2012) and 1-5 (Balasubramanian et al., 2000; Khanal et al., 2014). Both consumers and processors consider the colour retention of canned bean as an important attribute. However, navy beans are less likely to lose their colour during the canning process compared to the other market classes that show darker colours (Qureshi and Sadohara, 2019). Generally, consumers prefer canned beans with fewer splits because products with high percentages of splits are unappealing (Balasubramanian et al. 2000; Cichy et al., 2014).

Cultivars with high degree of clumping have unpalatable canning quality and are rejected by both breeders and processors. Figure 1.2 under the Introduction to thesis illustrates clumping in navy bean genotypes. However, the addition of calcium chloride in the canning medium reduces splitting and clumping of the canned product by increasing the firmness of the canned beans (Wang et al., 1988). Unfortunately, the addition of calcium has a disadvantage in that it tends to reduce the percent washed-drained weight (PWDW), an important trait to the processor (Wang et al., 1988). Therefore, the best approach will be to identify genotypes that are not prone to splitting and clumping during processing. Percent washed-drained weight, which also relates to processors' yield is another important parameter that is widely used by bean breeders and the canning industry. The PWDW is the weight of beans after they have been processed (cooked), rinsed and drained in a sieve (Hosfield and Uebersax, 1980). Therefore, following visual evaluations, the cooked bean samples are rinsed and drained to remove brine as well as wash away any macromolecules that could have extruded from the beans (Kelly and Cichy, 2012).

According to Walters et al. (1995) the WDW of dry beans is moderately heritable. A WDW of 240-280 grams for a sample of beans, equivalent to 90 g of initial total solids at a given moisture, is considered typical in bean breeding programs and by the processing industry (Mutari et al., 2021a). When expressed as a percentage, the desired PWDW is 60% (Balasubramanian et al., 2000) even though it varies in different countries. Another important parameter considered in breeding for canning quality is the texture (firmness or softness) of a bean sample after canning. Texture is measured by the Texture Analyzer as kilogram (kg) force required to shear 100 grams of processed beans (Kelly and Cichy, 2012). The textural standards established for processed navy beans are 50–60 kg (highly desirable/ideal), 40–70 kg (desirable/satisfactory), and < 40 kg and > 70 kg (undesirable/unsatisfactory) maximum force resistance per 100 grams of processed bean (Kelly and Cichy, 2012). Peak force values of < 40 kg indicate over-cooked or mushy samples, and peak force values of > 70 kg indicate under cooked or hard, intact samples (Kelly and Cichy, 2012). However, in the USA, the textural standard for the navy bean canning industry is 72 kg force per 100 grams of processed bean (Hosfield and Uebersax, 1980).

2.9 Breeding strategies for drought tolerance, canning and nutritional quality

The HarvestPlus thresholds for high Fe and Zn beans are 90 ppm and 40 ppm, respectively (International Center for Tropical Agriculture, 2008). However, according to Beebe (2020), for

a cultivar to be accepted as biofortified, dry beans breeders should target genotypes with 44 ppm and 22 ppm of seed Fe in long term (breeding goal) and short term (intermediate cultivar release goal), respectively above the levels in a local standard check cultivar. As for Zn, dry beans breeders should target genotypes with 17 ppm and 8.5 ppm of seed Zn content in long term and short term, respectively above the levels in a local standard check cultivar (Beebe, 2020).

It is important to note that there is lack of recombination between the middle-american and andean gene pools (Kornegay et al., 1992). This makes it difficult to improve complex traits in navy beans (middle-american gene pool), such as drought tolerance, canning and nutritional quality, using genetic diversity in the andean gene pool (Kornegay et al., 1992). However, considering that organisms' moderate Fe and Zinc uptake (homeostatic mechanisms), Beebe (2020) proposed the use of hybridizations between gene pools to "jumble" the genes for homeostasis. This is likely to result in recombinants with enhanced seed Fe and Zn concentrations. However, generally, most biofortification breeding programs develop a nutrient dense base population by crossing several high Fe and Zn parental lines among themselves to initiate recurrent selection (Blair et al., 2009). Queiroz et al. (2021) developed a base population by crossing ten micronutrient dense parental lines among themselves. The same concept of recurrent selection is also used when developing genotypes with the following traits; disease resistance, high grain yield potential, and canning quality. Other programs use the gamete selection technique from hybridizations (crossing of multiple parents) to F_8 or F_{10} to simultaneously combine multiple traits of interest into a single genetic background (Singh, 1994).

The gamete selection technique has also been used to improve grain yield and tolerance to bean rust, bean common mosaic virus, anthracnose, halo bacterial blight (*Pseudomonas syringae* pv. *phaseolicola*), white mould (*Sclerotinia sclerotiorum*), and common bacterial blight (Teran and Singh, 2009). Double-crosses with two or three micronutrient dense parents have also been used to simultaneously combine micronutrient density with market preferred grain types and desirable agronomic traits (Beebe, 2000). However, when improving the micronutrient density of a desirable cultivar (recurrent parent), a donor parent with high seed Fe and Zn content is crossed with the recurrent parent, followed by several cycles of backcrossing to the recurrent parent (Blair et al., 2009). Backcrossing is important to recover the farmers, processors and consumer's traits of interest such as maturity duration, taste, grain colour, grain size and growth

habit. On the other hand, Beebe (2020) proposed the inclusion of sister species of *Phaseolus vulgaris* such as the *Phaseolus coccineus* and *Phaseolus dumosus* in hybridizations when breeding for enhanced micronutrient density. According to Beebe (2020), sister species of *Phaseolus vulgaris* that evolved in environments that are deficient in Fe are likely to be more receptive to Fe uptake. Some of the most common parental sources of the high Fe trait in biofortification breeding programs from sister species are as follows; G10022, G23818B, G23823E, G40102, FEB226, G35575B, G35575A, and G14519 (Beebe, 2020).

Regarding drought resistance breeding, most dry beans breeding programs develop a population with drought resistance component traits by crossing several drought tolerant parental lines among themselves to initiate recurrent selection (Beebe et al., 2008). After initiating recurrent selection, a breeder can decide to use any of the dry beans breeding techniques such as the pedigree selection or the single-seed descent method to obtain fixed lines (Miklas et al., 2006). Other programs use the gamete selection technique to simultaneously introgress multiple traits of interest into a drought-resistant background as described earlier on (Singh, 1994; Beebe et al., 2013). Gamete selection involves complex and multiple hybridizations and selections among F_1 plants and F_1 derived families (Singh, 1994). Advanced backcrossing across gene pools is also used to improve drought tolerance traits (Beebe et al., 2013). With advanced backcrossing, multiple gene combinations can be transferred from the donor to the recurrent parent (Beebe et al., 2013). The race Durango is a major source of drought tolerance genes in most dry beans drought tolerance breeding programs globally (Teran and Singh, 2002; Beebe et al., 2013).

Interracial hybridizations between races Mesoamerica and Durango have been widely used in dry beans improvement programs when breeding for enhanced grain yield and drought tolerance (Beebe et al., 2008; Beebe et al., 2013). As reported by Beebe et al. (2013), hybridizations between the races Durango and Mesoamerica often result in transgressive segregation for drought tolerance due to the complimentary gene action. In addition, sister species of *Phaseolus vulgaris* such as the *Phaseolus acutifolius* which evolved in dryland environments are important sources of drought tolerance genes (Beebe et al., 2013). Some of the important drought resistance sources include BAT 477, A 195, BAT 1289 (White and Izquierdo, 1991), G40159, RAB650, SEA23, G40068 (Rao et al., 2004), and SER 16, SEA 5, SER 5 (Rao et al., 2006). Hybridizations have been attempted between race durango and andean types resulting in lines (SEQ, BRB and DRK series) with small genetic gain over the

cultivar ICA Quimbaya (International Center of Tropical Agriculture, 2006). However, drought tolerant lines with a wide range of seed coat colours have since been identified from the SEQ, BRB and DRK series lines (Beebe et al. 2013).

2.10 Screening strategies for drought tolerance, canning and nutritional quality

2.10.1 Drought tolerance

Screening for tolerance to drought stress in dry beans is usually done under rainout shelters, realistic production environments (main growing season), and in the field during off-season under controlled irrigation (Beebe et al., 2013). Rainout shelters are expensive to construct despite the fact that they can assure good terminal drought stress conditions (Beebe et al., 2013). The major limitation of evaluating genotypes for drought tolerance under realistic production environments is that, the timing and intensity of drought stress is unpredictable (Beebe et al., 2013). Therefore, most dry beans breeders prefer to evaluate genotypes for drought tolerance in the field under controlled irrigation. This is usually done during the cool dry season (off-season) when precipitation is unlikely. For example, drought tolerance breeding programs for different crops in Zimbabwe conduct trials in the lowveld region (Chisumbanje, Save valley and Chiredzi) during the dry winter season. Samson et al. (2006), Assefa et al. (2013b, 2017) evaluated navy bean breeding lines under drought stressed and non-stressed field conditions. The standard procedure followed when testing genotypes in the field under controlled drought stressed and non-stressed conditions to identify genotypes that are tolerant to drought stress (terminal) is briefly described below.

The drought stressed and non-stressed treatments are usually laid beside each other. Buffer zones ranging from 5 to 30 m are usually maintained between the drought stressed and non-stressed treatments to minimize the seepage of moisture from the non-stressed treatment to the drought stressed treatment. The best irrigation systems for use in drought tolerance bean breeding programs are the furrow and overhead sprinkler irrigations because it is possible to quantify the effects of drought stress on the crop (Beebe et al., 2013). In the non-stressed treatment, soil moisture is usually kept at field capacity during the crop growth period (Samson et al., 2006; Assefa et al., 2013b; Darkwa et al., 2016; Assefa et al., 2017). On the other hand, under the drought stressed treatment, soil moisture is usually kept at field capacity until when 80% (Assefa et al. 2017) of the plants have flowered. After that, drought stress is usually imposed up to physiological maturity by withholding irrigation water to a certain percentage of the field capacity (depending on the desired drought intensity) before re-irrigating on the

basis of readings from a tensiometer (Samson et al., 2006; Assefa et al., 2013b; Darkwa et al., 2016; Assefa et al., 2017).

During evaluation, key drought adaptive traits are recorded at the flowering [canopy temperature (CT), stomatal conductance (SC), leaf chlorophyll content (LCC), and days to 50% flowering (DFW)], mid-pod filling [stem biomass (SB), leaf biomass (LB), pod biomass (PB), total shoot biomass (TSB), CT, SC, LCC], and physiological maturity [days to physiological maturity (DPM), plant height (PH), dry weight of pod biomass (DPB), dry weight of stem biomass (DSB), dry weight of pod wall biomass (DPB), seed yield (GYD), and yield components] phases of growth (Beebe et al., 2013). The evaluation of genotypes under drought stressed and non-stressed environments allows for the calculation of quantitative indices of drought tolerance based on grain yield response under both environments. The most commonly used indices of drought tolerance include drought intensity index (DII), drought susceptibility index (DSI), geometric mean productivity (GMP), and percentage of grain yield reduction (%GYR) due to drought stress and drought tolerance index (DTI) (Fischer and Maurer, 1978).

2.10.2 Canning quality

It is usually expensive, laborious, and time-consuming to evaluate a large number of bean samples for canning quality using traditional selection methods (Walters et al., 1997; Posa-Macalincag et al., 2002; Kelly and Cichy, 2012; Mendoza et al., 2014). Furthermore, breeders are faced with challenges of limited quantities of seed in the early generations (Kelly and Cichy, 2012). Moreover, small quality differences among genotypes may not be detected with high precision when using the traditional selection methods (Walters et al., 1997). Phenotyping for canning quality is usually done using either the laboratory (for many breeding lines) or the industrial (few pre-release lines) canning protocol (Van Loggerenberg, 2004). However, most breeding programs follow the laboratory canning protocol that was developed by Hosfield and Uebersax (1980) when screening breeding lines for canning quality in the later generations. As time progressed, the laboratory canning protocol developed by Hosfield and Uebersax (1980) was slightly modified by Balasubramanian et al. (2000), De Lange and Labuschagne (2001), Van Loggerenberg (2004), and van der Merwe et al. (2006) for standardization of canning protocols within countries. The minor modifications were mainly on the following; beans are soaked and blanched (Balasubramanian et al. 2000) or blanched without soaking (De Lange and Labuschagne, 2001), filled into the can containing tomato sauce (De Lange and Labuschagne, 2001) or brine (Balasubramanian et al., 2000).

The advantage of the industrial canning protocol is that the canning regime (temperature, soak and retort times) of each genotype is determined, reducing the chances of over-cooking or under-cooking a genotype (van der Merwe et al., 2006). However, the major limitation of the industrial canning protocol is that a large sample size is required (e.g 50 kg per sample), which is impractical when dealing with breeding lines (Van Loggerenberg, 2004. Moreover, industrial processors are not willing to screen a large set of breeding lines that are usually handled in a breeding programme (Mutari et al., 2021a). Therefore, considering the limited seed availability before release and the large sets of breeding lines that are usually handled in breeding programs, dry-bean breeders resort to a small-scale laboratory canning protocol (Kelly and Cichy, 2012). However, the laboratory canning protocol also has its limitations. The major limitation is that, bean breeders are forced to standardize the canning protocol with respect to temperature and retort time, preventing multiple processing regimes from being applied to different breeding lines (Bassett et al., 2020). This approach has its own limitations, especially with respect to fast-cooking breeding lines, considering that most breeding programs rely on a 45-minute retort time to evaluate canning quality (Bassett et al., 2020). Fast-cooking genotypes would appear mushy and too soft with low texture scores since they would have been over-cooked at 45 minutes, resulting in biased evaluations (Nordstrom and Sistrunk, 1977; Davis et al., 1980).

Such challenges can be overcome through the indirect measurement of canning-quality traits using rapid genotyping tools and prediction models (Mendoza et al., 2017). This would enable highly efficient and accurate screening of genotypes for improved canning quality. Unfortunately, limited progress has been made in developing molecular markers that are linked to canning-quality traits, such as cooking time (Mutari et al., 2021a). According to Mendoza et al. (2014), the near-infrared spectroscopy (NIRS) can be potentially used by bean breeders as an alternative screening method to determine the canning quality (HC, visual colour ratings and WDW) of breeding lines (before canning) earlier in the breeding process when less seed is available. Even though the NIRS is an inexpensive and rapid screening tool, the prediction accuracies for visual appearance and texture of canned beans are poor (Mendoza et al., 2014). However, the major advantages of using the NIRS technique are that the seed can be planted after analysis and only a small sample size is required (Mendoza et al., 2014).

2.10.3 Nutritional quality

The micronutrient density (Fe and Zn concentrations) of breeding lines in biofortification breeding programs is determined using the following analytical techniques; X-ray fluorescence

(XRF), Atomic absorption spectrophotometer (AAS), and the Inductively Coupled Plasma Atomic Emission Spectrometry (ICP-AES) (Guild et al., 2017a). Both the ICP-AES and AAS have high accuracy and require sample digestion before analysis (Guild et al., 2017a). On the other hand, with XRF, a sample can be analysed in the form of milled flour or as whole grain (mostly for the small seeded crops) (Guild et al., 2017a). In order to increase the reproducibility of results between replicates, grinding grain to flour is recommended when screening grains larger than wheat (*Triticum aestivum* L.) such as dry beans, pigeon pea (*Cajanus cajan* (L.) Millsp.), maize (*Zea mays* L.), chickpea (*Cicer arietinum* L.) and groundnuts (*Arachis hypogaea* L.) (Guild et al., 2017b). Even though the ICP-AES analytical technique is capable of detecting contaminants from the soil, this analytical method is very expensive, involves extensive sample preparation, requires highly pure reagents and trained personnel (Guild et al., 2017b). Moreover, most biofortification breeding programs in developing countries send their materials to developed countries for ICP-AES analysis. For example, HarvestPlus sends pre-release dry beans genotypes to Flinders University in Australia for seed Fe and Zn confirmatory analysis using the ICP-AES method (Crop Breeding Institute, 2019). Consequently, many biofortification breeding programs use the XRF analytical method for preliminary analysis when screening many breeding lines for seed Fe and Zn concentrations.

Significant positive correlations have been reported between XRF and ICP-AES results with respect to Fe and Zn concentrations in dry beans, cowpea and maize flour (Guild et al., 2017b). Guild et al. (2017b) observed an average difference of ± 1 for both Fe and Zn between results from XRF and ICP-AES. Therefore, the XRF analytical technique is a rapid, inexpensive and accurate method for screening many breeding lines for micronutrient density (Guild et al., 2017b, 2017a). However, it is important to note that most biofortification breeding programs in developing countries do not have the XRF equipment. For example, most members of the Pan Africa Bean Research Alliance (PABRA) which comprises of 32-member countries send their materials either to the Alliance of Bioversity International and International Center of Tropical Agriculture (ABC) in Uganda, Democratic Republic of Congo or Colombia for preliminary seed Fe and Zn analysis. Blair et al. (2009) reported significant positive correlations between AAS and ICP-AES results with respect to seed Fe and Zn concentrations in dry beans. Therefore, both methods are reliable in determining seed Fe and Zn. However, the AAS analytical technique is less expensive compared to the ICP-AES with respect to operational costs as well as cost of equipment (Blair et al. 2009). Furthermore, the AAS

analytical technique requires smaller amounts of ground grain compared to the ICP-AES method (Blair et al. 2009).

2.11 Molecular breeding for drought tolerance, enhanced canning and nutritional quality in dry beans

2.11.1 Drought tolerance (Agronomic and physiological traits)

Several researchers have successfully used different types of deoxyribonucleic acid (DNA)-based marker systems in association mapping of polygenic traits in common beans. The most widely used marker systems include simple sequence repeats (SSRs; Perez-Vega et al., 2010; Pereira et al., 2019), amplified fragment length polymorphisms (AFLPs; Perez-Vega et al., 2010), single nucleotide polymorphisms (SNPs; Cichy et al., 2015; Kamfwa et al., 2015a; Katuuramu et al., 2018; Hoyos-Villegas et al., 2017; Dramadri et al., 2019) and microarray-based Diversity Arrays Technology (DArT; Cichy et al., 2014; Valdisser et al., 2020) markers. However, SNP markers are widely preferred because they exhibit high level of polymorphism and occur in abundance (cover the whole genome) as differences of individual nucleotides between individuals. To date, numerous genome wide association studies (GWAS) have been conducted in dry beans to identify molecular markers associated with the following; drought tolerance (Mukeshimana et al., 2014; Trapp et al., 2015; Hoyos-Villegas et al., 2017; Valdisser et al., 2020), disease and insect pest resistance (Tock et al., 2017; Tigist et al., 2019; Zia et al., 2022), nutritional composition-related traits (Katuuramu et al., 2018; Diaz et al., 2022), symbiotic nitrogen fixation (Kamfwa et al., 2015b), photosynthetic traits (Asfaw et al., 2012), agronomic traits (Kamfwa et al., 2015a; Hoyos-Villegas et al., 2017; Dramadri et al., 2019; Diaz et al., 2022) and cooking time (Cichy et al., 2015).

Even though several significant marker trait associations (MTAs) were identified in previous GWAS studies for agronomic traits in drought stressed environments, the use of very low thresholds ($-\log_{10}$ *p*-value ≥ 3.0) in most of the studies in determining significant quantitative trait loci (QTLs) might have resulted in many false positives. In addition, despite the fact that several QTLs or MTAs associated with agronomic traits have been identified in dry beans, further genetic studies are required using germplasm of different genetic backgrounds to reach a saturation point. Moreover, most of the reported putative genes for agronomic and physiological traits were detected under yield potential environments. Some of the previous mapping studies (Blair et al., 2006; Wright and Kelly, 2011; Mukeshimana et al., 2014; Hoyos-Villegas et al., 2017) conducted on agronomic and physiological traits used a small population

size and a limited number of molecular markers. This resulted in QTL with low resolution or poor estimation of marker effects, making it difficult to make inferences on candidate genes correlated with the identified QTL. In addition, some of the identified QTLs explained low total genetic variance (Asfaw et al., 2012), and were sometimes not stable across environments due to genotype by environment interaction (GEI) (Trapp et al., 2015). Thus, their potential for MAS in developing genotypes that are tolerant to drought stress was inconclusive. Therefore, additional studies are required to dissect the genetic basis of agronomic and physiological traits in dry beans under drought stressed and optimal environments for increased genetic gains.

2.11.2 Canning quality

At present, there is no application of molecular markers and genomic prediction/selection in canning-quality assessment in dry beans (Kelly and Bornowski, 2018). The current molecular-marker technologies mostly have application in selecting plants carrying genes associated with tolerance to diseases (Mukankusi et al., 2018). Thus, there is a dire need to fast-track the development of molecular markers that are linked to canning-quality traits. Studies have been conducted to identify QTL for improved canning quality in dry beans (Kelly and Cichy, 2012; Kelly and Bornowski, 2018). Previous studies on QTL for improved canning quality in navy, black and kidney beans identified QTL for colour retention and visual appearance, but the results were not validated for use in MAS (Walters et al., 1997; Posa-Macalincag et al., 2002; Wright and Kelly, 2011). Walters et al. (1997) identified several random amplified polymorphic DNA (RAPD) markers in three populations of navy bean that were associated with several canning-quality traits, such as visual appeal, texture and WDW of processed beans, but the results were also not validated for use in MAS.

As reported by Kelly and Bornowski (2018), limited progress has been made in developing useful markers for cooking time. In studies by Jacinto-Hernandez et al. (2003), the association between cooking time and RAPD marker UNAM 16 was low and did not support its use in MAS as an indirect selection tool. On the contrary, Cichy et al. (2015) revealed QTL on chromosomes *Pv1*, *Pv2*, *Pv3*, *Pv6*, and *Pv9* that have the potential to be explored further for their robustness for reduced cooking time and use in MAS. Cichy et al. (2014), working with the black bean market class, identified colour-related QTL for anthocyanin concentration in canned black beans. Perez-Vega et al. (2010), Cichy et al. (2014), and Kelly and Bornowski (2018) identified different QTLs for HC and water absorption in dry beans. However, these QTLs need further validation.

Bassett et al. (2021) conducted GWAS to reveal significant SNPs associated with several sensory attributes in cooked andean beans of different market classes. They identified many SNPs that were significantly associated with soak-water uptake, cooking time, total water uptake, cotyledon texture, and flavour, and most of these had not been previously associated with sensory attributes. Keller et al. (2022) identified a QTL for canning quality on chromosome *Pv07*, however this QTL needs further validation. In summary, there is a need to validate some of the molecular markers associated with canning quality traits that have been identified by several researchers, considering that most of them have not yet been validated.

2.11.3 Nutritional quality

Even though, several QTL studies have been conducted to identify genomic regions associated with enhanced seed Fe and Zn concentrations in dry beans, these results have not yet been used for marker assisted breeding (Izquierdo et al., 2018). Previous studies on QTL for enhanced seed micronutrient contents in dry beans identified QTL for high seed Fe and Zn (Cichy et al., 2009; Blair et al., 2009, 2010; Izquierdo et al., 2018; Diaz et al., 2022), but the results were not further validated for use in MAS. A recent GWAS analysis of three-bi-parental populations by Diaz et al. (2022) revealed 14 and 12 QTLs for seed Fe and Zn respectively, but these have not been validated for use in MAS. Keller et al. (2022) identified three significant MTAs for seed Fe using 1869 common bean lines from five breeding panels. However, the identified significant MTAs need further validation before use in marker-assisted breeding.

2.12 Combining ability analysis and gene action for drought tolerance in dry beans

To develop improved genotypes that are adapted to water deficit environments with significant genetic gain, knowledge of genetic variability of drought stress tolerance and its genetic basis is a pre-requisite. In addition, information on the inheritance of economic quantitative traits such as grain yield and yield attributing traits under drought stressed conditions and the identification of good general and specific combiners are the primary requirements. Combining ability is the breeding value of parental lines to produce desirable hybrids based on the performance of their progeny (Romanus et al., 2008). General combining ability (GCA – main effects) refers to the average performance of a parental line in a series of cross-combinations and is associated with additive gene effects and better segregants in later generations (Sprague and Tatum, 1942; Griffings, 1956). While, specific combining ability (SCA - interactions) is the average performance of certain cross-combinations relatively better or poorer than would

be expected on the basis of the average performance (GCA) of the other parental lines involved and is associated with non-additive/dominance gene effects (Su et al., 2017).

Crop Breeding Institute in Zimbabwe initiated a navy bean breeding program in 2018 targeting the development of cultivars that are tolerant to drought stress. Regrettably, the combining ability estimates of the navy bean germplasm at CBI that were introduced from ABC are not known. Furthermore, literature on combining ability and gene action controlling drought stress tolerance, grain yield and yield attributing traits is scanty among navy bean lines in Zimbabwe and globally. Assefa et al. (2013b, 2017) identified navy bean genotypes that were tolerant to drought stress. Unfortunately, the combining ability estimates of the drought tolerant navy bean genotypes that were identified by Assefa et al. (2013b, 2017) were never determined, making it difficult for bean breeders to use these genotypes as donors in drought tolerance breeding programs. Therefore, the scarcity of information regarding the GCA estimates of navy bean genotypes under drought stressed environments presents a challenge to the development of drought tolerant navy bean genotypes adapted to drought stressed environments in Zimbabwe.

On the other hand, the available limited information on other dry beans market classes other than navy beans regarding the inheritance of grain yield and yield component traits under drought stressed and non-stressed environments is contradictory (Amongi et al., 2015; Phiri, 2015; Senbetay and Tesfaye, 2015). Previous studies have shown that grain yield and yield component traits under drought stressed and non-stressed environments are controlled by both additive and non-additive gene action. Phiri (2015) reported the predominance of additive gene action over the non-additive gene action in controlling the number of pods per plant (NPPP), DFW, NSPP, hundred seed weight (SW) except for GYD under drought stressed environments. Amongi et al. (2015) reported that drought tolerance is governed by both additive and non-additive genes with predominance of additive gene effects for GYD, pod weight (PW), NSPP and NPPP. On the contrary, Makunde et al. (2007) reported the predominance of dominance effects for GYD, DFW and days to physiological maturity (DPM) under both drought stressed and non-stressed conditions. Therefore, evidence for the expression of GYD and its components under drought stressed environments is contradictory.

2.13 Genotype x environment interaction analysis

The interaction of genotypes with environments (G × E) can only occur if the test environments are divergent and the set of genotypes are of diverse genetic background (Kang et al., 2006). Considering that genotypes and environments are usually diverse in multi environment trials

(METs), in most cases, genotypes do not perform consistently across different environments. This makes breeding for enhanced tolerance to drought stress, canning and nutritional quality in dry beans a challenging task. According to Kang et al. (2006), the GEI presents both challenges and opportunities for geneticists and breeders. Therefore, bean breeders can exploit a significant GEI by selecting superior genotypes for each specific target test environment (breeding for specific adaptation). Furthermore, breeders can avoid GEI by selecting widely adapted and stable genotypes across diverse and multiple test environments (Kang et al., 2006).

Several studies have reported significant effect of GEI on common bean GYD (Kooshki et al., 2016; Tadesse et al., 2018), and seed Fe and Zn (Nchimbi-Msolla and Tryphone, 2010; Mukamuhirwa, 2013). According to Varner and Uebersax (1995), variability in canning-quality traits of navy bean genotypes from various locations was not only attributed to genotype differences, but also to environmental effects, such as soil moisture levels, soil type, and temperature. Thus, the final canning quality of dry beans is determined by the genetic make-up of the cultivar and its interaction with production environment (Balasubramanian et al., 1999; De Lange and Labuschagne, 2001; Kelly and Cichy, 2012), canning or processing factors (Hosfield, 1991) and storage conditions. In addition, several reports suggest non-significant genotype by year (G × Y) or genotype by location (G × L) interactions (Wassimi et al., 1990; Shellie and Hosfield, 1991), whereas other studies found these interactions to be significant (De Lange and Labuschagne, 2001; Khanal et al., 2014; Bassett et al., 2021).

In studies by De Lange and Labuschagne (2001), splits were significantly influenced by environment, genotype, and the G × L interaction. In contrast, De Lange and Labuschagne (1999) observed that splits in navy beans were not significantly influenced by G × L interaction. Bassett et al. (2021) observed significant genotype, environment, and G × L effects for many sensory attributes in cooked andean beans of different market classes. In summary, it can be concluded that there are conflicting reports with respect to the significance of genotype, environment and GEI effects on canning-quality traits. Moreover, most studies have investigated the effects of genotype, environment, and GEI on canning quality (De Lange and Labuschagne, 2001; Khanal et al., 2014; Amongi et al., 2021) and nutritional quality (Nchimbi-Msolla and Tryphone, 2010; Amongi et al., 2021) under stress free conditions yet most of the farmers are located in drought prone areas. Assefa et al. (2017) evaluated 36 navy bean genotypes for adaptation to drought stress at two locations for two seasons. However, the evaluation was not conducted across locations and seasons, making it difficult to identify stable

and specifically adapted genotypes. In Zimbabwe, there is no documented information regarding the adaptability and stability of the elite navy bean genotypes across diverse multi-environments. Thus, it is imperative to conduct studies on GYD, canning quality and seed micronutrient stability and GEI in multi-location trials under diverse agro-ecologies and seasons for devising ideal breeding strategies to adopt; either wide or specific adaptation.

2.14 Summary of research gaps identified and future prospects

From the literature search, it can be concluded that, in Zimbabwe, there is no documented participatory research on navy bean production status, biotic stress management strategies, farmers' perceived production, and marketing constraints, and cultivar trait preferences among the major navy bean growing regions in Zimbabwe. In addition, most of the biofortified dry beans cultivars that have been released in Africa belong to other market classes other than navy beans. Furthermore, no work has been conducted before in Zimbabwe related to breeding micronutrient dense navy bean genotypes for water deficit environments. The above makes it difficult for a breeder to make comprehensive and informed decisions regarding development of new product profiles.

The lack of biofortified navy bean cultivars has forced some of the bean processors in Zimbabwe to establish production lines for micronutrient dense dry beans cultivars of other market classes which generally do not have good canning-quality attributes. Therefore, it is imperative to develop and identify navy bean genotypes that combine drought tolerance with superior canning and nutritional quality traits. This is a reliable and cost-effective strategy. It can be concluded that most researchers do not simultaneously phenotype for drought tolerance, canning and nutritional quality yet most of the farmers are located in drought prone areas. In addition, most of the studies have focused on other market classes as well as on the effects of drought stress on agronomic traits other than on canning and nutritional quality traits. Consequently, limited information is available about the effects of drought stress on nutritional and canning quality in navy beans, and the available results are often inconclusive and contradictory. Therefore, it is imperative to conduct further studies under drought stressed environments across seasons and locations to determine the effects of drought stress on canning and nutritional quality in navy beans.

Marker assisted selection has the potential to facilitate the genetic improvement of several drought tolerance, canning and nutritional quality traits in dry beans. However, at present, there is no application of molecular markers and genomic prediction/selection in canning-quality

assessment in dry beans. Most of the QTLs that have been identified for drought tolerance, canning and nutritional quality traits have not been validated for use in MAS. Thus, there is a dire need to fast-track the validation and development of molecular markers that are linked to drought tolerance, canning and nutritional quality traits. The combining ability estimates of the navy bean germplasm at CBI that were introduced from ABC are not known. In addition, literature on combining ability and gene action controlling drought stress tolerance, grain yield and yield attributing traits is scanty among navy bean lines in Zimbabwe and globally. Moreover, the available limited information on other dry beans market classes other than navy beans regarding the inheritance of grain yield and its attributing traits under drought stressed and non-stressed conditions is contradictory. This necessitates the need to conduct further studies to elucidate the nature of gene action governing the inheritance of grain yield and yield related traits under drought stressed conditions.

It can be concluded that there are conflicting reports with respect to the significance of genotype, environment and GEI effects on canning and nutritional quality traits. Most studies have investigated the effects of genotype, environment, and GEI on canning quality and nutritional quality on other market classes other than navy beans, under stress free conditions yet most of farmers are located in drought prone areas. In Zimbabwe, there is no documented information regarding the adaptability and stability of the elite navy bean genotypes across diverse multi-environments. Thus, it is imperative to conduct studies on GYD, canning quality and seed micronutrient stability and GEI in multi-location trials under diverse agro-ecologies and seasons for devising ideal breeding strategies to adopt; either wide or specific adaptation.

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Chapter 3 [1]Farmers' perceptions of navy bean (*Phaseolus vulgaris* L.) production constraints, preferred traits, farming systems and their implications on bean breeding: A case study from south east lowveld region of Zimbabwe

Abstract

Navy bean (*Phaseolus vulgaris* L.) production in Zimbabwe is limited by multiple constraints including biotic, abiotic and socio-economic. This study aimed at identifying farmers' production constraints, preferred traits and cultivars of navy bean, and strategies used to mitigate some of these constraints. A Participatory Rural Appraisal approach was conducted in four villages of the Lowveld region of Zimbabwe. A total of 176 (75 males; M and 101 females; F) navy bean growing households were interviewed. The most important constraints to navy bean production were drought stress (F – 86%, M – 73%), heat stress (F – 58%, M – 55%), load shedding (F – 46%, M – 54%), poor soil fertility (F – 32%; M – 33%) and susceptibility to pod shattering (Females – 32%, Males – 43%). Mitigation strategies included mulching (18%), ridges (12%), reduced acreage (11%), and cultivating to retain more soil moisture (11%) for drought stress, while irrigating at night (32%), and adjusting planting dates (29%) were used to manage heat stress. Farmer-preferred traits included tolerance to drought and heat, early maturing varieties and disease resistance. Marketing constraints included non-payment for produce in hard currency, lack of diversity in terms of off-takers, high inflation, low grain producer price, and delayed payment. Adoption of improved navy bean cultivars can be increased if breeding programs address the aforementioned constraints and consider farmer-preferred traits when developing new cultivars. Breeders should work closely with extension officers to ensure that cultivars released are cultivated with appropriate agronomic packages for increased productivity and high adoption.

Keywords: Navy bean, participatory rural appraisal, production constraints, preferred traits, marketing constraints

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3.1 Introduction

Globally, common bean (*Phaseolus vulgaris* L.) is an important food and nutritional security pulse crop that provides a cheap source of vegetable proteins, and micronutrients (iron and zinc, and vitamins) and dietary fibre (Akibode and Maredia, 2011). In addition, it serves as an income generating crop thereby supporting many livelihoods, especially in sub-Saharan Africa (SSA). Common bean is widely cultivated and the largest volumes of the crop have come from SSA and Latin America, which accounts for more than 60% of the world production (Beebe et al., 2013). In southern and eastern Africa, the major producers are mainly smallholder farmers who primarily depend on beans for their livelihoods, household food, nutrition and income security (Beebe et al., 2013). Different market classes (sugar, red mottled, and navy bean) of common bean including landraces are grown by farmers in the Lowveld region of Zimbabwe (Katungi et al., 2017).

Navy beans (dry oval pea sized white haricot bean) locally called Michigan pea bean, is a distinct cultigen under common bean which is grown for both income and food security. Due to its high market value compared to the other bean market classes, smallholder farmers in the South East (SE) Lowveld region grow it mostly for income generation. This is exclusively for the bean canning industry under contractual agreements with canning companies, including Cairns Foods Limited, Olivine Industries Limited, Africa Preserves, and National Foods. Although this is not documented, information gathered during various field days with navy bean farmers indicate that farmers retain around 10% of the produce for household consumption, and 90% is delivered to the processor for income generation [Personal Observation, April 2019]. Even though navy bean is an important food security crop, the high market value associated with the crop forces farmers to deliver a greater percentage of the produce to the processor in search of income.

Although navy bean is a major cash crop, its production, productivity and market supply in Zimbabwe has declined in recent years due to several constraints (Mukweza, personal communication, 20 May, 2018[1]). The challenges include low grain yield, high susceptibility to diseases, unavailability of locally bred improved cultivars, drought and heat stress, damages by field pests including bean stem maggot (*Ophiomia phaseoli* sp.), aphids (*Aphis fabae*) and storage pests (*Acanthoscelides obtectus*) (Katungi et al., 2017). The unavailability of improved cultivars results in farmers planting old cultivars which are low yielding and susceptible to new

[1] = Head Research & Development at Cairns Foods Limited (One of the biggest navy bean canning companies)

races of diseases. On the other hand, insect pests (cause grain damage), diseases (cause grain discolouration), drought and heat stress (reduce grain size) affect the canning quality of the grain resulting in the rejection of the commodity by food processors. If a commodity is rejected by a food processor due to the above-mentioned constraints, the farmer would have lost income. This makes it difficult for a farmer to plant the next subsequent crop due to lack of running capital. Consequently, navy bean farmers have accumulated indigenous knowledge and experience over time on production systems and how to cope with a wide range of biotic, abiotic and socio-economic constraints. It is, therefore, important to utilize this knowledge from the farmers during cultivar development to improve the adoption rate of newly developed navy bean cultivars.

Participatory rural appraisal (PRA) relies on participation of the community (local people) and considers the value of stakeholders' knowledge, skill, experience, their needs, preferences, abilities, and innovation (Chandra, 2010). Participatory rural appraisal has been extensively used to identify production constraints of many crops (Derera et al., 2006; Mongi et al., 2016; Nduwumuremyi et al., 2016; Ngailo et al., 2016; Sheikh et al., 2017; Abady et al., 2019). Morris and Bellon (2004) reported that the participation of farmers' in the initial breeding process provides insight into cultivar trait preferences, production and marketing constraints, so that they can be addressed during the breeding process and hence enhance the adoption rate of newly developed cultivars. Information from PRA helps the breeder to design focussed breeding pipelines that result in genetic gains in farmers' fields and more income to the farmers (Danial et al., 2007). Mukankusi (2008) and Ojwang et al. (2009) successfully used information from PRA in the breeding process to develop common beans with resistance to fusarium root rot and bean stem maggot. According to my knowledge, there is no documented participatory research on navy bean production status, biotic stress management strategies, farmers' perceived production, and marketing constraints, and cultivar trait preferences among the major navy bean growing regions in Zimbabwe. Although Katungi et al. (2017) conducted a similar study in 2016 in Zimbabwe, the focus was not on the navy bean market class, but on common bean in general.

Furthermore, gender sensitive breeding has been reported to improve the adoption of released cultivars in Africa (Asfaw et al., 2012; Assefa et al., 2014; Ngailo et al., 2016). Danial et al. (2007) reported that the adoption of new agricultural technologies such as improved cultivars is also affected by gender. Thus, the information from the baseline study will be used to develop

an effective gender responsive, demand led and participatory plant breeding programme which considers the users' views (needs and preferences). The results from the PRA will guide bean breeders in Zimbabwe in defining important traits and constraints, and in developing comprehensive breeding strategies to develop improved high yielding cultivars that are tolerant to biotic and abiotic stresses and preferred by value chain actors (consumers, traders, processors, and farmers). Therefore, the objectives of this study were to: (i) identify major navy bean marketing and production constraints; (ii) identify navy bean cultivars and traits that are preferred by farmers; (iii) assess the production system of navy bean; and (iv) identify the strategies used by farmers to manage drought and heat stress, and their combined implications for breeding navy bean cultivars for Zimbabwe.

3.2 Materials and methods

3.2.1 Study area, sampling procedure and participants

The study was conducted in Chimanimani and Chipinge districts in the South East Lowveld region of Manicaland Province, Zimbabwe in November 2019. The area is a semi-arid region characterised by high temperatures, low, unpredictable and poorly distributed rainfall (Derera et al., 2006). The two districts were selected based on prior information on their experience of growing navy beans and on being the major navy bean growing areas in Zimbabwe. In these areas, navy bean production occurs during the dry winter season (April to July) mainly under flood irrigation as a source of both food and income (Mubako, personal communication, 13 May, 2018[1]). Using a purposive sampling procedure (Changaya, 2007) to ensure good representativeness of navy bean grower households in the study, a list of six major navy bean-growing villages namely Musikavanhu, Nenhowe, Nyanyadzi, Gudyanga, Maunganidze and Tonhorai located in the two districts were selected. These six villages were selected on the basis of their current high levels of navy bean production. Due to limited resources, the study could not be conducted in all the six villages. Therefore, out of the six villages which were used as the sampling frame, four villages [Nenhowe, Gudyanga, and Tonhorai (Chimanimani district) and Maunganidze (Chipinge district)] were chosen randomly for interviewing farmers, surveys and focus group discussions (Changaya, 2007). The global positioning system (GPS) location of the study areas, minimum and maximum temperatures, soil texture, and mean rainfall totals are indicated in Table 3.1.

[1] = Agricultural Extension Supervisor for Nenhowe, Gudyanga, Nyanyadzi, Chakohwa and Tonhorai villages

Table 3.1 Geographical description of the study locations.

District	Village	Geographical location		Altitude (m.a.s l)	M.A.R (mm)	Soil type	Temperature (ºC)	
		Latitude	Longitude				Max	Min
Chimanimani	NW	-19.73976	32.43407	541	415	Sandy loamy	40	15
Chimanimani	GD	-19.89719	32.38190	491	450	Clay loamy	39	18
Chimanimani	TH	-19.93702	32.37236	492	430	Clay	40	16
Chipinge	MD	-19.95341	32.35402	499	120	Sandy loam	38	15

m.a.s.l meters above the sea level, *M.A.R* mean annual rainfall, *mm* millimetres, *ºC* degrees Celsius, *Max* maximum, *Min* minimum, *NW* Nenhowe, *GD* Gudyanga, *TH* Tonhorai, *MD* Maunganidze.

Source: Pambuka, personal communication, 11 November, 2019[1]; Matsenure, personal communication, 12 November, 2019[2]; Mukwakwami, personal communication, 13 November, 2019[3]; Masimura, personal communication, November 14, 2019[4]

For farmer surveys and focus group discussions (FGDs), a systematic sampling method was followed to identify navy bean farmers in the selected villages from lists provided by the local extension stuff (Derera et al., 2006). During the mobilization of farmers, which was done with the assistance of local agricultural extension workers, gender balance was considered accordingly to ensure that at least 50% of the participating farmers were females. A total of 176 (75 males and 101 females) navy bean growing households were interviewed (Table 3.2).

Table 3.2 Number of farmers who participated in the individual household interviews and focus group discussions.

Village	Household Interviews			Focus Group Discussions		
	Males	Females	Total	Males	Females	No. of FGD conducted
Tonhorai	19(37.3%)	32(62.7%)	51	10	12	2
Maunganidze	22(44.9%)	27(55.1%)	49	10	10	2
Gudyanga	17(34.7%)	32(65.3%)	49	10	12	2
Nenhowe	17(63.0%)	10(37.0%)	27	10	11	2
Total	75(42.6%)	101(57.4%)	176	40	45	8

FGDs focus group discussions. The values in parenthesis indicate the percentage of male or female farmers who participated in the individual household interviews.

[1] Extension staff for Gudyanga
[2] Extension staff for Nenhowe
[3] Extension staff for Maunganidze
[4] Extension staff for Tonhorai

This was a representative sample of farmers who grow navy beans in the above-mentioned villages.

3.2.2 Data collection and analysis

Data were collected using various PRA techniques which included transect walk, problem listing, ranking and analysis (Derera et al., 2006) with key informants and corroborated by formal household interviews using a semi-structured questionnaire. Both formal and informal research approaches were used in order to obtain high evidential value, to improve the precision, for validation and to create a solid foundation for drawing conclusions (Derera et al., 2006). The questionnaire had five components namely, demographic information, navy bean cropping systems (sole cropping, mono cropping, inter cropping and mixed cropping), farmers' trait preferences of navy bean cultivars, navy bean production constraints and, strategies used to mitigate some of these constraints. To eliminate gender dominance in FGDs and gain an in-depth understanding of men and women farmer experiences in navy bean production and marketing, the FGDs were conducted separately for men and women with a group of community members. The group of community members in each village comprised of key informants, elders, women group representatives, community-based organization representatives, farmers, and village leaders. These farmers were selected based on; their interest in the navy bean crop, they had grown navy beans in the last two consecutive years, knowledge of navy bean production, knowledge of the village history, and farmers' influence in the village. In each of the four villages, two FGDs (one for men and one for women) were conducted. The number of participants in the FGDs in each village by gender is outlined in Table 3.2.

Issues discussed under the focus groups were: navy bean farming systems, crop production practices, cropping calendar, preferred navy bean cultivars and reasons for preference within the community, ranking of production constraints, major diseases in order of importance, and heat and drought stress management strategies. Interviews were conducted in Shona, the local language with the help of enumerators that had been selected from these villages. Transect walks were conducted in three selected fields after the FGDs to promote discussion amongst farmers about the navy bean production systems and the associated constraints. The collected information was translated to English. The data that was obtained through FGDs, problem listing and transect walk was used for triangulation, to validate and support the data gathered from the individual semi-structured household questionnaire. Both qualitative and quantitative

data from household interviews and FGDs were coded and subjected to analyses using cross-tabulation procedure and contingency chi-square values were calculated for significant tests using the statistical package for social scientists (SPSS) (Release 21) computer package (SPSS, 2021). The data were classified as ordinal or nominal for the SPSS spreadsheet. The farmers' production and marketing constraints and trait preferences were ranked according to the frequency of citation by respondents (percentage of respondents who selected the respective constraint and trait) at village level and across the villages (Nduwumuremyi et al., 2016). Charts were constructed in Microsoft Office Excel 2013.

3.3 Results

3.3.1 Demographics and household characteristics of respondents

As an economic activity, navy bean production is carried out by people of different ages in the villages sampled (Table 3.3). The age group, 41–50 years had the highest respondents and accounted for 28% of the surveyed population (Table 3.3). There were also respondents above 70 years that were involved in navy bean production in all the areas surveyed.

Table 3.3 Distribution of respondents' age in the study areas.

Age interval (Years)	**District**					
	Chimanimani			**Chipinge**		
	Villages			**Village**		
	Nenhowe	**Gudyanga**	**Tonhorai**	**Maunganidze**	**Overall**	***P*- value**
<30	1% (2)	3% (5)	3% (5)	1% (2)	8% (14)	0.294
31 – 40	2% (4)	10% (17)	5% (8)	3% (6)	20% (35)	0.001*
41 – 50	5% (8)	7% (13)	7% (12)	9% (16)	28% (49)	0.104
51 – 60	3% (6)	5% (9)	11% (19)	6% (10)	25% (44)	0.001*
61 – 70	2% (3)	2% (3)	3% (5)	6% (10)	12% (21)	0.098
>70	2% (4)	1% (2)	1% (2)	3% (5)	7% (13)	0.429

*Denotes that the villages differed significantly at $p \leq 0.05$. The values in parenthesis indicate the actual numbers per age group.

3.3.2 Navy bean production, farming systems and important crops grown

The formal survey revealed that maize (*Zea mays* L.), navy beans, onions (*Allium cepa* L.), wheat (*Triticum aestivum* L.), tomatoes (*Solanum lycopersicum* L.), velvet beans (*Mucuna pruriens* L.), sorghum (*Sorghum bicolor* L.), lablab (*Lablab purpureus* L.), and okra (*Abelmoschus esculentus* L.) were the major food crops grown in the study areas (Table 3.4).

Sunflower (*Helianthus annuus* L.), groundnut (*Arachis hypogaea* L.), and bambara groundnut (*Vigna subterranea* L.) were ranked as minor crops across all the villages. Most of the navy bean was grown during the dry winter season under irrigation using the scarce irrigation water resources alongside horticultural crops (onions and tomatoes) and wheat. Navy bean summer production was constrained by high temperatures and drought, even though some of the farmers grew navy beans in small plots for household consumption.

3.3.3 Ranking of food crops based on cultivation area

Maize (81%), navy bean (44.4%), tomatoes (23.1%), onions (16.3%) and sorghum (14.1%) were the major crops grown by both male and female farmers in the study areas in terms of cultivation area (Table 3.4). In each of the villages, maize was ranked first by more than 50% of both male and female respondents. In Nenhowe and Tonhorai villages, navy bean ranked second with 44.4% (males) and 29.6% (females), 39.2% (males), and 70.4% (females) of respondents, respectively, while at Maunganidze village, it was ranked equally with maize in importance (65.2%) among women farmers.

3.3.4 Ranking of food crops based on cash income

Based on cash income, and in order of ranking by the male and female farmers, navy bean, maize, tomatoes, onions, and wheat (*Triticum aestivum* L.) were the major crops grown in the study areas (Table 3.4). In all the four villages, navy bean was ranked first by 49-65.2% of the respondents, while in Maunganidze, Nenhowe and Tonhorai villages, it ranked second after maize among female farmers only. In contrary to women, male farmers in all the villages ranked navy bean as the most important cash crop ahead of maize, tomatoes, onions and wheat. The ranking for the other crops is shown in Table 3.4.

Table 3.4 Important crops in terms of cultivation area, cash income and food security (percentage of respondents).

		Villages															
		Gudyanga (%)			Maunganidze (%)			Nenhowe (%)			Tonhorai (%)			Overall Mean			
		Sex															
Criterion	**Crop**	**M[a]**	**F[b]**	**Mean**	**M**	**F**	**Mean**	**M**	**F**	**Mean**	**M**	**F**	**Mean**	**M**	**F**	**Mean**	***P* value**
Cultivation Area	Maize	48.8[1]	100.0[1]	74.4[1]	89.6[1]	65.2[1]	77.4[1]	100.0[1]	74.0[1]	87.0[1]	70.4[1]	100.0[1]	85.2[1]	77.2[1]	84.8[1]	81.0[1]	0.039*
	Beans	16.4[3]	57.2[2]	36.8[2]	32.8[2]	65.2[1]	49.0[2]	44.4[2]	29.6[2]	37.0[2]	39.2[2]	70.4[2]	54.8[2]	33.2[2]	55.6[2]	44.4[2]	0.044*
	Wheat	16.4[3]	16.4[4]	16.4[4]	0.0	0.0	0.0	29.6[3]	0.0	14.8[4]	8.0[4]	0.0	4.0[6]	13.5[6]	4.1[7]	8.8[6]	0.052
	Onions	24.4[2]	8.4[5]	16.4[4]	8.0[5]	40.8[3]	24.4[4]	14.8[5]	0.0	7.4[5]	8.0[4]	23.6[4]	15.8[4]	13.8[5]	18.2[4]	16.0[4]	0.050*
	Tomatoes	16.4[3]	48.8[3]	32.6[3]	32.8[2]	24.44[4]	28.6[3]	14.8[5]	0.0	7.4[6]	8.0[4]	39.2[3]	23.6[3]	18.0[3]	28.1[3]	23.1[3]	0.047*
	Sorghum	0.0	5.6[7]	2.8[7]	16.4[4]	8.0[5]	12.2[5]	29.6[3]	29.6[2]	29.6[3]	15.6[3]	8.0[5]	11.8[5]	15.4[4]	12.8[5]	14.1[5]	0.052
	Lab Lab	0.0	0.0	0.0	0.0	8.0[5]	4.0[6]	0.0	14.8[4]	7.4[6]	0.0	0.0	0.0	0.0	5.7[6]	2.9[8]	0.052
	Velvet beans	16.4[3]	8.0[6]	12.2[6]	0.0	8.0[5]	4.0[6]	0.0	0.0	0.0	0.0	0.0	0.0	4.1[7]	4.0[8]	4.1[7]	0.052
Cash Income	Maize	0.0	40.8[4]	20.4[4]	24.4[3]	65.2[1]	44.8[2]	44.4[2]	59.2[1]	51.8[2]	31.2[2]	70.4[1]	50.8[2]	25.0[2]	58.9[2]	42.0[2]	0.043*
	Beans	40.8[1]	89.6[1]	65.2[1]	40.8[1]	57.2[2]	49.0[1]	100.0[1]	29.6[2]	64.8[1]	54.8[1]	62.8[2]	58.8[1]	59.1[1]	59.8[1]	59.5[1]	0.044*
	Wheat	16.4[4]	8.0[6]	12.2[6]	24.4[3]	32.8[3]	28.6[3]	14.8[5]	14.8[3]	14.8[4]	8.0[5]	15.6[6]	11.8[5]	15.9[6]	17.8[5]	16.9[5]	0.051
	Onions	16.4[4]	48.8[3]	32.6[3]	24.4[3]	0.0	12.2[7]	29.6[3]	14.8[3]	22.2[3]	8.0[5]	8.0[7]	8.0[7]	19.6[4]	17.9[6]	18.8[4]	0.049*
	Tomatoes	32.8[2]	57.2[2]	45.0[2]	32.8[2]	24.4[4]	28.6[3]	0.0	14.8[3]	7.4[6]	31.2[2]	39.2[3]	35.2[3]	24.2[3]	33.9[3]	29.1[3]	0.047*
	Lab Lab	32.8[2]	0.0	16.4[5]	8.0[7]	8.0[7]	8.0[8]	29.6[3]	0.0	14.8[5]	0.0	23.6[5]	11.8[5]	17.6[5]	7.9[7]	12.8[6]	0.050
	Velvet beans	0.0	0.0	0.0	16.4[6]	16.4[5]	16.4[5]	14.8[5]	0.0	7.4[6]	15.6[4]	0.0	7.8[8]	11.7[7]	4.1[8]	7.9[8]	0.052
	Okra	0.0	16.4[5]	8.2[7]	8.0[7]	16.4[5]	12.2[6]	0.0	14.8[3]	7.4[6]	0.0	31.2[4]	15.6[4]	2.0[8]	19.7[4]	10.9[7]	0.050*
Food Security	Maize	100[1]	100.0[1]	100[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	100.0[1]	NS
	Beans	8.0[2]	24.0[2]	16.0[2]	8.0[3]	16.4[2]	12.2[4]	14.8[2]	29.6[2]	22.2[2]	8.0[3]	23.6[3]	15.8[3]	11.6[3]	23.4[2]	17.5[2]	0.052
	Sorghum	0.0	0.0	0.0	16.4[2]	16.4[2]	16.4[2]	14.8[2]	14.8[3]	14.8[3]	15.6[2]	31.2[2]	23.4[2]	11.7[2]	15.6[3]	13.7[3]	0.051
	Wheat	0.0	8.0[3]	8.0[3]	16.4[2]	16.4[2]	16.4[2]	0.0	0.0	0.0	15.6[2]	8.0[4]	11.8[4]	8.0[3]	8.1[4]	8.1[4]	0.052

M male, *F* female, *NS* not significant. The values in parentheses indicate the percentage of respondents who selected the respective particular crop and the superscript indicates the relative rank of the crop. *Denotes that the villages differed significantly at $p \leq 0.05$.

3.3.5 Ranking of food crops based on food security

Regarding food security, maize (100% of respondents), navy beans (17.5%), sorghum (13.7%) and wheat (8.1%) were the major crops as indicated by both men and women (Table 3.4). In Gudyanga and Nenhowe villages, navy bean was ranked second by 8.0% and 14.8% of the male respondents, respectively, while in Maunganidze village among men, it occupied the third (8.0%) place after sorghum and wheat, which were ranked equally (16.4%). Sorghum (31.2%) occupied the second place at Tonhorai village among women, while navy bean occupied the same place at Nenhowe (29.6%) and Gudyanga villages among women.

3.3.6 Land size and navy bean production yield

Sole cropping was the predominant (100%) cropping system in all the surveyed villages (Table 3.5). Farmers cultivated navy bean farming on small land holdings (mean = 0.27 ha). The average land size allocated to navy bean production was not significantly different among the villages from 0.23 (Gudyanga) to 0.32 ha (Nenhowe) (Table 3.5). On average the total land size per household was 0.75 ha, with the smallest being 0.69 ha (Gudyanga) and the largest being 0.77 ha (Tonhorai). The average grain yield of navy bean varied significantly ($p < 0.05$) from village to village with Gudyanga having the highest yields (Table 3.5). Focus group discussions reported average grain yields of 2.45, 2.76, 2.19 and 2.42 t ha^{-1} in Tonhorai, Gudyanga, Nenhowe and Maunganidze villages, respectively.

Table 3.5 Land size and navy bean cropping system in across four villages.

Village	**Average land size**		**Farming system (%)**				**Estimated Yield (t ha^{-1})**
	ALSH (ha)	**ALSAB (ha)**	**SC**	IC	MC	MOC	
Tonhorai	0.77	0.27	100.00	0.00	0.00	0.00	2.45^{bc}
Gudyanga	0.69	0.23	100.00	0.00	0.00	0.00	2.76^{d}
Nenhowe	0.79	0.32	100.00	0.00	0.00	0.00	2.19^{a}
Maunganidze	0.76	0.26	100.00	0.00	0.00	0.00	2.42^{b}
Mean	0.75	0.27	100.00				2.45
LSD	0.11	0.05	NS	-	-	-	0.26
F pr	0.08^{NS}	0.09^{NS}	NS	-	-	-	0.04^{*}

ALSH average land size per household, *ALSAB,* average land size allocated to navy bean per household, *SC* sole cropping, *IC* inter cropping, *MC* mixed cropping, *MOC* mono cropping, *LSD* least significant differences of means (5 % level*), F pr* probability value (5% level), *NS* not significant, * $p < 0.05$. The % indicates the percentage of respondents who are using the respective farming system. Means followed by the same letter are not significantly different.

3.3.7 Navy bean production constraints

Navy bean production was hampered by many constraints. Challenges ranged from biotic, abiotic and socio-economic constraints (Table 3.6). The perception of the constraints affecting navy bean production in the study locations was not different within and across villages as well as between men and women within the villages. The ranking of the constraints among both male and female farmers across all the locations did not differ much. Drought stress, heat stress, load shedding/power outages, susceptibility to pod shattering, poor soil fertility, insect pests, seed availability and diseases were the main constraints of navy bean production across all the villages according to both male and female farmers.

The most challenging insect pests across all the locations were the black bean aphid, bean stem maggot and harvester termites [*Hodotermes mossambicus* (Hagen) (Isoptera: Hodotermitidae)]. Diseases mainly comprised of bean rust (*Uromyces appendiculatus*), angular leaf spot (*Pseudocercospora griseola*), and common bacterial blight (*Xanthomonas axonopodis* pv. *phaseoli*). Drought stress was the second most challenging constraint in Nenhowe (68%) and Tonhorai (64%) villages among male farmers, while heat stress ranked the same at Gudyanga (60%), Maunganidze (64%), Nenhowe (48%) and Tonhorai (60%) villages among female farmers. Farmers reported that drought stress mainly occurred during the reproductive stage of growth and heat stress was common in the late planted crop for a short period of time. The other major constraints reported by both male and female farmers were lack of access to transport, low yielding cultivars, and shortage of labor.

3.3.8 Management strategies for drought and heat stress

The strategies used by farmers to alleviate the effects of drought stress are summarized in Table 3.7. A total of 40, 38, 33 and 43% of farmers in Gudyanga, Maunganidze, Nenhowe and Tonhorai villages, respectively, did not use any strategy to manage/control drought stress. However, soil mulching, reduced acreage, use of ridges, cultivating to retain more soil moisture, adjusting planting dates, and watering of plants at night are the strategies that were used by the other farmers to alleviate the effects of drought stress. Soil mulching was the most widely used method of managing drought stress at Gudyanga (29% of respondents), Maunganidze (16%) and Tonhorai (14%). During FGDs, farmers in all the four villages highlighted the importance of soil mulching in suppressing and reducing weed infestation and fungal disease pressure.

Table 3.6 Navy bean production constraints experienced by farmers.

		Villages										
Sex	**Constraint**	**Gudyanga (%)**	**Rank**	**Maunganidze (%)**	**Rank**	**Nenhowe (%)**	**Rank**	**Tonhorai (%)**	**Rank**	**Mean (%)**	**Overall Rank**	***P* - Value**
Females	Heat stress	60	2	64	2	48	2	60	2	58	2	0.046*
	Drought stress	84	1	80	1	100	1	80	1	86	1	0.025*
	Susceptibility to pod shattering	32	5	32	4	28	5	36	4	32	4	0 208
	Poor soil fertility	36	4	24	6	40	3	28	7	32	4	0.042*
	Diseases	24	7	24	6	28	5	28	7	26	8	0.417
	Insect pests	28	6	32	4	28	5	32	5	30	6	0.417
	Seed availability	24	7	24	6	28	5	32	5	27	7	0 152
	Low yielding cultivars	20	10	20	10	20	10	20	9	20	10	0 591
	Power outages	48	3	52	3	44	4	40	3	46	3	0.083
	Shortage of labor	20	10	20	10	20	10	16	11	19	11	0 556
	Lack of access to transport	24	7	24	6	24	9	20	9	23	9	0 556
Males	Heat stress	48	3	44	2	60	1	68	1	55	2	0.018*
	Drought stress	76	1	84	1	68	2	64	2	73	1	0.028*
	Susceptibility to pod shattering	44	4	44	2	36	4	44	4	42	4	0 139
	Poor soil fertility	28	5	40	5	36	4	28	7	33	6	0.062
	Diseases	24	7	24	7	28	6	32	6	27	9	0 152
	Insect pests	28	5	28	6	28	6	36	5	30	8	0 139
	Seed availability	24	7	24	7	24	8	20	8	23	10	0 556
	Low yielding cultivars	20	10	20	10	20	9	16	10	19	11	0 556
	Power outages	60	2	44	2	14	3	14	3	54	3	0.046*
	Shortage of labor	80	10	20	10	16	11	16	10	33	6	0.417
	Lack of access to transport	96	7	24	7	20	9	20	8	40	5	0.417

The % indicates the percentage of respondent; * denotes that the villages differed significantly at $p < 0.05$.

Table 3.7 Management strategies for drought and heat stress across four villages.

Stress	Strategy	Village				Average (%)	*P* - value
		Gudyanga (%)	Maunganidze (%)	Nenhowe (%)	Tonhorai (%)		
Moisture	Soil mulching	29(2)	16(2)	6(7)	14(2)	18(1)	0.040*
	Reducing acreage	11(3)	5(6)	17(3)	14(2)	11(3)	0.051
	Use of ridges	9(5)	14(3)	22(2)	9(5)	12(2)	0.049*
	Cultivating to retain more moisture in soil	6(5)	14(3)	11(4)	14(2)	11(3)	0.053
	Adjusting planting dates	0(7)	8(5)	0(7)	3(6)	3(6)	0.053
	No control strategy	40(1)	38(1)	33(1)	43(1)	39(NC)	0.052
	Watering of plants at night	6(6)	5(6)	11(4)	3(6)	6(5)	0.053
Heat	Adjusting planting dates	18(4)	22(2)	56(1)	38(1)	29(2)	0.006*
	Irrigating at night	24(2)	49(1)	25(2)	21(3)	32(1)	0.027*
	No control strategy	24(2)	16(3)	6(4)	25(2)	19(NC)	0.042*
	Mulching	33(1)	14(4)	13(3)	17(4)	20(3)	0.041*

NC no control/management strategy (represents percentage of farmers who reported that they do not use any control or management strategy). The % indicates the percentage of respondents using that respective strategy. *denotes that the villages differed significantly at $p < 0.05$.

At Nenhowe village, the most common method was the use of ridges (22%) followed by cultivating to retain more soil moisture. Overall (18%), soil mulching was the most common method of managing drought stress as reported by 29, 16, 14 and 6% of farmers interviewed at Gudyanga, Maunganidze, Tonhorai and Nenhowe villages, respectively. Ridges (12%) were the second most widely used strategy, followed by reducing acreage (11%) and cultivating to retain more soil moisture (11%). Less common strategies of managing drought stress included adjusting planting dates (3%) and watering of plants at night (6%). The strategies used by farmers to alleviate the effects of heat stress are summarized in Table 3.7. Irrigating at night (reported by 32% of respondents), adjusting planting dates (29%), and mulching (20%) are the methods that were used by farmers to alleviate the effects of heat stress. However, overall, 19% of the farmers across all the villages did not use any heat stress management/control strategy. A total of 56, 38, 22 and 18% of farmers at Nenhowe, Tonhorai, Maunganidze and Gudyanga villages, respectively, confirmed using the strategy of adjusting planting dates to alleviate the effects of heat stress. At Gudyanga and Maunganidze, the most commonly used methods were mulching (33%) and irrigating at night (49%) respectively. Overall (32%), irrigating at night was the most common method of alleviating the effects of heat stress as reported by 49, 25, 24 and 21% of farmers interviewed at Maunganidze, Nenhowe, Gudyanga and Tonhorai villages, respectively.

3.3.9 Navy bean marketing constraints

Navy bean production was hampered by many constraints among which are: lack of diversity in terms of buyers/off-takers, non-payment for produce in hard currency, delayed payment by contractor, low grain producer price, and inflation eroding the value of the produce (Table 3.8). Non-payment for produce in hard currency was the top most challenging constraint among both male and female farmers at Gudyanga, Nenhowe and Tonhorai, while lack of diversity in terms of buyers/off-takers (92% of male respondents) and low grain producer price (100% of female respondents) were ranked the same at Maunganidze. The other major challenging constraints among both male and female farmers were lack of transport to ferry produce, non-transparent grading, expensive packaging material and breach of contract by contractor.

Table 3.8 Navy bean marketing constraints experienced by farmers.

Sex	Constraint	Village				Mean (%)	Rank	*P* - Value
		Gudyanga (%)	Maunganidze (%)	Nenhowe (%)	Tonhorai (%)			
Male	Delayed payment by contractor	72	60	24	68	56	3	0.033*
	Breach of contract by contractor	0	0	0	64	16	7	0.022*
	Low grain producer price	36	28	96	44	51	4	0.019*
	Lack of diversity in terms of buyers/off-takers	48	92	84	64	72	2	0.081
	None	0	0	0	20	5	NC	0.107
	Expensive packaging material	48	20	0	0	17	7	0.021*
	Non-payment for produce in hard currency	100	52	100	96	87	1	0.062
	Inflation eroding the value of the produce	48	56	48	44	49	5	0.421
	Lack of transport to ferry produce	24	72	12	0	27	6	0.033*
	Non-transparent grain grading	24	20	24	0	17	7	0.081
Female	Delayed payment by contractor	72	64	20	56	53	3	0.054
	Breach of contract by contractor	24	28	0	44	24	6	0.065
	Low grain producer price	64	100	60	36	65	2	0.050*
	Lack of diversity in terms of buyers/off-takers	64	28	40	76	52	4	0.056
	None	0	0	30	24	13.5	NC	0.003*
	Expensive packaging material	28	0	40	0	17	7	0.028*
	Non-payment for produce in hard currency	100	40	100	100	85	1	0.148
	Inflation eroding the value of the produce	0	44	80	24	37	5	0.009*
	Lack of transport to ferry produce	24	28	0	0	13	9	0.157
	Non-transparent grain grading	0	48	0	12	15	8	0.025*

NC not a constraint (represents percentage of farmers who reported that they do not experience any marketing constraint). The % indicates the percentage of respondents experiencing the respective constraint. * denotes that the villages differed significantly at $p < 0.05$.

3.3.10 Farmer preferred traits for improvement during navy bean breeding

Across all the locations, farmers concurred that there was need for improvement of certain traits in the current cultivars. The farmer-preferred traits for improvement are summarized in Table 3.9. Tolerance to heat (72% of the respondents), and drought (72%), resistance to diseases (72%), and insect pests (71%), maturity period (71%), grain yield (71%), pod size (69%), grain size (68%), and resistance to pod shattering (68%) were identified as the most important traits that needed enhancement by both male and female farmers across all the locations. Canning quality (26%) and nutritional value (iron and zinc) (28%) were the least important traits for improvement among both male and female farmers across all the villages. Generally, no gender differences were observed for farmers' trait preferences across the villages.

3.3.11 Sources of seed supply and cultivar preferences by farmers

The major source of navy bean seed was the canning company (94%) as a business venture (Figure 3.1).

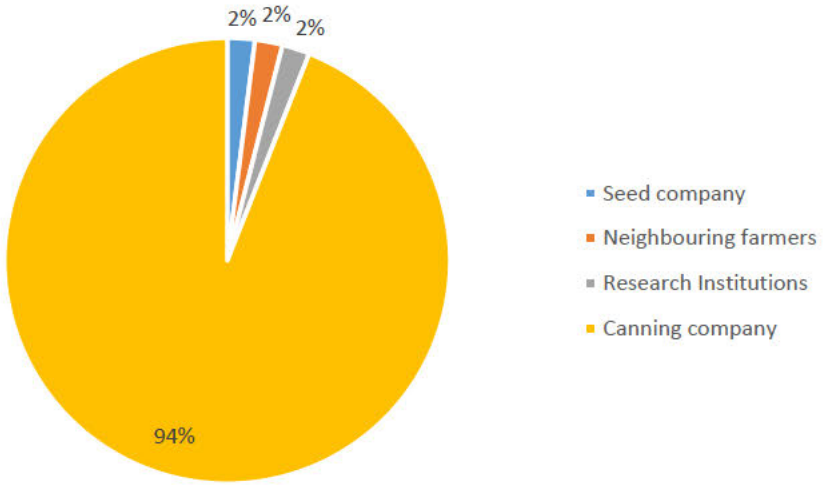

Figure 3.1 Sources of navy bean seed in south east lowveld region of Zimbabwe in 2019.

For household consumption especially during summer season, the neighbouring farmers, research institutions, and seed companies were a critical seed source.

Table 3.9 Farmers' trait preference of a navy bean cultivar by sex for improvement during breeding.

	Village														
	Gudyanga (%)			Maunganidze (%)			Nenhowe (%)			Tonhorai (%)					
Cultivar characteristic	**M**	**F**	**Mn**	**M**	**F**	**Mn**	**M**	**F**	**Mn**	**M**	**F**	**Mn**	**Mean (%)**	**Overall Rank**	***P*-Value**
Heat stress tolerance	76(1)	68(6)	72(2)	68(8)	67(9)	68(9)	71(1)	70(1)	71(1)	75(1)	75(2)	75(2)	72	1	0.125
Drought stress tolerance	70(3)	73(1)	72(2)	71(1)	75(1)	73(1)	71(1)	70(1)	71(1)	74(3)	69(8)	72(3)	72	1	0.083
Disease tolerance	70(3)	72(3)	71(4)	71(1)	75(1)	73(1)	71(1)	70(1)	71(1)	72(4)	72(4)	72(3)	72	1	0.059
Insect pest tolerance	68(5)	68(6)	68(6)	69(6)	66(10)	68(9)	71(1)	70(1)	71(1)	75(1)	76(1)	76(1)	71	4	0.985
Canning quality	30(16)	27(17)	29(16)	31(16)	30(16)	31(16)	33(16)	20(17)	27(17)	21(16)	11(17)	16(17)	26	17	0.011*
Short cooking time	68(5)	67(8)	68(6)	68(8)	63(11)	66(11)	69(7)	66(7)	68(7)	62(11)	73(3)	68(10)	68	8	0.116
Grain yield	68(5)	72(3)	70(5)	71(1)	75(1)	73(1)	71(1)	66(7)	69(6)	72(4)	68(9)	70(5)	71	4	0.469
Maturity period	72(2)	73(1)	73(1)	71(1)	75(1)	73(1)	64(11)	70(1)	67(9)	68(7)	71(6)	70(5)	71	4	0.221
Nutritional value iron, zinc	22(17)	34(16)	28(17)	29(17)	19(17)	24(17)	21(17)	59(11)	40(16)	21(16)	19(16)	20(16)	28	16	0.012*
Growth habit	44(15)	40(15)	42(15)	39(15)	35(15)	37(15)	44(15)	43(13)	44(15)	35(15)	46(15)	41(15)	41	15	0.019*
Plant height	54(12)	49(12)	52(12)	53(12)	50(12)	52(12)	50(12)	43(13)	47(12)	58(12)	52(12)	55(12)	52	12	0.560
Resistance to pod shattering	68(5)	65(10)	67(8)	68(8)	71(7)	70(6)	67(10)	63(10)	65(10)	66(9)	72(4)	69(8)	68	8	0.200
Pod size	68(5)	64(11)	66(9)	69(6)	69(8)	69(8)	69(7)	70(1)	70(5)	68(7)	71(6)	70(5)	69	7	0.854
Grain size	62(10)	69(5)	66(9)	71(1)	75(1)	73(1)	69(7)	66(7)	68(7)	66(9)	65(11)	66(11)	68	8	0.714
Grain taste	46(13)	46(14)	46(14)	44(13)	42(13)	43(13)	46(13)	47(13)	47(12)	48(14)	47(13)	48(14)	46	14	0.025*
Storability	62(10)	67(8)	65(11)	65(11)	75(1)	70(6)	71(1)	59(11)	65(10)	70(6)	68(9)	69(8)	67	11	0.504
Easy of shelling	46(13)	47(13)	47(13)	44(13)	41(14)	43(13)	46(13)	47(13)	47(12)	50(13)	47(13)	49(13)	47	13	0.521

M male, *F* female, *Mn* average. The number in parentheses () indicates the rank of the respective trait. * denotes that the villages differed significantly at $p < 0.05$.

Most of the respondents were not well informed of the existence of improved navy bean cultivars such as Protea and Teebus. Zimbabwe White Bean formerly called Michigan pea bean was the most widely grown navy bean cultivar among both men and women farmers at Nenhowe (70% of respondents), Gudyanga (85%), Tonhorai (82%), and Maunganidze (90%) (Table 3.10). The second most widely cultivated navy bean cultivar was Teebus (Nenhowe – 25%, Gudyanga – 11%, Tonhorai – 18%, and Maunganidze – 10%).

Table 3.10 Navy bean cultivars grown in the study areas.

		Village						
Gender	**Cultivar**	**Gudyanga**	**Maunganidze**	**Nenhowe**	**Tonhorai**	**Total**	**OR**	**P-value**
Females	Zimbabwe White Bean	54%	58%	15%	54%	49%	1	0.032*
	Teebus	8%	3%	10%	15%	9%	2	0.003*
	Caledon	3%	0%	0%	0%	1%	3	0.638
Males	Zimbabwe White Bean	31%	32%	55%	28%	34%	1	0.015*
	Teebus	3%	6%	15%	3%	5%	2	0.021*
	Caledon	3%	0%	5%	0%	1%	3	0.042*

OR overall rank. The number in parenthesis () indicates the cultivar rank in terms of the number of respondents cultivating the cultivar. The % indicates the percentage of respondents who are growing the respective cultivar. * denotes that the villages differed significantly at $p < 0.05$.

3.3.12 Farmers' desirable and undesirable characteristics of the navy bean cultivars

About 45% and 13% of the farmers across all the locations desired high grain yield and disease tolerance of the Zimbabwe White Bean cultivar, respectively (Figure 3.2). However, more than 15% of the farmers indicated they did not like any attribute of the Zimbabwe White Bean and Teebus cultivars, but they were the only available cultivars that were offered by the contractor/canning company. Even though Caledon was not widely grown, 2% of the farmers who cultivated the cultivar liked the high grain yield potential of the cultivar. The undesirable characteristics of the navy bean cultivars grown by farmers across the four villages are presented in Figure 3.3. Results indicated that susceptibility to pod shattering (3% of respondents), susceptibility to insect pests (45%), susceptibility to diseases (27%), susceptibility to heat stress (8%), small seed size (2%), low grain yield potential (15%), and susceptibility to drought stress (10%) were some of the undesirable traits of Zimbabwe White Bean cultivar. The cultivar Caledon had only one undesirable characteristic across all the locations which was susceptibility to insect pests (2%), mainly the black bean aphid.

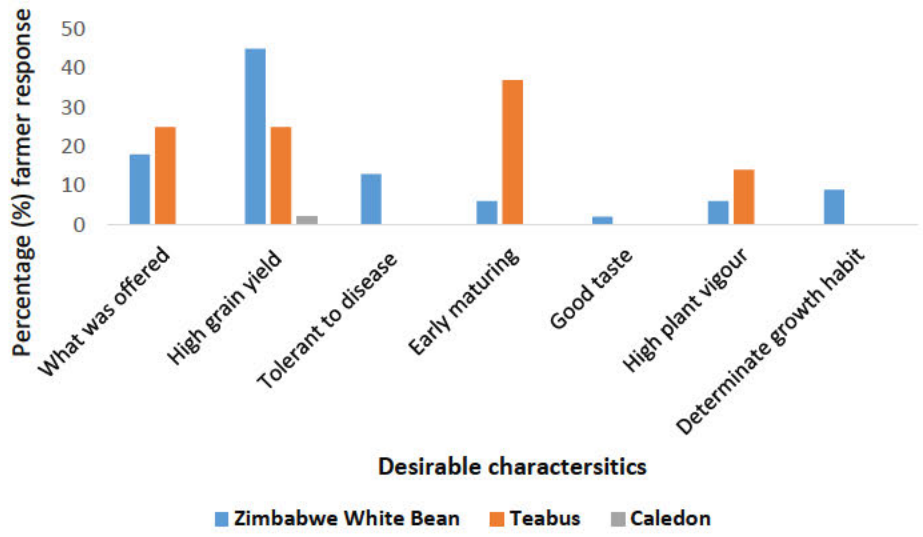

Figure 3.2 Desirable characteristics about the cultivars grown by farmers across the four villages.

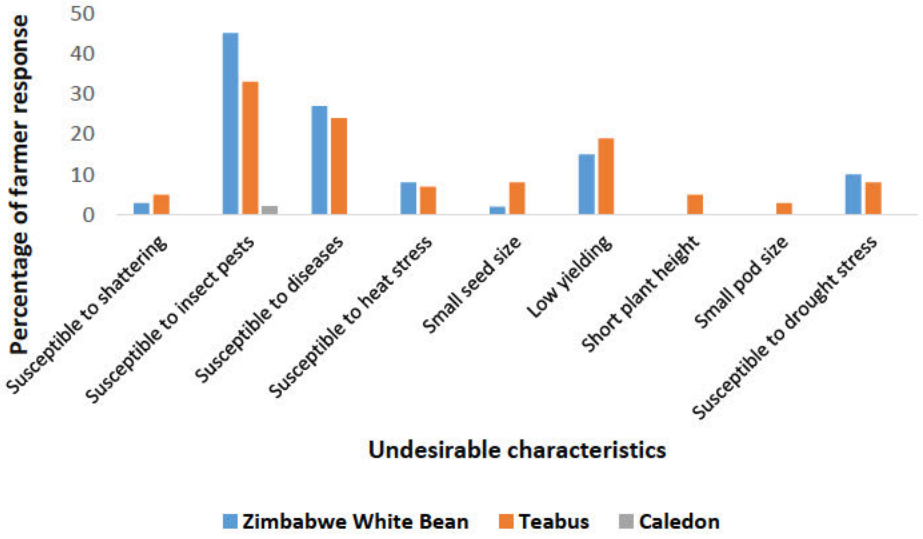

Figure 3.3 Undesirable characteristics about cultivars being grown by farmers across four villages.

With regards to Teebus, some of the undesirable characteristics across the four villages were; susceptibility to pod shattering (5%), susceptibility to insect pests (33%), susceptibility to diseases (24%), susceptibility to heat stress (7%), small seed size (8%), low grain yield potential (19%), short plant height (5%), small pod size (3%), and susceptibility to drought stress (8%).

3.4 Discussion

3.4.1 Gender and age distribution of respondents

The majority of navy bean farmers were females except at Nenhowe where women cultivate green mealies as a cash crop since it fetches a high market price (Banziger et al., 2002). Traditionally, bean is considered a women's crop in Zimbabwe. However, due to the profitability of navy bean production men are slowly involved in the cultivation of the crop. A very small percentage of the farmers were aged below 30 years since most of the youths were engaged in diamond mining which is associated with quick cash returns. The socio-economic constraints associated with navy bean production also hindered the participation of youths in navy bean production. Njenga et al. (2012) reported that agricultural activities were unattractive to youths due to the input and time investment.

3.4.2 Important crops grown

Farming enterprises were business oriented evidenced by the type of crops grown which ranged from horticultural crops, cereals, and others. The diversification of crops protected farmers from natural hazards such as drought, guaranteeing food, nutrition, and income security at farm level. Maize, navy bean and sorghum featured prominently among the most important food crops for household consumption and income generation. Both maize, sorghum, and navy beans are complementary to each other within the farming households, navy bean is a cheap source of proteins, and farmers often consume it with "sadza/isitshwala" (thick porridge made from maize/sorghum flour). Furthermore, navy bean is a short season crop which allows relay-cropping with green mealies and its market is guaranteed since it is grown under contract farming. Income generated from navy bean sales is used to purchase farming inputs and livestock (goats, and cattle), household food, and to pay school fees. Sorghum, a drought tolerant crop was grown by farmers during the summer season under rain-fed conditions as a coping strategy for adapting to drought stress and guaranteeing both human food and animal feed. These findings agree with Chidoko and Zhou (2012) and Nassary et al. (2020) who reported maize and dry beans as important food and cash crops in many parts of the world, including SSA. The majority of men ranked navy bean (average of US$800 per tonne) as the most important crop for cash income ahead of maize (average of US$235 per tonne) which was ranked first by women. This was because men were in charge of

navy bean sales with the contractor and women were in charge of green mealies (boiled, roasted) sales.

3.4.3 Land size and navy bean production yield

The average land size of 0.27 ha per household allocated to navy bean production was comparable to the observation made by Katungi et al. (2017) that the majority of dry beans farmers in Natural Region V allocated an average of 0.271 ha to dry beans production. Generally, navy bean was cultivated in small fields because most contracting companies availed seed which was enough to cover an area of 0.25 ha per farmer. This was used as a risk management strategy against biotic, abiotic and socio-economic constraints coupled with the unavailability of seed. Sole cropping was the most common cropping system because other crops (wheat, tomatoes, and onions) which the farmers cultivate during the dry winter season are not compatible for intercropping with navy bean. Furthermore, the weather conditions during the winter season are not favourable for the cultivation of other main food crops which are compatible to intercrop with navy beans such as maize. This is corroborated by Njoki (2013) and Katungi et al. (2017) who found that dry beans were grown as a sole crop in Zimbabwe and Kiambu County of Kenya, respectively. However, some authors, Fageria et al. (2010), and Mongi et al. (2016) reported that dry beans were grown by smallholder farmers in intercropping and mixed cropping systems in African countries. Gudyanga had the highest average navy bean grain yield (2.76 t ha^{-1}) per hectare because farmers practiced good agricultural practices (GAPs) (optimum fertilizer application, pesticide application, and herbicide application) despite the socio-economic constraints. In contrary, Nenhowe had the least average navy bean grain yield per hectare due to frequent breakdown of irrigation pumps which resulted in farmers applying an average of two irrigation cycles instead of five cycles per navy bean growing season. The significant yield gap between farmers' yield and yield potential could be attributed to drought stress, heat stress, susceptibility to fungal diseases, and socio-economic constraints such as unavailability of seed of improved cultivars.

3.4.4 Navy bean production constraints

The results revealed that drought stress, heat stress, pod shattering, poor soil fertility, insect pests, diseases, and seed availability were the major production constraints. This is corroborated by Katungi et al. (2017) who found that insect pests, diseases, and drought stress are the most challenging dry beans production constraints in Zimbabwe. A similar study carried out by

Chemining'wa et al. (2014) in Kenya also reported that insect pests, diseases, drought and transport are challenging constraints of navy bean production. Many scientists (Thung and Rao, 1999; Singh, 2001; Beebe et al., 2010) have reported that about 60% of cultivated beans worldwide are grown under the risk of either terminal or intermittent drought. Drought stress and heat stress were the most important constraints because farmers are not able to grow navy beans during the main cropping season due to erratic rainfall totals (less than 450 mm) coupled with high temperatures (more than 32 ℃). Load shedding (power cuts) in winter was also an important constraint because it affected the frequency of irrigation cycles resulting in the crop experiencing prolonged periods of drought stress. Farmers were forced to irrigate at night when electricity was available, a strategy which was often a challenge to women farmers due to household responsibilities/duties. Tackling the effects of load shedding on irrigation cycles needs much more effort and a holistic approach; the government of Zimbabwe and private sector must invest in solar energy to minimize the effects of drought stress when electricity is not available emanating from increased demand.

Susceptibility to pod shattering was an important constraint because despite experiencing significant grain yield losses, farmers spent a lot of time and labor in picking the small seeded grains from the ground. Farmers reported susceptibility to diseases as an important production constraint because some of the diseases infect the grain, and diseased grains are discarded by the contractor during grading since they do not meet the canning quality standards. This results in significant income losses on the part of the farmer since payment is based on the quantity of "clean" grain. Similar findings were reported by Njoki (2013) and Mongi et al. (2016) who found that diseases such as angular leaf spot were important dry beans production constraints in the southern highlands of Tanzania and Kiambu County in Kenya, respectively. The high susceptibility to diseases was exacerbated by the unavailability of seed of improved navy bean cultivars in the market. This was due to the absence of newly released cultivars and the lack of formal seed system (production of breeders, foundation and certified seed) for Zimbabwe White Bean to inject disease free seed into the system since this two-decade old cultivar was never formally released (Tsiko, 2018). This results in continued recycling of infected seed, a scenario which increases the prevalence of seed borne diseases such as angular leaf spot.

Similarly, Chemining'wa et al. (2014) reported that navy bean seed systems in Kenya were informal. On the other hand, studies conducted by Fourie (2011) revealed that the South African

cultivar "Teebus" was highly susceptible to common bacterial diseases. As a result, this cultivar has since been replaced in South Africa due to high susceptibility to bacterial and fungal diseases such as common bacterial blight and bean rust, respectively [Fourie, personal communication, January 2020[1]]. The unavailability of improved navy bean seed in Zimbabwe is due to the fact that the first improved navy bean cultivar (Protea) in Zimbabwe was released in 2018 (Tsiko, 2018) such that seed companies are still bulking foundation and certified seed. This compels canning companies to rely on Zimbabwe White Bean and importation of Teebus seed from South Africa) increasing production costs). Consequently, the majority (94%) of farmers sourced their seed from canning companies due to the unavailability of seed in agro-dealer shops. This is corroborated by Chemming'wa et al. (2014) who found that contracting companies in Kenya (Nakuru County) gave navy bean seed to farmers to grow the crop for them due to unavailability of seed. The challenge of the unavailability of navy bean seed and informal seed system can be partly addressed through the establishment of community-based seed production organizations (CBSPO). This will ensure that high quality seed of improved cultivars is available within the communities at affordable prices (Setimela et al., 2004).

Poor soil fertility frequently appeared as an important constraint probably due to soil nutrient imbalances since most of the farmers applied basal and top-dressing fertilizers without conducting soil nutrient analysis. Similar findings were reported by Njoki (2013) and Mongi et al. (2016) who found that poor soil fertility was an important dry beans production constraint in the southern highlands of Tanzania and Kiambu County in Kenya respectively. This finding is also consistent with Vanlauwe et al. (2016) who observed that unbalanced soil fertilization resulted in poor fertilizer response in maize. It is therefore of paramount importance for bean breeders to develop cultivars that are adapted to poor soils, particularly cultivars that are capable of producing acceptable grain yields under low nitrogen conditions.

3.4.5 Farmer's trait preferences

There was a fair level of consistency in trait preference rankings by both men and women probably because all the farmers experienced the same production and marketing constraints. This result is not in agreement with the findings of Asfaw et al. (2012) who reported differences in trait

[3] = Dry Bean Breeder at Agricultural Research Council, South Africa

preferences among both men and women dry beans farmers in Ethiopia. Tolerance to storage weevils, grain taste and cooking traits were not considered as important traits for improvement because farmers grow navy beans for income generation, and also deliver most (90%) of the produce to the contractor, and reserve 10% for consumption. This prompts them not to value or put more weight on them. The high market value (US$800 per tonne) of navy beans compared to other subsistence crops such as maize prompts farmers to reserve less for household consumption in search of income. These findings contradict with Asfaw et al. (2012, Njoki (2013), Balcha and Tigabu (2015), Katungi et al. (2017) and Sheikh et al. (2017) who reported a significant number of farmers who preferred common bean cultivars with a good taste and short cooking duration in their studies. Farmers did not value the importance of invisible traits such as nutritional value (Fe and Zn) and canning quality probably due to the unfamiliarity with the nutritional and health benefits of consuming bio fortified cultivars in these two districts. Therefore, capacity building and bio fortified bean awareness creation campaigns should be intensified in these two districts to strengthen farmers' knowledge on nutrition.

Generally, farmers showed strong preference for drought and heat stress tolerance ahead of high grain yield potential, suggesting that they are prepared to trade off a high yielding cultivar for a drought tolerant cultivar. This emphasizes that farmers perceived drought and heat stress as an urgent matter which the plant breeding program needs to address as a priority. Similar findings were reported by Derera et al. (2006), who found that maize farmers in Mutare West of Zimbabwe selected the drought tolerance trait ahead of grain yield. These findings also concur with Assefa et al. (2005), Asfaw et al. (2012), Njoki (2013), Assefa et al. (2014), Umar (2015) and Siri et al. (2020) who reported that farmers preferred drought tolerant dry beans genotypes for drought escape during their studies. Farmers preferred early maturing cultivars for early household food security, drought escape and the reduction of the number of irrigation cycles due to insufficient water resources for irrigation. Early maturing cultivars can also be grown during the main short rainfall season in summer, and in winter, they escape heat stress and bean rust disease by maturing before temperatures begin to rise in July. Assefa et al. (2005), Asfaw et al. (2012), Balcha and Tigabu (2015) and Siri et al. (2020) reported that dry beans farmers considered earliness as an important selection criterion in drought prone areas. Farmers preferred cultivars that are tolerant to pod shattering to reduce the amount of time and labor spent in picking the small seeded grains from the ground. This is corroborated by Asfaw et al. (2012) who reported that farmers in Ethiopia

preferred dry beans genotypes that were tolerant to pod shattering. Tolerance to diseases was one of the most preferred traits due to high costs of fungicides and the need to reduce the amount of labor and time spent on processing diseased grain, which was often done by women. High grain yield was an important trait that was preferred by farmers because navy beans are mainly grown under contract farming, and high productivity usually translates to high income. These findings were consistent with Asfaw et al. (2012), and Balcha and Tigabu (2015), who reported that high grain yield was an important selection trait of dry beans farmers in Ethiopia. Farmers preferred cultivars with an indeterminate growth habit because they had more than one flash of flowering periods which increased chances of drought stress escape.

3.4.6 Cultivars grown by farmers

There was a narrow variability in terms of navy bean cultivars being grown by farmers partially due to the unavailability of seed of improved navy bean cultivars in the market. The majority of farmers predominantly grow Zimbabwe White Bean since the year 2000 because this is what was being offered by canning companies, but reckoned that it was not the ideal cultivar due to a number of undesirable characteristics. Teebus was grown by a small fraction of farmers due to the limited quantities of seed available emanating from the high costs associated with the importation of seed from South Africa. On the other hand, the cultivar Caledon was only grown by very few individuals at Gudyanga and Nenhowe because the cultivar had not been officially released into the market. The private seed company Seed Co released Caledon in December 2019, therefore farmers who grew Caledon might have obtained the seed through on-farm variety pre-release demonstration plots.

3.4.7 Management strategies for drought and heat stress

Soil mulching with maize stover was widely used as a drought and heat stress management strategy to conserve soil moisture and regulate soil temperature respectively due to its multi beneficial effects. As reported by Telkar et al. (2017), Kader et al. (2019), and Iqbal et al. (2020), soil mulching improves the water infiltration and retention capacity of the soil, and also reduces surface evaporation resulting in higher water use efficiency. Many scientists (Long et al., 2001; Lamont, 2005; Bodner et al., 2015; Telkar et al., 2017; Kader et al., 2019; Iqbal et al., 2020) report that mulches protect the soils from extreme temperatures by lowering soil surface temperatures thereby keeping the plant root zone cooler and preventing soil temperature fluctuations, which is beneficial

for overall crop growth. Farmers revealed that soil mulching had many other beneficial effects which included a reduction in the incidence of fungal diseases and weed infestation.

Despite the wide use of soil mulching, it attracted harvester termites which reduced plant stand in navy bean by feeding on the plant. This agrees with Long et al. (2001) and Nyagumbo et al. (2015), who reported that the application of crop residues or organic mulches increases the activity of termites as a result of the moist conditions in the underlying soil. This suggests that breeding for tolerance to drought stress must be a priority in navy bean breeding programs. Irrigating at night was an important drought and heat stress management practice because it resulted in more water penetrating the soil due to the reduction in water losses from evaporation. However, female farmers found it difficult to irrigate at night due to the cultural household roles and responsibilities such as cooking. The strategy of irrigating at night agrees with Mahmoud and El-Bably (2019) who reported that night time irrigation improved water productivity by reducing losses of evaporation. Dong et al. (2016) reported that the application of irrigation water at night reduced the root-zone soil temperature by 0.6 ℃ in maize resulting in improved plant growth.

Farmers frequently cultivated their fields with hoes as a drought stress management strategy to retain more soil moisture since more water penetrates into the soil instead of running away over the soil surface during irrigation. However, they highlighted that this method was very laborious. This agrees with Leslie (2013) who reported that cultivation can be employed to retain more soil moisture bank levels for use by the crop. Farmers reduced the acreage under navy beans as a drought management strategy because this shortened the irrigation cycle turn-over despite its negative implications on the overall production (output). The farmers often adjusted the planting dates (early planting in March) to avoid high temperature stress during the reproductive stages of development in July and August based on weather forecast information obtained from agricultural extension officers. This is corroborated by Asseng et al. (2011), Chapman et al. (2012), Akter and Islam (2017), and Sandhu et al. (2018) who reported that the effects of heat stress can be managed through the adjustment of relevant agronomic practices such as the adjustment of planting dates.

3.4.8 Navy bean marketing constraints

Farmers revealed that most of the navy bean contractors were paying an average of US$800 per tonne, a price which they feel was low compared to what middlemen were paying (average of US$1200) for the sugar bean grain market class. This could be due to lack of diversity in terms of

buyers/off-takers in the navy bean market. It was mainly the canning companies who were contracting farmers to produce navy bean grain and subsequently purchasing the grain from them such that there was no competition from other players/off-takers/middlemen. Most of the canning companies only purchase the navy bean grain if the source of seed is from them since the grain is meant for canning purposes such that canning quality is very important. These findings were consistent with Chemining'wa et al. (2014) who found that common bean farm gate prices were higher than the prices of navy bean in Kenya. Additionally, some of the contractors would frequently breach the signed contract by deviating from the agreed buying price per tonne in preference of a low buying price during grain collection time. Moreover, some of the farmers produced navy bean grain under contract farming without signing any contract, making it difficult to tackle disputes. This gave room to the contractor to manipulate the price of the inputs (seed) that would have been advanced to the farmer under contract farming and the buying price to his/her own advantage.

Farmers mentioned that the breach of contract and low grain producer price forced some of them to withdraw from contractual agreements with canning companies in preference of bean seed production, also under contract with various seed companies. Similarly, Chemining'wa et al. (2014), reported that the navy bean farmer – processor contractual agreements collapsed in Kenya in 1994 due to low grain producer prices that could not cover production costs. The constraint of low grain producer price was exacerbated by the delayed payment for the grain by the contractor coupled with inflation. Farmers highlighted that by the time the contractor processed their payments, the money would have lost value due to inflation thus negatively affecting their purchasing power. Delayed payment for the produce meant that most of the farmers did not have enough running capital to purchase inputs for the summer cropping season. Due to the acute shortage of hard currency (local Zimbabwean dollar) in Zimbabwe (Chikonyora, 2020), most of the contractors have not been able to pay for the produce in hard currency. Payments to navy bean farmers are made through bank transfers inform of Real Time Gross Transfer (RTGS). However, most of the farmers in the study villages do not own bank accounts such that they receive their payments through mobile money platforms such as EcoCash, Telecash and One Money. Some of the EcoCash agents are charging excessive premiums (Herald, 2019) above the authorized commission levels, up to 55% (Chingwere, 2019) of the mobile money being cashed out, eroding the farmers' earnings.

3.4.9 Farmers' desirable and undesirable characteristics of the navy bean cultivars

Farmers highlighted that Zimbabwe White Bean was only tolerant to diseases when planted early, meaning that the cultivar was not tolerant but "escaped" disease infection. The early maturity trait of Zimbabwe White Bean ensured early returns and cropping fit since the farmers produced green mealies after harvesting navy beans. On the other hand, some of the farmers did not like any attribute on Zimbabwe White Bean and Teebus but they are cultivating the cultivars due to lack of options to select suitable cultivars for production. Caledon was preferred because of its tolerance to pod shattering, a trait which reduced labor in picking the grains from the ground and grain losses due to shattering.

Farmers highlighted that both Teebus and Zimbabwe White Bean were highly susceptible to drought and heat stress because both cultivars were not bred for production under heat and drought stressed environments. Therefore, there is need to disseminate improved navy bean cultivars in the Lowveld region that are tolerant to multiple biotic and abiotic constraints (drought, heat, and fungal diseases). In addition, farmers did not like the small seed size (< 25 grams per 100 seeds) of Zimbabwe White Bean and Teebus because it presented challenges during grading (removal of chuff). Furthermore, the small seeded navy been cultivars require more grain to fill a 50 kg bag compared to the large seeded cultivars (> 40 grams per 100 seeds) which required less. Unfortunately, most of the navy bean cultivars with good canning qualities are small seeded (< 25 grams per 100 seeds), and seed size is an important quality parameter for consideration during canning quality analysis due to consumer preferences (Loggerenberg, 2004).

3.5 Conclusions and recommendations

The main marketing constraints were non-payment for produce in hard currency, lack of diversity in terms of off-takers, delayed payment by the contractor, and low grain producer price. Farmers identified drought stress, heat stress, diseases, insect pests, unavailability of seed of improved cultivars, susceptibility to pod shattering and poor soil fertility as the major navy bean production constraints. Drought tolerance, heat tolerance, disease tolerance, insect pest tolerance, grain yield, resistance to pod shattering and early maturity were the major-farmer preferred traits. Improving seed size, pod shattering tolerance, fungal disease tolerance, drought tolerance, and heat tolerance of the cultivar "Zimbabwe White Bean" predominantly grown in the Lowveld region without compromising on its short maturity duration, short cooking time, and sweet taste would potentially

have a large impact on farmers' livelihoods in the study areas. Navy bean was frequently grown under contract farming across the studied locations reducing the burden of sourcing inputs on the part of the farmer. These findings imply that plant breeders should employ participatory plant breeding strategies and conventional approaches to improve existing cultivars and also develop improved climate smart cultivars. Therefore, navy bean improvement programs should consider and integrate the farmer-preferred traits, marketing, and production constraints during the development of improved cultivars.

There is urgent need to hasten seed multiplication, dissemination of improved navy bean cultivars and extension services in awareness creation among farmers about improved navy bean cultivars in the Lowveld region. This is important considering that most of the respondents were not well informed of the existence of improved navy bean cultivars such as Protea and Teebus despite the fact that participatory variety selection was conducted in the Lowveld region. There is also a need for breeders to develop cultivars that are adapted to low soil fertility, particularly cultivars that are capable of producing acceptable grain yield under low nitrogen conditions. Breeding programs should also consider traders and processors trait preferences during cultivar development. Where navy bean breeding cannot incorporate all the preferred traits, the key attributes should be included in particular cultivars, making sure that maturity duration is short and there is no grain yield penalty since both are essential traits for farmers. Early maturing cultivars (i.e. less than 75 days) with tolerance to drought and heat stress are recommended for deployment in the very dry and hot areas such as the Lowveld region. Since navy bean is mainly utilized in the canning industry, the product profile should have cooking characteristics that meet industry demand. Agronomic practices such as irrigating at night, mulching, ridges, reduced acreage, and cultivating the soil to increase the water infiltration rate must be adopted by farmers to mitigate the effects of biotic and abiotic stresses. There is need to train navy bean farmers on contract farming and Community Based Seed Production Organizations should be established to increase the availability of seed. Lastly, community seed banks should be established to improve access to seed reserves when cultivars fail, protect knowledge related to diverse local cultivars adapted to local conditions and reduce dependence on seed sources from outside the region. Irrigation schemes must be solarized to reduce the effects of power cuts on irrigation scheduling.

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Chapter 4 [1]Genotype x environment interaction and stability analyses of grain yield and micronutrient (Fe and Zn) concentrations in navy bean (*Phaseolus vulgaris* L.) genotypes under varied production environments

Abstract

Development of stable, high yielding and micronutrient dense bean cultivars offers a sustainable solution to the challenge of malnutrition in developing countries. The objectives of this study were to evaluate the effects of genotypes, environments and genotype by environment (GEI) on iron (Fe) and zinc (Zn) in the seed and grain yield (GYD) in navy bean genotypes, and identify genotypes with high adaptability and stability for high seed Fe, seed Zn and GYD. Eighty-four breeding lines and check cultivars were field-tested using a 12 x 7 alpha lattice design, in four locations over two seasons (2018/19 and 2019/20). The GEI was highly significant ($p < 0.001$) for grain yield but not significant for seed iron and zinc. Grain yield ranged from 2002 (G48) to 2501 (ZABRA16575-26F22) kg/ha and was largely influenced by environment (38.87%) and the GEI (39.48%). The largest variance was observed on seed iron, which ranged from 86.5 (SAB791) to 119.78 ppm (ZABRA16575-51F22). Highly significant and positive associations ($r = 0.52$, $p < 0.001$) were observed between Fe and Zn. Stability analysis using additive main effects and multiplicative interaction (AMMI), AMMI stability value (ASV) and Yield Stability Index, identified six genotypes (G14, G49, G37, ICA BUNSIxSXB405/3C-1C-1C-8, NAE70 and CZ108-53) with high GYD, good GYD stability and desirable seed iron and zinc concentrations above breeding targets of 90 and 40 ppm, respectively. These genotypes should be used as parents for crossing with other cultivars to improve micronutrient density, GYD and GYD stability. The ZABRA16575-26F22, ICA BUNSIxSXB405/4C-1C-1C-8 and NAE13 combined specific adaptation and high GYD with desirable micronutrient density. These genotypes could be recommended for deployment in their respective mega-environments.

Keywords: genotype x environment interaction, stability parameters, grain yield, iron, zinc

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4.1 Introduction

Dry beans (*Phaseolus vulgaris* L.) has a high nutritive value and is one of the inexpensive sources of micronutrients (Khanal et al., 2014). It is an important and affordable source of high protein (17% to 30%), dietary fibre and can provide 15% of daily requirements of micronutrients such as iron (Fe) and zinc (Zn) (Pujola et al., 2007). Among the different dry beans market classes, navy bean is a modern and market-oriented dry beans market class with major impacts on household food, nutrition, and income security in several countries in Africa. Micronutrient malnutrition is affecting billions of people worldwide (Welch and Graham, 2004). Iron and Zn are the most common nutritional deficiencies (Stein, 2010). According to Bouis (2003) and Bouis and Welch (2010), the immense uptake of staple food crops, mainly cereals with low dietary intake of Fe and Zn contributes to micronutrient malnutrition. In Zimbabwe, Fe deficiency is common in children under the age of 5 years, estimated to be at 72% (World Health Organization, 2015). In addition, the prevalence of anemia is high in this group, estimated to be 31% (World Health Organization, 2015; Kairiza et al., 2020). Moreover, according to Kairiza et al. (2020), Fe deficiency is also high, among infants of 6 to 11 months old, estimated to be 81%.

Various approaches, which include dietary diversification, nutrient supplementation, and food fortification have been practised in many countries for decades to alleviate the challenge of malnutrition (Kairiza et al., 2020; Philipo et al., 2021). A cost-effective and reliable compliment to the aforementioned approaches is genetic biofortification (Bouis and Islam, 2011; Philipo et al., 2021). One of the approaches to improve the level of Fe and Zn in processed tinned products such as baked/canned beans is to exploit the genetic variation in navy beans. Previously in Zimbabwe, most public and private bean breeding programs focused on developing cultivars of the sugar and calima market classes with desirable agronomic traits but little effort was put towards developing market-demanded, micronutrient dense and high yielding navy bean cultivars. Consequently, the first navy bean cultivar “Protea”, which was released in Zimbabwe by Crop Breeding Institute in May 2018 for canning purposes is not biofortified (Tsiko, 2018). Furthermore, the seed micronutrient concentrations of the elite navy bean genotypes at Crop Breeding Institute are not known, hampering efforts to promote the widespread production and consumption of biofortified bean cultivars in Zimbabwe.

In Zimbabwe, the production of navy bean is done under diverse environmental conditions regarding weather conditions, soil structure, disease pressure, latitude, soil fertility, altitude, seasonal variation, temperature, planting times and rainfall (Katungi et al., 2017). Given the diverse and wide ecologies in Zimbabwe, genotypes are predisposed to the effect of genotype by environment interaction (GEI). Several studies have reported significant effect of GEI on common bean grain yield (Torga et al., 2013; Kooshki et al., 2016; Tadesse et al., 2018) and seed Fe and Zn (Nchimbi-Msolla and Tryphone, 2010; Mukamuhirwa, 2013; Firew, 2017). This makes it necessary to evaluate promising genotypes in diverse environments, which requires plant breeders to conduct stability and adaptability analysis to identify the best performing genotypes across or within specific environments. Contextually, there is no documented information regarding the adaptability and stability of the elite navy bean genotypes across diverse multi-environments in Zimbabwe. Thus, there is a need to conduct studies on grain yield and seed micronutrient stability and GEI in multi-location trials under diverse agro-ecologies and seasons for devising ideal breeding strategies to adopt; either wide or specific adaptation.

Many different methods have been applied by past researchers to conduct stability and adaptability analysis of genotypes in multi-environment yield trials (MET) (Ribeiro et al., 2009; Pereira et al., 2009, 2011). Some of the commonly used methods include genotype, genotype by environment (GGE) biplot (Yan, 2001) and the Additive Main effects and Multiplicative Interaction (AMMI) analysis (Gauch and Zobel, 1997). Considering the increasing demand for navy beans, low productivity and the diverse production environments in Zimbabwe, the development of genotypes which combine high grain yield stability with superior nutritional quality will contribute to increased productivity, production, and commercialization of navy beans in Zimbabwe. Therefore, the objectives of this study were to; (i) evaluate the effects of genotypes, environments and the genotype x environment interaction (GEI) on seed Fe, Zn and GYD in navy bean genotypes; (ii) identify promising genotypes with high adaptability and stability for high seed Fe, Zn and yield and (iii) study the associations among seed Fe, Zn, days to physiological maturity and grain yield.

4.2 Materials and methods

4.2.1 Experimental sites and germplasm

The field experiments were conducted in four locations during the 2018/19 and 2019/20 rainy season from January to April in Zimbabwe. Chiredzi research station and Chisumbanje experiment

station are located in the lowveld region of Zimbabwe and are representative of low potential environments. On the other hand, Harare research station and Gwebi variety testing center are located in the highveld region of Zimbabwe and are representative of high potential environments. Detailed characteristics of the eight environments (site by year combinations) are outlined in Table 4.1. In general, agro-ecological characteristics, soil types, soil micronutrient profiles, and climatic conditions of the study environments vary considerably. The study comprised of 84 navy bean genotypes that were sourced from the Ethiopian Institute of Agricultural Research (EIAR; Ethiopia), Crop Breeding Institute (Zimbabwe), and the Alliance of Bioversity International and International Center of Tropical Agriculture (ABC; Malawi, Colombia and Uganda) (Appendix 4.1). The cultivar SMC16 with average seed Fe and Zn concentrations of 115 and 43 ppm, respectively (Crop Breeding Institute, 2019) was used as a micronutrient check while Protea, a production reference cultivar in Zimbabwe (Mukweza personal communication, May 2018)[1] was used as a grain yield check

4.2.2 Experimental design, field management, and phenotyping

The trial layout was a 12 x 7 alpha lattice design with two replications at each location under rain-fed conditions. Sowing was done by hand in 5.4 m^2 plots comprising of 4 rows, 3 m long with an inter-row spacing of 0.45 m. An in-row spacing of 0.2 m was used. Compound D (7N: 14P: 7K) and ammonium nitrate (34.5% N) fertilizers were applied at recommended rates for each location at sowing and before the flowering stage, respectively, in each season. Insect pests and fungal diseases were controlled using insecticides and fungicides, respectively. Hand weeding was practised when necessary. The number of days from planting to physiological maturity (DPM) was recorded from the two middle rows of each plot. This was recorded as the number of days after planting to when 95% of pods in a plot had lost their green pigmentation. As for GYD, harvesting was done by hand from the two middle rows in each plot.

[1] Head Research & Development at Cairns Foods Limited in Zimbabwe

Table 4.1 Description of locations and environments used for evaluation of the 84 bean genotypes in 2018/19 and 2019/20 seasons.

Parameter	2018 season				2019 season			
	Hara	GVTC	Chisu	Chire	Hara	GVTC	Chisu	Chire
pH (Calcium Chloride)	5.50	6.20	5.50	5.80	5.70	5.90	5.30	5.60
OM (%)	2.20	2.00	0.80	2.40	2.50	2.30	0.50	2.10
N (ppm)	20.00	19.00	14.00	23.00	18.00	21.00	17.00	21.00
P (ppm)	74.00	68.00	71.00	78.00	70.00	73.00	66.00	66.00
Ca (mg/100g)	9.00	10.80	8.60	9.10	9.60	11.60	8.10	10.30
Mg (mg/100g)	5.70	6.40	6.80	6.00	4.80	5.60	7.30	5.20
K (mg/100g)	0.30	0.40	0.30	0.40	0.30	0.30	0.30	0.30
Zn (ppm)	2.40	1.50	0.60	2.20	1.60	2.10	1.90	1.10
Fe (ppm)	13.10	10.30	6.10	7.10	15.30	11.60	5.60	10.90
Soil type	Clay	Clay loam	Basalt clays	Sand Clay Loam	Clay	Clay loam	Basalt clays	Sand Clay Loam
Rainfall received (mm)	504.70	571.50	441.90	416.50	436.30	578.50	434.80	419.20
Latitude	$17^0$48’S	$17^0$68’S	$20^0$80’S	$20^0$85’S	$17^0$55’S	$17^0$68’S	$20^0$80’S	$21^0$02’S
Longitude	$31^0$03’E	$30^0$86’E	$32^0$24’E	$31^0$12’E	$31^0$76’E	$30^0$86’E	$32^0$23’E	$31^0$57’E
Altitude (m.a.s.l)	1508	1450	399	513	1512	1449	413	422

Hara Harare Research Station, *GVTC* Gwebi Variety Testing Center, *Chisu* Chisumbanje Experiment Station, *Chire* Chiredzi Research Station *OM* organic matter content, *masl* meters above sea level, *mm* millimetres, *ppm* parts per million, *mg/100g* milligram equivalents per 100g.

A total of 30 well-filled above ground pods were harvested randomly from the two inner rows in all the plots and replications when 95% of the pods in a plot had reached physiological maturity. Grain yield data was adjusted to kg ha^{-1} at 12.5% moisture content. Milled bean seed samples (20 g) were used in the Fe and Zn analysis using the atomic absorption spectrophotometer model Varians AA-1275 following the procedure described by Shar et al. (2002). Micronutrient analysis was conducted in the food laboratory at the Department of Research and Specialist Services (DR&SS) in Harare, Zimbabwe.

4.2.3 Statistical analysis

The homogeneity of error variances between the environments was tested using Bartlett's chi-square test (Steel and Torrie, 1998). Initially, Bartlett's test revealed heterogeneity ($p < 0.05$) of residual variance for grain yield and homogeneity ($p > 0.05$) of residual variance for seed Fe and Zn (Appendix 4.2). As a result, square root transformation was applied to grain yield data to improve normality of the residuals and reduce the effects of non-additivity. This was further confirmed by the residual plots for grain yield, Fe and Zn which were normally distributed. In the first step of analysis, the analysis of phenotypic data from four sites across two seasons was performed for the mixed effect model using residual (or restricted) maximum likelihood (REML) in Genstat® Discovery 18th Edition (Payne et al., 2018). This was done to check the possibility of treating the location by year combinations as individual environments. The residual effect, genotypic effect and its interactions with environments (genotype by location, genotype by year, genotype by year by location) were treated as random effects (Yan, 2021). The environment main effects (location, year, and location by year), replication and block were treated as fixed effects (Piepho and Mohring, 2007; Yan, 2021). The following model was used:

$$Y_{ijklm} = \mu + G_i + L_j + Y_k + R_{l(jk)} + B_{m(jkl)} + GL_{ij} + GY_{ik} + LY_{jk} + GLY_{ijk} + e_{ijklm} \quad (1)$$

where Y_{ijklm} = response of the ith genotype in jth location and lth replication within year and mth block within location, μ = grand mean, G_i = random effect of the ith genotype, L_j = fixed effect of the jth location, Y_k = fixed effect of the year effect k, $R_{l(jk)}$ = fixed effect of the replicate l nested within location j in year k, $B_{m(jkl)}$ = fixed effect of the block m nested within location j in year k and replicate l, GL_{ij} = random effect of the interaction between genotype i and location j, GY_{ik} = random effect of the interaction between genotype i and year k, LY_{jk} = random effect of the interaction between location j and year k, GLY_{ijk} = random effect of the genotype by location by year interaction, and e_{ijlkm} = random error. Since the "location x year interaction" exhibited highly

significant ($p < 0.001$) effects on GYD, seed Fe and Zn (Appendix 4.3), each location x year combination was treated as an environment resulting in eight environments. In the second step of analysis, the phenotypic data of each individual environment were analysed using a linear mixed model to generate adjusted genotype means for use in the third step of analysis (across environment analysis). In this model, blocks and genotypes were treated as random effects, whereas replicates were taken as fixed effects (Singh and Ceccarelli, 1995; Piepho and Mohring, 2007; Schmidt et al., 2019). The following model was used:

$$Y_{ijl} = \mu + g_i + r_j + b_{Ij} + e_{ijl} \quad (2)$$

where Y_{jkl} = phenotypic observations of the trait of interest, μ = grand mean, g_i = random effect of the *i*th genotype, r_j = fixed effect of the *j*th replicate, b_{lj} = random effect of the *I*th block nested within the *j*th replicate, and e_{ijl} = residual effect. In the third step of analysis, an across environment analysis was done for eight test environments using adjusted genotype means derived from the analysis of individual environments to determine the significance level of genotype, environment and GEI. In the across environment analysis, a mixed effect model was used whereby blocks within replications, replications within environments, genotypes and their interactions with environments (GEI) were considered as random effects (Singh and Ceccarelli, 1995). Environments (combination of locations and years) were considered as fixed effects (Singh and Ceccarelli, 1995). The following model was used:

$$Y_{ijkl} = \mu + G_i + E_j + R_{k(j)} + B_{l(jk)} + GE_{ij} + e_{ijlk} \quad (3)$$

where Y_{ijkl} = response of the *i*th genotype in *j*th environment and *k*th replication within environment and *I*th block within replication and environment, μ = grand mean, G_i = random effect of the *i*th genotype, E_j = fixed effect of the *j*th environment, $R_{k(j)}$ = random effect of the replicate *k* nested in environment *j*, $B_{l(jk)}$ = random effect of the *I*th block nested in environment *j* and replicate *k*, GE_{ij} = random effect of genotype by environment interaction, and e_{ijlk} = random error. The statistical analysis of the second and third steps was done using the Breeding Management Systems (BMS) statistical analysis software version 18 (The Integrated Breeding Platform's BMS, 2021). Subsequently, the AMMI analysis was carried out in R software version 4.0.1 (R Core Team, 2022) to dissect the GEI across the eight environments. The significance of statistical differences among the genotypes was tested using Tukey's honest significant difference test to control the family-wise error rate. When the variance structure is unbalanced (data from trials laid out in incomplete blocks), the conventional broad-sense heritability (H^2) equation $H^2 = \frac{\sigma_G^2}{\sigma_G^2 + \frac{\sigma_{GL}^2}{l} + \frac{\sigma_\varepsilon^2}{rl}}$ (4)

does not hold (Piepho and Mohring, 2007). Therefore, H^2 estimates for seed Fe, Zn and GYD were estimated on an entry-mean basis using the VHERITABILITY command within the REML procedure in Genstat® Discovery 18th Edition (Payne et al., 2018). The REML method was applied in order to estimate the mean variance of the predicted values for each trait. According to Wright et al. (2020), VHERITABILITY in a REML analysis of unbalanced data employs a H^2 calculation approach suggested by Cullis et al. (2006) and Piepho and Mohring (2007);

$$H^2 = 1 - \frac{\bar{\upsilon}BLUP}{2\sigma_G^2} \quad (5)$$

where σ_G^2 = genotypic variance and $\bar{\upsilon}$BLUP = mean variance of adjusted treatment means (best linear unbiased prediction) over *l* locations and *y* years with *r* replicates per trial (Talbot, 1984; Piepho and Mohring, 2007). Associations among GYD, DPM, seed Fe, and Zn across the eight environments were established by the Pearson's correlation coefficient (r) using adjusted genotype means of the genotypes across environments. The correlation analysis was done using Genstat® Discovery 18th Edition (Payne et al., 2018). Since the GEI was significant for GYD, there was need to conduct stability and adaptability analysis of the genotypes. Stability and adaptability parameters of the genotypes were estimated using various statistical stability models such as AMMI, GGE biplot, yield stability index (YSI) and AMMI stability value (ASV) using the BMS statistical analysis software version 18 (The Integrated Breeding Platform's BMS, 2021). The AMMI bi-plot analysis was conducted using 21 best performing genotypes (25% of the genotypes) that were selected from the first four AMMI selections per test environment. This was done to improve the visualization of the bi-plots. With the AMMI bi-plot, stable genotypes have close to zero PC scores and are located near the bi-plot origin (Gauch and Zobel, 1996). The ASV was calculated to simultaneously quantify genotypic stability and rank genotypes according to their GYD stability as described by Purchase et al. (2000) using:

$$\text{ASV} = \sqrt{\left[\frac{IPCA1_{some\ of\ square}}{IPCA2_{some\ of\ square}}\ (IPCA1_{score})\right]^2 + (IPCA1_{score})^2} \quad (6)$$

where: IPCA1 and IPCA2 is the first and the second interaction principal component axes, respectively. Smaller ASV scores indicate low GEI and a relatively more stable genotype across environments (Purchase et al., 2000). The YSI model simultaneously provides a single measure of yield and GYD stability by adding the ranks of a genotype across environments with respect to GYD and ASV. According to Purchase et al. (2000), genotypes with the lowest YSI are high

yielding and most stable. The GGE biplot analysis was also conducted using only 21 genotypes (25% of the genotypes) that were selected from the first four AMMI selections per environment. The performance and stability of genotypes was visualized on the genotype-focused bi-plot through the average environment coordinate as described by Yan and Kang (2003). Mega-environments (which-won-where pattern) were identified using GGE biplots as described by Yan (2001). With mega environment analysis, genotypes can be recommended for deployment to specific mega environments.

4.3 Results

4.3.1 Grain yield, micronutrient concentrations, and broad sense heritability

The predicted genotype values ($\hat{G}$) of the 10 best and 10 worst performing navy bean genotypes for GYD, Fe and Zn are presented in Table 4.2 while the average performance of all the genotypes is shown in Appendix 4.4. Phenotypic variability was observed among the evaluated genotypes regarding seed Fe, Zn and GYD. Mean GYD ranged from 2002 kg/ha (G65) to 2501 kg/ha (G27), with a grand mean GYD of 2256 kg/ha, and 42.9% of the genotypes had mean GYD that was greater than the average. Mean seed Fe content was 106.90 ppm, and 58.3% of the genotypes had mean seed Fe content that was greater than the average. Mean seed Zn content was 42.83 ppm and 46.4% of the genotypes had mean seed Zn content that was above the average. Seed Fe concentrations ranged from 86.5 (G63) to 119.78 ppm (G37) while mean seed Zn content ranged from 34.3 (G53) to 51.6 ppm (G76). Although G27 and G79 were the highest yielding genotypes, these two were not among the top performers with respect to seed Fe and Zn concentrations (Table 4.2 and Appendix 4.4). The H^2 estimates for micronutrients ranged from moderate for seed Fe (0.40) and GYD (0.60) to high for Zn (0.82) (Table 4.2). A total of 53, 28, and 6 genotypes performed better than the standard checks regarding GYD, seed Fe and Zn respectively (Table 4.2 and Appendix 4.4).

4.3.2 Restricted maximum likelihood combined analysis for grain yield and nutritional quality traits

The REML combined ANOVA of GYD, Fe and Zn of 84 navy bean genotypes evaluated in eight environments is presented in Table 4.3. Significant differences were observed among the genotypes with respect to seed Fe ($p < 0.05$) and Zn ($p < 0.001$). The effects of replication within an environment Rep(Env) and incomplete block within an environment Block(Env*Rep) were highly significant ($p < 0.001$).

Table 4.2 Mean performance of the top and bottom ten yielding navy bean genotypes across eight environments based on predicted genotype values ($\hat{G}$).

Genotype	GYD (kg/ha)	Rank	Genotype	Iron (ppm)	Rank	Genotype	Zinc (ppm)	Rank
				Top ten				
	$\hat{G}$			$\hat{G}$			$\hat{G}$	
G27	2501^{f}	1	G37	119.75^{f}	1	G76	51.63^{h}	1
G79	2488^{e-f}	2	G42	118.75^{ef}	2	G74	50.13^{gh}	2
G64	2445^{d-f}	3	G44	118.00^{ef}	3	G21	49.50^{f-h}	3
G56	2438^{c-f}	4	G38	117.50^{d-f}	4	G28	49.25^{e-h}	4
G41	2430^{c-f}	5	G5	117.50^{d-f}	4	G5	49.25^{e-h}	4
G34	2427^{c-f}	6	G70	115.88^{c-f}	6	G75	48.88^{d-h}	6
G43	2420^{c-f}	7	G2	115.38^{c-f}	6	G73	48.75^{c-h}	7
G24	2401^{b-f}	8	G7	114.50^{c-f}	8	G40	47.63^{c-h}	8
G47	2396^{b-f}	9	G77	114.50^{c-f}	8	G84	46.63^{c-h}	8
G30	2396^{b-f}	10	G21	113.88^{c-f}	10	G6	46.50^{c-h}	10
				Bottom ten				
G54	2153^{a-f}	75	G69	98.00^{a-f}	75	G15	39.75^{a-g}	75
G71	2134^{a-f}	76	G31	97.63^{a-f}	76	G72	39.50^{a-g}	76
G70	2132^{a-f}	77	G23	97.50^{a-f}	77	G1	38.75^{a-f}	77
G32	2126^{a-f}	78	G15	96.00^{a-f}	78	G23	38.75^{a-f}	77
G48	2116^{a-e}	79	G9	95.13^{a-e}	79	G56	38.38^{a-e}	79
G31	2092^{a-d}	80	G78	94.75^{a-e}	80	G31	38.00^{a-d}	80
G68	2079^{a-d}	81	G62	93.38^{a-d}	81	G11	37.88^{a-c}	81
G67	2057^{a-c}	82	G65	92.38^{a-c}	82	G59	37.88^{a-c}	81
G77	2019^{ab}	83	G72	88.88^{ab}	83	G2	34.38^{ab}	83
G65	2002^{a}	84	G63	86.50^{a}	84	G53	34.25^{a}	84
Mean	2256.90			106.90			42.83	
Min	1854.00			41.00			22.00	
Max	3548.00			136.00			68.00	
CV (%)	11.30			24.80			17.00	
LSD	176.82			18.42			5.06	
H^2	0.60			0.40			0.82	
H^2 (%)	60.00			40.00			82.00	
SD	254.70			23.96			7.29	

$\hat{G}$ predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *CV* coefficient of variation, H^2 broad-sense heritability, *LSD* least significance difference at 0.05, *SD* standard deviation, *ppm* parts per million, *Min* minimum, *Max* maximum. Means with different letters in the same column are significantly different.

The GEI effects were not significant for both seed Fe and Zn. The genotype (G), environment (E) and genotype x environment (GEI) interaction effects were highly significant ($p < 0.001$) for GYD. This suggested that there was GEI influencing the GYD performance of navy bean genotypes across environments. Therefore, there was a need for further analyses to determine the stability of the genotypes and the magnitude of GEI for GYD.

Table 4.3 Restricted maximum likelihood (REML) combined analysis of variance for grain yield, seed iron and seed zinc concentrations of 84 navy bean genotypes evaluated across eight environments in Zimbabwe during 2018 and 2019 cropping seasons.

		Wald statistic		
Source of variation	df	Grain Yield (kg/ha)	Iron (ppm)	Zinc (ppm)
Env	7	828.36***	761.71***	260.11***
Rep(Env)	8	384.59***	1743.58***	1348.90***
Block(Env*Rep)	96	117.83***	352.65***	160.60***
Gen	83	241.04***	339.85*	773.88***
Gen*Env	581	721.54***	601.08	434.23

Env environment, *Rep(Env)* Replications nested in environments, *Block(Env*Rep)* incomplete block within an environment, *Gen* genotype, *Gen*Env* genotype by environment interaction, *df* degrees of freedom, *ppm* parts per million. *, **, *** indicate significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively.

4.3.3 Genotype and environmental variance using AMMI model for grain yield

The combined AMMI ANOVA of GYD response of the 84 navy bean genotypes across eight environments is presented in Table 4.4. Highly significant differences ($p < 0.001$) were observed among the genotypes with respect to GYD ($p < 0.001$). Combined analysis showed significant main effects ($p < 0.05$) among the study environments regarding GYD. The GEI effects significantly ($p < 0.001$) affected the GYD performance of the navy bean genotypes across the study environments. The effects of replication within an environment [Rep(Env)] and incomplete block within an environment Block(Env*Rep) were highly significant ($p < 0.001$). The main effects of the environment and genotypes regarding GYD contributed 38.87%, and 13.40% of the observed total variation, respectively while GEI contributed 39.48% of the observed variation (Table 4.4). Furthermore, the GEI effects for GYD were partitioned into principal component (PC): PC1, PC2, PC3, PC4, PC5, PC6 and PC7. All the PCs were highly significant ($p < 0.001$), contributing 35.30, 18.90, 13.80, 10.50, 9.80, 7.90 and 3.80% of the total GEI variation, respectively (Table 4.4). The AMMI analysis identified the top four performing navy bean genotypes in each test environment with respect to GYD (Table 4.5). Genotypes such as G34, G22,

G78, G17, G41, G71, G81, G75, G33, G64, G58, and G2 showed specific adaptation, appearing among the top four in only one environment (Table 4.5). Conversely, genotypes such as G27, G24, G61, G63, G30, G47, G30, G79, G12, and G43 were among the top 4 ranked genotypes in at least two or more environments (Table 4.5).

Table 4.4 Additive main effects and multiplicative interaction (AMMI) analysis of variance for grain yield of 84 navy bean genotypes tested across eight environments in Zimbabwe, during the 2018 and 2019 cropping seasons.

Source of variation	GYD (kg/ha)			
	df	SS	MS	Total variation explained (%)
Env	7	3.80e + 07	5432257*	38.87
Rep(Env)	8	1.77e + 07	2206839***	1.81
Block(Rep*Env)	96	6.30e + 06	65608***	6.44
Gen	83	1.31e + 07	158411***	13.40
Gen*Env	581	3.86e + 07	66491***	39.48
PC1	89	1.36e + 07	153335***	(35.30)
PC2	87	7.28e + 06	83714***	(18.90)
PC3	85	5.33e + 06	62654***	(13.80)
PC4	83	4.05e + 06	48794***	(10.50)
PC5	81	3.79e + 06	46789***	(9.80)
PC6	79	3.05e + 06	38605***	(7.90)
PC7	77	1.49e + 06	19299***	(3.80)
Residuals	568	1.98e + 07	34852	-

GYD grain yield, *df* degrees of freedom, *SS* mean sum of squares, *MS* mean square error, *PC* principal component axis, *ENV* environment, *Gen* genotype, *Rep(Env*) replication within an environment, *Block (Rep*Env)* incomplete block within an environment, *Gen*Env* genotype by environment interaction. Values between brackets indicate Genotype x Environment percentage explained by PC. *, **, *** indicate significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively.

The standard checks for GYD (G1; Protea) and micronutrient density (G73; SMC16) were not among the best four selections in all the test environments (Table 4.5). Among the high potential environments, Harare Research Station in 2019 (Hara2019) had the highest mean GYD followed by Gwebi Variety Testing Center in 2019 (GVTC2019) (Table 4.5). On the other hand, among the low potential environments, Chisumbanje Experiment Station in 2018 (Chisu2018) had the highest mean GYD followed by Chisumbanje Experiment Station in 2019 (Chisu2019) (Table 4.5).

Table 4.5 The first four additive main effects and multiplicative interaction (AMMI) selections of navy bean genotypes for grain yield in each of the eight environments.

Environment	Environment mean	Score	Genotype Rank			
	Grain yield (kg/ha)		1st	2nd	3rd	4th
Hara2018	2335	-28.81	G27	G41	G30	G43
GVTC2018	2272	-1.96	G24	G47	G79	G81
Chisu2018	2334	16.71	G61	G27	G63	G75
Chire2018	1934	12.63	G63	G24	G12	G33
Hara2019	2484	-15.78	G79	G27	G43	G64
GVTC2019	2424	-13.20	G34	G78	G61	G58
Chisu2019	2166	22.10	G22	G61	G71	G2
Chire2019	2107	8.32	G30	G17	G12	G47

Hara harare research station, *GVTC* gwebi variety testing center, *Chisu* chisumbanje experiment station, *Chire* chiredzi research station. 2018 and 2019 denotes the cropping season.

4.3.4 Stability analysis using IPCA scores, yield stability index and AMMI stability value

With respect to IPCA1 scores, genotypes: G4, G31, G54, G65, G67, G68, G70, G71, G74, G76 and G77 showed large and positive interaction with the study environments (Appendix 4.5). On the other hand, genotypes such as G16, G20, G27, G30, G34, G35, G37, G41, G43, G47, G56, G64, and G79 exhibited large and negative interaction with the study environments (Table 4.6 and Appendix 4.5). The genotypes: G14, G18, G24, G38, G39, G44, G46, G69, G80, and G82 had the lowest and positive interaction with the study environments (Table 4.6 and Appendix 4.5). On the other hand, genotypes G6, G12, G36, G40, G59, and G66 exhibited the lowest and negative interaction with the study environments. Results of stability analysis for GYD using YSI and ASV are presented in Table 4.6 and Appendix 4.5. The ASV of the genotypes across environments ranged from 0.62 (G44) to 21.57 (G68). Based on ASV, the most stable (low ASV and GEI) genotypes were G44, G40, G82, G12, G39, G66, G69, G46, G38, G5, G2 and G3 while genotypes such as G70, G79, G43, G77, G41, and G68 were the least stable (high ASV and GEI). The concurrent selection of the genotypes for GYD and stability performances (YSI) showed G12 as the most stable and adapted genotype, followed by G2, G3, G36, G66, G39, G69, G14, G17, G80 and G38. G54, G67, G68, G70 and G77 were the least stable genotypes based on YSI.

Table 4.6 Interaction principal component axes (IPCA) scores and stability analyses for grain yield (kg/ha) of top twenty and bottom five yielding genotypes tested in eight environments.

No.	Genotype	IPCAg1	IPCAg2	GYD	GYD Rank	ASV	ASV Rank	YSI	YSI Rank
Top twenty yielding genotypes									
1	G27	-13.88	8.66	2501	1	20.87	83	84	46
2	G79	-10.47	1.41	2488	2	14.40	77	79	38
3	G64	-9.10	2.98	2445	3	12.80	70	73	32
4	G56	-11.73	1.93	2438	4	16.17	79	83	44
5	G41	-13.59	4.28	2430	5	19.08	82	87	47
6	G34	-9.72	-4.66	2427	6	14.09	75	81	41
7	G43	-12.15	4.67	2420	7	17.27	80	87	48
8	G24	0.23	-13.39	2401	8	13.39	72	80	39
9	G47	-7.06	1.97	2396	9	9.86	61	70	30
10	G30	-5.83	10.95	2396	10	13.55	73	83	43
11	G61	2.17	-5.54	2386	11	6.29	40	51	14
12	G78	-4.09	-4.83	2385	12	7.39	44	56	19
13	G72	-5.91	-2.63	2369	13	8.50	54	67	28
14	G12	-0.78	-0.83	2355	14	1.35	4	18	1
15	G2	1.31	-0.72	2353	15	1.93	12	27	2
16	G63	3.62	6.08	2341	16	7.84	48	64	25
17	G3	1.49	0.24	2332	17	2.05	14	31	3
18	G17	-0.62	4.04	2315	18	4.13	27	45	9
19	G14	0.02	-4.09	2312	19	4.09	26	45	8
20	G36	-0.26	2.00	2312	20	2.03	13	33	4
Bottom five yielding genotypes									
22	G31	5.14	3.35	2092	80	7.79	47	127	74
23	G68	14.79	7.47	2079	81	21.57	84	165	84
24	G67	9.79	3.97	2057	82	13.97	74	156	82
25	G77	12.83	7.33	2019	83	19.03	81	164	83
26	G65	5.64	2.31	2002	84	8.06	51	135	78

IPCAg1 interaction principal component axes for genotypes 1, *IPCAg2* interaction principal component axes for genotypes 2, *GYD* grain yield, *ASV* AMMI stability value, *YSI* yield stability index.

Generally, the YSI statistical model showed comparable result with that of the ASV statistical model with respect to stability ranking. For example, both YSI and ASV statistical models identified G12, G66, G69, G39, G38, G2 and G3 among the most stable genotypes in terms of GYD (Table 4.6 and Appendix 4.5). In addition, both statistical models identified G70, G77 and G68 among the most unstable genotypes in terms of GYD.

4.3.5 Inter-relationship amongst environments and discriminating power of environments

Figure 4.1 shows interrelationship amongst environments and discriminating ability of the eight test environments for GYD. The bi-plot accounted for 60.43% of the total variation regarding G and GEI with PC1 and PC2 explaining 42.81% and 17.62%, respectively. As reported by Yan and

Kang (2003), the ability of a test environment to discriminate the genotypes is measured by the length of the environmental vector from the bi-plot origin. Based on the length of the environmental vectors (Figure 4.1), Harare Research Station during 2018 (Hara2018) and Gwebi Variety Testing Center in 2019 (GVTC2019) were the most discriminating (large positive PC1 scores, longest vector) test environments. The environments could be ranked as follows with respect to discrimination of the genotypes; Hara2018 > GVTC2019 > GVTC2018 = HaraC2019 > Chisu2019 > Chisu2016 > Chire2018 = Chire2019. Correlations among the test environments were also visualized from the GGE bi-plot in Figure 4.1. According to Yan (2002), interrelationships between two test environments can be estimated through the cosine of the angle between vectors of the respective test environments. The cosine of the angles between vectors of environments GVTC2018/GVTC2019 and Hara2019, and environments Chisu2018/Chisu2019 and Chire2018 were less than 90^{o} (Figure 4.1).

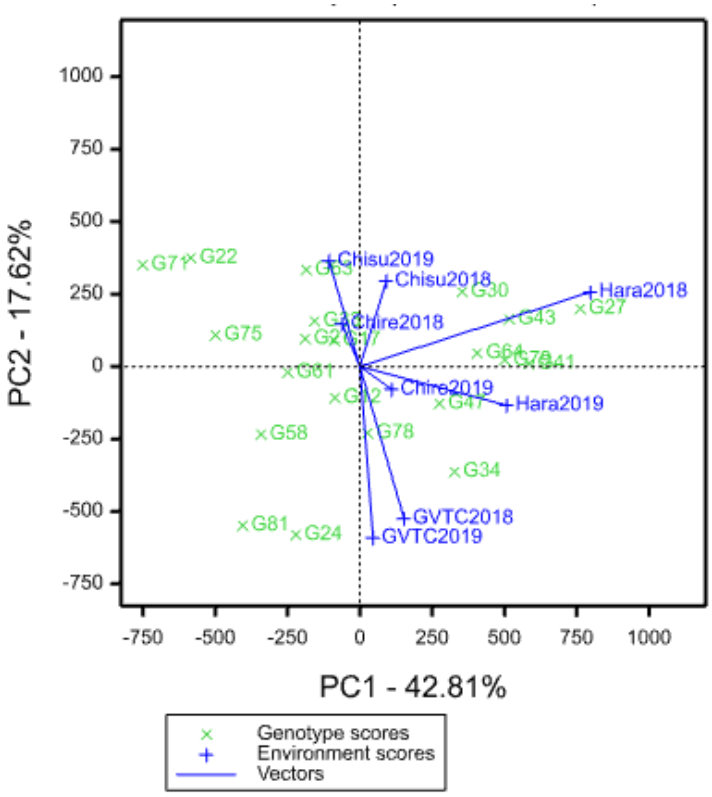

Figure 4.1 Genotype, genotype by environment (GGE) biplot showing interrelationship amongst environments and discriminating ability of the environments for grain yield.

Conversely, the cosine of the angles between vectors of GVTC2018/GVTC2019 and three other test environments (Chisu2018, Chisu2019, and Chire2018) were more than 90^{o} (Figure 4.1).

4.3.6 Mega-environments and genotype response to specific and wider adaptation

Figure 4.2 shows results of "which-won-where" polygon-view of the GGE biplot for GYD under each sector. The vertex genotypes have the longest vectors and are therefore located at the corners of the polygon. Accordingly, the vertex genotypes (G24, G34, G22, and G27) were among the most responsive (either best or worst) to environmental interactions for GYD in their corresponding directions in a given sector. The rays of the GGE biplot from the origin divided the plot into seven sectors. However, only three of the sectors had environments in them, indicating the presence of three different mega-environments (Figure 4.2).

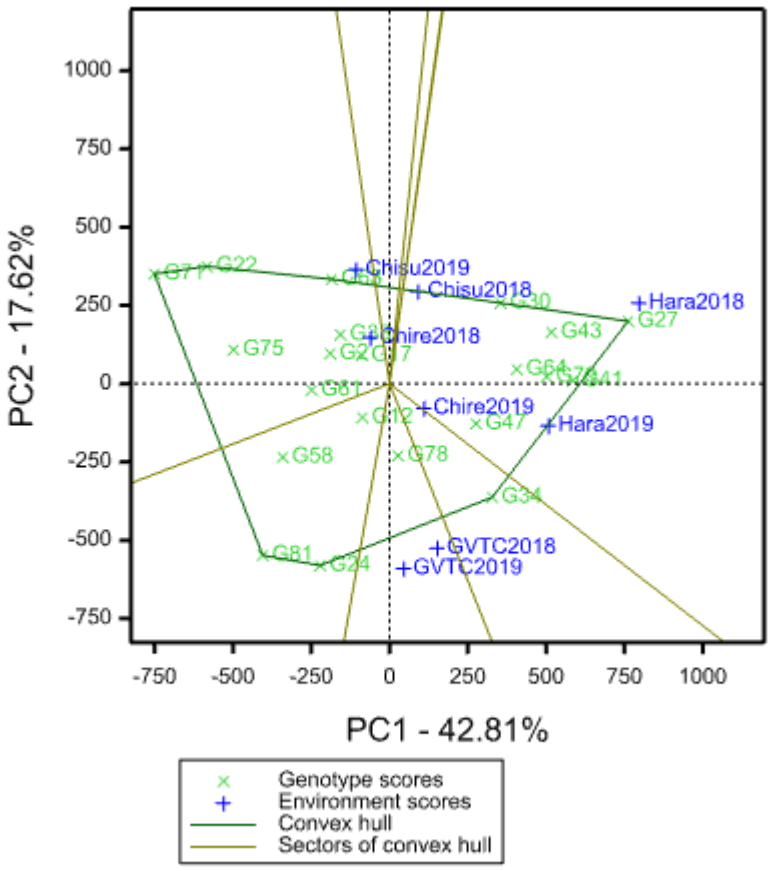

Figure 4.2 A Genotype, genotype by environment (GGE) biplot view for grain yield (kg/ha) showing "which-won-where". See codes of the test environments in Table 4.1.

The first sector comprised of four test environments (Hara2018, Hara2019, Chiredzi2019 and Chisu2018) and G27 was the best-yielding vertex winning genotype in this sector. Environments GVTC2018 and GVTC2019 constituted the second sector, and G24 was the best-yielding vertex winning genotype. The third sector comprised of two environments (Chisu2019 and Chire2018) located in the lowveld region, and G22 was the best-yielding winning genotype in this sector. The genotype G12 which is located close to the biplot origin was relatively stable (widely adapted). This genotype had similar GYD rankings across all the test environments. The first two PC (PC1 and PC2) of the AMMI model explained 58.31% of the observed variation (Figure 4.3).

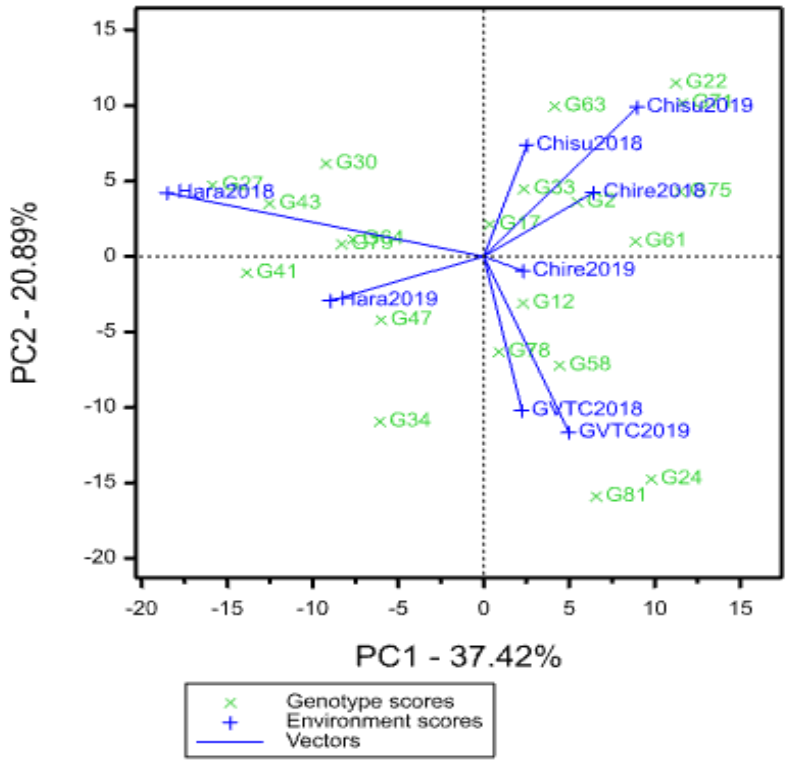

Figure 4.3 Additive main effects and multiplicative interaction (AMMI) 2 biplot for grain yield (kg/ha) showing means of genotypes (1-84) and test environments plotted against their respective scores of interaction principal component axes (IPCA) 1. See codes of environments in Table 4.1.

The magnitude of GEI is proportional to the length of an environmental vector from the origin of the biplot. The environments near the bi-plot origin with shorter vectors elicit weak interactive forces, whereas those with longer vectors (far from the biplot origin) elicit strong interactive forces. Environment Hara2018 exhibited the strongest interactive forces (most discriminating) followed by GVTC2019 and Chisu2019 (Figure 4.3). The environment

Chire2019 had the weakest interactive forces (least discriminating) followed by Chire2018. Genotypes such as G17 and G12 located near the bi-plot origin are insensitive to environmental interactions, widely adapted and more stable in GYD performance across the study environments (Figure 4.3). On the other hand, genotypes located far away from the bi-plot origin are sensitive to environmental interaction. For example, an environment and genotype with markers in opposite directions from the biplot origin have a negative GEI interaction, and in same direction a positive GEI. Thus, genotypes G22, G75, G71 and G24 had positive GEI with environments Chisu2019, Chire2019, Chisu2019 and GVTC2018, respectively, indicating that they were specifically adapted. On the other hand, genotypes G34, G47 and G30 had negative GEI with Chisu2018, Chiredzi 2018, and GVTC2019, respectively. Genotypes that are clustered together in the AMMI2 bi-plot exhibited similar GYD responses across diverse environments. Thus, genotypes G22 and G21, G81 and G24, had similar GYD performances across the study environments (Figure 4.3). Generally, the AMMI2 biplot showed similar results with that of the YSI statistical model in terms of stability ranking. For example, both YSI model and AMMI2 biplot identified G12 (most stable) and G17 among the most stable genotypes in terms of GYD.

4.3.7 Correlation among traits

The correlation coefficients among seed Fe, Zn, DPM and GYD across the environments are presented in Table 4.7. Generally, all the studied traits (DPM, GYD, Fe content, and Zn content) were positively associated across the environments.

Table 4.7 Pearson correlation coefficients among different traits using average data of 84 navy bean genotypes across eight different environments.

Traits	GYD	Iron	Zinc
DPM	0.16^{***}	0.07^{**}	0.01
GYD	-	0.06^{*}	0.16^{***}
Iron		-	0.52^{***}

DPM days to physiological maturity, *GYD* grain yield. *, **, *** indicate significance at $P < 0.05$, $P < 0.01$ and $P < 0.001$, respectively.

The highest, significant and positive correlation ($r = 0.52$, $p < 0.001$) was found between seed Fe and seed Zn. Conversely, the association was low, positive and significant between seed Fe and DPM ($r = 0.07$, $p < 0.01$), seed Fe and GYD ($r = 0.06$, $p < 0.05$), Zn and GYD ($r = 0.16$, $p < 0.001$). Very weak, positive and non-significant association was observed between seed Zn and DPM ($r = 0.01$, $p > 0.05$).

4.4 Discussion

4.4.1 Variability in grain yield, micronutrient concentrations, and broad sense heritability

In the current study, wide genetic variation was observed among the study genotypes as revealed by GYD and seed Zn which expressed high genotypic main effect ($p < 0.001$) and high H^2 estimates. The high H^2 estimates for GYD and seed Zn suggest strong genetic control, predominance of additive gene action and the potential of high response to selection given that a greater percentage of the observed phenotypic variation was due to genetic variance. Conversely, seed Fe exhibited low genotypic main effect ($p < 0.05$) and moderate H^2 estimates (0.40). These findings agree with Gomez-Becerra et al. (2010) who reported that H^2 also indicates genetic differentiation among genotypes in a given population. High seed Fe concentrations (G37 – 120 ppm; G42 – 119 ppm; G44 – 118 ppm) and Zn (G76 – 52 ppm; G74 – 50 ppm; G21 50 ppm) were observed in this study. According to Blair et al. (2010), Akond et al. (2011) and Mukamuhirwa (2013), dry beans genotypes of the middle-american gene pool such as navy beans have been found to contain higher levels of seed Fe and Zn concentrations as compared to bean genotypes of the andean gene pool. This suggests that the middle-american gene pool constitute important genetic resources for developing dry beans cultivars with improved levels of seed Fe and Zn concentrations. These findings agree with Akond et al. (2011) who reported high concentrations of Fe and Zn (112 mg kg-1 of Fe and 49.2 mg kg-1 of Zn) in dry beans seed of the middle-american gene pool.

The micronutrient dense genotypes identified in this study should be validated through the Inductively Coupled Plasma Atomic Emission Spectrometry (ICP-AES) which is capable of detecting Fe and Zn contaminants. Furthermore, the effects of the environment on seed Fe and Zn concentrations can be reduced through the use of molecular markers that are linked to high seed Fe and Zn. Unfortunately, the bean community is not yet using any molecular markers for genotypic selection for high seed Fe content (Izquierdo et al., 2018; Mukankusi personal communication[1], August 2021). There was some progress made by Dr Bodo Raatz (ABC in Colombia) who identified three markers (SdFe6.2_GT_22265290, SdFe6.2_GT_22340161 and SdFe6.2_TG_22844368) linked to high seed Fe but the findings were not conclusive and the identified markers haven not been validated (Mukankusi personal communication, August 2021).

[1] Dry bean breeder at ABC in Uganda

4.4.2 Genotype by environment interaction

In the present study, the GEI for seed Fe and Zn was small and not significant suggesting that the ranking of genotypes across environments regarding seed Fe and Zn remained relatively the same despite the changes in seed micronutrient levels across environments. According to Welch and Graham (2004) and Beebe (2020), these findings suggest that the traits responsible for genetic improvement in seed Fe and Zn contents are relatively stable across test environments resulting in similar genotype rankings over environments. The current findings imply that the evaluation of genotypes for seed Fe and Zn can be conducted in fewer and reliable sites thus reducing trial evaluation costs. The AMMI analysis of variance for GYD revealed that the genotypes, environments and GEI were highly significant indicating differential GYD response and rankings across the diverse conditions of the test environments. Furthermore, the environments (38.87%) and GEI (39.48%) contributed the largest percentage to the total variation explained, suggesting that most of the observed variation regarding GYD was contributed by the environmental conditions. This concurs with Katuuramu et al. (2020) who reported that GYD stability in dry beans was affected by divergent environmental conditions which resulted in high GEI.

In other studies, Ashango et al. (2016), Molosiwa et al. (2019), and Mndolwa et al. (2019) reported a higher contribution of environments to the total variation with values of 81.06 %, 36.83%, and 46%, respectively. On the contrary, Philipo et al. (2021) and Ligarreto-Morenoa and Pimentel-Ladino (2021) reported a higher contribution of genotype main effect to the total variation with values of 39.3% and 53.14%, respectively. According to Yan and Kang (2003) and Yan and Tinker (2006), breeders can exploit GEI by (i) evaluating genotypes within a mega-environment, (ii) identifying an ideal genotype which combines both high GYD performance and stability across diverse environments (wide adaptation), and (iii) identifying genotypes that are adapted to specific environments. All the aforementioned options of exploiting GEI were explored in this study. The changes in rankings of genotypes across environments was also confirmed by the first four AMMI selections for GYD which had different winning genotypes in most of the test environments. This signified the presence of cross-over type of GEI (Figure 4.2 and Table 4.5) which complicates the selection of genotypes. The cross-over GEI could be attributed to genetic variability among the test genotypes and diverse conditions of the study environments such as rainfall, soil type and temperature. Evidently, the eight study environments were characterized by differences in soil types, soil micronutrient profiles, altitude, latitude, and longitude (Table 4.1). Ashango et al.

(2016), Katuuramu et al. (2020) and Philipo et al. (2021) also reported the presence of crossover GEI for GYD in their studies across different environments. The presence of a cross-over GEI also indicates the existence of different mega-environments from which different winning genotypes per environment could be selected (Yan et al., 2007). Accordingly, in this study, three mega-environments were identified for GYD, indicating that there are at least three navy bean mega-environments in Zimbabwe for the evaluation, selection, and subsequent deployment of different navy bean genotypes. The existence of different mega environments in this study was also confirmed by the GEI effects for GYD which were higher than the genotypic effects. Since the GEI effect for GYD was significant, there was need to identify and select stable and widely adapted genotypes.

4.4.3 Genotype adaptability and stability

Assessment of the environmental stability of GYD, seed Fe and seed Zn concentrations is important in navy bean breeding programs focussed on enhancing the GYD and micronutrient density potential of breeding lines and released cultivars. According to Yan and Tinker (2006), if there is a significant cross-over type of GEI for a specific trait, it is important to conduct stability analysis. The top two high yielding genotypes G27 (2502 kg/ha) and G79 (2488 kg/ha) were relatively not stable in GYD across environments indicating inconsistent GYD response of genotypes across diverse environments due to the strong influence of GEI. Earlier studies by Assefa et al. (2013) and Gereziher et al. (2017) on G79 (Awash Melka/ICA Bunsi) classified G79 as a high yielding cultivar under optimum conditions. The current findings are also consistent with previous findings by Katuuramu et al. (2020) who reported that the highest yielding dry beans genotypes in their study were not stable across nine on-farm environments. Earlier studies by Assefa et al. (2013) and Gereziher et al. (2017) on G79 (Awash Melka/ICA Bunsi) also classified G79 as a high yielding cultivar under optimum conditions. The vertex genotypes G27 and G24 were specifically adapted to agro-ecological conditions of the testing environments in mega-environment 1 (Hara2018, Hara2019, Chisu2018, and Chire2019) and mega-environment 2 (GVTC2018 and GVTC2019), respectively as revealed by the "which-won-where" polygon-view of GGE biplot. Specific adaptation (temporal stability) is a desirable attribute to farmers who are mainly concerned with how a cultivar performs in their locality or region (Kang, 1998). Considering that G27 and G24 also had seed Fe and Zn concentrations above the breeding targets of 90 and 40 ppm respectively, these genotypes could be recommended for narrow adaptation (deployment) in mega-environments 1 and 2 respectively, where they performed relatively well.

Overall, both YSI and ASV statistical models identified seven promising genotypes (G12, G66, G69, G39, G38, G2 and G3) which combined high GYD with stability across different environments. Among the identified genotypes, G12 was classified as widely adapted by AMMI. Widely adapted cultivars (spatial stability) are preferred by breeders and seed companies for seed production because of reduced vulnerability to environmental and seasonal changes. However, considering the three strongly differing mega-environments identified in this study, widely adapted genotypes are not very useful. On the other hand, G2 had positive GEI with all the environments in the lowveld region suggesting that it was resistant to environmental changes and specifically adapted to low potential environments. Thus, G2 could be considered for deployment in low potential environments and utilization in navy bean breeding programs as a source of high GYD, stability and specific adaptation alleles. However, G2 should be evaluated further in farmers' fields to confirm the current findings. In another study, Mutari and Hodzi (2015) reported three out of fifteen dry beans genotypes being specifically adapted to low potential environments and identified two out of fifteen genotypes that were widely adapted. According to Ceccareli (1996), genotypes with high GYD stability and adaptability have a positive effect on farmers' income security and contribute to food security at household and national level.

Interestingly, the seven promising genotypes (G12, G66, G69, G39, G38, G2 and G3) which combined high GYD with stability also had seed Fe and Zn concentrations above the breeding targets of 90 and 40 ppm except for G2. These genotypes were also comparable with the micronutrient (G73 - SMC17) and grain yield (G1 – Protea) checks, in terms of seed Fe and seed Zn and GYD respectively. This suggested that these genotypes combined high GYD stability and adaptability with desirable micronutrient density. Nutritional quality traits (Fe and Zn) are important attributes that are highly valued by bean processors and policy makers in Zimbabwe and other countries given the mandatory national food fortification strategy that was launched in 2015 (World Health Organization, 2015). Therefore, G12, G66, G69, G39, G38 and G3 should be prioritized for use in navy bean breeding programs as parental genotypes for crossing with other cultivars to improve micronutrient (Fe and Zn) density, in addition to GYD and GYD stability. Furthermore, these genotypes could also appeal to policy makers, breeders, farmers, traders, processors, schools (feeding programs) and non-governmental organizations (NGOs) because they combined high GYD and high GYD stability with desirable above average seed Fe and Zn concentrations. Moreover, they outperformed the standard checks with respect to GYD, seed Fe and Zn concentrations. However, as highlighted earlier on, before

these genotypes can be recommended for deployment in target environments, it is important to evaluate them under farmer managed conditions.

Generally, the YSI statistical model consistently showed results comparable with those of ASV statistical model with respect to stability ranking. This indicates that the two stability analysis methods employed in this study accurately identified stable and unstable genotypes. However, the utilization of YSI statistical model was advantageous in this study because it combined both high yielding and stability traits into a single index, unlike the ASV which in some instances ranked low yielding genotypes among the most stable. Thus, the YSI statistical model complements the AMMI method for identifying highly adaptable and stable genotypes. Therefore, the YSI statistical model is recommended for use in MET for the simultaneous identification of high yielding and stable genotypes.

4.4.4 Associations among traits, grain yield and nutritional quality trade-off

Interestingly, the top five ranked genotypes with respect to seed Fe concentrations (G37 – 120 ppm; G42 – 119 ppm; G44 – 118 ppm, G38 – 118 ppm; G5 – 118 ppm) were not among the top yielding genotypes across environments (G42 – 2283 kg/ha; G38 – 2250 kg/ha; G5 – 2218 kg/ha; G3 – 2213 kg/ha; G44 – 2183k g/ha). This could be attributed to the dilution effect of seed Fe and Zn owing to the increased translocation of carbohydrates to the seed, a scenario common in high yielding genotypes (Diaz et al., 2022). Other studies have attributed the observed trade-offs between GYD and seed micronutrient concentrations to mechanisms more complex than dilution such as nutrient uptake by the root system, nutrient translocation, redistribution, followed by remobilization and accumulation into the seed (Kobayashi and Nishizawa, 2012; Marcos-Barbero et al., 2021). Similar results were reported in dry beans (Raatz, 2018; Beebe, 2020; Diaz et al., 2022), chickpea (*Cicer arietinum* L.) (Diapari et al., 2014), rice (*Oryza sativa* L.) (Inabangan-Asilo et al., 2019) and bread wheat (Marcos-Barbero et al., 2021). Therefore, improved seed micronutrient density in navy beans can be realized at the expense of GYD. The current findings suggest that it would be a challenging task for breeders to package into one genotype genes containing micronutrient density and high GYD genes when breeding biofortified beans. These findings agree with Beebe et al. (2020) who reported that it is a challenge for breeders to combine micronutrient density with high grain yield. Therefore, bean breeders could probably aim to develop genotypes that combine micronutrient density with ‘acceptable’ GYD potential. Another alternative will be to make use of middle american-andean inter-gene pool hybridization and segregation which produces distinct genes for homeostatic mechanisms, thereby disrupting homeostasis and creating

genetic variability (Beebe, 2020). Homeostasis is a mechanism which regulates the uptake, translocation and redistribution of Fe in plants to prevent toxicity by maintaining its concentration within biologically acceptable levels (Morrissey and Guerinot, 2009).

Considering that bioavailability of Fe and Zn in dry beans varies with genotype, market class and processing method (Elobeid et al., 2014; Wiesinger et al., 2020), it is recommended to assess the bioavailability of seed Fe and Zn in micronutrient dense genotypes identified in this study. The present study also demonstrated the existence of a strong and significant positive association between seed Fe and Zn concentration suggesting that an increase in seed Fe concentration would significantly increase the seed Zn concentration visa vis. Therefore, it is possible to select for high seed Fe and Zn simultaneously with "acceptable GYD potential" through conventional breeding practices. Earlier studies have also reported significant, strong, and positive association between seed Fe and Zn concentration in dry beans (Blair et al., 2009; Cichy et al., 2009; Mukamuhirwa et al., 2015; Amongi et al., 2018; Katuuramu et al., 2021; Diaz et al., 2022; Keller et al. 2022). The strong positive associations observed in this study between seed Fe and Zn concentrations suggest that both micronutrients have similar mechanisms of assimilation to the seed (Hacisalihoglu and Kochian, 2003). Welch and Graham (2004), Blair et al. (2009) and Beebe (2020) also attributed this correlation to the co-localization or co-segregation of quantitative trait loci (QTL) for seed Fe and Zn, increasing the possibility of improving both traits simultaneously through marker assisted selection. However, the co-localization of QTL for seed Zn and Fe would need to be tested.

4.4.5 Interrelationship among environments and discriminating ability of the environments for grain yield

The correlation coefficients of less than 90^{o} observed between vectors of environments GVTC2018/GVTC2019 and Hara2019, and environments Chisu2018/Chisu2019 and Chire2018 indicate that these environments were relatively similar in their differentiation of the study genotypes. However, to select for GYD as well as seed Fe and Zn content, all the three mega-environments must be represented per year. This implies that when evaluating navy bean genotypes in Zimbabwe, a breeder has to select both HRS and GVTC in the highveld region (high potential environments) since they appeared in different mega-environments as well as either CRS or CES in the lowveld region (low potential environments) as sites for phenotyping. This is because equally or more informative information on genotype performance could be obtained from fewer but better test environments (Yan and Kang, 2003). Even though both GVTC and HRS appeared in different mega-environments despite exhibiting

strong association, GVTC is known to have a higher incidence of bean stem maggot (*Ophyiomia phaseoli*), common bacterial blight caused by *Xanthomonas axonopodis* pv. *phaseoli* (Xap), bean rust caused by *Uromyces appendiculatus* and angular leaf spot caused by *Phaeoisariopsis griseola*, making it a better preference for evaluating genotypes than HRS when resources are limiting. As for the low potential environments, CRS is good for screening drought and heat tolerance compared to CES. Thus, this strategy could significantly reduce evaluation costs under limited human (labor) and financial resources, thereby ultimately improving efficiency of the breeding programme.

The HRS environment in 2018 (Hara2018) and CES in 2019 (Chisu2019) had stronger interactive forces whilst CRS in 2018 (Chire2018) had weaker interactive forces. Furthermore, HRS in 2019 (Hara2019) had the highest mean GYD among the eight environments despite having received less rainfall than GVTC in both seasons. Therefore, considering that the GEI was significant, HRS can be considered as the best test environment for the genetic differentiation of breeding lines when breeding for the highveld region (high potential environments). This concurs with Mutari and Hodzi (2015) who recommended HRS as a good location for conducting MET targeting high potential environments. The superiority of HRS over the other locations could be attributed to the presence of deep, well-drained fertile soils and receipt of adequate seasonal rainfall that was evenly distributed throughout the growing season.

Likewise, when breeding for the lowveld region (targeting low potential environments), CES can be considered as the best test environment for the genetic differentiation of breeding lines. This is because, among the environments located in the lowveld region, CES had longer environmental vectors and higher GYD than CRS in both 2018 and 2019 seasons. Locations such as CRS which had the weakest interactive forces and the lowest mean GYD during both seasons should be excluded from hosting multi environment yield trials to save on time and costs. This is important considering that environments with weak interactive forces do not provide additional information on GEI. However, CRS is good for screening drought and heat tolerance. The current findings agree with Mohammadi and Haghparast (2011) who reported that genotypes selected at ideal sites would have the highest probability of representing desirable genotypes that perform well across the target environments in the production region. However, it is important to highlight that, since the GEI was significant in this study, a better understanding of performance of genotypes across diverse environments would be obtained using the 3 mega-environments identified in this study.

4.5 Conclusions, recommendations, and implications

The study revealed some outstanding genotypes with respect to seed Fe [G37 (ZABRA16575-51F22), G42 (SMB30) and G44 (G99)], seed Zn [G76 (SMC17), G74 (SMC21), and G21 (ICA BUNSIxSXB405-1C-1C)], and GYD [G27 (ZABRA16575-26F22), G41 (ZABRA16575-73F22), G79 (Awash melka) and G41 (ZABRA16575-73F22)] that could be used as parents to simultaneously improve the respective traits in navy beans. However, there is a need to pyramid high GYD and nutritional quality traits (Fe and Zn) into a single genetic background considering that the best performing genotypes for GYD, Fe, and Zn were different. Most importantly, bean breeders could probably aim to develop genotypes that combine micronutrient density with "acceptable GYD potential" taking into consideration the 'dilution effects'. This entails designing an appropriate breeding strategy for micronutrient density and acceptable GYD, selection strategies, and screening procedures. Cross-over GEI was observed for GYD. Stability analysis using AMMI, YSI and ASV identified six promising genotypes [G12 (G14), G66 (G49), G69 (G37), G39 (ICA BUNSIxSXB405/3C-1C-1C-8), G38 (NAE70) and G3 (CZ108-53)] with high GYD, good GYD stability and desirable seed Fe and Zn concentrations above breeding targets of 90 and 40 ppm, respectively. These genotypes should be used as parents for crossing with other cultivars to improve micronutrient density, GYD and GYD stability. The vertex genotypes G27 (ZABRA16575-26F22), G24 (ICA BUNSIxSXB405/4C-1C-1C-8) and G33 (NAE13) combined specific adaptation and high GYD with desirable micronutrient density as revealed by the "which-won-where" polygon-view of GGE biplot. These genotypes could be recommended for deployment in their respective mega-environments. However, before the selected genotypes can be considered for release, there is a need to evaluate their preference among different stakeholders such as farmers, traders, bean processors, and consumers. Additionally, these genotypes should be subjected to on-farm multi-environment testing, bioavailability studies, canning quality analysis, and confirmatory micronutrient analysis using the ICP-AES. The environments, "GVTC2018/GVTC2019 and Hara2019" and "Chisu2018/Chisu2019 and Chire2018" were highly correlated among themselves implying that either GVTC or HRS and CES or CRS could be dropped to save resources since they are likely to give same information about the genotypes. Highly significant and positive associations were observed between seed Fe and Zn suggesting that both traits can be improved simultaneously. The genotypic selection for high seed Fe and Zn through the use of molecular markers that are linked to these nutritional quality traits would be more reliable and efficient in biofortification programs.

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Appendix 4.1 List of navy bean genotypes used in the study and their sources.

No.	Genotype	Code	Source
1	Protea (Grain yield check)	G1	ABC Malawi
2	CZ108-52	G2	ABC Malawi
3	CZ108-53	G3	ABC Malawi
4	SMB31	G4	ABC Colombia
5	NAE60	G5	ABC Colombia
6	NAE19	G6	ABC Colombia
7	NAE87	G7	ABC Colombia
8	NAE78	G8	ABC Colombia
9	SAA12	G9	ABC Malawi
10	SAA1	G10	ABC Malawi
11	G54	G11	ABC Colombia
12	G14	G12	ABC Colombia
13	AWASH-1	G13	EIAR Ethiopia
14	NAE40	G14	ABC Colombia
15	SAB792	G15	ABC Colombia
16	ZABRA16573-25F22	G16	ABC Malawi
17	SAA2	G17	ABC Colombia
18	RAZ-36	G18	ABC Malawi
19	ZABRA16575-57F22	G19	ABC Malawi
20	DAB562	G20	ABC Colombia
21	ICA BUNSIxSXB405-1C-1C	G21	ABC Colombia
22	G550	G22	ABC Colombia
23	CZ113-13	G23	ABC Malawi
24	ICA BUNSIxSXB405/4C-1C-1C-8	G24	ABC Colombia
25	NAE80	G25	ABC Colombia
26	SAB-662	G26	ABC Colombia
27	ZABRA16575-26F22	G27	ABC Malawi
28	NAE24	G28	ABC Colombia
29	NAIN DEKYONDO	G29	AB Malawi
30	CZ108-27	G30	ABC Malawi
31	SAB793	G31	ABC Colombia
32	RAZ-44	G32	ABC Malawi
33	NAE13	G33	ABC Colombia
34	NAVY LINE-48	G34	ABC Malawi
35	G30	G35	ABC Colombia
36	ICA BUNSIxSXB405/9C-1C-1C-3	G36	ABC Colombia
37	ZABRA16575-51F22	G37	ABC Malawi
38	NAE70	G38	ABC Colombia
39	ICA BUNSIxSXB405/3C-1C-1C-8	G39	ABC Colombia
40	G32	G40	ABC Colombia
41	ZABRA16575-73F22	G41	ABC Malawi
42	SMB30	G42	ABC Colombia
43	NAVY LINE-60	G43	ABC Malawi
44	G99	G44	ABC Colombia
45	G6	G45	ABC Colombia
46	G24	G46	ABC Colombia
47	NAVY LINE 22	G47	ABC Malawi
48	CIM-NAV02-35-1	G48	ABC Malawi
49	SAA18	G49	ABC Malawi
50	CIM-NAV02-17-3	G50	ABC Malawi
51	SAA17	G51	ABC Malawi
52	SAA7	G52	ABC Malawi

No.	Genotype	Code	Source
53	NAVY46	G53	ABC Malawi
54	G90	G54	ABC Colombia
55	G100	G55	ABC Colombia
56	CANPSULA	G56	ABC Malawi
57	ZABR-16576-20	G57	ABC Malawi
58	G738	G58	ABC Colombia
59	NAVY19	G59	ABC Malawi
60	UBR(92)25	G60	ABC Malawi
61	G16	G61	ABC Colombia
62	SAA19	G62	ABC Malawi
63	SAB791	G63	ABC Colombia
64	CIM-NAV02-10-1	G64	ABC Malawi
65	G48	G65	ABC Colombia
66	G49	G66	ABC Colombia
67	G70	G67	ABC Colombia
68	G40	G68	ABC Colombia
69	G37	G69	ABC Colombia
70	G34	G70	ABC Colombia
71	G27	G71	ABC Colombia
72	CIM-DWRF-CLIM01-1-1	G72	ABC Malawi
73	SMC16 (Micronutrient check)	G73	ABC Colombia
74	SMC21	G74	ABC Colombia
75	RWR2154	G75	ABC Malawi
76	SMC17	G76	ABC Colombia
77	Ex-rico	G77	CBI Zimbabwe
78	Chercher	G78	ABC Uganda
79	Awash melka	G79	EIAR Ethiopia
80	Awash 2	G80	EIAR Ethiopia
81	RAZ 42	G81	ABC Uganda
82	RAZ11	G82	ABC Uganda
83	CAB 2	G83	ABC Uganda
84	G53	G84	ABC Uganda

CBI crop breeding institute, *ABC* Alliance of Bioversity International and International Center of Tropical Agriculture, *EIAR* ethiopian institute of agricultural research.

Appendix 4.2 Bartlett's test for homogeneity of error variances.

		Grain yield			
Environment	**Error variance**	**Degrees of freedom**	**Chi-square**	**Degrees of freedom**	**Probability**
Chire2019	84959				
Chire2018	66689				
Chisu2018	78798				
Chisu2019	96433				
GVTC2018	77964				
GVTC2019	88256				
Hara2018	100671				
Hara2019	91395				
Bartlett's test		167	10.04	7	0.186
		Seed iron			
Environment	Error variance	Degrees of freedom	Chi-square	Degrees of freedom	Probability
Chire2019	323.3				
Chire018	405.2				
Chisu2018	337.9				
Chisu2019	324.9				
GVTC2018	305.4				
GVTC2019	296.5				
Hara2018	386.9				
Hara2019	253.6				
Bartlett's test		167	12.8	7	0.077
		Seed zinc			
Environment	Error variance	Degrees of freedom	Chi-square	Degrees of freedom	Probability
Chire2019	55.9				
Chire2018	51.9				
Chisu2018	42.8				
Chisu2019	39.6				
GVTC2018	44.9				
GVTC2019	36.9				
Hara2018	38.6				
Hara2019	44.3				
Bartlett's test		167	12.4	7	0.090

Hara harare research station, *GVTC* gwebi variety testing center, *Chisu* chisumbanje experiment station, *Chire* chiredzi research station. 2018 and 2019 denotes the cropping season.

Appendix 4.3 Restricted maximum likelihood combined analysis for grain yield, seed iron and zinc concentrations of 84 navy bean genotypes evaluated in two seasons across four locations.

		Wald statistic		
Source	**Degrees of freedom**	**Grain yield (kg/ha)**	**Iron (ppm)**	**Zinc (ppm)**
Location	3	785.64***	360.52***	260.11***
Genotype	83	241.04***	339.85***	773.88***
Year	1	42.72***	0.24	0.49
Location.Genotype	249	721.54**	299.37*	434.23*
Genotype.Year	83	306.00***	174.70***	12.39***
Location.Year	3	237.12***	401.20***	1077.31***
Location.Genotype.Year	249	484.27**	301.71*	14.28
Location.Replication	4	384.59***	1743.58***	1348.90***
Location.Replication.Block	96	117.83***	352.65***	160.60***

ppm parts per million.

Appendix 4.4 Mean performance of the 84 navy bean genotypes across eight environments based on predicted genotype values ($\hat{G}$).

Genotype	GYD	Rank	Genotype	Fe	Rank	Genotype	Zn	Rank
G27	2501^{f}	1	G37	119.75^{f}	1	G76	51.63^{h}	1
G79	2488^{e-f}	2	G42	118.75^{e-f}	2	G74	50.13^{gh}	2
G64	2445^{d-f}	3	G44	118.00^{e-f}	3	G21	49.50^{f-h}	3
G56	2438^{c-f}	4	G38	117.50^{d-f}	4	G28	49.25^{e-h}	4
G41	2430^{c-f}	5	G5	117.50^{d-f}	4	G5	49.25^{e-h}	4
G34	2427^{c-f}	6	G70	115.88^{c-f}	6	G75	48.88^{d-h}	6
G43	2420^{c-f}	7	G2	115.38^{c-f}	6	G73	48.75^{c-h}	7
G24	2401^{b-f}	8	G7	114.50^{c-f}	8	G40	47.63^{c-h}	8
G47	2396^{b-f}	9	G77	114.50^{c-f}	8	G84	46.63^{c-h}	9
G30	2396^{b-f}	10	G21	113.88^{c-f}	10	G6	46.50^{c-h}	10
G61	2386^{b-f}	11	G46	113.63^{c-f}	11	G66	46.00^{c-h}	11
G78	2385^{b-f}	12	G50	113.50^{c-f}	12	G55	45.88^{c-h}	12
G72	2369^{a-f}	13	G19	113.25^{c-f}	13	G38	45.38^{c-h}	13
G12	2355^{a-f}	14	G28	113.13^{b-f}	14	G27	45.25^{b-h}	14
G2	2353^{a-f}	15	G39	112.75^{b-f}	15	G65	45.00^{a-h}	15
G63	2341^{a-f}	16	G45	112.63^{b-f}	16	G14	44.88^{a-h}	16
G3	2332^{a-f}	17	G16	112.38^{b-f}	17	G58	44.88^{a-h}	16
G17	2315^{a-f}	18	G32	112.25^{b-f}	18	G24	44.75^{a-h}	18
G14	2312^{a-f}	19	G48	111.50^{b-f}	19	G25	44.75^{a-h}	18
G36	2312^{a-f}	20	G10	111.38^{b-f}	20	G39	44.63^{a-h}	20
G35	2311^{a-f}	21	G34	111.00^{b-f}	21	G52	44.63^{a-h}	20
G33	2311^{a-f}	22	G35	110.88^{b-f}	22	G42	44.50^{a-h}	22
G10	2310^{a-f}	23	G1	110.75^{a-f}	23	G45	44.50^{a-h}	22
G18	2305^{a-f}	24	G75	110.75^{a-f}	23	G4	44.38^{a-h}	24
G80	2297^{a-f}	25	G40	110.63^{a-f}	25	G3	44.25^{a-h}	25
G26	2294^{a-f}	26	G18	110.38^{a-f}	26	G71	44.13^{a-h}	26
G60	2292^{a-f}	27	G74	110.38^{a-f}	26	G83	44.13^{a-h}	26
G73	2292^{a-f}	28	G57	109.63^{a-f}	28	G7	44.00^{a-h}	28
G75	2286^{a-f}	29	G73	109.38^{a-f}	29	G44	44.00^{a-h}	28
G53	2283^{a-f}	30	G25	109.25^{a-f}	30	G26	43.75^{a-h}	30
G6	2283^{a-f}	31	G26	109.25^{a-f}	30	G57	43.63^{a-h}	31
G42	2283^{a-f}	32	G41	109.25^{a-f}	30	G46	43.50^{a-h}	32
G66	2282^{a-f}	33	G80	109.13^{a-f}	33	G22	43.25^{a-h}	33
G15	2270^{a-f}	34	G13	108.88^{a-f}	34	G41	43.25^{a-h}	33
G69	2263^{a-f}	35	G84	108.88^{a-f}	34	G8	43.25^{a-h}	33
G39	2257^{a-f}	36	G64	108.75^{a-f}	36	G82	43.25^{a-h}	33
G84	2254^{a-f}	37	G30	108.63^{a-f}	37	G34	43.13^{a-h}	37
G23	2254^{a-f}	38	G4	108.63^{a-f}	37	G16	43.00^{a-h}	38
G55	2252^{a-f}	39	G82	108.50^{a-f}	39	G63	42.88^{a-h}	39
G11	2251^{a-f}	40	G11	108.38^{a-f}	40	G19	42.75^{a-h}	40
G38	2250^{a-f}	41	G43	108.25^{a-f}	41	G81	42.75^{a-h}	40
G50	2249^{a-f}	42	G53	107.75^{a-f}	42	G51	42.50^{a-h}	42
G9	2247^{a-f}	43	G27	107.38^{a-f}	43	G61	42.50^{a-h}	42
G16	2247^{a-f}	44	G56	107.25^{a-f}	44	G80	42.50^{a-h}	42
G83	2245^{a-f}	45	G59	107.25^{a-f}	44	G47	42.25^{a-h}	42
G82	2243^{a-f}	46	G60	107.13^{a-f}	46	G67	42.25^{a-h}	42
G22	2237^{a-f}	47	G24	107.00^{a-f}	47	G78	42.25^{a-h}	42
G46	2235^{a-f}	48	G29	107.00^{a-f}	47	G32	42.13^{a-h}	48
G52	2233^{a-f}	49	G76	107.00^{a-f}	47	G48	42.00^{a-h}	49
G7	2232^{a-f}	50	G55	106.88^{a-f}	50	G77	42.00^{a-h}	49
G58	2230^{a-f}	51	G61	106.88^{a-f}	50	G37	42.00^{a-h}	49
G59	2230^{a-f}	52	G36	106.63^{a-f}	52	G18	41.88^{a-h}	52
G21	2228^{a-f}	53	G47	106.38^{a-f}	53	G20	41.75^{a-h}	53
G1	2222^{a-f}	54	G81	106.38^{a-f}	53	G60	41.75^{a-h}	53
G81	2222^{a-f}	55	G6	105.75^{a-f}	55	G54	41.63^{a-h}	55
G40	2219^{a-f}	56	G17	105.63^{a-f}	56	G50	41.50^{a-h}	56
G5	2218^{a-f}	57	G67	105.38^{a-f}	57	G79	41.50^{a-h}	56

Genotype	GYD	Rank	Genotype	Fe	Rank	Genotype	Zn	Rank
G62	2217^{a-f}	58	G8	104.75^{a-f}	58	G17	41.38^{a-h}	58
G37	2213^{a-f}	59	G14	104.63^{a-f}	59	G64	41.38^{a-h}	59
G28	2212^{a-f}	60	G83	104.50^{a-f}	60	G35	41.25^{a-h}	60
G25	2208^{a-f}	61	G49	104.38^{a-f}	61	G13	41.13^{a-h}	61
G4	2203^{a-f}	62	G54	104.00^{a-f}	62	G36	41.13^{a-h}	61
G8	2203^{a-f}	62	G22	103.75^{a-f}	63	G69	41.00^{a-h}	63
G20	2200^{a-f}	64	G71	103.50^{a-f}	64	G10	40.88^{a-h}	64
G74	2192^{a-f}	65	G33	103.25^{a-f}	65	G62	40.88^{a-h}	64
G29	2192^{a-f}	66	G79	102.63^{a-f}	66	G9	40.88^{a-h}	64
G19	2190^{a-f}	67	G58	102.50^{a-f}	67	G12	40.63^{a-g}	67
G57	2189^{a-f}	68	G12	102.38^{a-f}	68	G49	40.63^{a-g}	67
G44	2183^{a-f}	69	G68	100.88^{a-f}	69	G70	40.50^{a-g}	69
G45	2182^{a-f}	70	G20	100.75^{a-f}	70	G30	40.25^{a-g}	70
G49	2177^{a-f}	71	G51	100.75^{a-f}	70	G43	40.13^{a-g}	71
G76	2169^{a-f}	72	G66	98.88^{a-f}	72	G33	40.00^{a-g}	72
G51	2160^{a-f}	73	G52	98.63^{a-f}	73	G29	39.88^{a-g}	73
G13	2155^{a-f}	74	G3	98.13^{a-f}	74	G68	39.88^{a-g}	73
G54	2153^{a-f}	75	G69	98.00^{a-f}	75	G15	39.75^{a-g}	75
G71	2134^{a-f}	76	G31	97.63^{a-f}	76	G72	39.50^{a-g}	76
G70	2132^{a-f}	77	G23	97.50^{a-f}	77	G1	38.75^{a-f}	77
G32	2126^{a-f}	78	G15	96.00^{a-f}	78	G23	38.75^{a-f}	77
G48	2116^{a-e}	79	G9	95.13^{a-e}	79	G56	38.38^{a-e}	79
G31	2092^{a-d}	80	G78	94.75^{a-e}	80	G31	38.00^{a-d}	80
G68	2079^{a-d}	81	G62	93.38^{a-d}	81	G11	37.88^{a-c}	81
G67	2057^{a-c}	82	G65	92.38^{a-c}	82	G59	37.88^{a-c}	81
G77	2019^{ab}	83	G72	88.88^{ab}	83	G2	34.38^{ab}	83
G65	2002^{a}	84	G63	86.50^{a}	84	G53	34.25^{a}	84
Mean	2256.90			106.90			42.83	
Min	1854.00			41.00			22.00	
Max	3548.00			136.00			68.00	
CV (%)	11.30.00			24.90			17.00	
LSD	176.82			18.46			5.06	
H^2	0.60			0.40			0.82	
H^2 (%)	60.00			40.00			82.00	
SD	254.70			26.60			7.29	

GYD grain yield (kg/ha*), Fe* iron (ppm), *Zn* zinc (ppm), $\hat{G}$ predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *CV* coefficient of variation (%), H^2 broad-sense heritability (%), *LSD* least significance difference at 0.05, *SD* standard deviation, *ppm* parts per million, *Min* minimum, *Max* maximum. Means with different letters in the same column are significantly different.

Appendix 4.5 IPCA scores and stability analyses for grain yield (kg/ha) of eight-four genotypes tested in eight environments during 2018 and 2019.

No.	Genotype	IPCAg1	IPCAg2	GYD	GYD Rank	ASV	ASV Rank	YSI	YSI Rank
1	G1	4.52	9.83	2222	54	11.61	69	123	73
2	G2	1.31	-0.72	2353	15	1.93	12	27	2
3	G3	1.49	0.24	2332	17	2.05	14	31	3
4	G4	6.43	-0.78	2203	62	8.83	56	118	70
5	G5	1.35	-0.04	2218	57	1.85	10	67	27
6	G6	-0.20	5.43	2283	31	5.44	35	66	26
7	G7	3.83	-6.08	2232	50	8.03	50	100	59
8	G8	1.23	-1.89	2203	63	2.53	16	79	37
9	G9	-1.82	-2.46	2247	43	3.50	21	64	24
10	G10	-2.22	-3.29	2310	23	4.48	30	53	15
11	G11	4.20	-10.03	2251	40	11.56	68	108	65
12	G12	-0.78	-0.83	2355	14	1.35	4	18	1
13	G13	1.84	-1.47	2155	74	2.92	18	92	51
14	G14	0.02	-4.09	2312	19	4.09	26	45	8
15	G15	3.79	-4.07	2270	34	6.59	42	76	33
16	G16	-5.55	1.61	2247	44	7.76	46	90	49
17	G17	-0.62	4.04	2315	18	4.13	27	45	9
18	G18	0.79	-5.68	2305	24	5.78	36	60	23
19	G19	-1.29	1.95	2190	67	2.63	17	84	45
20	G20	-5.58	0.89	2200	64	7.69	45	109	66
21	G21	3.18	-4.75	2228	53	6.44	41	94	55
22	G22	7.75	2.80	2237	47	10.97	67	114	69
23	G23	-2.81	5.70	2254	38	6.88	43	81	40
24	G24	0.23	-13.39	2401	8	13.39	72	80	39
25	G25	5.41	-5.70	2208	61	9.34	60	121	71
26	G26	-3.26	-1.92	2294	26	4.86	33	59	22
27	G27	-13.88	8.66	2501	1	20.87	83	84	46
28	G28	2.08	-3.55	2213	60	4.55	31	91	50
29	G29	1.81	4.50	2192	66	5.14	34	100	60
30	G30	-5.83	10.95	2396	10	13.55	73	83	43
31	G31	5.14	3.35	2092	80	7.79	47	127	74

No.	Genotype	IPCAg1	IPCAg2	GYD	GYD Rank	ASV	ASV Rank	YSI	YSI Rank
32	G32	-2.48	-1.43	2126	78	3.68	23	101	61
33	G33	1.37	4.23	2311	22	4.63	32	54	17
34	G34	-9.72	-4.66	2427	6	14.09	75	81	41
35	G35	-9.30	-2.34	2311	21	12.94	71	92	52
36	G36	-0.26	2.00	2312	20	2.03	13	33	4
37	G37	-5.70	3.21	2213	59	8.43	53	112	68
38	G38	0.73	-1.54	2250	41	1.84	9	50	12
39	G39	0.50	-1.29	2257	36	1.46	5	41	6
40	G40	-0.43	0.56	2219	56	0.81	2	58	20
41	G41	-13.59	4.28	2430	5	19.08	82	87	47
42	G42	-4.97	7.46	2283	32	10.09	62	94	56
43	G43	-12.15	4.67	2420	7	17.27	80	87	48
44	G44	0.13	-0.59	2183	69	0.62	1	70	29
45	G45	-2.17	-5.52	2182	70	6.27	39	109	67
46	G46	0.19	-1.67	2235	48	1.69	8	56	18
47	G47	-7.06	1.97	2396	9	9.86	61	70	30
48	G48	1.57	-0.45	2116	79	2.20	15	94	57
49	G49	1.88	2.40	2177	71	3.52	22	93	54
50	G50	-3.29	-7.55	2249	42	8.79	55	97	58
51	G51	7.18	3.52	2160	73	10.44	64	137	79
52	G52	2.73	-2.46	2233	49	4.47	29	78	35
53	G53	-1.02	-3.89	2283	30	4.13	28	58	21
54	G54	6.74	4.11	2153	75	10.10	63	138	80
55	G55	1.35	-0.51	2252	39	1.92	11	50	13
56	G56	-11.73	1.93	2438	4	16.17	79	83	44
57	G57	4.49	0.21	2189	68	6.15	38	106	64
58	G58	-2.23	-7.54	2230	51	8.13	52	103	62
59	G59	-0.87	3.17	2230	52	3.39	20	72	31
60	G60	-3.00	9.82	2292	27	10.64	65	92	53
61	G61	2.17	-5.54	2386	11	6.29	40	51	14
62	G62	-1.08	2.62	2217	58	3.01	19	77	34
63	G63	3.62	6.08	2341	16	7.84	48	64	25
64	G64	-9.10	2.98	2445	3	12.80	70	73	32

No.	Genotype	IPCAg1	IPCAg2	GYD	GYD Rank	ASV	ASV Rank	YSI	YSI Rank
65	G65	5.64	2.31	2002	84	8.06	51	135	78
66	G66	-0.42	-1.52	2282	33	1.63	6	39	5
67	G67	9.79	3.97	2057	82	13.97	74	156	82
68	G68	14.79	7.47	2079	81	21.57	84	165	84
69	G69	0.49	1.49	2263	35	1.63	7	42	7
70	G70	10.34	0.14	2132	77	14.15	76	153	81
71	G71	6.69	-0.18	2134	76	9.16	58	134	77
72	G72	-5.91	-2.63	2369	13	8.50	54	67	28
73	G73	2.52	-1.55	2292	28	3.78	25	53	16
74	G74	6.67	0.40	2192	65	9.14	57	122	72
75	G75	4.98	-4.02	2286	29	7.91	49	78	36
76	G76	6.72	0.03	2169	72	9.20	59	131	75
77	G77	12.83	7.33	2019	83	19.03	81	164	83
78	G78	-4.09	-4.83	2385	12	7.39	44	56	19
79	G79	-10.47	1.41	2488	2	14.40	77	79	38
80	G80	0.46	-3.66	2297	25	3.71	24	49	10
81	G81	-3.02	-13.95	2222	55	14.55	78	133	76
82	G82	0.78	-0.54	2243	46	1.20	3	49	11
83	G83	1.31	5.72	2245	45	5.99	37	82	42
84	G84	-7.15	-4.86	2254	37	10.92	66	103	63

IPCAg1 interaction principal component axes for genotypes 1, *IPCAg2* interaction principal component axes for genotypes 2, *GYD* grain yield, *ASV* AMMI stability value, *YSI* yield stability index.

Chapter 5 [1]Drought stress impact on agronomic, shoot, physiological, canning and nutritional quality traits of navy beans under field conditions in Zimbabwe

Abstract

Climate change has increased the frequency of terminal drought stress substantially in navy bean (*Phaseolus vulgaris* L.) growing regions. The objectives of this study were to investigate the impact of terminal drought stress on agronomic and shoot traits, canning and nutritional quality of navy beans, and to identify drought tolerant genotypes with good canning and nutritional quality. For this purpose, 110 genotypes were evaluated in 2019 and 2020 at Save Valley Experiment Station, Zimbabwe under drought stressed (DS) and well-watered, non-stressed (NS) field conditions, resulting in four environments. Combined analysis showed significant genotype and genotype x environment interaction (GEI) effects ($p < 0.001$; $p < 0.05$) for most of the evaluated traits. Under DS conditions, the the predicted genotype values ($\hat{G}$) for seed micronutrient concentrations ranged from 72.3 (NAVY LINE-48) to 120 ppm (ZABRA16575-51F22) for Fe; 31.3 (Navy 46) to 60.8 ppm (NAE70) for Zn, while washed drained weight (WDW) varied from 224.8 (Protea) to 310 g (G24), and grain yield (GYD) ranged from 494 (SIRAJ) to 2619 kg/ha (ZABRA16573-78F22). Terminal drought reduced mean stomatal conductance (SC), leaf chlorophyll content (LCC), GYD, number of mature pods per plant, number of seeds per pod, number of seeds per plant and 100-seed weight by 80, 42, 28, 26, 3, 30 and 3%, respectively. Seed Fe concentration and leaf temperature increased by 1.4% and 34.2% in the DS environments, respectively, whereas seed Zn decreased by 0.9%. Terminal drought stress adversely impacted the canopy biomass, pod harvest index, hydration coefficient, WDW, uniformity, shape of seed and degree of splitting. The genotypes ZABRA16575-86F22 and CIM-NAV08-1 had better mean ranks across four GYD based drought tolerance indices, canning and nutritional quality traits under DS compared to the standard checks. These two genotypes are potential candidates for release and genetic analysis.

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5.1 Introduction

Different market classes of dry beans exist and these include navy bean, red kidney, sugars, small reds, large whites, yellows and small blacks, among many others. Navy bean (middle-american gene pool) is an important commercial commodity for processing into canned beans globally. In the United States of America (USA), Ethiopia, Kenya, South Africa, Zambia and Zimbabwe, navy bean is extensively processed in tomato sauce or brine as canned beans. Sometimes it is marketed as dry packed beans. In North America, about 85% of the total navy bean production is destined for the bean canning industry (Khanal et al., 2014). Similarly, in South Africa, navy beans constitute 80% of dry beans that are utilized by the bean processing industry (De Lange and Labuschagne, 2001). The increasing market price of cooking fuels, electricity and fast-growing urban populations of Africa, including Zimbabwe are driving a greater demand for processed and ready-made products such as baked beans in brine or tomato sauce.

The ideal navy bean cultivar must meet the required canning quality standards, micronutrient density and agronomic performance regardless of the production environment. Significant research has been conducted to identify the traits necessary to enhance dry beans canning quality. Notably, most dry beans processing companies in Africa opt for biofortified navy bean grain for canning purposes (Mutari et al., 2022b). This is due to the food fortification policies that have been implemented in many countries in Africa to reduce micronutrient deficiency. Unfortunately, the navy bean cultivars that are currently being processed in SSA are not biofortified (Mutari et al., 2022b). The lack of micronutrient dense navy bean cultivars in African markets has forced dry beans canning companies in countries such as Zimbabwe to process nutrient dense beans of other market classes with poor canning quality attributes (Mutari et al., 2022b). In addition to micronutrient malnutrition, terminal drought stress is another important challenge affecting farmers in Zimbabwe and Sub-Saharan Africa (SSA).

The reproductive stages (flower formation, full flowering, pod formation, and grain filling) of dry beans are extremely sensitive to terminal drought stress. Terminal drought stress adversely affects grain yield, grain quality and the market value of the grain (Rainey and Griffiths, 2005). Smallholder farmers who produce most of the dry beans in Africa are located in marginal areas where seasonal rainfall fluctuates. In addition, terminal drought stress can result in grain yield losses of 50% or more (Katungi et al., 2009; Beebe et al., 2013). Furthermore, farmers with

irrigation facilities in SSA are not spared from the effects of drought due to the declining ground water tables emanating from the increased prevalence of multi-year droughts. Therefore, a cost-effective and reliable strategy for terminal drought stress management is to explore navy bean germplasm to develop drought tolerant genotypes. A study conducted by Mutari et al. (2021) in Zimbabwe identified terminal drought stress as the major abiotic constraint affecting navy bean production. Regrettably, progress in improving drought tolerance in navy beans has been limited compared to the other commercial classes of small seeded middle-american beans (Assefa et al., 2017). Furthermore, the best navy bean cultivars that are currently being processed in Zimbabwe are not tolerant to terminal drought stress (Mutari et al., 2022b).

As reported by Mutari et al. (2022b), most scientists do not simultaneously study drought tolerance, canning and nutritional quality due to high phenotyping costs, yet most of the farmers are located in drought prone areas. According to Beebe et al. (2010), about 60% of cultivated beans worldwide are grown under the risk of either terminal or intermittent drought. Most studies have investigated the effects of genotype, environment, and their interaction (GEI) on canning quality (De Lange and Labuschagne, 2001; Khanal et al., 2014; Amongi et al., 2021; Mukankusi et al., 2022) and nutritional quality (Nchimbi-Msolla and Tryphone, 2010; Amongi et al., 2021) under stress free or high yield potential conditions despite most of the farmers being located in drought prone areas. As a result, limited information is available regarding the effects of drought stress on nutritional and canning quality, and the available results are often inconclusive Mutari et al. (2022). Amongi et al. (2021) phenotyped 578 dry beans genotypes comprising of different market classes for canning and nutritional quality under optimum conditions. However, in their work, important canning quality traits such as the seed shape, uniformity, washed drained weight (WDW), percent washed drained weight (PWDW), degree of clumping and splitting were not determined. Assefa et al. (2013) identified high yielding navy bean breeding lines under drought stressed (DS) and non-stressed (NS) conditions in Ethiopia. However, the canning and nutritional quality attributes of the superior breeding lines were not reported.

Assefa et al. (2017) also screened 36 navy bean breeding lines under DS and NS conditions for two seasons and at two locations in Ethiopia. However, phenotyping for canning quality was done using 24 high yielding genotypes which had been selected from the second year's drought experiment. Thus phenotyping for canning quality was done for a single season, making it difficult

to identify genotypes with stable canning quality across seasons. In summary, given the increased prevalence of drought and micronutrient malnutrition in SSA, it is important that we identify micronutrient dense, high yielding and drought tolerant navy bean genotypes with acceptable canning quality. Therefore, the objectives of this study were to (i) investigate the effects of terminal drought stress on some agronomic, shoot, physiological, canning and nutritional quality traits in navy beans; (ii) investigate the associations among canning, nutritional, shoot, physiological and agronomic traits when grown under drought-stressed and non-stressed conditions; and (iii) identify drought tolerant genotypes with high grain yield, superior canning and nutritional quality.

5.2 Materials and methods

5.2.1 Experimental sites and weather data

The drought stressed (DS) and non-stressed (NS) field trials were carried out at Save valley experiment station (SVES) in Zimbabwe during the dry season (from April to August in both 2019 and 2020) when rainfall was unlikely. In both seasons, prior to sowing navy bean trials, the experimental fields had been previously planted with maize (*Zea mays* L.) crop. Save valley experiment station is characterised by well-drained deep (120 cm) clay loam soils, and is situated in the drier lowveld agro-ecological zone of Zimbabwe (Table 5.1). The area receives an annual average rainfall of 450 mm that is distributed mainly in the growing season (December to April). The soil micronutrient profiles of SVES are provided in Table 5.1. The daily average maximum and minimum weather parameters such as temperature (°C) and relative humidity (%) (Table 5.1) were recorded throughout the crop growing season by an automated weather station which was located near the experiment field at SVES (Table 5.1). No rainfall was received during the trial evaluation period in either season.

5.2.2 Description of plant materials used

A set of 110 navy bean genotypes were used in the study (Appendix 5.1). The initial set of germplasm comprised of 220 genotypes. However, to ensure synchronization of flowering time, the 220 genotypes were pre-assessed during the 2018 season to group the genotypes according to their maturity group.

Table 5.1 Weather conditions and soil characteristics during the trial evaluation period at Save valley experiment station, Zimbabwe (April to July, 2019 and 2020).

Parameter		2019 season				2020 season			
		April	May	June	July	April	May	June	July
Temperature (ºC)	Max	33.00	29.00	28.00	30.00	31.00	28.50	27.00	32.00
	Min	9.00	9.50	10.00	12.00	11.50	8.00	8.5.00	12.50
Relative Humidity (%)	Max	82.00	95.00	69.00	91.00	74.00	85.00	69.00	71.00
	Min	42.00	56.00	44.00	25.00	46.00	59.00	50.00	30.00
		Soil micronutrient profiles							
		2019 season	2020 season						
pH (Calcium Chloride)		5.6	5.4						
OM (%)		2.6	2.2						
N (ppm)		18.0	20.0						
P (ppm)		69.0	76.0						
Ca (mg/100g)		9.8	9.2						
Mg (mg/100g)		5.5	4.4						
K (mg/100g)		0.32	0.37						
Zn (ppm)		1.67	2.30						
Fe (ppm)		11.03	8.07						
		Global positioning system location							
		2019 season	2020 season						
Latitude		20°48′S	20°51′S						
Longitude		33°03′E	33°01′E						
Altitude (m.a.s.l)		450	453						

OM organic matter content (%), *masl* meters above sea level, *ppm* parts per million, *mg/100g* milligram equivalents per 100g, *Max* maximum, *Min* minimum.

A total of 180 genotypes were grouped in the medium maturity group (average of 100 – 103 days to physiological maturity). Thus, the 110 genotypes used in this study were randomly selected from the medium maturity group. The improved genotypes were sourced from the Alliance of Bioversity International and International Center of Tropical Agriculture (ABC) in Malawi (45 entries), ABC in Colombia (43 entries), ABC in Uganda (17 entries), Ethiopian Institute of Agricultural Research (EIAR) in Ethiopia (3 entries) and Crop Breeding Institute (CBI) in Zimbabwe (2 entries) (Appendix 5.1). The commercial navy bean cultivar Protea (G1) from CBI was used as a standard check for agronomic traits (under NS conditions only) and superior canning quality, while SMC16 (G73) was the standard check for seed Fe and Zn concentrations. SMC16 has an average seed Fe and Zn concentration of 115 and 43 ppm, respectively (Crop Breeding Institute, 2019). The cultivar Protea was developed for production under non-stressed conditions. As a result, it was not used as a standard check for agronomic traits under DS conditions. Therefore, the standard check for drought tolerance and agronomic traits under DS conditions was G40 (G68). G40 resulted from a cross between ICA Bunsi and SXB405, and was among the drought tolerant genotypes that were identified by Assefa et al. (2013). Furthermore, the cultivar ICA Bunsi (navy bean) which has good canning qualities is also called Awash-1 in Ethiopia where it was released. SXB405 (cream seeded) combines high grain yield potential with drought tolerance (Assefa et al., 2013).

5.2.3 Experimental design and procedure

One hundred and ten (110) genotypes were evaluated in two treatments, DS and NS (control) conditions. The DS and NS treatments were laid beside each other using a 10 x 11 rectangular lattice design with two replications. A 30 m buffer zone was maintained between the two treatments to minimize the seepage of moisture from the NS treatment to the DS treatment. The genotypes were hand planted in four-row plots of 2.5 m in length, with a spacing of 0.45 m between rows resulting in a gross plot area of 4.5 m^2 (2.5 m x 4 rows x 0.45 m). In each row, two seeds were planted per hole at an intra-row spacing of 0.20 m. An intra-row spacing of 0.2 m was used instead of the traditional 0.1 m since most navy bean genotypes have type III prostrate growth habit (Soltani et al., 2016). The seedlings were thinned to one plant per hill at 12 days after emergence resulting in 50 plants per plot. Compound D (N = 7%, P = 14%, K = 7%) was applied as basal fertilizer during planting in both treatments at a rate of 300 kg/ha. An overhead sprinkler irrigation system was used in both treatments. Soil moisture was monitored using tensiometers.

Two tensiometers of two different lengths (0.5 m and 1 m depths near each other per station) were installed at four stations in each treatment (DS and WW fields). In the NS treatment, soil moisture was kept at field capacity during the crop growth period. Under the DS treatment, soil moisture was kept at field capacity until 80% of the plants had flowered. After that, DS was imposed up to physiological maturity (Darkwa et al., 2016). Terminal DS was imposed by withholding irrigation water to 30% of the field capacity before re-irrigating on the basis of readings from tensiometers (Darkwa et al., 2016). Six irrigation cycles amounting to 252 mm and 246 mm, respectively (each cycle with roughly 42 mm) were applied to the DS experiments in 2019 and 2020. On the other hand, the NS treatment was kept at field capacity throughout the crop duration. As a result, 10 cycles of irrigation were applied to the NS experiments in 2019 (420 mm) and 2020 (416 mm), each cycle with roughly 42 mm). Across both treatments, ammonium nitrate (34.5% N) fertilizer was applied 4 weeks after emergence (before flowering) at a rate of 100 kg/ha. During growth, pests such as insects, diseases and weeds were controlled using insecticides, fungicides and by hand weeding, respectively.

5.2.4 Data collection

5.2.4.1 Phenotyping in drought and non-stressed treatments

At mid-pod filling, the total dry canopy biomass (CB; leaf biomass + stem biomass + pod biomass including reproductive structures) was determined in both DS and NS treatments. Canopy biomass was determined at the mid-pod filling stage when CB is at its maximum. Destructive sampling was done on a 0.5 m row segment from the two center rows in each plot with about three plants to determine the CB (Beebe et al., 2013). The leaves, stems and pods were subsequently dried in an oven at 70 ℃ for 48 hours to establish the CB in kg/ha. At mid-pod filling, leaf temperature (LT; ℃), stomatal conductance (SC; mmol m^{-2} s^{-1}) and leaf chlorophyll (LCC) content were recorded in all plots in both treatments. The LT and SC data were recorded from the surface of the uppermost fully expanded young leaf between 11:00 am to 14:00 pm using an infrared thermometer (Everest Interscience, Tucson, AZ, USA) and leaf porometer (Decagon Devices®, Pullman, WA, USA), respectively. Three readings were collected on three plants, randomly selected from each plot per replicate in both treatments. An average of the three recordings was taken to obtain one final reading per plot. Phenotyping for LT and SC was done for six days on clear, sunny days with minimal wind. Leaf chlorophyll content was measured using a soil and plant analysis development

(SPAD) chlorophyll meter (SPAD-502*Plus*, Konica-Minolta, Osaka, Japan) on two fully developed leaves of three plants in each plot. Then, the average value was calculated.

At physiological maturity, the following traits were recorded from the two center rows of each plot (net plot area of 2.025 m^2 with about 23 plants) in both DS and NS treatments: days from planting to physiological maturity (DPM), number of mature pods per plant (NMPP), number of seeds per pod (NSP), number of seeds per plant (NSPP), grain yield (GYD; kg/ha) and 100-seed weight (SW; g). The NMPP, NSP and NSPP were averaged from three randomly chosen plants per plot. Pod weight was determined by weighing in grams the weight of all the pods in each plot using a beam balance weighing scale. The DPM were recorded as the number of days after planting (from first date of irrigation) to when 95% of pods in a plot lost their green pigmentation. Grain yield which is the weight of clean seed harvested from the two center rows in each plot was measured using a grain weighing scale. The GYD was subsequently converted from grams/plot to kilograms per hectare (kg/ha) after adjusting to 12.5% moisture content. After recording GYD, 100 seeds were selected randomly from each plot harvest and weighed using a beam balance weighing scale to determine SW. The pod harvest index (PHI; %) was determined using the following formula;

$$\text{PHI (\%)} = \frac{\text{Dry weight of seed at physiological maturity (g)}}{\text{Dry weight of pods at physiological maturity (g)}} \text{ x } 100 \quad (1)$$

5.2.4.2 Determination of canning quality

Phenotyping for canning quality was done in the food laboratory at the Department of Research and Specialist Services (DR&SS) in Harare, Zimbabwe. Due to the labor and high costs associated with phenotyping for canning quality using the laboratory protocol, samples (two replicates) were only taken from the DS treatments in both seasons. The initial seed moisture content (MC; %) of each cleaned genotype sample from DS and NS treatments was obtained using a draminski moisture meter model Twist Grain Pro. Based on the seed MC (%), the quantity of bean seed (fresh) equivalent to 90 g bean grain solids required to fill each jar was determined using the formula:

$$\text{Fresh weight to yield required solids} = \frac{\text{90 g (i.e.solids required)}}{1-(\frac{MC}{100})} \quad (2)$$

where MC = moisture content. Canning quality analysis was conducted following the method described by Kelly and Cichy (2012) with minor modifications. Briefly, triplicate seed samples of

each genotype with weights equivalent to 90 g solids were weighed, placed into cotton mesh bags, soaked for 30 minutes in a stainless-steel water bath with cool water at room temperature. After soaking, the samples were weighed and blanched (hot soaked) for 30 minutes at 87 ℃ in pre-heated water containing 100 ppm Ca^{++}. Seed samples were then cooled in water at room temperature for 5 minutes, followed by the draining of water for 10 minutes, after which the bean seed samples were weighed. Hydration coefficient (HC) was calculated using the weight (g) gained by imbibition during cold soaking and blanching as follows:

$$\text{HC} = \frac{\text{Weight of hot soaked beans after cooling in cold water (g)}}{\text{Original fresh weight (g) of beans equivalent to 90 g solids}} \quad (3)$$

A HC of 1.8 is considered optimum. Bean samples were transferred into coded heat resistant console jars which were subsequently filled with hot brine sauce [1.56% (wt/vol) sugar, 100 ppm Ca^{++} and 1.3% (wt/vol) NaCl], leaving 0.5 cm headspace. Console jars were then tightly sealed and auto-claved in an auto clave for 30 minutes at 121℃. Console jars were stored for 4 weeks at room temperature prior to canning quality evaluation. After 4 weeks, console jars were weighed to establish the mass of cooked seeds in brine. Each console jar was opened and the contents were unloaded onto a number 8 mesh screen to drain the brine. The magnitude of clumping was recorded using a 1-7 visual hedonic scale (1 = very much clumping in the bottom of the can and 7 = no/very little clumping) in reference to the compact mass of beans clumped to the bottom of the jar (Uebersax and Hosfield, 1985; Warsame and Kimani, 2014). Cooked seeds were washed gentle with slow flowing tap water on a mesh screen and let to drain for 2 minutes. The seeds that remained on the mesh screen were recorded as the WDW (g) after weighing. The WDW is the mass of the thermally processed (cooked) bean, rinsed, and drained. Based on existing canning standards, the WDW for a sample of beans equivalent to 90 g solids should be 240 – 280 grams (Mutari et al., 2022b). When expressed as a percentage, the PWDW was calculated using the formula:

$$\text{PWDW (\%)} = \frac{\text{Washed drained weight (g)}}{\text{Net weight of cooked bean in brine (g)}} \text{ x } 100 \quad (4)$$

The PWDW value should be no less than 60% (Balasubramanian et al., 2000). Physical traits and appearance of the processed beans were also studied during and after the draining and rinsing of the processed bean samples. The investigated traits included uniformity of seed (1 = very variable

and 7 = very uniform seed), and degree of splitting (1 = completely broken and 7 = seeds intact without cracks) (Uebersax and Hosfield, 1985; Warsame and Kimani, 2014).

5.2.4.3 Determination of seed iron and zinc concentrations

Phenotyping for nutritional quality was done in the food laboratory at DR&SS in Harare, Zimbabwe. At physiological maturity, 30 above ground and well-filled pods were harvested randomly from the two center rows in each plot. The concentrations of Fe and Zn in the milled samples were determined using the atomic absorption spectrophotometer model Varians AA-1275 following the protocol described by Shar et al. (2002). The breeding targets of Fe and Zn are 90 ppm and 40 ppm, respectively.

5.2.5 Statistical analysis

5.2.5.1 Analysis of variance

Bartlett's chi-square test was used to test the homogeneity of residual variances between the environments before combined analysis was performed. Among the studied traits, Bartlett's test revealed heterogeneity of residual variance for GYD, DPM, LCC, LT, NMPP, NSP, PHI, SC, SW, clumping, HC and splitting. Therefore, square root transformation was applied to the above-mentioned traits to improve normality of the residuals and reduce the effects of non-additivity. We considered two environments as combinations of years (DS 2019 and DS 2020 or NS 2019 and NS 2020) for within/separate/individual irrigation treatments (DS or NS). For combined data analysis (across irrigation treatments), the year-water regime combinations (DS 2019, DS 2020, NS 2019 and NS 2020) were considered as individual environments resulting in four environments. A linear mixed effect model from which the best linear unbiased predictors [BLUPs – predicted genotype values ($\hat{G}$) and predicted genotype effects ($\hat{g}$)] for each of the studied traits were obtained was used for analysis of variance (ANOVA). In this model, incomplete blocks within replications, replications within environments, genotypes and their interactions with environments (GEI) were considered as random effects (Singh and Ceccarelli, 1995). Environments were considered as fixed effects (Singh and Ceccarelli, 1995). The following model was used:

$$Y_{ijkl} = \mu + G_i + E_j + R_{k(j)} + B_{l(jk)} + GE_{ij} + e_{ijlk} \quad (5)$$

where Y_{ijkl} = observation of the *i*th genotype in *j*-th environment and *k*th replication within environment and *I*-th incomplete block within replication and environment, μ = general mean, G_i

= random effect of the *i*-th genotype, E_j = fixed effect of environment *j*, $R_{k(j)}$ = random effect of replicate *k* nested in environment *j*, $B_{l(jk)}$ = random effect of incomplete block *I* within replicate *k* in environment *j*, GE_{ij} = random effect of genotype by environment interaction, and e_{ijlk} = error (residual) associated with observation *ijlk*. All statistical analysis was carried out using Genstat® Discovery 18th Edition (Payne et al., 2018).

5.2.5.2 Determination of broad–sense heritability

Broad-sense heritability (H^2) estimates on entry mean basis across environments for shoot, agronomic, physiological, canning and nutritional quality traits were calculated as described by Mutari et al. (2022a).

5.2.5.3 Indices of drought tolerance and association among traits

Three quantitative indices of drought tolerance were calculated using the $\hat{G}$ based on GYD under DS and NS conditions. Drought intensity index (DII), geometric mean productivity (GMP) and percentage of seed yield reduction (%SYR) due to DS were calculated as indicated by Fischer and Maurer (1978);

$$\text{DII} = \left(1 - \left(\frac{T\hat{G}_{DS}}{T\hat{G}_{NS}}\right)\right) \quad (6)$$

$$\%\ \text{SYR} = \left(1 - \left(\frac{\hat{G}_{DS}}{\hat{G}_{NS}}\right)\right) x\ 100 \quad (7)$$

$$\text{GMP} = \sqrt{\hat{G}_{DS} x\ \hat{G}_{NS}} \quad (8)$$

where $T\hat{G}_{DS}$ and $T\hat{G}_{NS}$ = average predicted genotype values for GYD of all genotypes under drought stressed and non-stressed conditions, respectively and $\hat{G}_{DS}$ and $\hat{G}_{NS}$ = predicted genotype value ($\hat{G}$) for GYD of a genotype in drought stressed and non-stressed conditions, respectively. Regarding the %SYR, stable genotypes across both DS and NS conditions have relatively low %SYR values. Genotypes with a high GMP value are desirable (Schneider et al., 1997). A ranking method was used for the overall judgement to identify desirable stress tolerant genotypes by calculating the mean rank of each genotype across multiple drought tolerance indices.

5.2.5.4 Genotype by trait associations and associations among traits

Associations [genetic correlation coefficients (r)] among the studied traits between and under DS and NS conditions were estimated directly from the data using multi-variate analyses. The genotype by trait (GT) associations were estimated based on singular value decomposition using the genotype plus genotype by environment (GGE) biplot model following Yan and Rajcan (2002). This was done in Genstat® Discovery 18th Edition (Payne et al., 2018) using the $\hat{G}$ under DS and NS environments, and $\hat{G}$ computed from across all environments. To further explore the findings in graphical form, a two-dimensional scatterplot of SYD under DS and NS conditions was completed using the $\hat{G}$ for GYD for two seasons at SVES. Vertical and horizontal lines in the scatterplot represent the trait mean in the trial under DS (x-axis) or NS (y-axis) conditions and thus dividing the genotypes into four response groups. The four groups are as follows; genotypes suitable for both DS and NS environments, those suitable for DS environments; genotypes suitable for NS environments; and genotypes not suitable for either NS or DS environments.

5.3 Results

5.3.1 Effect of genotype, environment and genotype x environment interaction (G x E) on physiological, agronomic, shoot and nutritional quality traits

The combined ANOVA of physiological traits for 110 genotypes across four environments (year-water regime combinations - DS 2019, DS 2020, NS 2019 and NS 2020) are presented in Table 5.2. Significant ($p < 0.001$; $p < 0.05$) genotypic (Gen) and environmental (Env) differences were observed for LCC, LT and SC across environments. The GEI effects under both environments (DS as well as NS) were also significant ($p < 0.001$; $p < 0.05$) for all the studied physiological traits. Most of the variance observed, as indicated in Table 5.2, was attributed to GEI effect rather than the genotypic main effect. The coefficient of variation (CV) across environments ranged from 10.5% (LT) to 23.3% (LCC) (Table 5.2).

Table 5.2 Restricted maximum likelihood (REML) combined analysis for physiological traits of 110 navy bean genotypes under drought stressed and non-stressed conditions over two seasons (2019 and 2020) at Save valley experiment station, Zimbabwe.

		Wald statistic of traits		
Source of variation	DF	LCC	LT (°C)	SC (mmol m^{-2} s^{-1})
Gen	109	317.73***	153.93*	976.63***
Env	3	810.64***	2556.42***	3209.18***
Gen*Env	327	416.54**	362.33*	2020.15***
Env.Rep	4	21.15***	304.23***	121.52***
Env.Rep.Block	80	91.69	148.02***	145.54***
CV (%)		23.29	10.46	22.05

Rep replication, *Env* environment, *Gen* genotype, *Rep(Env)* replications nested in environments, *Block(Env*Rep)* incomplete block within an environment, *Gen*Env* genotype by environment interaction, *Df* degrees of freedom, *CV* coefficient of variation, *LCC* leaf chlorophyll content, *LT* leaf temperature, *SC* stomatal conductance, *, **, *** indicate significance at P ≤ 0.05, P ≤ 0.01, and P ≤ 0.001, respectively. **NB**: In REML combined analysis, the year-water regime combinations (DS 2019, DS 2020, NS 2019 and NS 2020) were considered as individual environments resulting in four environments.

The ANOVA of shoot, agronomic and nutritional quality traits for 110 genotypes evaluated in four environments are presented in Table 5.3. Significant ($p < 0.001$; $p < 0.05$) genotypic (Gen) and environmental (Env) differences were observed for shoot, agronomic and nutritional quality traits across environments. The GEI effects under both environments were also significant ($p < 0.001$; $p < 0.05$) for all the studied traits except for PHI. Most of the variance observed, as indicated in Table 5.3, was attributed to genotypic main effect rather than the GEI. Coefficient of variation (CV) for GYD across environments was 50.5%, while other CVs ranged from 2% (DPM) to 49.8% (NSPP) (Table 5.3).

5.3.2 Effect of genotype, environment and genotype x environment interaction (G x E) on canning quality traits

The significant tests and Wald statistic values of the canning quality traits and 110 genotypes evaluated in two DS environments (year – DS 2019 and DS 2020) are presented in Table 5.3. Genotypic differences were highly significant ($p < 0.001$) with respect to clumping, HC, splitting, PWDW, WDW and uniformity. The environment effects were significant ($p < 0.001$; $p < 0.05$) for all the canning quality traits except for PWDW and WDW.

Table 5.3 Restricted maximum likelihood (REML) combined analysis for shoot traits, seed yield, yield-attributing traits, canning and nutritional quality traits of 110 navy bean genotypes under drought stressed and non-stressed conditions over two seasons (2019 and 2020) at Save valley experiment station, Zimbabwe.

Wald statistic of shoot, agronomic and nutritional quality traits across environments (drought stressed and non-stressed conditions)											
Source of variation	DF	GYD (kg/ha)	NMPP	NSP	NSPP	DPM	SW (g)	CB (kg/ha)	PHI (%)	Fe (ppm)	Zn (ppm)
Gen	109	368.66***	366.89***	498.69***	444.13***	4749.26***	921.31***	195.79***	170.52***	1171.59***	2027.29***
Env	3	235.21***	300.48***	70.84***	237.67***	52567.59***	8.83*	35.96***	34.23***	71.87***	242.83***
Gen*Env	327	555.11***	429.97**	454.54***	432.45**	8854.50***	616.43***	411.14*	382.68	680.84***	706.52***
Rep(Env)	4	53.65***	41.63***	19.70***	45.27***	3483.76***	12.75*	20.51***	2.69	122.91***	298.54***
Block(Env*Rep)	80	108.65*	148.50*	103.62	127.49**	75.15	86.43	123.88**	108.67*	291.38***	179.62***
CV (%)		50.50	44.00	15.20	49.80	2.00	26.40	45.70	19.00	11.00	7.80

Wald statistic of canning quality traits under terminal drought stress conditions							
Source of variation	DF	Clumping	HC	Splitting	PWDW (%)	WDW (g)	Uniformity
Gen	109	5280.90***	165985.38***	3044.76***	1352020.45***	233993.86***	7577.43***
Env	1	928.37***	6.98**	798.66***	0.30	0.01	684.14***
Gen*Env	109	0.53	12.46	0.67	0.01	1.61	0.82
Rep(Env)	2	5195.89***	6493.17***	4327.37***	57720.45***	2425.76***	4680 30***
Block(Env*Rep)	40	35.99	1400.52***	424.56***	5917.73***	90.31***	628.64***
CV (%)		8.51	3.59	16.70	0.30	1.38	10.60

Rep replication, *Env* environment, *Gen* genotype, *Rep(Env)* replications nested in environments, *Block(Env*Rep)* incomplete block within an environment, *Gen*Env* = genotype by environment interaction, *Df* degrees of freedom, *CV* coefficient of variation, *GYD* grain yield, *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seed per plant, *DPM* days to physiological maturity, *SW* 100-seed weight, *CB* canopy biomass, *PHI* pod harvest index, *HC* hydration coefficient, *WDW* washed drained weight, *PWDW* percentage washed drained weight, *Fe* iron, *Zn* zinc, *, **, *** indicate significance at $P \leq 0.05$, $P \leq 0.01$, and $P \leq 0.001$, respectively.

NB: In the first REML combined analysis (table on top), the year-water regime combinations (DS 2019, DS 2020, NS 2019 and NS 2020) were considered as individual environments resulting in four environments. In the second REML combined analysis with canning quality traits (bottom table) which were only recorded in the DS experiment, the years (DS 2019 and DS 2020) were considered as individual environments resulting in two environments.

However, the GEI effects were not significant for all the canning quality traits. Coefficient of variation (CV) for WDW under DS environments was 1.38%, while other CVs ranged from 0.30% (PWDW) to 16.70% (degree of splitting) (Table 5.3).

5.3.3 Performance of genotypes under drought stressed and non-stressed conditions

5.3.3.1 Predicted genotype values and genotypic effects for nutritional and canning quality traits

The predicted genotype values ($\hat{G}$) and predicted genotypic effects ($\hat{g}$) of the genotypes regarding canning and nutritional quality traits are presented in Table 5.4 and Appendix 5.2. Variability was observed among the genotypes for seed Fe and Zn concentrations, WDW, PWDW, uniformity, degree of clumping, and degree of splitting. Among the best 12 (G70, G35, G91, G93, G29, G50, G108, G20, G30, G53, G19 and G105) yielding genotypes under DS conditions, two (G50 and G108) presented desirable positive $\hat{g}$ for HC under DS conditions (Table 5.4). In addition, all the best 12 yielding genotypes under DS had positive (desirable) $\hat{g}$ for WDW and PWDW. Furthermore, all of them showed positive (desirable) $\hat{g}$ for uniformity (except for G70), degree of clumping (except for G20), and degree of splitting (except for G70, G35, G29, G20 and G105) (Table 5.4). Regarding seed Zn content under DS and NS conditions, all the top 12 high yielding genotypes had desirable positive $\hat{g}$ except for G53 under both conditions. On the other hand, regarding seed Fe content under DS and NS conditions, all the top 12 yielding genotypes had positive (desirable) $\hat{g}$ except for G35, G29, G50 and G30 under both conditions (Table 5.4).

The $\hat{G}$ for HC of all the genotypes over 2 seasons ranged from 0.5 (G87) to 2.1 (G75, G96 and G102) under DS treatments. Regarding the degree of splitting, $\hat{G}$ ranged from 1.0 (G11; G39; G40; G93; G73; G75; G80) to 5.0 (G81), and from 1.0 (G20; G36; G63) to 5.0 (G7; G81; G109) under DS conditions, respectively. The $\hat{G}$ under DS conditions ranged from 224.8 g (G1) to 310 g (G46) for WDW and from 1.0 (G39) to 5.9 (G82) for uniformity. G63 had the highest degree of clumping (2.0) and G37, G79, G92 and G109 had the lowest (7.0). Generally, the standard check cultivar Protea (G1) exhibited poor canning quality under DS conditions compared to the test genotypes. Terminal drought stress significantly affected HC and the degree of splitting as evidenced by few genotypes that met the required industrial canning quality standards for these three traits under DS conditions.

Table 5.4 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 12 highest yielding and the 6 lowest yielding genotypes in drought treatment over two seasons (2019 and 2020), for canning (under drought stressed conditions) and nutritional quality (under drought stressed and non-stressed conditions) traits at Save valley experiment station, Zimbabwe.

Best 12 yielding genotypes under drought stress																				
Geno	DS												Fe (ppm)				Zn (ppm)			
	HC		WDW (g)		PWDW (%)		Uniformity		Clumping		Splitting		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G70	1.5	-0.1	229	4.4	56.2	1.4	1.4	-0.6	**4.0**	**1.3**	1.5	-0.7	**113.8**	**44.5**	**120.3**	**40.0**	39.8	12.4	42.3	7.0
G35	1.4	-0.2	**254**	**30.3**	**64.2**	**9.0**	3.1	0.5	**4.8**	**1.5**	2.3	-0.4	76.5	-11.8	61.3	-19.0	38.3	6.0	37.0	1.4
G91	1.3	-0.3	**246**	**22.0**	**60.5**	**5.7**	**4.4**	**2.2**	**6.0**	**3.2**	4.5	2.2	91.8	14.7	87.3	14.1	37.0	4.0	37.3	2.8
G93	1.2	-0.4	231	6.6	56.2	1.9	**3.9**	**2.3**	**4.0**	**1.2**	4.0	2.3	93.5	22.4	93.3	13.0	40.0	8 2	39.3	3.8
G29	1.5	-0.2	233	7.9	57.5	2.2	2.9	0.2	3.0	0.2	2.0	-0.9	83.8	-7.1	73.8	-14 9	40.0	8 9	41.3	5.1
G50	1.7	0.1	233	7.9	57.3	2.2	**4.6**	**2.2**	**6.8**	**4.2**	4.8	2.2	79.8	-0.25	76.3	-4.1	39.0	10.0	41.3	5.8
G108	1.7	0.1	**276**	**51.1**	**67.8**	**13.1**	**4.4**	**2.3**	**4.0**	**1.3**	2.5	0.3	96.0	31.0	96.3	16.0	42.8	12.9	43.3	8.0
G20	1.0	-0.5	237	13.1	58.0	3.3	2.1	0.1	2.3	-0.9	1.0	-1.9	99.0	18.4	98.3	14.2	45.0	11.1	45.0	10.1
G30	1.4	-0.2	**254**	**29.6**	**64.2**	**9.0**	3.1	0.7	**4.8**	**1.6**	2.3	-0.4	83.0	-5.5	85.5	-20.8	38.3	6 3	41.5	0.1
G53	1.0	-0.6	230	5.6	56.2	1.6	**4.1**	**2.1**	**6.8**	**4.1**	4.3	2.1	98.5	21.2	100.3	21.0	31.3	-0.5	32.3	-4.0
G19	1.2	-0.4	**256**	**31.6**	**62.7**	**8.1**	**4.1**	**2.2**	**5.8**	**3.3**	4.3	2.3	81.3	3.6	79.8	-9.9	43.8	13.2	45.8	5.0
G105	1.6	-0.1	**256**	**30.7**	**63.2**	**8.0**	2.9	0.4	3.0	0.3	2.0	-0.6	101.3	39.7	94.8	10.0	39.3	7.0	38.3	0.0
Lowest 6 yielding genotypes under drought stress																				
G94	1.2	-0.4	**292**	**67.9**	**71.5**	**17.3**	1.9	0.3	**4.0**	**1.3**	**4.0**	**2.3**	101.3	42.1	**110.8**	**25.1**	45.8	19.0	49.3	8.9
G67	1.5	-0.2	**254**	**29.5**	**64.4**	**9.1**	3.4	0.7	**4.5**	**1.7**	2.5	-0.2	98.8	21.2	93.3	13.0	49.5	22.5	53.3	17.9
G10	1.2	-0.5	**284**	**59.7**	**70.4**	**15.1**	2.9	0.2	3.0	0.2	2.0	-0.9	99.0	26.3	102.8	8.1	42.8	12.8	44.8	5.1
G23	1.1	-0.5	**270**	**45.4**	**66.**	**11.5**	**4.4**	**2.1**	**6.0**	**3.1**	**4.5**	**2.1**	90.8	9.9	89.3	-17 9	37.5	2.7	36.3	-2.0
G98	1.2	-0.4	**290**	**65.8**	**71.0**	**16.7**	1.9	0.3	**4.0**	**1.2**	2.0	0.2	101.5	37.6	**112.3**	**25.0**	47.8	19.7	49.8	12.8
G106	**2.0**	**0.8**	**296**	**71.5**	**73.3**	**18.0**	**4.9**	**2.1**	**4.0**	**1.1**	2.0	-0.8	96.3	38.7	106.3	17.0	39.0	9.7	40.8	2.9
Mean	1.4		257.0		63.4		3.3		4.5		2.4		97.1(1.4)		95.7		42.7(0.9)		44.2	
H^2 (%)	99.4		99.3		99.2		98.6		98.4		97.3		52.7		29.6		59.0		61.0	
LSD	0.04		4.95		0.27		0.49		0.53		0.56		20.12		6.33		7.94		2.80	

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *HC* hydration coefficient, *WDW* washed drained weight, *PWDW* percentage washed drained weight, *Fe* iron, *Zn* zinc, ppm parts per million, *DS* drought stressed, *NS* non-stressed, *LSD* Least significant difference (0.05), H^2 broad-sense heritability. The value in brackets under the mean which corresponds to Fe and Zn represents the percentage (%) increase and decrease respectively in drought stressed conditions. **NB:** Values in bold were above the breeding target and the respective genotype outperformed the standard check

Overall, 11.8%, 56.4%, 71.8%, 46.6%, 78.2% and 12.7% of the test genotypes had values above the breeding target and greater Ĝ for HC, WDW, PWDW, uniformity, degree of clumping and degree of splitting under DS conditions, respectively in comparison to the check (G1). Some of the entries (G20, G10, G95 and G107) which had very low Ĝ for HC (less than 1.2) were prone to clumping. Seed Fe and Zn concentrations varied significantly among the test genotypes under both DS and NS conditions. The Ĝ for seed Fe ranged from 72.3 (G34) to 120 ppm (G37 and G84) under DS conditions and 61.3 (G35) to 122.3 ppm (G102) under NS conditions. Seed Zn ranged from 31.3 (G53) to 60.8 ppm (G38) under DS conditions and 31.8 (G54) to 68.3 ppm (G38) under NS conditions. About, 6.4% of the test genotypes (G21, G38, G42, G46, G76, G84 and G101) had seed Zn concentrations greater than the standard check (G73 - 50.5 ppm) and above the breeding target (40 ppm) under DS conditions. The seed Zn concentrations within this group ranged from 51.5 (G76, G84 and G101) to 60.8 ppm (G38). On the other hand, 17.3% of the evaluated genotypes had seed Fe concentrations above the standard check (G73 – 105.5 ppm) and breeding target (90 ppm) under DS conditions. These genotypes had seed Fe concentrations ranging from 106.6 (G74) to 120.8 ppm (G37 and G71). Notably, seed Fe concentration increased by 1.4% in the DS environments, whereas seed Zn concentration decreased by 0.9% (Table 5.4).

Generally, the H^2 estimates for canning quality traits were high, ranging from 97.3 (split) to 99.4% (HC) under DS conditions (Table 5.4). As for nutritional quality traits, seed Zn had moderate to high H^2 estimates under DS (59%) and NS (61%) treatments, respectively (Table 5.4). Seed Fe had low to moderate H^2 estimates under NS (29.6%) and DS (59.0%) treatments, respectively (Table 5.4).

5.3.3.2 Predicted genotype values and genotypic effects for agronomic, shoot and physiological traits

The Ĝ and ĝ of the genotypes regarding agronomic, shoot and physiological traits under both DS and NS treatments are presented in Table 5.5 and Appendix 5.3 (agronomic traits) and Table 5.6 and Appendix 5.4 (shoot and physiological traits). Phenotypic variability was observed among the study genotypes with respect to GYD, NMPP, NSPP, SW and PHI under DS and NS environments. Among the 10 (G91, G93, G29, G50, G108, G20, G30, G53, G19 and G105) highest yielding genotypes under DS, all of them showed positive (desirable) ĝ for GYD under DS conditions and SW under NS conditions (Table 5.5).

Table 5.5 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 10 highest yielding and 6 lowest yielding genotypes in terminal drought stress treatment over two seasons (2019 and 2020), for agronomic traits evaluated under terminal drought stressed and non-stressed conditions at Save valley experiment station.

Best 10 yielding genotypes under terminal drought stress environment																								
Geno	GYD (kg/ha)				NMPP				NSP				NSPP				DPM				SW (g)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G91	**2067**	**874**	1663	-1867	**25.0**	**-8.0**	32.0	-22.4	7.0	-0.2	7.0	-0.7	**122**	**-22.0**	124	-112	103	1	113	8	**21**	**-6.0**	**22**	**2**
G93	**2081**	**697**	2330	-11	**38.0**	**-0.4**	26.0	-9.3	6.0	-1.2	7.0	-0.2	**113**	**-12.2**	101	-47	103	0	110	0	**25**	**2.0**	**27**	**4**
G29	**2115**	**553**	**2541**	**123**	**41.0**	**5.3**	38.0	-2.6	8.0	-0.1	7.0	-0.7	**139**	**30.3**	133	-25	103	1	107	-2	**22**	**-0.3**	**24**	**5**
G50	**2196**	**1558**	1422	-1582	**44.0**	**27.0**	36.0	-14.9	7.0	0.1	**7.0**	**0.5**	**156**	**70.9**	74	-92	99	-4	109	0	**24**	**3.0**	21	2
G108	**2219**	**666**	2089	-1093	**28.0**	**-17.5**	**44.0**	**-12.1**	6.0	-0.4	**8.0**	**-0.3**	**115**	**-49.9**	169	-104	104	0	109	0	20	-3.0	20	1
G20	**2244**	**2135**	1811	257	15.0	-25.7	30.0	-5.3	6.0	-1.5	6.0	-1.8	38	-75.7	72	-107	102	1	108	0	**29**	**0.3**	**52**	**33**
G30	**2289**	**2446**	2322	-756	**34.0**	**-10.8**	**47.0**	**1.9**	7.0	0.0	6.0	0.2	**92**	**-16.3**	171	5.6	102	0	108	-1	**23**	**1.0**	21	3
G53	**2448**	**2017**	1959	-447	**25.0**	**-6.5**	34.0	-7.4	6.0	-1.2	6.0	-0.3	80	-13.9	109	-51	102	0	108	-2	25	2.0	26	4
G19	**2526**	**1451**	**2515**	**-1066**	**26.0**	**-17.1**	27.0	-10.4	7.0	-0.5	7.0	0.0	**85**	**-61.2**	95	-91	103	1	109	0	**24**	**3.0**	**23**	**5**
G105	**2619**	**1162**	**2933**	**124**	**37.0**	**-0.3**	34.0	-11.9	7.0	-0.1	**7.0**	**-0.2**	**158**	**10.8**	139	-37	102	-1	110	-1	**23**	**-0.8**	**25**	**3**
Lowest 6 yielding genotypes under terminal drought stress environment																								
G94	493	-565	1830	-989	13.0	-18.7	34.0	-5.6	5.0	-2.1	6.0	-1.7	41	-75.9	112	-76	103	0	113	5	**27**	**3.0**	**24**	**0**
G67	507	-289	941	-1211	15.0	-9.8	23.0	-11.8	7.0	-0.5	5.0	-1.2	45	-22.7	72	-82	103	0	110	3	**23**	**-2.0**	21	1
G10	679	-601	874	-1579	12.0	-28.8	6.0	-20.6	5.0	-1.9	4.0	-0.6	23	-101.0	11	-131	102	1	109	3	**36**	**2.0**	**55**	**38**
G23	685	-237	1215	-1117	7.0	-24.0	11.0	-23.4	5.0	-1.3	6.0	1.5	17	-86.0	35	-116	102	-1	109	0	**27**	-9.0	**40**	14
G98	744	-220	**2815**	**-1239**	14.0	-19.1	**46.0**	**6.6**	7.0	-1.2	**7.0**	**-0.2**	67	-62.5	95	-40	103	1	109	-1	19	-11.0	18	3
G106	748	-608	1515	-1347	**30.0**	**-18.0**	**44.0**	**-6.9**	6.0	-1.4	6.0	-1.6	72	-59.6	77	-114	104	1	115	6	20	-8.0	**23**	**1**
Mean	1393		1940		22.0		29.9		6.2		6.4		75.9		106 9		102		109.6		24.9		26	
H^2	42.1		25		60.0		33.0		63.0		53		66		46		29		15		80		85	
LSD	745 3		1142.0		13.3		18.2		1.4		1.3		49.2		75.2		ns		1.0		4.0		5.7	

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *GYD* seed yield, *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100-seed weight, *DS* drought stressed, *NS* non-stressed, *LSD* least significance difference at 0.05, H^2 Broad-sense heritability (%), ns not significant. **NB:** Values in bold were above the breeding target and the respective genotype outperformed the standard check.

Table 5.6 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 10 highest yielding and 6 lowest yielding genotypes in terminal drought stress treatment over two seasons (2019 and 2020), for shoot and physiological traits evaluated under terminal drought stress and non-stressed conditions at Save valley experiment station.

Best 10 yielding genotypes under terminal drought stress environment																				
Geno	GYD	LCC				LT				SC				CB				PHI			
	DS	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G91	**2067**	36.6	-3.5	41.8	-5.5	26.8	1.9	18.9	-0.5	68.9	15.6	152.8	11.0	**2550**	**-496**	2325	-2094	63.3	2.5	69.6	-8.0
G93	**2081**	39.6	3.7	31.2	-14.6	23.3	0.5	20.8	1.7	77.4	43.7	155.7	16.9	**3375**	**323**	**2775**	**-97**	**72.9**	**6.4**	65.8	-8.2
G29	**2115**	**36.4**	**3.0**	**38.5**	**-13.0**	**29.4**	**4.2**	**19.8**	**-0.4**	**43.3**	**-42.5**	**183.6**	**44.9**	**4200**	**1112**	2850	22	57.7	7.8	75.8	-7.0
G50	**2196**	29.6	1.0	43.9	0.9	25.6	4.2	19.3	2.2	25.5	-65.5	97.1	-30.0	**3525**	**2089**	1425	-2159	**68.2**	**-2.5**	66.4	0.4
G108	**2219**	38.3	-0.3	34.6	-12.0	27.0	2.7	18.2	1.5	56.9	-0.5	158.5	-4.9	**2400**	**-853**	2850	-1010	**64.1**	**-0.7**	73.9	-16.1
G20	**2244**	31.5	0.9	42.4	-4.0	27.8	2.8	19.5	1.5	120.8	11.4	200.5	58.8	2175	-1026	2850	920	59.8	-5.7	67.1	-16.2
G30	**2289**	35.4	-5.8	40.3	-9.7	27.5	1.9	20.7	1.7	51.9	-8.6	110.9	-8.5	**2265**	**-351**	3300	-54	63.1	2.0	64.4	-3.6
G53	**2448**	6.8	-32	25.2	-10.2	26.5	2.3	20.8	2.2	34.7	-42.1	155.2	6.8	1950	-242	2115	-1037	67.0	8.6	66.1	-2.7
G19	**2526**	**34.6**	**-8.3**	**45.0**	**-2.8**	**26.9**	**2.1**	**18.2**	**-2.0**	**53.6**	**-51.3**	**158.5**	**-2.6**	**2700**	**-748**	1875	-1068	62.0	-1.7	70.9	-23.4
G105	**2619**	**39.9**	**4.8**	**39.7**	**-5.9**	**26.8**	**2.5**	**19.4**	**-0.4**	**70.1**	**-41.1**	**146.2**	**1.5**	**3705**	**176**	**2925**	**-333**	**69.8**	**1.4**	74.1	-9.6
Lowest 6 yielding genotypes under terminal drought stress environment																					
G94	493	33.8	-4.7	34.9	-9.8	26.2	3.2	19.9	-0.1	66.5	-81.5	76.5	-71.6	1140	-1363	2475	-223	54.2	-4.9	69.2	-25.9
G67	507	33.6	-3.4	35.5	-10.1	25.1	0.9	21.8	2.6	69.4	24.9	140.4	-18.4	1281	-585	1125	-1539	57.3	-14.7	83.0	-19.1
G10	679	27.5	4.8	43.9	-3.3	34.1	8.7	22.8	1.4	86.6	62.4	141.7	35.7	1494	-1602	1650	-1760	61.5	5.4	46.5	-22.7
G23	685	23.6	-2.8	35.0	-26.3	27.7	3.3	20.7	2.4	62.4	13.3	109.2	-29.4	1215	-1378	2010	-240	52.5	-4.4	66.4	-18.9
G98	744	**29.3**	**1.0**	**42.4**	**-5.9**	**27.8**	**3.6**	**22.6**	**3.7**	**78.4**	**49.3**	**126.9**	**-79.5**	1560	-964	2925	-138	64.1	0.9	62.4	-21.6
G106	748	42.6	7.8	45.9	-0.7	27.7	4.5	19.4	1.5	76.0	-9.4	109.3	28.8	**2355**	**-920**	2415	-1372	49.8	-11.2	52.1	-30.1
Mean	1393.0	23.1		39.6		26.3		19.6		26.6		135.0		2110.0		2403		61.9		65.0	
H^2 (%)	42.1	31.0		33.0		27.0		21.0		26.0		31.0		51.1		27.8		21.7		8.1	
LSD	745.3	13.1		9.4		4.1		26		28.7		32.5		1173.0		ns		12.3		20.6	

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *GYD* seed yield (kg/ha), *LCC* leaf chlorophyll content, *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%), *DS* drought stressed, *NS* non-stressed, ns not significant, *LSD* least significance difference at 0.05 , H^2 broad-sense heritability. **NB:** Values in bold were above the breeding target and the respective genotype outperformed the standard check.

However, among them, only G29, G20 and G105 had positive ĝ for SYD under NS conditions. High yielding genotypes such as G29 and G50 had positive (desirable) ĝ for NMPP and NSPP, under DS conditions (Table 5.5). All the highest yielding genotypes expressed positive ĝ for DPM under DS conditions except for G50 and G105. Among the best and lowest yielding genotypes under DS conditions, none of them had desirable negative ĝ for LT under DS conditions (Table 5.6). High yielding genotypes presented desirable positive ĝ for SC (G91, G93 and G20), CB (G93, G29, G50 and G105), PHI (G91, G93, G29, G30, G53 and G105), and LCC (G93, G29, G50, and G20) under DS conditions (Table 5.6). The Ĝ ranged for NSPP from 15.3 (G51) to 156.3 (G50), and from 11.2 (G10) to 243.2 (G59); for DPM from 99 (G50) to 104 (G106 and G87), and from 106 (G2) to 115 (G95 and G106); for SW (g) from 15.3 (G85) to 52.5 (G17), and from 16 (G85) to 54.8 (G10) under DS and NS treatments, respectively (Table 5.5 and Appendix 5.3). The Ĝ for NSP ranged from 3 (G9) to 8 (G68) under DS and from 4 (G10) to 8 (G72) under NS conditions. Furthermore, the Ĝ for GYD (kg/ha) among 110 genotypes varied from 494 (G94) to 2619 (G105), and 615 (G22) to 3344 (G103) under DS and NS conditions, respectively. Thus, the range in GYD was substantially wide under DS and NS treatments. Furthermore, G3, G11, G12, G16, G19, G20, G24, G35, G40, G41, G50, G53, G62, G84, G101, G102 and G108 exhibited an increase in GYD under DS in comparison to NS conditions (Table 5.5 and Appendix 5.3). The Ĝ for NMPP ranged from 9 (G62) to 43.5 (G50) under DS and 5.8 (G10) to 47 (G30) under NS conditions. The Ĝ for PHI (%) ranged from 49 (G78) to 75.4 (G85) under DS and from 42.9 (G11) to 84 (G38 and G86) under NS conditions (Table 5.6 and Apendix 4.4).

As for CB (kg/ha), Ĝ ranged from 1125 (G76) to 4200 (G29) under DS and from 1125 (G67) to 4050 (G59) under NS conditions. The Ĝ ranged for LCC from 11.6 (G35) to 45.2 (G41), and from 20.7 (G2) to 46.9 (G77); for SC (mmol m^{-2} s^{-1}) from 14.8 (G11) to 143.8 (G62), and from 29.2 (G25) to 202.7 (G45); for LT (°C) from 22.8 (G56) to 34.1 (G10), and from 17.5 (G13) to 22.8 (G10) under DS and NS treatments, respectively (Table 5.6 and Table 5.4). Generally, the standard check G68 performed better than 50% of the test genotypes under DS conditions with respect to NSPP, CB (kg/ha) and PHI (%). For example, only 40, 39 and 43.6% of the entries had superior Ĝ for NSPP, CB and PHI under DS conditions, respectively in comparison to the standard check. On the other hand, 50.9 and 74.5% of the entries had superior Ĝ for NMPP and SW under DS conditions, respectively in comparison to the standard check G68. Only 25.5% of the entries had

GYD levels above the standard check (G68 – 1593 kg/ha) under DS conditions (Figure 5.1, Table 5.5 and Appendix 5.3).

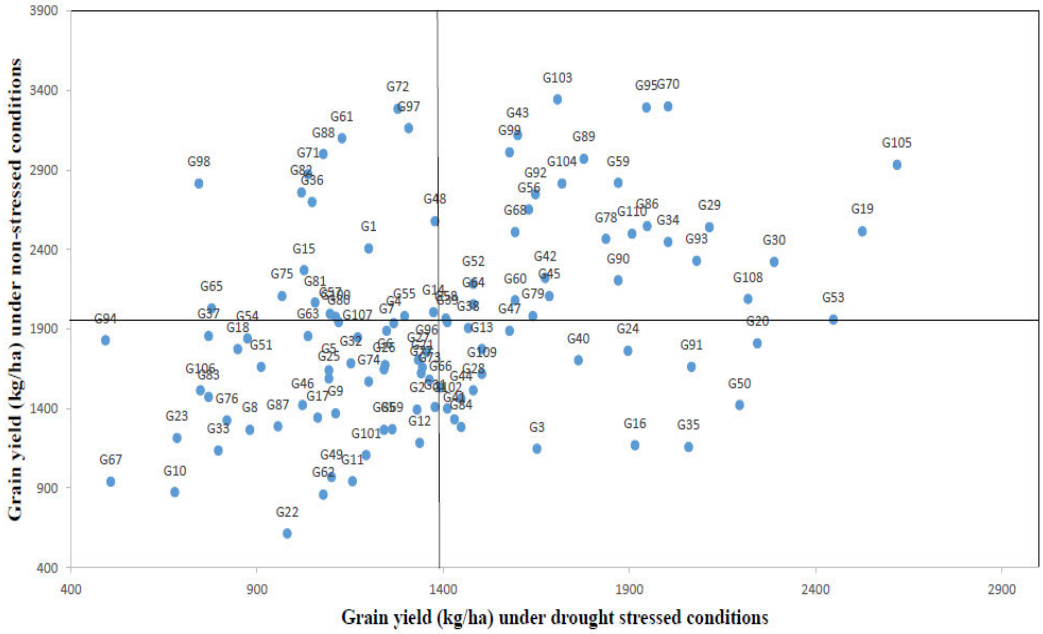

Figure 5.1 Classification of 110 navy bean genotypes based on average grain yield (kg/ha) of genotypes under drought stressed and non-stressed environments at Save valley experiment station. Best yielding genotypes under both environments are located in the upper, right-hand quadrant.

The eight highest yielding entries under DS conditions were G29, G50, G108, G20, G30, G53, G19, and G105 (Figure 5.1, Table 5.5 and Appendix 5.3). Genotypes G29, G19 and G105 were also good performers under NS conditions, with GYD ranging from 2515 (G19) to 2933 kg/ha (G105) in comparison to the standard check for NS conditions (G1 - 2407 kg/ha) (Figure 5.1, Table 5.5 and Appendix 5.3). In addition, all the top eight yielding genotypes under DS had superior PHI than the standard check (G68) even though they were not significantly different from each other. However, among the top eight yielding genotypes under DS conditions, G29, G50, G108, G30, G19 and G105 had more CB in comparison to the standard check G68 under DS conditions. Broad-sense heritability estimates were higher in DS conditions for GYD, NSP, NMPP, NSPP, CB, LT and PHI, while SW, LCC and SC presented higher values under NS conditions (Table 5.5 and Table 5.6). Under DS conditions, H^2 estimates ranged from low (PHI – 22%, SC – 26, LT – 27%

and DPM - 28.8%), moderate (LCC – 31%, SC – 31%, GYD - 42.1% and CB - 51.1%) to high (NMPP - 60.4%, NSP - 63.4%, NSPP - 65.7% and SW - 79.7%) (Table 5.5 and Table 5.6). On the other hand, under NS conditions, H^2 estimates ranged from low (PHI, LT, CB, GYD, DPM, CB and PHI), moderate (LCC, SC, NMPP, NSP, NSPP and CB) to high (SW) (Table 5.5 and Table 5.6).

5.3.4 Drought stress indices and performance of genotypes under combined environments

5.3.4.1 Predicted genotype values and genotypic effects for agronomic traits, shoot traits, and physiological traits

The $\hat{G}$ and $\hat{g}$ of the genotypes regarding agronomic, shoot and physiological traits under combined environments (DS plus NS conditions) are presented in Table 5.7 and Appendix 5.5 (agronomic traits) and Table 5.8 and Appendix 5.6 (shoot and physiological traits). All the best 10 yielding genotypes under DS conditions had positive (desirable) $\hat{g}$ for SW under combined environments (Table 5.7). Furthermore, high yielding genotypes under DS conditions presented desirable positive $\hat{g}$ for GYD (G29, G43, G70 and G105), NMPP (G30, G59, G43, G95, and G70), NSP (G30, G29, G59, G43, G19, and G70), NSPP (G30, G59, G43, and G101) (Table 5.7). However, the highest yielding genotype (G105) under combined environments expressed a negative $\hat{g}$ for DPM. Among the 10 highest yielding genotypes under DS conditions, only two (G105 and G70) of them exhibited positive (desirable) $\hat{g}$ for PHI under combined environments, and the low yielding genotype G62 also showed a positive $\hat{g}$ (Table 5.8). In addition, high yielding genotypes under DS conditions expressed desirable positive $\hat{g}$ for LCC (G89 and G70), SC (G29, G59, G43, G103, G95, G70 and G105), and CB (G29, G59, G43 and G70) under combined environments (Table 5.8).

Significant variation was observed among 110 genotypes regarding GYD, NMPP, NSP, NSPP, DPM and SW (Table 5.7 and Appendix 5.5), CB, LCC, SC, LT and PHI across environments (Table 5.8 and Appendix 5.6). Combined $\hat{G}$ for GYD over 2 seasons at SVES ranged from 724 (G67) to 2652 kg/ha (G70) (Table 5.7 and Appendix 5.5). On average, GYD, NMPP, NSPP, DPM and SW were 28.2, 26.4, 29.8, 6.9 and 2.7% lower, respectively, under DS conditions compared to NS conditions (Table 5.7). On the other hand, CB, PHI, LCC and SC were 12.0, 4.8, 41.7 and 80.3% lower, respectively, under DS conditions compared to NS conditions (Table 5.8). Leaf temperature increased by 34.2% in the DS environments (Table 5.8).

Table 5.7 Grain yield-based drought tolerance indices and predicted genotype values (Ĝ) and genotypic effects (ĝ) of 10 highest yielding and 6 lowest yielding genotypes for agronomic traits evaluated under combined environments at Save valley experiment station in 2019 and 2020.

Best 10 performing genotypes across environments															
Geno	GYD (kg/ha)		NMPP		NSP		NSPP		DPM		SW (g)		GMP	%SYR	MR
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ			
G30	2306.0	-756	41	1.9	7.0	0.2	132.0	5.6	105.0	-1.0	22	3.1	2305.0	1.4	**15**
G29	2328.0	123	40	-2.6	7.0	0.3	136.0	-25.3	105.0	-2.0	23	4.9	2318.0	16.8	**21**
G59	2344.0	-100	40	6.4	7.0	0.8	174.0	60.6	106.0	0.0	20	3.1	2296.0	33.7	**38**
G43	2359.0	255	29	6.1	7.0	0.0	115.0	25.0	106.0	0.0	23	6.7	2233.0	48.7	50
G89	2374.0	-517	31	-4.3	7.0	-0.5	129.0	-19.6	106.0	3.0	22	3.5	2298.0	40.1	**12**
G19	2520.0	-1066	27	-10.4	7.0	0.0	90.0	-91.2	106.0	0.0	24	5.5	2520.0	-0.4	**12**
G103	2526.0	-234	44	-9.1	6.0	-0.3	179.0	-62.3	105.0	0.0	23	1.3	2389.0	49.0	48
G95	2619.0	-423	38	1.6	5.0	-1.7	115.0	-28.3	109.0	7.0	26	4.2	2531.0	49.0	**42**
G70	2652.0	1519	29	19.2	7.0	0.2	124.0	101.0	106.0	0.0	24	5.3	2571.0	39.3	**39**
G105	2776.0	124	35	-11 9	8.0	-0.2	149.0	-37.0	106.0	-1.0	24	3.3	2771.0	10.7	**16**
6 lowest yielding genotypes across environments															
G67	724.0	-1211	19	-11.8	7.0	-1.2	59.0	-82.2	107.0	3.0	22	1.4	690.7	46.1	95
G10	776.0	-1579	9	-20.6	5.0	-0.6	17.0	-130.6	106.0	3.0	46	38.3	770.4	22.3	75
G22	798.0	-1433	21	-9.6	5.0	-0.7	45.0	-104.3	105.0	-1.0	47	24.4	776.7	-59.5	54
G23	950.0	-1117	9	-23.4	6.0	1.5	26.0	-116.3	105.0	23.0	34	14.2	912.3	43.6	93
G33	967.0	-1536	20	-17.3	6.0	1.5	80.0	-86.5	107.0	2.0	20	1.8	951.3	30.0	82
G62	969.0	-485	14	0.3	5.0	-1.7	36.0	-66.2	105.0	-1.0	43	27.4	962.3	-25.5	54
Mean	1667.0		25.9		6.3		91.4		105.8		25.5		1617.2	22.8	
Reduction (%)	28.2		26.4		3.1		29.8		6.9		2.7				
H^2 (%)	34.5		44.9		57.4		50.9		27.9		68.5				
LSD (5%)	679.6		11.2		0.9		44.8		0.5		6.2				

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* = predicted genotypic effect of genotype, *SYD* seed yield, *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100 seed weight (g), *GMP* geometric mean productivity, *%SYR* percentage seed yield reduction, *MR* mean rank of a genotype across all the drought tolerance indices, *LSD* least significance difference at 0.05, H^2 broad-sense heritability. **NB:** Values in bold indicate that the respective genotype outperformed the standard check.

Table 5.8 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 10 highest yielding and 6 lowest yielding genotypes for shoot and physiological traits evaluated under combined environments.

Best 10 performing genotypes across environments											
Geno	GYD	LCC		SC		LT		CB		PHI	
	Ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G30	2306.0	37.8	-9.7	81.4	-8.5	24.1	1.7	2783.0	-54	63.6	-3.6
G29	2328.0	37.4	-13.0	113.5	44.9	24.6	-0.4	3525.0	22	66.6	-7.0
G59	2344.0	33.1	-8.9	104.8	9.3	23.2	-0.3	3338.0	1020	69.5	-4.6
G43	2359.0	36.5	-3.4	91.8	33.1	22.4	0.8	2603.0	691	60.6	-6.6
G89	2374.0	44.3	0.4	115.1	-13 3	23.1	1.1	2438.0	-1046	61.9	-23.3
G19	2520.0	39.8	-2.8	106.0	-2.6	22.5	-2.0	2288.0	-1069	66.4	-23.4
G103	2526.0	34.7	-6.1	130.2	13.2	23.1	0.0	3488.0	-860	68.3	-14.0
G95	2619.0	37.4	-8.2	112.7	20.1	24.2	2.8	2698.0	-594	67.2	-1.3
G70	2652.0	38.2	1.1	103.2	22.0	24.2	1.9	3240.0	2568	69.8	2.4
G105	2776.0	39.4	-5.9	108.1	1.5	23.1	-0.4	3315.0	-333	69.1	9.6
6 lowest yielding genotypes across environments											
G67	724.0	34.6	-10.1	104.9	-18.4	23.4	2.6	1203.0	-1539	70.2	-19.1
G10	776.0	35.7	-3.3	114.2	35.7	28.4	1.4	1572.0	-1760	54.1	-22.7
G22	798.0	30.0	-16.3	100.8	-21 1	24.5	2.5	1613.0	-428	56.9	-18.7
G23	950.0	29.3	-26.3	85.8	-29.4	243.2	2.4	1612.0	-240	59.4	-18.9
G33	967.0	29.5	-10.5	66.7	-16.8	23.4	0.0	1800.0	-1169	62.6	-17.8
G62	969.0	29.2	-11.2	123.4	7.0	22.0	0.8	1665.0	-339	63.6	6.4
Mean	1667.0	29.9		67.1		22.1		2257.0		63.4	
Reduction (%)	28.2	41.7		80.3		-34.2		12.0		4.8	
H^2 (%)	34.5	57.1		31.5		32.8		23.2		14.5	
LSD (5%)	679.6	8.04		21.6		2.5		1015.0		11.8	

Geno – genotype, $\hat{G}$ predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], $\hat{g}$ predicted genotypic effect of genotype, GYD seed yield (kg/ha), *LCC* leaf chlorophyll content, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%), *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *LSD* least significance difference at 0.05, H^2 broad-sense heritability. **NB:** Values in bold were above the breeding target and the respective genotype outperformed the standard check.

Heritability estimates ranged from low (CB, PHI and DPM), moderate (SC, LT, SYD, NMPP, NSPP and LCC) to high (SW) under combined environments (Table 5.7 and Table 5.8). The drought tolerance indices for the 110 genotypes based on Ĝ GYD are summarised in Table 5.7 and Appendix 5.5). The severity of terminal drought stress at SVES across the 2 seasons of evaluation was moderate (DII of 0.28). Among the evaluated genotypes, G35, G16, G22, G50, G3, G53, G91, G20 and G1 were less sensitive to DS based on their low DSI and %GYR. These genotypes had DSI values ranging from -2.8 (G35) to - 0.8 (G11) and %GYR ranging from -77.7 (G35) to - 22.5 (G11). On the whole, 20 genotypes had %GYR values below zero.

On the other hand, 4 genotypes (G69, G44, G102 and G19) had %GYR values that were close to zero and 17 genotypes had %GYR of more than 50%. Geometric mean productivity confirmed the earlier results from the scatterplot that G105, G70, G95, G19, G103, G29, G30, G89, G59 and G43 were the top performers under both treatments. Overall, 40 genotypes were ranked higher than the standard check G68 and were considered tolerant to DS based on their mean ranks across all the studied drought tolerance indices. Genotypes G53, G19, G30, G20, G105, G108, G91, G50, G29 and G93 were among the top 10 drought stress tolerant genotypes.

5.3.5 Genotype by trait analysis

5.3.5.1 Identification of superior genotypes combining good agronomic traits with desirable shoot, physiological, canning and nutritional quality traits

The GT biplot is useful for visualizing how the genotypes performed with respect to multiple traits (trait profiles of the genotypes) and their associations under DS, NS and combined environments. Furthermore, the results of GT biplot analysis are substantiated by the performance of the genotypes under DS, NS and across environments outlined in Table 5.4 and Appendix 5.2, Table 5.5 and Appendix 5.3, Table 5.6 and Appendix 5.4, Table 5.7 and Appendix 5.5, and Table 5.8 and Appendix 5.6.

5.3.5.1.1 Under drought stressed environments

The GT biplot under DS conditions was drawn using two-seasons data from 5 agronomic, 6 canning, 2 shoot, 3 physiological and 2 nutritional quality traits of 110 genotypes across two DS environments. Fifty-five percent of the total variation was explained by the biplot, with principal components (PC) 1 and PC2 accounting for 32.8 and 22.7%, respectively (Figure 5.2). The "which-won-where" polygon-view of the GGE biplot was divided by rays into ten sectors. G38, G102, G105, G50, G15, G75 and G10 located at the corners of the polygon were the vertex genotypes (Figure 5.2). The vertex genotypes were among the most responsive (either the best or worst) in terms of expression of one or more specific traits in a given sector. Among the ten sectors, only five had traits in them (Figure 5.2). The NMPP, GYD, CB, PHI, degree of clumping, degree of splitting, and uniformity fell in the same sector, NSP, DPM, SC, LCC, and HC fell in the same sector. The PWDW, WDW and seed Zn fell in the same sector, SW and LT also fell in the same sector while seed Fe was in its own sector (Figure 5.2). Genotypes that are in the same sector or associated with a specific trait or group of traits had the highest values of the specific trait or group of traits.

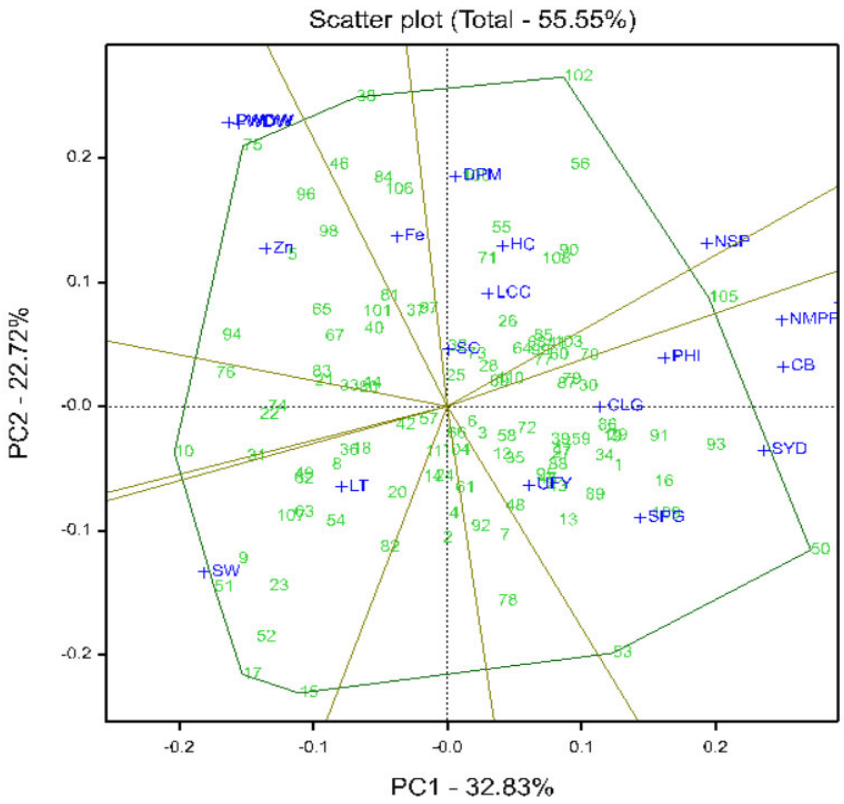

Figure 5.2 The which-won-where polygon-view of the genotype-by-trait biplot to highlight genotypes with outstanding multiple-trait profiles under drought stressed environments over two seasons. *SYD/GYD* grain yield (kg/ha), *LCC* leaf chlorophyll content, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%), *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100 seed weight (g), *HC* hydration coefficient, *WDW* washed drained weight, *PWDW* percentage washed drained weight, *Fe* iron, *Zn* zinc, *CLG* clumping, *UFY* uniformity, *SPG* splitting. Genotypes are represented by numbers and traits are represented by plus signs.

This reveals higher or lower utility and performance in that specific trait or group of traits depending on how the trait is interpreted. Furthermore, genotypes that are close to the biplot origin did not show a considerable reaction to different traits. G50, G105, G93, G16, G91 and G53 were found to be highly associated with higher scores (desirable) for canning quality traits (uniformity, degree of clumping and degree of splitting) and higher performance for agronomic and shoot traits (NMPP, CB, PHI, and GYD) (Figure 5.2). Furthermore, the same genotypes were associated with lower values (undesirable) for seed Zn, seed Fe, PWDW and WDW, and lower values (desirable) for DPM and LT. On the contrary, G75, G96, G98, G5, G94, G66 and G65 were found to be highly associated with lower scores (undesirable) for canning quality traits (degree of clumping, uniformity and degree of splitting) and lower values for shoot and

agronomic traits (PHI, NMPP, CB, GYD and NSP) (Figure 5.2). However, the same lines were found to be highly associated with higher values (desirable) for seed Zn, WDW and PWDW (Figure 5.2). Genotypes G102 and G56 were observed to be highly associated with higher values (undesirable) for DPM, higher values (desirable) for NSP, LCC, SC and HC, and lower values for LT (desirable) and SW (undesirable).

The genotypes G75, G96, G65, G98 and G5 were found to be highly associated with higher values (desirable) for seed Zn, WDW and PWDW, and lower scores (desirable) for uniformity, degree of clumping, degree of splitting, and lower values (undesirable) for GYD, CB and NMPP (Figure 5.2). In addition, G38, G46, G84 and G106 were highly associated with higher values (desirable) for seed Fe, and lower values (undesirable) for GYD, uniformity, degree of clumping and degree of splitting, and lower values values (desirable for LT (Figure 5.2). Furthermore, G57, G11, G6 and G66 were located close to the biplot origin, indicating that they did not show a considerable reaction to different traits. Regarding genotypes that combine high seed GYD with desirable seed Fe content, twenty-three genotypes had above average GYD (1393 kg/ha) and seed Fe concentration (97.1 ppm) under DS conditions (Figure 5.3).

Notably, among these, G42, G45, G59, G70, G103 and G110 performed better than both standard checks with respect to GYD (G68 – 1593 kg/ha) and seed Fe concentration (G73 – 105.5 ppm) under DS conditions (Figure 5.3). These six genotypes had GYD ranging from 1674 (G42) to 2004 kg/ha (G70) and seed Fe concentration ranging from 108.8 (G110) to 118 ppm (G42) under DS conditions (Table 5.5, Appendix 5.2 and Appendix 5.3). Among the six genotypes that combined high GYD and acceptable seed Fe concentration (above the standard checks), only G103 met the required industrial canning quality standards in more than 50% of the studied traits under DS conditions (Table 5.5 and Appendix 5.2). In all, G103 met the required canning quality standards in 71.4% of the studied traits, respectively. Therefore, G103 (ZABRA16575-86F22) combined high GYD with desirable canning and nutritional quality under DS compared to the standard checks.

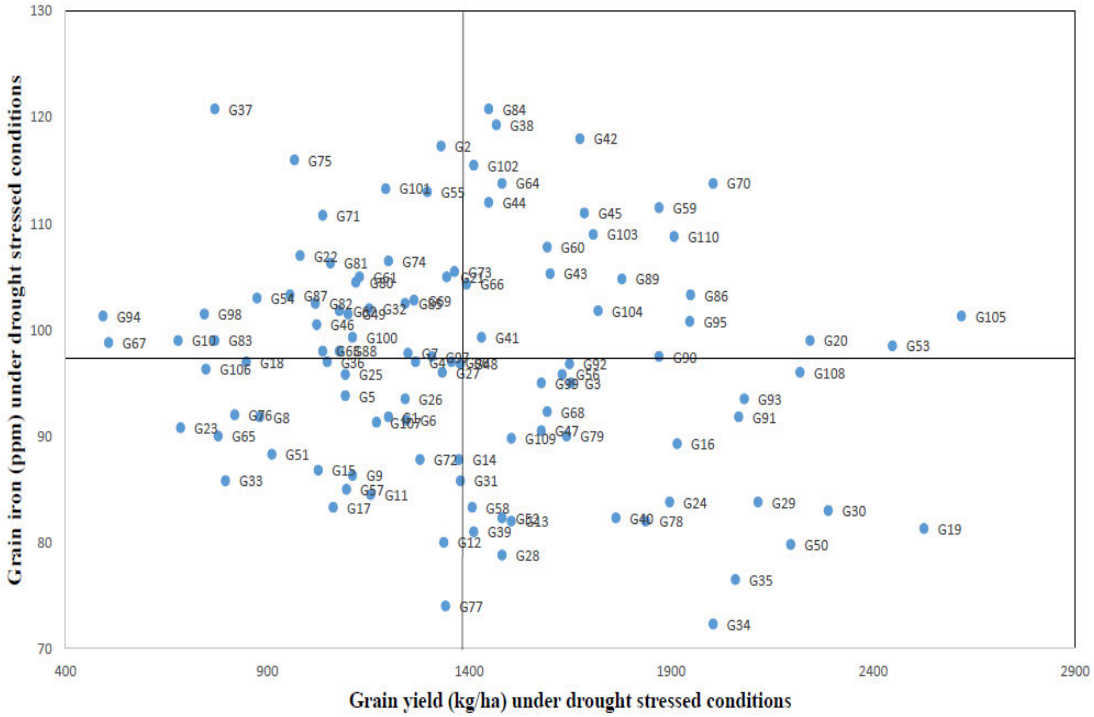

Figure 5.3 Classification of 110 navy bean genotypes based on mean grain yield (kg/ha) and seed iron (ppm) concentration under DS environments at Save valley experiment station, Zimbabwe. Vertical and horizontal lines represent trial mean grain yield (kg/ha; x-axis) and seed Fe concentration (ppm; y-axis), respectively under DS conditions. Genotypes with superior GYD and seed Fe content are located in the upper, right-hand quadrant.

5.3.5.1.2 Under non-stressed environments

The GT biplot under NS conditions was constructed using two-seasons data from 6 agronomic, 2 shoot, 3 physiological and 2 nutritional quality traits of 110 genotypes across two NS environments. Fifty-nine percent of the total variation was explained by the biplot, with PC1 and PC2 accounting for 37.2 and 22.2%, respectively (Figure 5.4). The "which-won-where" polygon-view of the GGE biplot was divided by rays into nine sectors. G10, G38, G103, G1, G39, G11 and G88 located at the corners of the polygon were the vertex genotypes, and hence the most responsive in non-stressed conditions (Figure 5.4). Among the nine sectors, only three had traits in them (Figure 5.4). The NMPP, NSPP, NSP, GYD, CB, PHI, and LCC fell in the same sector, SW and LT fell in the same sector. Furthermore, seed Zn, seed Fe, DPM and SC fell in the same sector (Figure 5.4). Genotypes G103, G59, G82, G95, G89, G70 and G82 were found to be highly associated with higher values (desirable) for GYD, CB, NMPP, NSPP, PHI, NSP and LCC and lower values for LT (desirable) and SW (undesirable) (Figure 5.4).

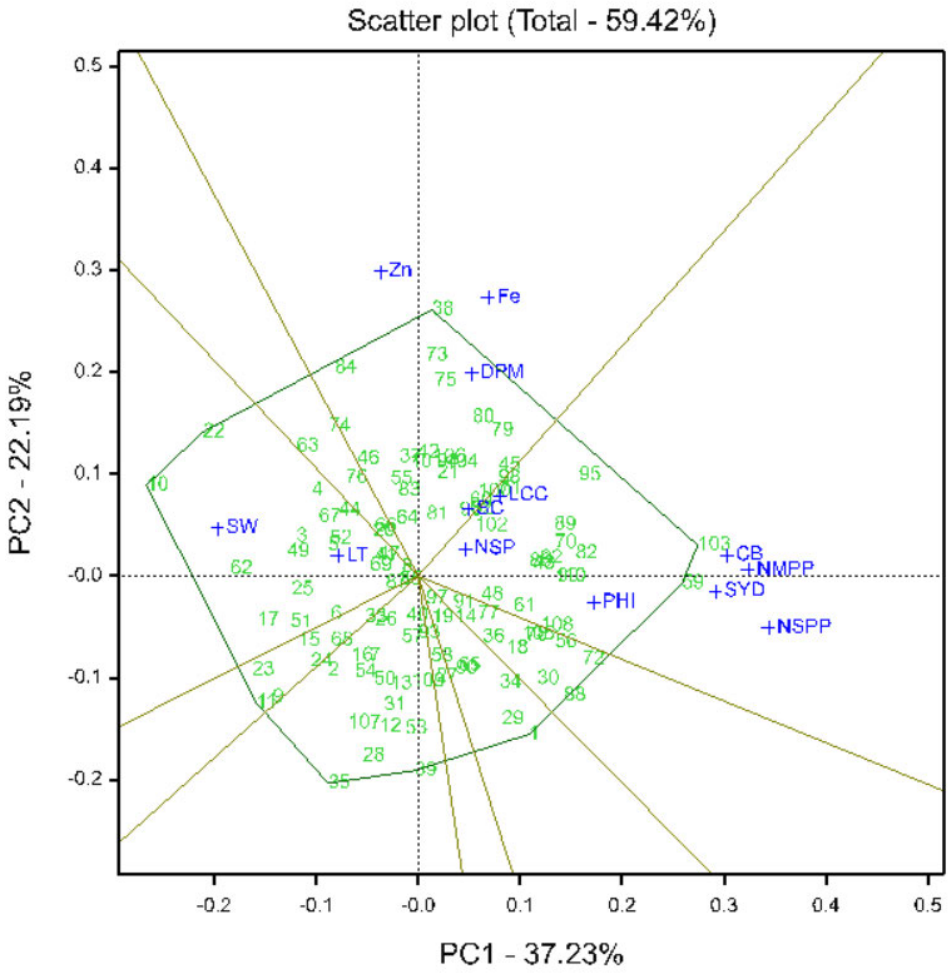

Figure 5.4 The which-won-where polygon-view of the genotype-by-trait biplot to highlight genotypes with outstanding multiple-trait profiles under non-stressed environments over two seasons. *SYD/GYD* grain yield (kg/ha), *LCC* leaf chlorophyll content, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%), *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100 seed weight (g), *Fe* iron, *Zn* zinc. Genotypes are represented by numbers and traits are represented by plus signs.

The genotypes G38, G73, G75, G80 and G79 were highly associated with higher values (desirable) for seed Zn, seed Fe, DPM and SC, while G10 and G22 were highly associated with higher values for SW (desirable) and LT (undesirable) (Figure 5.4).

5.3.5.1.3 Under combined environments

The GT biplot under combined environments was constructed using data from 6 agronomic, 2 shoot, 3 physiological and 2 nutritional quality traits of 110 genotypes across four environments. Sixty-two percent of the total variation was explained by the biplot, with principal components (PC) 1 and PC2 accounting for 37.6 and 24.5%, respectively (Figure 5.5). The "which-won-where" polygon-view of the GGE biplot was divided by rays into ten

sectors. G75, G85, G103, G29, G23, G10 and G50 located at the corners of the polygon were the vertex genotypes, and hence the most responsive across environments (Figure 5.5). Among the ten sectors, seven had traits in them (Figure 5.5). The seed Fe content, DPM, SC and LCC fell in the same sector, PHI, CB and NMPP fell in the same sector while NSPP, LT, SW and seed Zn content each fell in its own sector (Figure 5.5). Grain yield and NSP fell in the same sector. G73, G38, G85, G60, G95, G79 and G106 were found to be highly associated with higher values (desirable) for seed Fe, DPM, SC and LCC, and lower values (desirable) for LT (Figure 5.5).

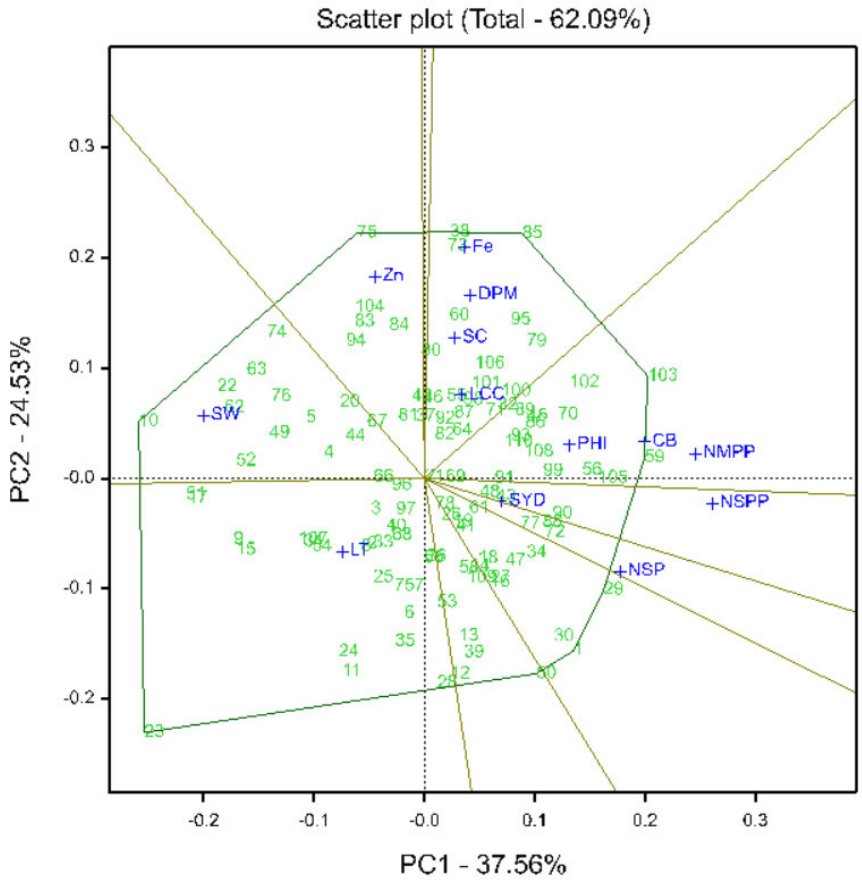

Figure 5.5 The which-won-where polygon-view of the genotype-by-trait biplot to highlight genotypes with outstanding multiple-trait profiles under combined environments (drought plus non-stressed conditions). *SYD/GYD* grain yield (kg/ha), *LCC* leaf chlorophyll content, *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%), *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100 seed weight (g), *Fe* iron, *Zn* zinc. Genotypes are represented by numbers and traits are represented by plus signs.

Furthermore, G103, G59, G105, G102, G56 and G70 were observed to be highly associated with higher values (desirable) for PHI, CB and NMPP, and lower values (undesirable) for SW (Figure 5.5). On the other hand, G77, G88 and G72 were highly associated with higher values

(desirable) for GYD and NSP, and lower values (undesirable) for SW and seed Zn. In addition, genotypes G10, G62, G22, G63 and G52 were associated with higher values (desirable) for SW, and lower values for GYD, NSP, NSPP, NMPP, CB and PHI (Figure 5.5). Furthermore, G96, G97 and G78 were located close to the biplot origin, indicating that they did not show a considerable reaction to different traits (Figure 5.5).

5.3.6 Association among traits

5.3.6.1 Genetic correlations among canning and nutritional quality traits under drought stressed conditions

The coefficients of genetic correlation among canning and nutritional quality traits under DS conditions are summarised in Table 5.9. Significant and positive associations were observed for PWDW ($r = 0.30$, $p < 0.001$) and WDW ($r = 0.30$, $p < 0.01$) with seed Zn content under DS conditions. The degree of clumping was significantly and positively associated with HC ($r = 0.18$, $p < 0.05$), degree of splitting ($r = 0.49$, $p < 0.001$) and uniformity ($r = 0.22$, $p < 0.05$).

Table 5.9 Genetic correlation coefficients (r) among canning and nutritional quality trait combinations based on 110 genotypes under drought stressed conditions in 2019 and 2020, at Save valley experiment station, Zimbabwe.

Trait	Clumping	Fe	HC	PWDW	Splitting	Uniformity	WDW	ZN
Clumping	1	-0.05	0.18*	-0.08	0.49***	0.22*	-0.09	-0.18
Fe		1	0.15	0.10	-0.04	0.02	0.11	0.41***
HC			1	0.09	-0.05	0.00	0.06	0.04
PWDW				1	-0.25**	-0.10	……	0.30***
Splitting					1	0.46***	-0.24*	-0.28**
Uniformity						1	-0.09	-0.10*
WDW							1	0.30**
Zn								1

Fe iron (ppm), *Zn* zinc (ppm), *HC* hydration coefficient, *WDW* washed drained weight (g), *PWDW* percentage washed drained weight (%), *, **, *** indicate significance at $P \leq 0.05$, $P \leq 0.01$, and $P \leq 0.001$, respectively. **NB:** …… indicates same trait.

Seed Fe concentration was significantly ($p < 0.001$) and positively ($r = 0.41$) correlated with seed Zn concentration under DS conditions.

5.3.6.2 Genetic correlations among shoot, physiological, agronomic and nutritional quality traits under drought and non-stressed conditions

The coefficients of correlation among agronomic, shoot and nutritional quality traits under DS and NS conditions are shown in Table 5.10.

Table 5.10 Genetic correlation coefficients (r) among shoot, agronomic, physiological and nutritional quality trait combinations based on 110 genotypes under drought stressed and non-stressed conditions, in 2019 and 2020, at Save valley experiment station, Zimbabwe.

Under drought stressed conditions (DS)													
Trait	CB	DPM	Fe	LCC	LT	NMPP	NSP	NSPP	PHI	SC	SW	GYD	Zn
CB	1												
DPM	0.02	1											
Fe	-0.08	0.20*	1										
LCC	0.22*	0.26**	0 10	1									
LT	-0.09	-0.08	-0.08	-0.01	1								
NMPP	0.65***	0.01	0.04	0.10	-0.22*	1							
NSP	0.38***	0.11	0.03	0.02	-0.14	0.38***	1						
NSPP	0.28**	0.01	0.06	-0.05	0.05	0.31***	0.30***	1					
PHI	0.27**	0.01	0.08	0.05	-0.16	0.31***	0.22*	0.20*	1				
SC	0.09	0.09	0 11	0.31***	-0.10	0.03	0.00	0.01	0.10	1			
SW	-0.19*	-0.22*	-0.06	-0.03	0 10	-0.38***	-0.54***	-0.25**	-0.26**	0.12	1		
GYD	0.62***	-0.03	-0.15	0.02	-0.10	0.47***	0.31***	0.30***	0.35***	0.15*	-0.20*	1	
Zn	-0.24*	0.01	0.41***	0.05	-0.16	-0.19*	-0.01	-0.10	-0.05	0.09	0.24*	-0.20*	1
Under non-stressed conditions (NS)													
Trait	CB	DPM	Fe	LCC	LT	NMPP	NSP	NSPP	PHI	SC	SW	GYD	Zn
CB	1												
DPM	0.13	1											
Fe	0.13	0.16	1										
LCC	0.13	0.19*	-0.02	1									
LT	-0.14	-0.11	0.07	-0.16	1								
NMPP	0.71***	0.12	0 16	0.14	-0.13	1							
NSP	0.03	-0.03	0.07	-0.05	0 13	0.12	1						
NSPP	0.71***	0.01	0 12	0.06	-0.14	0.83***	-0.14	1					
PHI	0.22*	0.01	0.07	0.05	-0.14	0.19*	0.00	0.35***	1				
SC	0.14	-0.05	0 15	0.13	-0.19*	0.09	-0.10	0.01	0.09	1			
SW	-0.12	-0.11	0.04	-0.04	0.09	-0.45***	-0.19*	-0.55***	-0.23*	0.12	1		
GYD	0.64***	0.02	0 16	0.21*	-0.02	0.52***	0.03	0.64***	0.41***	0.10*	0.24*	1	
Zn	-0.04	0.22*	0.46***	0.06	0.08	-0.06	0.08	-0.15	-0.04	-0.01	0.02	-0.14	1

GYD grain yield (kg/ha), *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100-seed weight (g), *CB* canopy biomass (kg/ha), *PHI* pod harvest index (%), *Fe* iron (ppm), *Zn* zinc (ppm), *LCC* leaf chlorophyll content, *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *, **, *** indicate significance at $P \leq 0.05$, $P \leq 0.01$, and $P \leq 0.001$, respectively.

The strongest association under DS conditions was observed between CB and NMPP (r = 0.65, p < 0.001). Stomatal conductance exhibited positive and significant genotypic correlations with LCC (r = 0.31; p < 0.001) and GYD (r = 0.15; p < 0.05). The NMPP presented significant positive correlations with GYD (r = 0.47, p < 0.001), PHI (r = 0.31, p < 0.001), NSPP (r = 0.31, p < 0.001), and NSP (r = 0.38, p < 0.001) under DS conditions. Grain yield showed significant positive correlations with NSPP (r = 0.30, p < 0.001), PHI (r = 0.35, p < 0.001) and CB (r = 0.62, p < 0.001) under DS conditions. Furthermore, the NSPP was significantly (p < 0.05) and positively associated with PHI (r = 0.20) and CB (r = 0.28) under DS conditions. There existed

slightly negative associations between GYD and seed Fe (r = - 0.15, p > 0.05) and seed Zn (r = - 0.20, p < 0.05) concentrations under DS conditions. Under NS conditions, the strongest association was observed between NSPP and NMPP (r = 0.83, p < 0.001). There were also significant and positive associations for NMPP (r = 0.71, p < 0.001), NSPP (r = 0.71, p < 0.001), PHI (r = 0.22, p < 0.05), and GYD (r = 0.64, p < 0.001) with CB. Furthermore, GYD presented significant positive correlations with LCC (r = 0.21, p < 0.05), NMPP (r = 0.52, p < 0.001), NSPP (r = 0.64, p < 0.001), PHI (r = 0.41, p < 0.001) and SW (r = 0.24, p < 0.05). Seed Fe concentration showed a significant (p < 0.001) and positive (r = 0.46) correlation with seed Zn concentration under NS conditions. There existed a significant (p < 0.05) and negative (r = - 0.55) association between NSPP and SW.

5.3.6.3 Genetic correlations between traits under drought and non-stressed conditions

The associations between traits under DS and NS conditions varied widely (Table 5.11). The highest positive and significant ($p < 0.001$) correlations were observed for seed Zn content, seed Fe content, and SW between DS and NS conditions. Furthermore, the expression of CB, LCC, NMPP, NSPP, DPM, and GYD were significantly (p < 0.001; p < 0.05) and positively correlated between DS and NS conditions.

Table 5.11 Genetic correlation coefficients (r) between drought stressed and non-stressed conditions in the growing seasons of 2019 and 2020 for shoot, agronomic and nutritional quality traits, at Save valley experiment station, Zimbabwe.

Trait	Correlation coefficient
Iron (ppm) (Fe)	0.91***
Zinc (ppm) (Zn)	0.94***
Stomatal conductance (mmol m^{-2} s^{-1}) (SC)	0.16
Canopy biomass (kg/ha) (CB)	0.22*
Leaf chlorophyll content (LCC)	0.50***
Leaf temperature (°C) (LT)	-0.22
Pod harvest index (%) (PHI)	0.18
Number of mature pods per plant (NMPP)	0.40***
Number of seeds per plant (NSPP)	0.51***
Number of seeds per pod (NSP)	0.04
Days to physiological maturity (DPM)	0.24*
100-seed weight (SW)	0.74***
Grain yield (kg/ha) (GYD)	0.36***

, * indicate significance at P ≤ 0.01, and P ≤ 0.001, respectively.

5.4 Discussion

5.4.1 Terminal drought stress adaptability analysis

The net water requirement for optimum growth and development of a bean crop in a season ranges from 350 to 500 mm, depending on climatic factors, genetic make-up, soil type and agronomic management (Darkwa et al., 2016). However, in the current study, plants in the DS experiments received less than 300 mm of water in each of the two seasons, exposing the plants to terminal drought stress. The observed DII was moderate (0.28) despite the DS experiments receiving inadequate moisture during the reproductive growth stage, suggesting that DII also depends on the type and diversity of germplasm used. Similarly, Schneider et al. (1997) and Darkwa et al. (2016) reported DII of 0.26 and 0.30, respectively, in dry beans drought screening experiments. The experimental lines evaluated in this study are of the Mesoamerican race, which has the highest level of drought tolerance in dry beans, after the race Durango (Padilla-Ramirez et al., 2005).

Reductions in GYD differed among the evaluated genotypes, signifying their differential response to drought stress. In this study, 20 genotypes had negative %GYR and DSI values indicating that they had higher GYD under DS compared to NS conditions. This suggests that mechanisms that contribute to improved GYD performance under DS and NS environments differ. It may be valuable to establish the genetic basis of high GYD under DS compared to NS conditions in these 20 genotypes that set them apart from the rest of the genotypes. Similar findings were reported in dry beans (Darkwa et al., 2016) and sorghum (*Sorghum bicolor* [L.]) Moench) (Mwamahonje et al., 2021). It should be noted that among the genotypes which had negative %GYR and DSI values, G35, G12, G84, G40, G11 and G20 have the drought tolerant breeding line SXB405 in their pedigree. As reported by Assefa et al. (2013), SXB405 combines high GYD with drought tolerance. Overall, four genotypes (G69, G44, G102 and G19) had %GYR values close to zero suggesting that they were stable and maintained their GYD levels across both treatments. Grain yield stability under both DS and NS environments is an important indicator of tolerance to drought stress in dry beans (Assefa et al., 2014).

Considering that drought conditions in SSA vary widely from season to season, genotypes that perform well under both DS and NS conditions (high GMP values) are preferred. Genotypes G105, G70, G95, G19, G103, G29, G30, G89 and G68 had high GMP values, suggesting that they might have combined the two mechanisms that contribute to high GYD under both DS and NS conditions. Furthermore, G68 (G40), the drought tolerant check was previously found

to possess high levels of drought tolerance (Assefa et al., 2013). The most drought tolerant genotypes (G53, G19, G30, G20 and G105) based on their mean ranks across the indices would serve as valuable genetic resources in breeding for stable and high yielding genotypes under DS and NS environments. Furthermore, these genotypes are promising candidates for use in genetic and physiological studies to comprehend the genetic basis of drought tolerance in navy beans.

5.4.2 Grain yield, yield components, shoot attributes and physiological traits

The high coefficient of variation values observed in this study for GYD, NMPP and NSPP across environments might be due to the differential performance of genotypes across the contrasting environments. On the other hand, H^2 increased in DS conditions for GYD, NSP, NMPP, NSPP, CB, LT and PHI compared to NS conditions. This reflects the wider genetic variability in agronomic and shoot traits among the tested genotypes that was generated by terminal drought stress (Gomez-Becerra et al., 2010; Assefa et al., 2013). The results show that terminal drought stress had severe impacts on shoot traits, yield components, physiological traits and GYD, indicating that the intensity of drought was sufficient to discriminate the genotypes. Similar findings were reported by Androcioli et al. (2020) and Papathanasiou et al. (2022). The considerable reduction in SC and LCC, and increase in LT under DS conditions were caused by the closure of stomata. This is the first reaction undertaken by plants when subjected to drought stress to reduce water loss through transpiration. The closure of stomata results in low SC, decreases the amount of CO_2 available in the leaves, and consequently the rate of photosynthesis (Tardieu et al., 2018). On the other hand, the decreased rate of transpiration through the closure of stomata affects transpiration cooling of the plant, resulting in increased leaf temperature.

The considerable reductions in the NMPP and NSPP under DS conditions were caused by the increased flower, seed and pod abortion due to drought stress. Similar findings were reported in navy beans (Assefa et al., 2017), chickpea (*Cicer arietinum* L.) (Behboudian et al., 2001) and lentil (*Lens culinaris* Medikus) (Choukri et al., 2020). Consequently, GYD (28.2%) and SW (2.7%) were significantly reduced under DS conditions, which is consistent with earlier findings in dry beans by Beebe et al. (2008), Urrea et al. (2009), Beebe et al. (2010), Assefa et al. (2013), Darkwa et al. (2016), Assefa et al. (2017), Papathanasiou et al. (2022) and Smith et al. (2022). This is attributed to the direct stress effects on the development of reproductive organs, poor assimilation of photo-assimilates, reduced seed sink capacity and poor

partitioning of carbohydrates to the developing seed under DS conditions (Muñoz-Perea et al., 2006).

Meanwhile, most of the test genotypes exhibited a significant reduction in CB under DS environments, corroborating previous findings (Rao et al., 2009; Assefa et al., 2013, 2017; Polania et al., 2016; Smith et al., 2022). Notably, terminal drought stress accelerated phenological growth stages, with genotypes maturing on average seven days earlier in DS treatments compared to NS treatments. This was further supported by the two (G105 and G50) highest yielding genotypes which had negative genotypic effects for DPM under DS conditions. The current findings are in accordance with earlier reports in dry beans by Assefa et al. (2014), Darkwa et al. (2016), Assefa et al. (2017) and Smith et al. (2019). The current observation suggests that drought tolerant genotypes hasten their maturity by rapidly changing from vegetative to reproductive stages such that they are able to reach maturity before the depletion of soil moisture. However, it is important to note that among the highest yielding genotypes under DS conditions, only G105 and G50 presented negative genotypic effects for DPM, suggesting that they had greater assimilate remobilization potential of photo-assimilates and partitioning to the developing seed. This helped the two genotypes to compensate for their short growth cycle, which usually reduces SYD potential. Similar findings were reported by Polania et al. (2016) in dry beans under DS conditions. Therefore, efficiency in partitioning dry matter to the developing seed is an important drought tolerance mechanism in dry beans.

The significant GEI effects for GYD and all yield components under both DS and NS conditions suggests that the environments influenced the genetic expression of these traits. The observed GYD results are comparable to the reports by Assefa et al. (2013) who observed GYD (kg/ha) ranging from 1433 (DS conditions) to 2775 (NS conditions), and SW (g) ranging from 24.9 (NS conditions) to 21.9 (DS conditions) for G40. I hypothesize that genotypes G19, G20, G29, G30, G50, G70, G91, G93, G105 and G108 that combined high CB with high GYD, highlight their superiority and efficiency in photosynthesis, water use and remobilizing photo-assimilates from vegetative parts to the pods and from pod walls to the developing seeds (Rao et al., 2009; Beebe et al., 2010; Polania et al., 2016). Similar results were reported by Assefa et al. (2017) who identified six navy bean genotypes that combined high CB with high GYD under DS conditions. Genotypes G50, G53, G56, G93, G95, G104 and G105 combined high PHI with high GYD under DS conditions suggesting that they were better and more efficient in remobilizing photo-assimilates from vegetative parts to the developing pods and from pod walls to the developing seeds during water deficit (Assefa et al., 2013; Polania et al., 2016;

Smith et al., 2019). Therefore, these genotypes are promising parents in breeding for improved PHI under DS conditions. Interestingly, the two drought susceptible genotypes G94 and G67 had larger SW under DS conditions compared to NS conditions. Similar findings were observed by Singh (2007) who attributed this to the partial abortion of pods and seeds and remobilization of photosynthates to the remaining pods and developing seeds by the drought susceptible genotypes in DS environments.

5.4.3 Canning quality traits

In this study, it was not feasible to phenotype for canning quality under both DS and NS environments due to high costs associated with the analysis (Walters et al., 1997; Posa-Macalincag et al., 2002; Kelly and Cichy, 2012; Mendoza et al., 2014). Therefore, there is need to fast-track the development and validation of molecular markers that are associated with canning quality parameters (Mutari et al., 2022b). However, the use of the available recommended canning quality standards guided the identification of lines whose canning quality was not affected by drought stress. Significant genotypic differences were observed among the evaluated genotypes regarding canning quality traits under DS conditions. This indicates the presence of wide genetic variability for improving canning quality under DS conditions. Similarly, Assefa et al. (2017) observed wide genetic variability among navy bean genotypes under DS conditions regarding canning quality parameters. On the other hand, Balasubramanian et al. (2000), Gathu et al. (2012), Warsame and Kimani (2014) and Mukankusi et al. (2022) reported significant genetic variation in canning quality parameters among dry beans genotypes under optimal conditions. The GEI effects were not significant for all the studied canning quality traits, suggesting the influence of the environment in the genetic expression of these traits was minimal, also confirmed by the high H^2 estimates (> 95%). However, these results contradict with Balasubramanian et al. (1999) and Khanal et al. (2014) who found that the GEI significantly influenced WDW in dry beans genotypes. The high H^2 estimates (> 95%) observed for all the canning quality traits under both DS and NS conditions further suggest that these traits can be improved through selection under either DS or NS conditions.

Few genotypes had HC, uniformity, and degree of splitting values that met the required industrial canning quality standards under DS conditions. These findings suggest that these traits are highly sensitive to drought stress, whereas PWDW and degree of clumping are the least sensitive. The observed variation could be attributed to genetic variability among the

studied genotypes or to the genetic nature of the traits. Balasubramanian et al. (2000) and van der Merwe et al. (2006) reported poor estimates of HC among navy bean genotypes using the laboratory canning quality evaluation protocol. However, when they used the industrial canning quality protocol, the same genotypes produced good estimates of HC. This is because, during industrial canning, the soaking time of each genotype is determined, while in the laboratory canning, all genotypes are soaked using the same time (van der Merwe et al., 2006). Therefore, to avoid the possibility of discarding germplasm with desirable HC values, genotypes such as G7, G19, G33 and G34, which exhibited low HC values but were superior in other canning quality traits should be subjected to industrial canning quality assessment. Another alternative will be to use molecular markers that are closely linked with superior canning quality traits.

Hydration coefficient has an economic impact to the processor since it directly affects the "can or processor yield" (Mutari et al., 2022b). Genotypes with low HC values result in more costs per can to the canning company since they require more quantities of seed to fill a given can volume, affecting the profitability of the canning operation (Khanal et al., 2014). Therefore, genotypes with low HC (< 1.8) values after the confirmatory industrial canning quality analysis will be discarded. In this study, genotypes such as G20, G10, G95 and G107 which had very low HC values were prone to clumping because they imbibed additional water during cooking and storage. Clumping reduces the quality of the canned bean, affecting consumer acceptability of the product. In this study, genotypes exhibited WDW (g) values ranging from 224.8 – 310 under DS conditions. A similar finding was reported for WDW variability among dry beans germplasm by Warsame and Kimani (2014) and Assefa et al. (2017). Washed drained weight is an important economic canning quality trait which affects the profitability of the canning bean industry. Therefore, genotypes such as G1, G13 and G17, which combined very low WDW values with high rates of clumping might have had excessive exudation of carbohydrates into the brine medium during thermal cooking and storage (Khanal et al., 2014; Qureshi and Sadohara, 2019). These genotypes will be discarded.

5.4.4 Nutritional quality traits

Significant genotypic differences were observed among the evaluated genotypes regarding seed Fe and Zn concentrations under DS and NS environments. This suggests that there is wide genetic variation among the studied genotypes for improving nutritional quality under DS and NS conditions. These results, however, contradict those reported by Smith et al. (2022) where no genotypic variation in seed Fe and Zn among twelve dry beans genotypes under DS and NS

environments was detected. On the other hand, Beebe et al. (2000), Pereira et al. (2014) and Amongi et al. (2021) reported wide genetic variability among dry beans genotypes under optimum conditions regarding seed Fe and Zn concentrations.

Under terminal drought stress, the availability of nutrients in the soil as well as uptake by plant roots is reduced (Kheradmand et al., 2014). This consequently reduces the concentration of nutrients in plant tissues such as the seed, explaining the observed trend with respect to seed Zn concentration. On the other hand, the observed reduction in seed Zn concentration and increase in seed Fe concentration under DS conditions suggests that both Fe and Zn have different accumulation mechanisms in response to drought stress. Furthermore, the shrinkage effect (small grains) of seeds under DS could have contributed to the observed reduction in seed Zn concentration. Magallanes-López et al. (2017) reported similar findings in bread wheat (*Triticum aestivum* L.) under DS conditions. However, reports are contradictory for dry beans seed Fe and Zn concentrations in response to drought stress. Smith et al. (2019) reported that drought stress had no negative effect on the accumulation of Fe and Zn in dry beans seeds. Pereira et al. (2014) and Smith et al. (2022) found that terminal drought stress increased seed Fe and Zn concentrations in dry beans. On the other hand, Ghanbari et al. (2013, 2015) reported a significant decrease in both seed Fe and Zn concentrations under DS conditions. Therefore, the findings agreed with Pereira et al. (2014) and Smith et al. (2022) with respect to increased seed Fe concentration under DS conditions, but contradicted on increased seed Zn concentration. Differences in population structure and size, genetic backgrounds of genotypes used and drought intensity could be the reasons for the inconsistency in results. The specific mechanism on how drought stress increases seed Fe concentration nor decreases Zn concentration is not entirely clear, and needs further investigation.

Most of the genotypes which had above average GYD (1940 kg/ha) under NS conditions had low concentrations of seed Fe suggesting that there are trade-offs that must be made when simultaneously selecting genotypes for improved GYD and nutritional quality traits under NS conditions. Similar observations were reported in a range of crops including dry beans (Raatz, 2018; Beebe, 2020; Diaz et al., 2022), chickpea (Diapari et al., 2014), rice (*Oryza sativa* L., Inabangan-Asilo et al. (2019) and bread wheat (Marcos-Barbero et al., 2021; Devate et al., 2022). Devate et al. (2022) and Diaz et al. (2022) attributed this scenario to the dilution effect of seed Fe and Zn concentrations resulting from the increased translocation of carbohydrates to the seed in high yielding genotypes under optimum conditions. Genotypes such as G11, G18, G38 and G110, which had seed Fe and Zn concentrations above the standard check (G73) in

both DS and NS conditions are useful genetic resources for improving genetic gains in seed Fe and Zn in navy bean improvement programs.

5.4.5 Identification of superior genotypes combining good agronomic traits with desirable shoot, physiological and nutritional quality traits

Cultivar trait preferences vary among navy bean value chain actors. Farmers and seed companies are interested in productivity, whereas bean canning companies are interested in productivity, canning and nutritional quality. Thus, to enhance the adoption rates of navy bean cultivars along the value chain, breeders should consider the canning quality of navy beans together with their nutritional and agronomical attributes. In this study, only one genotype (G103) combined multiple traits (agronomic, shoot, physiological, nutritional and canning quality) of interest suggesting that it is a challenge to develop and identify high yielding and micronutrient dense genotypes with superior canning quality. However, before G103 can be considered for commercial release and canning on an industrial scale, it is important to evaluate their preference among different stakeholders through participatory variety evaluation. Furthermore, the genotype should be subjected to confirmatory seed Fe and Zn analysis using the Inductively Coupled Plasma Atomic Emission Spectrometry (ICP-AES) which is capable of detecting contaminants from the soil. Even though navy beans have low levels of tannins (Beebe et al., 2000), which inhibit the absorption of iron, it might be worthwhile to measure the bioavailability of both Fe and Zn in G103.

Genotypes such as G105, G93, G50, G16, G91, G102, G56, G103, and G38 were found to be superior under DS in some of the yield components, physiological, agronomic and nutritional quality traits, thus may result in high yielding genotypes if used in hybridization programs targeting drought tolerance and superior nutritional quality. On the other hand, the genotypes G75, G96, G98, G5, G38, G106, G105, G93, G50, G16 and G91 could also be used in navy bean hybridization programs (recurrent selection) to form base populations with improved canning quality under DS environments considering that they were associated with superior canning quality in some of the studied traits. Furthermore, considering that the superior genotypes identified in this study did not combine most of the studied traits, the use of the gamete selection technique to simultaneously combine multiple traits into a single genetic background is recommended. According to Singh (1994), breeding programs use the gamete selection technique from hybridizations (crossing of multiple parents) to F_8 or F_{10} to simultaneously combine multiple traits of interest into a single genetic background. However, the breeding values (combining ability) of the genotypes that exhibited superior values for

agronomic, shoot, nutritional, physiological and canning quality traits should be determined before their use in hybridization programs.

5.4.6 Genotypic correlations among traits and broad-sense heritability

In this study, the observed positive and significant genotypic correlations for seed Fe content, seed Zn content, LCC, NMPP, NSPP, CB, SW, SYD and DPM between DS and NS conditions suggest that the genetic effects were relatively consistent under both conditions. Thus, some genotypes performed consistently under DS and NS conditions with respect to these traits. For example, four genotypes (G69, G44, G102 and G19) had %SYR values close to zero, suggesting that they were stable and maintained their GYD levels across both DS and NS conditions. Therefore, NS conditions to identify promising genotypes may be ideal for selecting superior genotypes with respect to traits (seed Fe, seed Zn and SW) which showed significant and very strong genotypic correlations between NS and DS conditions. The current findings validate previous reports by Assefa et al. (2014) with respect to SYD, NMPP, NSPP, CB and SW.

Significant positive associations were found between GYD and traits such as PHI, CB, NMPP and NSPP under DS and NS environments corroborating previous reports on dry beans (Darkwa et al., 2016; Polania et al., 2016; Assefa et al., 2017; Berny Mier y Teran et al., 2019; Smith et al., 2022). This suggested that it is feasible to improve these traits simultaneously by direct and indirect selection under both DS and NS environments. The H^2 of CB under NS was low (27.8%), implying that CB may not be an effective selection criterion to indirectly select for GYD under NS conditions. As for PHI, indirect selection of GYD using this trait might also not be very effective taking into consideration the low H^2 estimates observed in this study for this trait under both DS (21.7%) and NS (8.1%) conditions. Contrary to the current results, Assefa et al. (2013) reported a moderate H^2 estimate (48%) for PHI under DS conditions in navy beans. Differences in the method of calculation, population structure and size, genetic backgrounds of genotypes used and number of test environments and replications could be the explanations for the inconsistency in results.

The significant and positive correlation observed between PHI with NMPP, NSPP and SYD under DS conditions suggest that the evaluated genotypes had superior SYD mainly due to remobilization of the bulk of photo-assimilates from pod walls to the developing seeds during terminal drought stress. The observed high H^2 estimates of all the studied canning quality traits under DS conditions indicate the predominance of additive gene action. In addition, the

significant positive association observed between HC and WDW under DS conditions suggest that superior values of HC are associated with higher values of WDW. Furthermore, this implies that breeding programs without specialized equipment can use HC to predict WDW in early generations without conducting the actual thermal processing, saving on costs and time. Similar results were observed in navy beans by Khanal et al. (2014). Significant positive associations observed between the degree of splitting and degree of clumping under DS conditions corroborate previous reports by Lu and Chang (1996). When bean seed splits during cooking and storage, starch is released into the brine or tomato sauce, causing graininess of the canning medium and clumping of seeds at the bottom of the jar.

The significant positive association observed between seed Fe and Zn concentration under DS and NS conditions suggest that it is feasible to simultaneously select for high seed Fe and Zn using convectional plant breeding methods. Therefore, either seed Fe or seed Zn can be used as a selection tool for the trait, reducing the costs of phenotyping for both traits in trials. These findings are consistent with the results found in dry beans by Mukamuhirwa et al. (2015), Amongi et al. (2018), Katuuramu et al. (2021), Amongi et al. (2021), Diaz et al. (2022), Keller et al. (2022) and Mutari et al. (2022a). The strong correlation might be due to co-segregation of quantitative trait loci (QTL) for seed Fe and Zn concentrations Beebe (2020), and common uptake pathways of these micronutrients (Sperotto et al., 2014). The negative association that was observed between GYD and seed Fe under DS conditions further confirms the trade-off reported earlier on in this study between GYD and seed Fe concentration. Many previous studies reported a negative correlation between GYD and seed Fe in bread wheat (Garvin et al., 2006; Peleg et al., 2008; Magallanes-López et al., 2017; Thapa et al., 2022; Govindan et al., 2022), pearl millet (*Pennisetum glaucum* [L.]; Kanatti et al., 2014) and dry beans (Amongi et al., 2021). The strong negative and significant association observed between NSPP and SW maybe attributed to the increased competition for photo-assimilates as the numbers of seeds increase in a plant, resulting in small seeds. The SW was the most highly heritable trait in this study under both DS and NS conditions, validating previous reports in dry beans (Schneider et al., 1997; Hoyos-Villegas et al., 2017) and bread wheat (Mathew et al., 2018). This indicates that selection for SW will be effective under DS and NS conditions. In contrast, the H^2 estimates for LT and PHI under DS and NS conditions were moderate, suggesting that selection for these physiological traits will be less effective under both conditions.

5.5 Conclusions and recommendations

Several genotypes were identified for use as parents in breeding for drought tolerance (NAE70, RAZ-34, ZABRA16575-86F22, ZABRA16573-78F22, ZABRA16574-37F22, and G34), superior canning quality (G2154, G19, G75, RAZ-34, `NAE70, NAE60, SIRAJ, G49, and G48) and nutritional (NAE70, SMC16, RAZ-34, ZABRA16575-86F22, and G34) quality. These superior genotypes require further investigations to understand the mechanism behind the observed 'minimal' impact of drought stress on their GYD, shoot traits, canning and nutritional quality. Overall, one genotype G103 (ZABRA16575-86F22) was identified that combined high GYD with acceptable canning and nutritional quality under DS and NS environments. The nutrient and water use efficiency of the drought tolerant and micronutrient dense genotypes identified in this study should be investigated. Furthermore, the bioavailability of Fe and Zn in micronutrient dense genotypes identified in this study should be determined. Grain yield, yield attributing traits and shoot traits were significantly and positively associated under DS and NS conditions across two seasons. Among the canning quality traits, important correlations were observed between HC and WDW, and degree of splitting and degree of clumping under DS environments. The significant associations observed in this study among canning, nutritional and agronomic traits will guide future selection efforts in navy bean breeding programs under DS and NS conditions. The results indicate that terminal drought stress significantly reduced GYD, CB, PHI and yield components in both seasons. We report a reduction in Zn (0.9%) and an increase in Fe (1.4%) concentrations in navy bean seeds under DS conditions. The impact of terminal drought stress was more severe on HC, WDW, uniformity, and degree of splitting compared to degree of clumping and PWDW. This resulted in trait means below the required industrial canning quality standards for these traits. Genotypes such as G10 (SAA1), G17 (SAA2), G52 (SAA7), G22 (G550) and G15 (SAB792) which exhibited SW of more than 30 g/100 seeds should be moved to their respective breeding pipelines.

5.6 References

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Appendix 5.1 List of navy bean genotypes used in the study and their sources.

No.	Genotype	Code	Source
1	Protea (Check for Agronomic Traits & Canning Quality)	G1	CBI Zimbabwe
2	CZ108-52	G2	ABC Malawi
3	CZ108-53	G3	ABC Malawi
4	SMB31	G4	ABC Colombia
5	NAE60	G5	ABC Colombia
6	NAE19	G6	ABC Colombia
7	NAE87	G7	ABC Colombia
8	NAE78	G8	ABC Colombia
9	SAA12	G9	ABC Malawi
10	SAA1	G10	ABC Malawi
11	G54	G11	ABC Colombia
12	G14	G12	ABC Colombia
13	AWASH-1	G13	EIAR Ethiopia
14	NAE40	G14	ABC Colombia
15	SAB792	G15	ABC Colombia
16	ZABRA16573-25F22	G16	ABC Malawi
17	SAA2	G17	ABC Colombia
18	RAZ-36	G18	ABC Malawi
19	ZABRA16575-57F22	G19	ABC Malawi
20	DAB562	G20	ABC Colombia
21	ICA BUNSIxSXB405-1C-1C	G21	ABC Colombia
22	G550	G22	ABC Colombia
23	CZ113-13	G23	ABC Malawi
24	ICA BUNSIxSXB405/4C-1C-1C-8	G24	ABC Colombia
25	NAE80	G25	ABC Colombia
26	SAB-662	G26	ABC Colombia
27	ZABRA16575-26F22	G27	ABC Malawi
28	NAE24	G28	ABC Colombia
29	NAIN DEKYONDO	G29	ABC Malawi
30	CZ108-27	G30	ABC Malawi
31	SAB793	G31	ABC Colombia
32	RAZ-44	G32	ABC Malawi
33	NAE13	G33	ABC Colombia
34	NAVY LINE-48	G34	ABC Malawi
35	G30	G35	ABC Colombia
36	ICA BUNSIxSXB405/9C-1C-1C-3	G36	ABC Colombia
37	ZABRA16575-51F22	G37	ABC Malawi
38	NAE70	G38	ABC Colombia
39	ICA BUNSIxSXB405/3C-1C-1C-8	G39	ABC Colombia
40	G32	G40	ABC Colombia
41	ZABRA16575-73F22	G41	ABC Malawi
42	SMB30	G42	ABC Colombia
43	NAVY LINE-60	G43	ABC Malawi
44	G99	G44	ABC Colombia
45	G6	G45	ABC Colombia
46	G24	G46	ABC Colombia
47	NAVY LINE 22	G47	ABC Malawi
48	CIM-NAV02-35-1	G48	ABC Malawi
49	SAA18	G49	ABC Malawi
50	CIM-NAV02-17-3	G50	ABC Malawi
51	SAA17	G51	ABC Malawi
52	SAA7	G52	ABC Malawi
53	NAVY LINE -46	G53	ABC Malawi
54	G90	G54	ABC Colombia
55	G100	G55	ABC Colombia
56	CANPSULA	G56	ABC Malawi
57	ZABR-16576-20	G57	ABC Malawi
58	G738	G58	ABC Colombia
59	NAVY19	G59	ABC Malawi
60	UBR(92)25	G60	ABC Malawi
61	G16 (Check for drought susceptibility)	G61	ABC Colombia
62	SAA19	G62	ABC Malawi
63	SAB791	G63	ABC Colombia

No.	Genotype	Code	Source
64	CIM-NAV02-10-1	G64	ABC Malawi
65	G48	G65	ABC Colombia
66	G49	G66	ABC Colombia
67	G70	G67	ABC Colombia
68	G40 (Check for drought tolerance)	G68	ABC Colombia
69	G37	G69	ABC Colombia
70	G34	G70	ABC Colombia
71	G27	G71	ABC Colombia
72	CIM-DWRF-CLIM01-1-1	G72	ABC Malawi
73	SMC16 (Check for seed Fe and Zn)	G73	ABC Colombia
74	SMC21	G74	ABC Colombia
75	RWR2154	G75	ABC Malawi
76	SMC17	G76	ABC Colombia
77	Ex-rico	G77	ABC Zimbabwe
78	Chercher	G78	ABC Uganda
79	Awash melka	G79	EIAR Ethiopia
80	Awash 2	G80	EIAR Ethiopia
81	RAZ-42	G81	ABC Uganda
82	RAZ-11	G82	ABC Uganda
83	CAB 2	G83	ABC Uganda
84	G53	G84	ABC Uganda
85	CHORE	G85	ABC Uganda
86	ARGENE	G86	ABC Uganda
87	NAZARETH2	G87	ABC Uganda
88	SWAT-09 (SELIAM 9)	G88	ABC Uganda
89	BIOFORT SMALL SEEDED 15	G89	ABC Uganda
90	SWAT-10 (SELIAM 10)	G90	ABC Uganda
91	SWAT-12 (SELIAM-11)	G91	ABC Uganda
92	R02/1	G92	ABC Uganda
93	BASABEER	G93	ABC Uganda
94	SIRAJ	G94	ABC Uganda
95	MUTWAKIL	G95	ABC Uganda
96	G19	G96	ABC Malawi
97	G22	G97	ABC Malawi
98	G75	G98	ABC Malawi
99	G97	G99	ABC Malawi
100	ICN BunsixSxB405/7C-1C-1C-5	G100	ABC Malawi
101	ZABRA16575-60F22	G101	ABC Malawi
102	ZABRA16574-37F22	G102	ABC Malawi
103	ZABRA16575-86F22	G103	ABC Malawi
104	WAJU	G104	ABC Uganda
105	ZABRA16573-78F22	G105	ABC Malawi
106	RAZ-34	G106	ABC Malawi
107	NAVY LINE-47	G107	ABC Malawi
108	NAVY LINE-52	G108	ABC Malawi
109	NAVY LINE-54	G109	ABC Malawi
110	CIM-NAV08-1	G110	ABC Malawi

CBI Crop Breeding Institute, *ABC* Alliance of Bioversity International and International Center for Tropical Agriculture, *EIAR* Ethiopian Institute of Agricultural Research.

Appendix 5.2 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 110 genotypes over two seasons (2019 and 2020) for canning (under drought stress conditions) and nutritional quality (under drought stressed and non-stressed conditions) traits of navy bean genotypes at Save valley experiment station, Zimbabwe.

Geno	DS												Fe (ppm)				Zn (ppm)			
	HC		WDW		PWDW (%)		Uniformity		Clumping		Splitting		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G1	1.7	-0.1	224.0	3.0	55.6	0.7	3.1	0.6	3.3	1.4	3.3	0 3	91.8	11.5	82.3	-15.2	37.5	5.8	34.3	3.1
G2	1.3	-0.3	239.0	14.8	58.9	3.8	**4.6**	**2.1**	**4.3**	1.0	2.8	0.0	**117.3**	**36.4**	**114.3**	**40.1**	37.3	6.7	39.3	4.1
G3	0.9	-0.7	**249.0**	**24.4**	**61.3**	**6.2**	2.6	0.1	3.3	0.1	1.8	-0.9	95.0	23.8	**98.8**	**-2.0**	**43.5**	**14.6**	**47.8**	**6.0**
G4	1.0	-0.7	**241.0**	**16.1**	59.3	4.3	2.6	0.2	3.3	0.2	1.8	-0.8	97.0	19.0	**96.3**	**-7.0**	**47.3**	**16.3**	**48.8**	**6.0**
G5	1.5	-0.1	309.0	84.4	**76.4**	**21.3**	**5.1**	**3.2**	**4.3**	1.1	1.8	-0.9	93.8	1.1	84.3	4.0	**45.3**	**13.9**	**46.3**	**11.0**
G6	1.5	-0.2	**254.0**	**30.2**	**64.4**	**9.1**	3.4[j]	0.5	**4.5**	1.5	2.5	-0.5	91.5	12.0	94.3	-6.0	**43.5**	**11.5**	**44.8**	**5.0**
G7	1.2	-0.5	**249.0**	**24.7**	**61.7**	**6.3**	**4.9**	**2.2**	**4.0**	1.2	**5.0**	2 1	**97.8**	**18.3**	94.8	-4.9	36.8	5.8	37.8	5.1
G8	1.4	-0.2	**254.0**	**29.8**	**63.9**	**9.1**	2.9	0.6	**4.5**	1.6	2.0	-0.4	91.8	13.8	88.8	-12.0	**43.0**	**17.1**	**50.3**	**6.0**
G9	1.1	-0.5	**272.0**	**47.3**	**66.8**	**12.1**	**4.4**	**2.2**	**4.0**	1.2	2.5	0 2	86.3	-3.0	74.3	-6.0	**44.0**	**8.8**	**41.3**	**6.0**
G10	1.2	-0.5	284.0	59.7	**70.4**	15.1	2.9	0.2	3.0	0.18	2.0	-0.9	**99.0**	**26.3**	**102.8**	**8.0**	**42.8**	**12.8**	**44.8**	**5.1**
G11	1.3	-0.3	**265.0**	**41.5**	**64.8**	**10.4**	1.9	0.1	**4.0**	1.1	2.0	0 1	84.5	-0.1	82.8	-16.8	36.8	1.1	37.5	-0.9
G12	1.6	-0.0	**253.0**	**29.0**	**61.7**	**7.3**	1.8	0.1	**4.0**	1.2	2.0	0 1	80.0	-19.1	65.3	-14.9	37.5	4.3	38.3	3.1
G13	1.4	-0.2	235.0	11.1	57.2	2.8	**3.9**	**2.1**	3.0	0.2	1.3	-0.8	82.0	2.3	76.3	-16.9	**40.5**	**9.5**	**42.8**	**3.0**
G14	1.4	-0.2	**253.0**	**29.4**	**62.9**	**8.6**	2.4	0.7	**4.5**	1.8	1.5	-0.2	87.8	4.1	80.3	-11.9	**43.0**	**13.7**	**46.3**	**6.0**
G15	0.9	-0.7	**247.0**	**22.4**	**60.9**	**5.7**	**4.6**	**2.2**	**4.3**	1.3	2.8	0 2	86.8	5.8	81.3	-17.9	**40.5**	**9.2**	**41.0**	**3.5**
G16	1.2	-0.4	**248.0**	**6.7**	56.8	1.6	**4.6**	**2.0**	**4.3**	1.1	2.8	0 1	89.3	9.5	90.8	-7.0	35.8	4.0	37.3	-0.0
G17	1.2	-0.4	227.0	8.0	57.2	2.1	1.6	-0.8	3.3	0.3	1.8	-0.8	83.3	11.8	87.3	-6.9	**42.0**	**13.2**	**45.3**	**0.0**
G18	1.4	-0.2	**254.0**	**29.7**	**63.7**	**9.0**	2.6	0.6	**4.8**	1.7	1.8	-0.3	**97.0**	**21.8**	**95.8**	**18.1**	**40.3**	**7.0**	**40.3**	**6.0**
G19	1.2	-0.4	**256.0**	**31.6**	**62.7**	**8.1**	**4.1**	**2.2**	**5.8**	3.3	**4.3**	2 3	81.3	3.6	79.8	-9.9	**43.8**	**13.2**	**45.8**	**4.6**
G20	1.1	-0.5	237.0	13.1	58.0	3.3	2.1	0.1	2.3	-0.9	1.0	-1.9	**99.0**	**18.4**	**98.3**	**14.2**	**45.0**	**11.1**	**45.0**	**10.1**
G21	1.6	-0.0	**270.0**	**45.3**	**66.3**	**11.5**	**4.4**	**2.1**	3.0	0.1	1.5	-0.9	**105.0**	**19.6**	**109.3**	**19.2**	**52.0**	**18.0**	**52.3**	**15.2**
G22	1.2	-0.5	285.0	60.3	**70.6**	**15.3**	**4.9**	**2.2**	3.0	0.2	2.0	-0.9	107.0	29.9	**110.8**	**22.1**	**49.0**	**21.9**	**54.3**	**6.1**
G23	1.1	-0.5	**270.0**	**45.4**	**66.3**	**11.5**	**4.4**	**2.1**	**6.0**	3.1	**4.5**	2 1	90.8	9.9	89.3	-17.9	37.5	2.7	36.3	-2.0
G24	1.5	-0.2	**254.0**	**29.3**	**64.4**	**9.1**	3.4	0.7	**4.5**	1.7	2.5	-0.4	83.8	4.9	85.8	-16.9	39.5	7.4	39.8	3.1
G25	1.0	-0.6	**262.0**	**37.5**	**64.4**	**9.6**	2.4	0.2	**4.0**	1.3	2.5	0 2	**95.8**	**15.7**	**97.3**	**-5.9**	**43.5**	**14.4**	**47.3**	**3.0**
G26	1.4	-0.2	**254.0**	**29.6**	**63.9**	**9.1**	2.9[-]	0.7	**4.5**	1.6	2.0	-0.4	93.5	**1.1**	88.8	**-3.8**	41.5	**8.8**	43.8	**7.1**
G27	1.0	-0.6	235.0	11.0	57.7	2.9	**4.4**	**2.1**	**4.0**	1.1	2.5	0 1	96.0	15.9	95.3	-8.9	37.8	0.7	34.8	3.0
G28	1.1	-0.5	283.0	58.5	**69.6**	**14.8**	1.4	-0.9	**4.0**	1.1	2.5	0 1	78.8	-25.5	64.3	-15.8	39.0	5.0	39.3	4.2
G29	1.5	-0.2	233.0	7.9	57.5	2.2	2.9	0.2	3.0	0.2	2.0	-0.9	83.8	-7.1	73.8	-14.9	40.0	8.9	41.3	5.1
G30	1.4	-0.2	**254.0**	**29.6**	**64.2**	**9.1**	3.1	0.7	**4.8**	1.6	2.3	-0.4	83.0	-5.5	85.5	-20.8	38.3	6.3	41.5	0.1
G31	0.6	-0.1	299.0	75.4	**73.6**	**19.0**	2.1	0.1	**4.3**	1.2	1.3	-0.8	85.8	10.2	78.3	-2.0	36.5	2.8	33.3	-2.1
G32	0.3	-1.3	**279.0**	**54.2**	**68.8**	**13.7**	2.6	0.1	**4.3**	1.1	1.8	-0.9	102.0	33.9	101.3	3.1	40.8	14.3	44.3	4.0
G33	1.3	-0.3	**276.0**	**52.5**	**67.8**	**13.2**	**4.1**	**2.0**	**4.3**	1.0	2.3	0 1	85.8	17.4	83.3	-13.0	42.3	13.6	44.8	4.0
G34	1.2	-0.4	**249.0**	**24.6**	**61.4**	**6.3**	**4.6**	**2.1**	**4.3**	1.1	2.8	0 1	72.3	-3.1	64.3	-16.0	39.8	9.3	39.3	4.0
G35	1.4	-0.2	**254.0**	**30.3**	**64.2**	**9.1**	3.1	0.5	**4.8**	1.5	2.3	-0.4	76.5	-11.8	61.3	-19.0	38.3	6.0	37.0	1.4
G36	1.6	0.0	**254.0**	**29.4**	**62.3**	**7.5**	2.4	0.1	3.0	0.1	1.0	-1.9	97.0	21.9	89.3	9.1	37.8	9.3	39.3	4.0
G37	1.5	-0.1	**261.0**	**37.3**	**63.7**	**9.4**	**3.9**	**2.1**	**7.0**	4.0	2.0	0 1	**120.8**	**47.0**	**119.0**	**40.1**	49.3	11.2	50.8	14.0
G38	1.2	-0.4	309.0	85.0	**76.1**	**21.3**	**4.4**	**2.0**	**4.0**	1.0	2.5	0 1	**119.3**	**49.9**	**120.3**	**40.0**	**60.8**	**37.1**	**68.3**	**32.9**
G39	1.5	-0.1	**246.0**	**22.5**	**60.1**	**5.8**	**3.9**	**2.2**	**6.0**	3.1	2.0	0 2	81.0	-3.0	67.3	-13.0	38.0	6.0	37.3	1.9
G40	**1.8**	**0.2**	284.0	60.5	**69.5**	**15.2**	1.0	-1.0	**7.0**	4.0	2.0	0 1	82.3	3.4	69.3	-11.0	48.8	19.1	50.3	14.9
G41	1.5	-0.1	**254.0**	**29.6**	**63.9**	**9.1**	2.9	0.6	**4.5**	1.6	2.0	-0.4	99.3	12.3	94.8	5.0	40.0	8.9	40.8	-1.0
G42	1.0	-0.6	**261.0**	**37.1**	**64.2**	**9.4**	**4.4**	**2.1**	3.0	0.1	2.5	0 1	**118.0**	**35.8**	**113.0**	**31.0**	54.5	23.3	51.3	14.0

Geno	DS												Fe (ppm)				Zn (ppm)			
	HC		WDW		PWDW (%)		Uniformity		Clumping		Splitting		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G43	1.3	-0.3	234.0	9.9	57.5	2.7	**4.4**	**2.2**	**6.0**	3.2	**4.5**	2 2	105.3	22.3	98.8	20.9	43.0	12.0	43.3	11.8
G44	1.4	-0.2	**254.0**	**29.7**	**63.9**	**9.1**	1.1	-3.4	**4.5**	1.6	2.0	-0.4	**112.0**	**34.2**	106.3	32.9	44.3	11.2	42.3	9.9
G45	1.6	0.0	231.0	6.7	56.7	1.9	**4.4**	**2.2**	3.0	0.2	2.5	0 2	**111.0**	**31.8**	**108.3**	**24.9**	48.8	19.5	50.8	13.8
G46	1.2	-0.5	310.0	85.5	**76.7**	**21.4**	1.9	-1.0	3.0	0.0	3.0	0 1	100.5	20.4	99.8	-0.1	51.8	23.6	**54.8**	**19.9**
G47	1.5	-0.2	239.0	14.3	59.0	3.7	**4.9**	**2.1**	**6.0**	3.1	3.0	0 1	90.5	13.2	89.8	-20.1	45.3	14.6	45.8	10.8
G48	1.4	-0.3	228.0	2.8	56.2	0.9	**4.9**	**2.2**	3.0	0.2	3.0	0 2	96.8	10.0	88.3	8.0	44.0	10.9	44.3	8.8
G49	1.5	-0.2	**254.0**	**30.1**	**64.4**	**9.1**	3.4	0.5	**4.5**	1.5	2.5	-0.4	101.5	21.4	100.8	1.9	42.5	12.1	43.3	5.9
G50	1.7	0.1	233.0	7.9	57.3	2.2	**4.6**	**2.2**	**6.8**	4.2	**4.8**	2 2	79.8	-0.25	76.3	-4.1	39.0	10.0	41.3	5.8
G51	0.6	-0.9	**263.0**	**39.3**	**64.6**	**9.9**	**4.1**	**2.1**	3.3	0.1	2.3	0 1	88.3	16.0	84.8	-19.1	41.3	11.8	43.8	7.9
G52	0.9	-0.7	**246.0**	**21.4**	**60.2**	**5.6**	2.1	0.2	3.3	0.2	1.3	-0.8	82.3	13.1	86.3	-18.1	48.3	16.6	48.8	14.8
G53	1.0	-0.6	230.0	5.6	56.2	1.6	**4.1**	**2.1**	**6.8**	4.1	**4.3**	2 1	98.5	21.2	100.3	21.0	31.3	-0.5	32.3	-4.0
G54	1.4	-0.2	**254.0**	**29.3**	**64.2**	**9.1**	3.1	0.7	**4.8**	1.7	2.3	-0.3	103.0	26.4	102.3	23.0	35.0	-1.1	31.8	-5.2
G55	1.4	-0.2	**254.0**	**29.5**	**63.7**	**9.1**	2.6	0.6	**4.8**	1.5	1.8	-0.5	113.0	38.1	**111.5**	**34.0**	47.5	18.4	50.0	16.0
G56	1.6	0.0	300.0	75.4	**73.8**	**10.5**	**4.4**	**2.1**	**6.0**	3.1	2.5	0 1	95.8	23.0	96.3	8.9	41.3	11.7	42.3	4.8
G57	0.9	-0.7	**265.0**	**41.0**	**64.8**	**2.4**	**3.9**	**2.2**	**4.0**	1.2	2.0	0 2	85.0	5.6	78.8	-10.1	42.3	11.1	43.3	3.8
G58	1.5	-0.1	233.0	8.6	57.2	2.5	2.4	0.3	**4.0**	1.3	1.5	-0.7	83.3	5.0	77.3	-14.1	44.0	12.6	45.3	12.0
G59	1.5	-0.1	234.0	9.7	57.3	2.5	2.4	0.0	**6.0**	3.0	2.5	0.0	**111.5**	**26.3**	102.3	38.9	41.3	13.2	45.3	4.9
G60	1.2	-0.4	236.0	11.7	57.5	3.2	1.9	0.3	**4.0**	1.1	2.0	0 2	**107.8**	**24.0**	101.3	39.9	46.0	16.1	47.3	10.8
G61	1.6	0.0	228.0	4.0	56.0	1.2	**4.4**	**2.2**	**6.0**	3.2	2.5	0 2	105.0	28.3	97.3	23.1	44.5	14.6	47.3	11.1
G62	1.5	-0.2	**254.0**	**29.5**	**64.4**	**9.1**	3.5	0.7	**4.5**	1.7	2.5	-0.2	101.8	30.3	102.3	27.0	46.0	14.5	45.3	12.9
G63	1.4	-0.2	233.0	8.4	57.2	2.4	2.4	0.4	2.0	-0.7	1.0	-1.7	98.0	28.5	104.3	9.0	46.0	17.9	47.8	8.0
G64	1.3	-0.3	**246.0**	**21.9**	**60.5**	**5.7**	1.4	-0.8	**4.0**	1.2	2.5	0 3	**113.8**	**40.8**	**118.8**	**38.1**	43.8	15.8	47.3	11.2
G65	1.4	-0.2	294.0	70.0	**72.5**	**17.7**	2.4	0.2	**4.0**	1.2	1.5	-0.8	90.0	4.3	89.5	-0.9	39.5	8.6	41.8	5.1
G66	1.5	-0.2	239.0	13.7	59.0	3.8	**4.9**	**2.4**	**6.0**	3.5	2.0	-0.5	104.3	27.7	98.8	17.0	49.5	20.4	51.8	17.0
G67	1.5	-0.2	**254.0**	**29.5**	**64.4**	**9.1**	3.4	0.7	**4.5**	1.7	2.5	-0.2	98.8	21.2	93.3	13.0	49.5	22.5	53.3	17.9
G68	1.4	-0.2	**254.0**	**29.0**	**63.9**	**9.1**	2.9	0.9	**4.5**	1.8	2.0	-0.2	92.3	6.5	82.3	2.0	41.0	11.4	41.3	6.0
G69	1.5	-0.2	**254.0**	**29.8**	**64.4**	**9.1**	3.4	0.6	**4.5**	1.7	2.5	-0.3	102.8	22.5	97.3	17.0	38.5	9.5	40.3	5.0
G70	1.5	-0.1	229.0	4.4	56.2	1.4	1.4	-0.6	**4.0**	1.3	1.5	-0.7	**113.8**	**44.5**	**120.3**	**40.0**	39.8	12.4	42.3	7.0
G71	**2.0**	**0.8**	**264.0**	**39.5**	**64.9**	**10.1**	1.4	-0.8	**6.0**	3.2	2.5	0 2	**110.8**	**44.8**	**120.8**	**40.0**	42.8	12.6	45.3	10.8
G72	1.4	-0.2	**250.0**	**24.9**	**61.3**	**6.6**	**4.4**	**2.3**	**6.0**	3.3	2.5	0 3	87.8	18.9	91.8	-2.1	37.0	8.2	40.3	0.9
G73	1.0	-0.6	**257.0**	**32.5**	**62.7**	**8.4**	**3.9**	**2.3**	**6.0**	3.2	2.0	0 2	105.5	33.5	107.3	14.9	50.5	22.2	53.8	17.8
G74	1.4	-0.2	**253.0**	**29.4**	**63.4**	**9.11**	2.4	0.6	**4.5**	1.6	1.5	-0.4	**106.5**	**20.6**	99.3	18.0	48.5	25.1	53.3	14.0
G75	**2.1**	**0.5**	297.0	72.9	**72.8**	**18.5**	1.9	0.3	3.0	0.2	1.3	-0.8	**116.0**	**42.8**	**120.3**	**39.9**	48.3	19.7	50.3	14.8
G76	1.1	-0.5	**276.0**	**51.3**	**67.9**	**13.2**	**4.4**	**2.3**	**4.0**	1.3	1.5	-0.7	92.0	11.4	84.3	3.9	**51.5**	**20.2**	52.8	18.0
G77	1.4	-0.2	**254.0**	**29.6**	**63.9**	**9.1**	2.9	0.6	**4.5**	1.6	2.0	-0.4	74.0	-1.5	70.8	-8.1	42.5	15.8	47.3	11.8
G78	**1.8**	0.2	223.0	-1.7	54.6	-0.2	2.4	0.2	**6.0**	3.2	**4.5**	2 2	82.0	10.8	86.3	7.0	42.5	10.6	44.3	14.8
G79	1.4	-0.2	**254.0**	**29.9**	**63.9**	**9.1**	1.4	-1.0	**7.0**	4.0	2.5	0 1	90.0	16.2	92.8	12.9	45.0	17.7	49.3	12.9
G80	1.4	-0.2	**246.0**	**22.1**	**60.1**	**5.8**	1.0	-0.7	**4.0**	1.2	1.3	-0.8	104.5	29.3	106.8	13.9	42.8	17.7	48.3	7.8
G81	**2.0**	**0.3**	285.0	60.4	**70.6**	**15.4**	**4.9**	**2.3**	**6.0**	3.3	3.0	0 3	106.3	55.2	**119.8**	**40.0**	42.0	16.3	46.3	14.0
G82	**1.8**	**0.1**	227.0	2.6	56.1	0.8	**5.9**	**3.2**	**4.0**	1.2	3.0	0 2	102.5	46.0	**113.3**	**25.1**	41.3	12.7	44.3	11.9
G83	1.5	-0.2	**254.0**	**29.9**	**64.4**	**9.1**	3.4	0.6	**4.5**	1.6	2.5	-0.4	99.0	31.2	96.8	32.0	43.5	16.4	45.8	12.9
G84	**1.9**	0.3	284.0	60.3	**70.0**	**15.2**	2.4	0.1	**4.0**	1.1	2.5	0 1	**120.8**	**48.8**	**120.3**	**40.1**	51.5	28.2	**57.8**	**22.1**
G85	0.9	-0.7	**256.0**	**31.7**	**62.9**	**8.2**	2.4	0.2	3.0	0.2	2.5	0 2	102.5	38.0	101.3	21.1	39.3	11.2	39.8	9.9
G86	1.3	-0.4	**240.0**	**15.4**	59.3	4.0	**4.9**	**2.2**	**6.0**	3.2	3.0	0 2	103.3	39.0	106.3	40.1	37.0	7.7	39.5	9.4
G87	0.5	-1.1	**264.0**	**39.2**	**64.8**	**10.0**	**4.4**	**2.3**	**6.0**	3.2	**4.5**	2 2	103.3	33.0	102.3	30.0	36.5	11.3	39.8	2.9
G88	**1.9**	**0.2**	228.0	3.7	56.3	1.0	**4.9**	**2.1**	**6.0**	3.1	3.0	0 1	98.0	29.7	95.3	31.0	35.8	6.4	35.8	2.9

Geno	DS												Fe (ppm)				Zn (ppm)			
	HC		WDW		PWDW (%)		Uniformity		Clumping		Splitting		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G89	1.5	-0.1	226.0	2.1	55.5	0.7	**5.4**	**3.2**	**4.0**	1.2	**4.5**	2 2	104.8	47.8	**113.3**	**27.0**	37.8	13.4	42.8	0.9
G90	**2.0**	0.7	280.0	55.9	**68.9**	**14.1**	2.9	0.6	**4.5**	1.6	2.0	-0.4	97.5	21.8	93.3	17.1	36.5	6.7	36.8	5.1
G91	1.3	-0.3	**246.0**	**22.0**	**60.5**	**5.7**	**4.4**	**2.2**	**6.0**	3.2	**4.5**	2 2	91.8	14.7	87.3	14.1	37.0	4.0	37.3	2.8
G92	1.2	-0.4	232.0	7.8	57.0	2.3	**4.3**	**2.3**	**7.0**	4.3	**4.5**	2 3	96.8	32.3	102.3	19.0	42.0	11.7	43.3	7.0
G93	1.2	-0.4	231.0	6.6	56.2	1.9	**3.9**	**2.3**	**4.0**	1.2	**4.0**	2 2	93.5	22.4	93.3	13.0	40.0	8.2	39.3	3.8
G94	1.2	-0.4	292.0	67.9	**71.5**	**17.3**	1.9	0.3	**4.0**	1.3	**4.0**	2 2	101.3	42.1	**110.8**	**25.1**	45.8	19.0	49.3	8.9
G95	1.1	-0.5	226.0	1.2	55.3	0.5	1.4	-0.8	3.0	0.2	2.5	0 2	100.8	33.7	106.3	23.1	42.0	8.0	41.3	7.8
G96	**2.1**	**0.5**	299.0	74.6	**73.7**	**19.0**	2.4	0.3	**4.0**	1.3	1.5	-0.7	97.0	33.3	103.3	29.0	46.8	17.7	48.8	15.9
G97	1.4	-0.2	**253.0**	**29.5**	**63.4**	9.1	2.4	0.6	**4.5**	1.6	1.5	-0.4	97.5	19.4	96.3	30.1	44.5	12.5	44.3	13.0
G98	1.2	-0.4	290.0	65.8	**71.0**	16.7	1.9	0.3	**4.0**	1.2	2.0	0 2	101.5	37.6	**112.3**	**25.0**	47.8	19.7	49.8	12.8
G99	1.4	-0.2	**254.0**	**29.4**	**63.9**	9.1	2.9	0.7	**4.5**	1.7	2.0	-0.3	95.0	28.7	101.3	12.1W	41.8	6.5	39.8	9.8
G100	**2.0**	0.4	280.0	55.9	**68.9**	14.1	2.4	0.1	**4.0**	1.1	1.5	-0.9	99.3	33.8	104.8	10.0	45.0	16.8	47.8	6.8
G101	1.4	-0.2	**254.0**	**29.3**	**63.9**	9.1	2.9	0.8	**4.5**	1.7	2.0	-0.2	**113.3**	**42.8**	**110.3**	**40.0**	**51.5**	**22.6**	53.8	19.9
G102	**2.1**	1.4	295.0	69.9	**73.0**	17.8	**4.9**	**2.4**	**6.0**	3.3	3.0	0.4	**115.5**	**55.7**	**122.3**	**42.0**	41.5	11.5	43.3	8.0
G103	0.9	-0.7	**265.0**	**40.7**	**65.2**	10.5	**4.4**	**2.3**	**4.0**	1.3	2.5	0 3	**109.0**	**46.5**	**111.8**	**24.0**	47.3	13.9	44.3	13.0
G104	1.4	-0.3	**255.0**	**30.4**	**63.1**	7.8	**4.9**	**2.2**	3.0	0.2	3.0	0 2	101.8	40.1	**109.3**	**19.1**	44.3	12.4	45.8	6.9
G105	1.6	-0.1	**256.0**	**30.6**	**63.2**	8.0	2.9	0.4	3.0	0.3	2.0	-0.6	101.3	39.7	94.8	10.0	39.3	7.0	38.3	0.0
G106	**2.0**	0.8	296.0	71.5	**73.3**	18.0	**4.9**	**2.1**	4.0	1.1	2.0	-0.8	96.3	38.7	106.3	17.0	39.0	9.7	40.8	2.9
G107	1.1	-0.5	**262.0**	**37.0**	**64.3**	9.5	**4.4**	**2.3**	3.0	0.2	1.5	-0.8	91.3	7.1	78.5	6.0	38.8	8.0	38.3	0.9
G108	1.7	0.1	**276.0**	51.1	**67.8**	13.1	**4.4**	**2.3**	**4.0**	1.3	2.5	**0 3**	96.0	31.0	96.3	**16.0**	42.8	**12.9**	43.3	**8.0**
G109	1.5	-0.2	237.0	11.9	58.5	3.3	**4.9**	**2.4**	**7.0**	4.3	**5.0**	**2.4**	89.8	19.7	**96.5**	**16.0**	**41.3**	**9.5**	**41.8**	**7.0**
G110	1.5	-0.2	**254.0**	**30.0**	**64.4**	**9.2**	**3.5**	**0.6**	**4.5**	1.6	2.5	**-0.4**	**108.8**	**26.0**	**96.3**	**40.0**	**42.8**	**12.1**	**43.3**	**9.0**
Mean	1.4		257.0		63.4		3.3		4.5		2.4		97.1(1.4%)		95.7		43.7(0.9%)		44.1	
H^2 (%)	99.4		99.3		99.2		98.6		98.4		97.3		52.7		29.6		59.0		61.0	
LSD (5%)	0.04		4.95		0.27		0.49		0.53		0.56		20.12		6.33		7.94		2.80	

Geno genotype, Ĝ predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *HC* hydration coefficient, *WDW* washed drained weight, *PWDW* percentage washed drained weight, *DS* drought stressed, *NS* non-stressed, *LSD* Least significant difference, H^2 broad-sense heritability, *Fe* iron, *Zn* zinc, *ppm* parts per million. The value in brackets under the mean which corresponds to Fe and Zn represents the percentage increase and decrease respectively in drought stressed conditions.

NB: Values in bold were above the breeding target and the respective genotype outperformed the standard check

Appendix 5.3 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 110 genotypes over two seasons (2019 and 2020) of navy bean genotypes for shoot, agronomic and nutritional quality traits evaluated under drought stressed and non-stressed conditions at Save valley experiment station, Zimbabwe.

Geno	GYD (kg/ha)				NMPP				NSP				NSPP				DPM				SW (g)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G1	1200	175	2407	-150	**30**	**-10.0**	40	19.0	7	0.3	7	0.6	**123**	**-24.5**	174	0.2	102	1	108	0	20.4	-3.6	21.2	1.4
G2	1330	-116	1393	-1828	**22**	**-25.4**	23	-26.6	6	-1.2	6	-0.7	56	-71.6	90	-151.0	101	0	106	-2	**26.3**	**2.1**	**25.3**	**7.0**
G3	**1652**	**460**	1148	-1390	**25**	**-11.1**	20	-22.5	7	-0.0	6	0.1	82	-29.4	73	-133.0	102	1	110	5	**27.5**	**3.6**	**30.3**	**10.6**
G4	1267	-155	1937	-922	**31**	**-8.3**	16	-19.8	7	-1.2	5	-1.3	83	-48.6	32	-144.0	100	-1	111	6	**34.5**	**15.1**	**27.3**	**8.3**
G5	1093	26	1641	-1942	18	-18.2	20	-24.6	6	-1.3	5	-2.8	46	-57.7	53	-120.0	103	1	112	5	**28.8**	**3.2**	**27.4**	**6.5**
G6	1244	282	1674	-1689	21	-12.5	20	-31.0	7	0.0	**7**	**0.5**	**91**	**-41.5**	80	-146.0	101	-1	108	0	21.0	-1.5	20.0	-5.0
G7	1248	-157	1889	-765	19	-22.3	24	-11.1	6	-1.4	6	0.4	80	-60.5	94	-69.0	101	-2	108	-2	20.3	**-3.3**	**31.1**	**1.8**
G8	881	-452	1267	-2301	13	-23.6	28	-32.0	6	-0.0	5	-2.9	49	-74.4	108	-162.0	101	-1	109	0	19.3	-4.4	20.5	0.6
G9	1111	15	1370	-588	16	-21.8	13	-21.3	3	-2.2	4	-0.3	31	-105.1	25	-149.0	102	-2	110	0	**38.5**	**32.1**	**34.3**	**23.3**
G10	679	-601	874	-1579	12	-28.8	6	-20.6	5	-1.9	4	-0.6	23	-101.1	**11**	**-130.0**	102	1	109	3	**36.3**	**2.2**	**54.8**	**38.3**
G11	1156	-310	944	-1891	**22**	-22.2	17	-28.3	7	-1.0	6	0.2	**86**	**-63.7**	69	-141.0	102	1	108	0	26.8	**0.3**	**22.5**	**2.1**
G12	1337	160	1185	-1676	20	-14.6	22	-24.0	7	0.4	7	-0.7	**94**	**-29.7**	105	-107.0	101	-2	111	5	**22.0**	**-1.6**	**21.8**	**3.9**
G13	1504	-179	1774	-1334	**29**	-11.4	28	-17.6	6	-1.3	7	0.4	**116**	**-30.0**	88	-98.9	100	-1	108	0	20.3	-5.2	20.5	0.7
G14	1374	-253	2007	-1273	19	-21.6	30	-8.9	5	-1.5	6	-0.5	79	-71.7	128	-60.7	101	-1	111	5	**23.5**	1.3	21.0	1.0
G15	1026	87	2270	-961	14	-19.1	15	-16.2	5	-2.7	5	-0.8	42	-66.6	43	-106.0	100	-2	109	0	**42.0**	**20.9**	**42.3**	**25.4**
G16	1915	680	1170	-1003	**34**	-2.4	27	-8.1	7	-1.3	7	-0.1	**122**	**-26.1**	89	-78.0	101	-1	109	0	18.5	-5.3	20.9	2.7
G17	1063	-202	1344	-1272	12	-24.6	11	-17.2	5	-2.2	4	-1.3	27	-84.6	26	-108.0	101	-2	107	-2	52.5	**30.9**	**34.0**	**27.0**
G18	848	-527	1774	-1148	18	-10.9	48	23.9	5	-0.8	6	-1.1	45	-60.5	137	2.2	102	0	108	0	**30.5**	14.8	19.8	0.7
G19	**2526**	**1451**	**2515**	**-1066**	**26**	**-17.1**	27	-10.4	7	-0.5	7	0.0	**85**	**-61.2**	95	-91.2	103	1	109	0	**24.0**	**2.8**	**23.0**	**5.5**
G20	**2244**	**2135**	1811	257	15	-25.7	30	-5.3	6	-1.5	6	-1.8	38	-75.7	72	-108.0	102	1	108	0	**28.8**	**0.3**	**51.9**	**33.1**
G21	1344	242	1659	-726	14	-19.2	34	1.3	6	-1.0	**8**	**0.8**	42	-52.3	118	-35.0	101	-2	111.0	6	**25.5**	1.7	19.9	5.8
G22	981	65	615	-1433	21	-15.7	21	-9.6	6	-1.1	5	-0.7	58	-53.7	33	-103.0	101	-2	109	-1	**47.0**	**30.2**	**47.3**	**24.4**
G23	685	-237	1215	-1117	7	-24.0	11	-23.4	5	-1.3	6	1.5	17	-86.1	35	-116.0	101	-1	109	0	**27.0**	**-9.4**	**40.1**	**14.2**
G24	1896	680	1763	-1877	13	-24.7	15	-22.1	7	-0.6	6	-1.2	56	-59.7	66	-116.0	102	0	108	-1	**21.1**	**-2.1**	**22.0**	**1.9**
G25	1093	-22	1589	-1286	**24**	**-18.7**	19	-20.7	7	-0.5	7	-0.9	**98**	**-32.8**	84	-103.0	103	0	109	3	**23.8**	**2.6**	**22.3**	**2.4**
G26	1241	180	1648	-1696	**27**	**-18.8**	36	-19.1	7	0.0	7	0.2	**87**	**-47.3**	118	-125.0	103	1	108	0	**25.5**	**1.6**	**25.9**	**3.6**
G27	1333	-59	1707	-947	**34**	**-12.0**	33	-9.4	7	-0.7	7	0.5	66	-36.6	122	-70.0	103	1	108	0	18.8	-5.4	19.0	0.2

Geno	GYD (kg/ha)				NMPP				NSP				NSPP				DPM				SW (g)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G28	1481	20	1515	-1423	**26**	**-16.7**	30	-13.8	7	-0.0	7	-0.2	**105**	**-38.3**	115	-88.0	101	-2	109	0	**21.5**	**-1.8**	**21.6**	**2.8**
G29	**2115**	**554**	**2541**	**123**	**4**	**5 3**	38	-2.6	8	-0.1	7	0.3	**139**	**30.3**	133	-25.0	103	1	107	-2	**22.0**	**-0.3**	**23.8**	**4.9**
G30	**2289**	**2447**	2322	-756	**34**	**-10.8**	**47**	**1.9**	7	0.0	6	0.2	**92**	**-16.3**	171	5.6.0	103	0	108	-1	**22.8**	1.1	20.8	3.1
G31	1378	554	1410	-601	14	-20.2	30	-7.1	5	-2.8	4	-2.4	29	-90.2	82	-88.0	101	0	110	0	**26.8**	**1.7**	**33.8**	**1.6**
G32	1152	-499	1685	-1659	**27**	**-6.2**	40	-16.4	7	-0.4	6	-1.2	84	-62.1	119	-97.0	101	0	112	3	19.0	**-3.2**	**22.5**	**4.0**
G33	796	-150	1137	**-1536**	16	-16.6	24	-17.3	6	-1.0	6	1.5	63	-44.1	96	-86.0	103	0	111	-2	19.8	-4.3	19.6	1.8
G34	**2004**	**538**	**2448**	-1096	**28**	**-10.7**	38	-11.9	7	-0.9	7	-0.2	**102**	**-34.1**	139	-73.0	102	-1	112	0	19.4	-3.2	20.6	2.0
G35	**2059**	**569**	1159	**-1613**	20	-14.5	20	-17.8	7	-0.5	6	-1.0	78	-44.6	80	-88.0	103	1	109	0	**22.0**	**-1.9**	**22.6**	**1.2**
G36	1048	-395	**2700**	-1741	16	-17.7	30	-20.9	7	-0.9	7	0.3	55	-64.1	141	-102.0	101	-1	112	5	**22.5**	**0.8**	**22.6**	**2.0**
G37	770	-718	1856	-1649	19	-18.3	26	-34.0	7	-1.2	7	-0.2	70	-62.8	88	-160.0	102	-2	110	-1	**22.3**	**-0.8**	**21.6**	**1.7**
G38	1467	51	1907	-751	18	-17.7	22	-14.8	7	-0.2	7	-0.7	**84**	**-32.8**	101	-67.0	103	0	109	0	**26.0**	0.2	20.8	0.3
G39	1411	327	1944	-1520	23	-10.4	33	-19.9	7	-0.3	7	-0.3	**94**	**-29.6**	126	-99.0	102	-1	109	0	**21.5**	**-0.9**	**21.6**	**2.1**
G40	1763	339	1704	-1395	15	-20.6	27	-18.8	6	-1.5	6	-0.5	51	-83.1	100	-99.0	102	0	109	0	**23.5**	**-1.3**	**22.8**	**4.8**
G41	1430	-142	1333	-2022	**27**	**-6.8**	30	-24.2	7	-0.4	7	-0.8	**99**	**-3.3**	89	-119.0	101	-2	112	5	20.0	**-4.5**	**23.7**	**0.0**
G42	**1674**	**721**	2222	-155	**34**	**17.1**	30	-3.0	6	-1.3	6	-1.3	58	-42.8	104	-72.0	100	-3	110	0	**25.8**	**0.4**	**25.0**	**6.8**
G43	**1600**	**1025**	**3119**	**255**	21	-6.0	37	6.1	7	-0.9	7	0.0	75	-29.6	156	25.0	102	0	111	0	**22.8**	**-4.7**	**23.6**	**6.7**
G44	1448	519	1463	-1709	12	-18.1	21	-17.8	6	-1.1	6	0.4	44	-69.1	72	-91.0	102	1	111	3	**27.5**	**4.9**	**24.3**	**5.4**
G45	**1685**	**1062**	2107	-323	**29**	**5.0**	35	8.6	6	-0.9	7	0.5	**101**	**5.9**	122	29.0	100	-4	110	1	**20.8**	-4.7	20.9	1.7
G46	1022	-474	1422	-1705	**25**	**-3.0**	28	-9.9	7	-0.1	7	0.8	77	-42.7	110	-51.0	103	1	112	0	**21.5**	**-2.2**	**21.6**	**2.3**
G47	1578	720	1889	-509	**24**	**-7.3**	28	-4.9	7	-0.3	7	-0.3	84	-23.9	106	-36.0	102	1	112	0	**23.5**	**-1.0**	**23.7**	**3.3**
G48	1378	159	**2578**	**-1164**	**26**	**-5.4**	33	-9.0	6	-0.9	7	-1.0	80	-72.0	115	0.1	102.	0	111	0	**23.8**	**-0.4**	**21.5**	**2.9**
G49	1100	304	970	-1090	12	-12.5	22	-15.9	5	-1.6	6	-1.6	28	-98.0	48	-1.2	102	0	109	0	**32.8**	**0.3**	**45.6**	**20.3**
G50	**2196**	**1558**	1422	-1582	**44**	**27.0**	36	-14.9	7	0.1	7	0.1	**156**	**92.0**	74	0.5	99	-4	109	0	**24.3**	3.3	20.5	1.7
G51	911	634	1663	-401	7	-22.8	16	-14.1	5	-3.0	5	-3.0	15	-97.0	42	-1.7	102	0	108	0	**38.3**	**26.8**	**43.7**	**19.6**
G52	1481	1140	2185	230	10	-17.2	27	-15.7	6	-1.7	6	-1.7	33	-77.0	42	-1.0	100	-3	109	0	**48.8**	**32.1**	**39.5**	**29.5**
G53	**2448**	**2017**	1959	-447	**25**	**-6.5**	34	-7.4	6	-1.2	6	-1.2	80	-51.0	109	-0.3	102	0	108	-2	**24.5**	**2.4**	**25.1**	**3.8**
G54	874	-363	1841	-2204	15	-19.1	20	-30.7	4	-1.8	6	-1.8	52	-135.0	83	-1.5	101	0	108	-1	**21.8**	**-2.0**	**30.4**	**-0.3**
G55	1296	318	1981	-1462	**26**	**-19.1**	23	-21.8	7	-0.7	7	-0.7	**98**	**-93.0**	79	-0.4	104	1	109	0	**21.8**	**-3.7**	**21.4**	**3.5**
G56	**1630**	**331**	**2652**	**-290**	**27**	**-9.5**	39	9.4	7	-0.2	6	-0.2	**130**	**28.0**	**177**	**-1.9**	103	0	108	0	**27.0**	**3.3**	**22.5**	**1.6**
G57	1096	-75	1996	-1674	18	-16.2	24	-21.2	7	-0.2	7	-0.2	72	-91.0	105	-0.5	101	-3	109	0	**21.5**	**-2.9**	**22.0**	**4.5**

Geno	GYD (kg/ha)				NMPP				NSP				NSPP				DPM				SW (g)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G58	1407	353	1967	-842	**23**	**-10.8**	30	-15.2	7	-0.9	**7**	**-0.9**	**99**	**-64.0**	**106**	**-1.0**	103	-1	109	-1	19.5	-5.8	18.1	0.9
G59	**1870**	**530**	**2819**	**-100**	**24**	**-0.7**	**56**	**6.4**	6	-2.5	**8**	**-2.4**	**104**	**51.0**	**243**	**0.8**	102	-1	109	0	20.4	-3.3	19.4	3.1
G60	1593	586	2081	-872	**27**	**-3.4**	31	-8.7	7	-0.3	**7**	**-0.3**	**102**	**-43.0**	121	-0.1	102	-2	111	3	19.8	-5.1	20.4	3.0
G61	1128	-169	**3100**	**1351**	13	-25.9	39	22.1	6	-1.5	**7**	**-1.5**	61	92.0	169	1.3	101	-2	109	0	**21.0**	**-3.8**	**23.4**	**6.8**
G62	1078	119	859	-485	9	-20.3	19	0.3	5	-2.5	5	-2.5	28	-66.0	44	-1.7	101	0	108	-1	**36.0**	**-1.7**	**49.5**	**27.4**
G63	1037	17.6	1856	444	11	-21.2	18	-4.3	6	-1.1	6	-1.1	29	-58.0	47	-0.8	100	-3	111	5	**33.3**	**0.8**	**48.3**	**31.3**
G64	1481	-232	2056	-857	**30**	**-15.3**	30	-11.1	7	-0.6	**7**	**-0.6**	**115**	**-65.0**	81	0.4	102	0	108	-1	**23.4**	**-1.2**	**23.1**	**3.6**
G65	778	-332	2030	-1079	15	-24.4	38	-10.4	7	-0.5	6	-0.5	67	-36.0	164	-0.2	102	1	108	0	**23.8**	**-2.8**	**33.5**	**6.8**
G66	1393	674	1533	-978	17	-10.1	24	-12.3	8	-0.2	7	-0.2	54	-37.0	97	0.2	101	-2	108	0	**25.0**	**-0.9**	**23.5**	**5.6**
G67	507	-289	941	-1211	15	-9.8	23	-11.8	7	-0.5	5	-0.5	45	-82.0	72	-1.1	103	0	110	3	**23.3**	-1.7	21.0	1.4
G68	1593	944	**2511**	**126**	21	-7.2	17	-11.8	8	0.4	7	0.4	84	-61.0	63	-0.3	102	-1	109	0	20.4	**-5.7**	**23.6**	**6.3**
G69	1263	51	1270	-1281	**22**	**-16.6**	28	-2.2	7	-0.3	6	-0.3	78	-49.0	86	-1.0	103	-1	112	0	**23.0**	**-2.4**	**21.3**	**2.9**
G70	**2004**	**573**	**3300**	**1519**	**21**	**-9.2**	37	19.2	7	0.4	**7**	**0.4**	**104**	**101.0**	144	0.2	104	1	109	0	**24.8**	**-2.1**	**22.6**	**5.3**
G71	1037	-497	**2874**	**-1499**	**27**	**-17.3**	31	-9.8	7	-1.6	**8**	**-1.6**	**100**	**-69.0**	135	-0.3	103	-1	110	0	**22.5**	**-5.4**	**25.3**	**3.4**
G72	1278	508	**3285**	**-86**	**21**	**-11.9**	39	8.3	7	-1.2	8	0.8	**93**	**-37.7**	**198**	**74.0**	102	-2	108	-1	**22.5**	**-2.2**	**22.4**	**6.6**
G73	1363	858	1581	-1451	**28**	**2.6**	**42**	**12.3**	6	-0.0	7	-0.3	66	-10.3	90	-63.0	103	-1	114	4	**32.8**	**9.3**	**32.0**	**13.7**
G74	1200	-35	1570	-1358	17	-14.2	22	-4.0	5	-4.1	7	-0.1	32	-65.5	51	-79.0	103	0	112	3	**39.0**	**16.1**	**33.5**	**17.0**
G75	967	-141	2107	-701	19	-15.6	33	10.8	6	-2.1	6	-1.8	42	-64.1	83	-27.0	104	1	112	-1	**31.3**	**2.1**	**29.4**	**7.7**
G76	819	34	1326	-1449	12	-17.9	29	-4.7	6	-2.2	6	-2.7	31	-70.2	70	-81.0	103	0	112	5	**32.0**	**6.3**	**26.3**	**10.6**
G77	1341	331	1622	-934	**27**	**-9.7**	**44**	**1.8**	7	-0.5	**8**	**0.4**	**104**	**-12.5**	123	-36.0	102	-1	109	0	19.5	-9.0	19.5	0.8
G78	**1837**	**1363**	**2467**	**-18**	**24**	**-7.8**	**43**	**9.2**	5	-2.1	7	-0.8	66	-35.0	154	11.6	101	0	108	-1	**26.5**	**0.1**	**24.5**	**8.9**
G79	**1641**	**989**	1981	-766	**37**	**0 1**	36	4.3	6	-1.8	7	-0.5	**95**	**-29.8**	122	-41.8	102	1	114	2	**26.5**	**-1.1**	**23.5**	**8.3**
G80	1119	200	1944	-1212	15	-10.1	32	-6.2	6	-1.1	7	-1.3	61	-24.1	123	-48.0	103	1	114	3	**21.8**	**-6.9**	**21.9**	**1.2**
G81	1056	-0.2	2067	-1552	16	-14.0	27	-21.8	6	-1.8	**7**	**-0.4**	55	-55.9	97	-95.0	102	-2	109	-1	20.0	-4.9	19.87	0.9
G82	1019	-71	**2759**	**-684**	14	-19.4	**41**	**-15.8**	6	-1.7	6	-2.0	44	-56.8	173	-74.0	103	-1	109	0	**23.3**	**-2.1**	**24.5**	**6.2**
G83	770	45	1474	-838	13	-17.3	24	-13.7	5	-2.6	7	0.1	55	-58.8	86	-86.0	105	4	113	3	**30.5**	**6.8**	**28.7**	**10.6**
G84	1448	294	1285	-1854	16	-15.3	21	-24.1	7	-0.6	**8**	**0.7**	61	-53.3	88	-126.0	103	0	112	2	**23.6**	-1.2	20.1	-1.2
G85	1241	66	1267	-1421	**33**	**0.23**	31	-15.0	6	-1.1	7	-0.0	**110**	**4.8**	106	-111.0	103	0	112	4	15.3	-8.3	16.0	-2.6
G86	**1948**	**633**	**2548**	**-1255**	**23**	**-6.88**	30	-21.8	7	-0.2	**7**	**0.0**	**92**	**5.7**	133	-105.0	103	0	112	6	17.8	-9.1	19.0	2.2
G87	956	-34	1289	-1219	**31**	**-1.2**	29	-3.8	6	-1.2	6	-1.0	**108**	**-8.9**	86	-62.0	104	1	109	0	18.3	-7.7	20.3	3.5

Geno	GYD (kg/ha)				NMPP				NSP				NSPP				DPM				SW (g)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G88	1078	-326	**3000**	**177**	**24**	**-7.3**	38	-1.7	7	-0.6	**8**	**1.2**	**101**	**-10.3**	**186**	**3.3**	103	0	109	0	**22.0**	**-2.7**	**24.0**	**3.1**
G89	1778	528	**2970**	**-517**	**24**	**-0.5**	39	-4.3	7	-0.6	7	-0.5	**90**	**-14.6**	169	-20.0	102	-1	111	3	**23.5**	-0.4	21.0	3.5
G90	**1870**	**-232**	2207	-1491	**39**	**-6.3**	33	-8.1	7	-1.1	**8**	**0.2**	**98**	**-25.3**	128	-68.0	103	1	109	0	20.1	**-5.2**	**22.7**	**2.3**
G91	**2067**	**697**	1663	-1867	**25**	**-8.3**	32	-22.4	7	-0.2	7	-0.7	**122**	**-22.0**	124	-112.0	103	1	113	8	**20.5**	**-6.4**	**22.1**	**2.2**
G92	**1648**	**1117**	**2748**	**554**	15	-12.0	**48**	**9.1**	6	-1.8	7	-0.7	42	-42.6	130	-57.0	104	1	110	0	**28.5**	**3.8**	**30.5**	**7.4**
G93	**2081**	**874**	2330	-11	**38**	**-0.4**	26	-9.3	6	-1.2	7	-0.2	**113**	**-12.2**	101	-48.0	103	0	110	0	**24.8**	**2.2**	**26.7**	**4.5**
G94	493	-565	1830	-989	13	-18.7	34	-5.6	5	-2.1	6	-1.7	40	-75.9	112	-76.0	103	0	113	5	**26.5**	**2.9**	**24.2**	**0.4**
G95	**1946**	**609**	**3293**	**-423**	**31**	**-6.3**	**45**	**1.6**	6	-1.2	6	-1.7	68	-71.0	161	-28.0	103	0	115	7	**27.5**	**1.6**	**25.0**	**4.2**
G96	1356	-98	1756	-1350	13	-19.5	34	-11.4	6	-1.8	67	-07	55	-81.6	127	-89.0	103	0	109	-1	17.3	-9.7	17.3	-1.6
G97	1307	-167	**3163**	**-199**	17	-18.7	24	-18.6	7	-1.7	**7**	**-0.0**	76	-69.9	106	-95.0	104	1	109	0	19.5	**-10.4**	**24.0**	**3.8**
G98	744	-221	**2815**	**-1239**	14	-19.1	**46**	**6.6**	7	-1.2	**7**	**-0.2**	67	-62.5	95	-40.0	103	1	109	-1	19.3	-11.5	17.8	3.0
G99	1578	-21	**3011**	**-504**	**27**	**-0.8**	35	-2.4	7	-0.7	**7**	**0.3**	**98**	**-30.0**	157	-15.0	102	0	112	5	19.3	-6.4	20.8	1.2
G100	1111	-245	1978	-502	**24**	-11.7	33	-0.32	7	-1.1	7	-0.6	**103**	**-43.0**	158	-9.0	103	1	112	5	**22.3**	**-5.5**	**26.5**	**2.1**
G101	1193	327	1107	-2152	19	-17.7	39	-13.9	7	-0.4	**7**	**-0.3**	55	-59.3	142	-53.0	102	0	110	3	18.3	-6.3	19.8	-0.6
G102	1411	162	1400	-1498	**34**	0 3	40	-13.4	8	-0.1	**8**	**-0.2**	**106**	**-16.2**	159	-79.0	104	1	108	-2	18.5	**-5.8**	**24.0**	**-2.7**
G103	**1707**	**-149**	**3344**	**-234**	**36**	**-11.0**	**53**	**-9.1**	7	-0.9	**7**	**-0.3**	**131**	**-26.9**	**227**	**-62.0**	101	0	109	0	**21.8**	**-1.6**	**23.8**	**1.3**
G104	**1719**	**424**	**2815**	**-793**	20	**-18.0**	24	-20.5	5	-2.0	5	-2.2	62	-48.1	81	-111.0	102	-1	111	0	**35.5**	**16.5**	**39.0**	**17.1**
G105	**2619**	**1162**	**2933**	**124**	**37**	**-0.3**	34	-11.9	7	-0.1	**7**	**-0.2**	**158**	**10.8**	139	-37.0	102	-1	110	-1	**23.0**	**-0.8**	**25.0**	**3.3**
G106	748	-608	1515	-1347	**30**	-18.0	**44**	**-6.9**	6	-1.4	6	-1.6	72	-59.6	77	-114.0	104	1	115	6	20.0	**-7.6**	**22.5**	**1.0**
G107	1170	810	1848	-454	15	-16.4	23	-19.9	4	-2.5	6	-2.3	35	-62.1	81	-115.0	103	-1	109	-1	**32.5**	**16.0**	**29.8**	**14.4**
G108	**2219**	**666**	2089	-1098	**28**	-17.5	**44**	**-12.1**	6	-0.4	**8**	**-0.3**	**115**	**-49.9**	169	-77.0	104	0	109	0	20.3	-2.6	20.0	1.3
G109	1504	-60	1619	-987	**25**	-8.8	37	-21.4	8	0.9	6	-1.2	**126**	**-15.7**	132	-104.0	101	-1	108	0	**23.5**	-1.8	20.5	-1.7
G110	**1907**	**-68**	**2500**	**-1038**	**24**	**-14.2**	36	-14.4	7	-1.7	7	-0.5	87	-53.4	159	-32.0	102	1	111	-1	**22.0**	-1.7	18.5	2.0
Mean	1393.0		1940.0		22.0		29.9		6 2		6.4		75.0		106 9		102		109.6		**24.9**		**25.6**	
H^2	42.1		24.8		60.4		33.1		63.4		53.3		65.7		45.7		28.8		15.4		**79.7**		84.9	
LSD	745.3		1142.0		13.3		18.2		1.4		1.3		49.2		75.2		ns		1.0		4.0		5.7	

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *GYD* seed yield, *NMPP* number of mature pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100 seed weight, *DS* drought stressed, *NS* non-stressed, ns not significant, *LSD* least significance difference at 0.05, H^2 broad-sense heritability (%). **NB:** Values in bold were above the breeding target and the respective genotype outperformed the standard check.

Appendix 5.4 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 110 genotypes over two seasons (2019 and 2020) of navy bean genotypes for shoot and physiological traits evaluated under drought stressed and non-stressed conditions at Save valley experiment station, Zimbabwe.

Geno	CB (kg/ha)				PHI (%)				LCC				SC (mmol m^{-2} s^{-1})				LT (°C)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G1	**2655**	**-700**	3075	956	63.5	2.1	60.3	-24 2	30.3	0.6	46.2	-3.2	56.8	-55.1	120.8	-15.4	26.0	0.1	19.4	0.3
G2	1770	-1716	1725	-2586	62.6	0.3	66.6	-14 3	17.0	-8.5	20.7	-34.4	59.6	10.0	158.4	21.5	26.2	3.0	20.5	1.9
G3	**2400**	**-643**	1725	-1843	61.7	1.7	57.8	-20 5	28.7	2.9	36.1	-9.6	53.5	-1.4	108.4	-2.7	25.1	2.3	19.9	0.3
G4	**2625**	**-538**	1725	-1426	56.9	-8.6	55.2	-21 5	24.3	-5.9	43.2	-5.4	43.3	-27.2	141.7	0.5	26.7	1.9	18.4	-0.8
G5	1803	-1040	1650	-1941	60.2	0.1	65.4	-22.8	25.7	-8.3	40	-1.9	94.1	40.2	143.5	10.9	27.0	3.4	19.2	0.6
G6	**2205**	**-600**	1950	-2700	61.5	6.5	50.8	-22.7	25.6	-5.8	37.6	-12.0	54.4	-4.8	110.5	6.9	28.6	3.6	20.2	0.4
G7	**2235**	**-1003**	1950	-560	61.4	5.3	66.7	-6.0	30.0	-10.3	43.5	-3.6	74.9	-51.4	111.9	-6.5	27.8	3.2	20.4	2.3
G8	1575	-1993	2805	-2833	50.0	-8.3	60.5	-25 5	21.1	0.9	39.7	-7.0	43.4	-21.6	118.3	-16.1	24.0	-1.0	19.2	1.7
G9	1950	-688	1980	-826	55.6	-3.6	68.3	-8.4	25.2	-7.7	32.4	-6.5	58.5	-33.8	60.0	-95.7	26.9	0.1	17.5	-1.2
G10	1494	-1602	1650	-1760	61.5	5.4	46.5	-22.7	27.5	4.8	43.9	-3.3	86.6	62.4	141.7	35.7	34.1	8.7	22.8	1.4
G11	2130	-1776	1500	-2530	60.3	-2.3	42.9	-33.7	23.6	-11.8	33.5	-19.6	14.8	-85.7	151.3	-3.8	30.6	6.8	20.5	1.2
G12	**2250**	**-615**	2325	-1881	**65.6**	**3.6**	72.1	**-26.7**	30.8	-0.4	38.8	-8.4	35.1	-47.0	85.0	-72.3	28.6	4.7	19.2	0.1
G13	**2265**	**-823**	2025	-1486	**72.1**	**8.4**	58.6	**-19 9**	28.9	5.0	40.9	-6.4	38.5	-37.5	137.6	21.6	26.4	3.2	17.5	-1.0
G14	**2400**	**-1198**	2625	-769	**63.8**	**0.1**	76.5	**-14 2**	23.2	-1.9	38.4	-5.4	36.8	-46.2	85.5	-6.2	26.2	3.4	20.1	1.3
G15	2010	-463	2055	-1254	52.7	-7.1	62.1	-17.0	22.3	-0.3	38.3	-9.2	78.7	40.4	134.1	-22.4	28.9	3.8	20.2	0.3
G16	**3225**	**-210**	1800	-1143	58.1	-10.0	58.0	-21 1	32.1	6.6	41.0	-6.0	105.2	-12.9	136.7	-20.3	27.5	2.8	20.4	-1.1
G17	1950	-1363	1425	-954	50.6	-5.6	72.5	-21 2	41.9	9.4	41.0	-6.5	94.8	-4.6	149.3	61.5	29.5	3.9	20.2	1.3
G18	1905	-1303	3375	1064	**66.0**	**10.8**	54.9	**-28.4**	36.3	8.6	40.5	-8.1	44.6	-81.6	112.4	-39.0	25.9	2.1	18.9	1.1
G19	**2700**	**-748**	1875	-1068	62.0	-1.7	70.9	-23.4	34.6	-8.3	45.0	-2.8	53.6	-51.3	158.5	-2.6	26.9	2.1	18.2	-2.0
G20	2175	-1026	2850	920	59.8	-5.7	67.1	-16 2	31.5	0.9	42.4	-4.0	120.8	11.4	200.5	58.8	27.8	2.8	19.5	1.5
G21	1575	-1140	2475	445	**68.8**	**11.3**	74.6	**-13.4**	25.8	-4.5	38.5	-9.7	25.3	-63.6	58.8	-39.3	28.3	3.4	21.8	4.1
G22	1875	-688	1350	-428	61.3	0.9	53.5[i]	-18.7	26.0	5.3	34.0	-16.3	70.2	26.4	131.4	-21.1	28.8	4.4	20.3	2.5
G23	1215	-1378	2010	-240	52.5	-4.4	66.4	-18 9	23.6	-2.8	35.0	-26.3	62.4	13.3	109.2	-29.4	27.7	3.3	20.7	2.4
G24	1665	**-1588**	1425	-1478	**64.5**	12.6	65.6	-23.7	30.4	5.5	46.4	-3.1	24.6	-64.8	102.8	17.9	31.8	4.6	22.4	4.3
G25	1950	-1123	1500	-993	**64.5**	2.3	46.	-24.6	21.5	-2.4	37.2	-5.0	60.7	-44.9	29.2	-99.3	28.1	2.7	20.6	1.6
G26	2100	**-801**	1650	-2004	**67.1**	3.3	48.1	-19 5	31.1	2.3	39.0	-8.8	137.1	7.0	165.2	41.3	23.6	1.8	19.9	1.4
G27	**2625**	**-628**	2175	-1110	58.0	-4.4	63.6	-16 5	36.6	2.7	42.2	-9.7	45.9	-44.6	174.4	33.1	26.3	1.8	20.2	0.1

Geno	CB (kg/ha)				PHI (%)				LCC				SC (mmol m^{-2} s^{-1})				LT (°C)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G28	**2250**	-1140	1575	-1505	60.8	-4.5	58.8	-20 9	26.7	-5.1	35.7	-12.5	61.6	-29.4	109.5	-27.0	25.8	3.2	19.6	0.9
G29	**4200**	**1112**	2850	22	57.7	7.8	75.8	-7.0	36.4	3.0	38.5	-13.0	43.3	-42.5	183.6	44.9	29.4	4.2	19.8	-0.4
G30	**2265**	**-351**	3300	-54	63.1	2.0	64.4	-3.6	35.4	-5.8	40.3	-9.7	51.9	-8.6	110.9	-8.5	27.5	1.9	20.7	1.7
G31	1845	-681	3300	1498	53.5	1.5	58.4	-20 5	33.2	7.3	36.3	-3.4	38.5	-38.6	142.2	-18.7	29.3	2.8	20.1	2.0
G32	**2625**	-396	2550	-1536	61.1	-3.5	65.3	-5.4	36.4	3.5	41.1	-3.2	120.8	62.9	168.1	14.4	28.1	2.8	18.9	0.6
G33	1425	-1236	2175	-1169	59.2	1.2	66.0	-17.8	21.9	-3.4	37.0	-10.5	52.6	-15.8	80.7	-16.8	27.2	1.9	19.6	0.0
G34	**2400**	-546	2775	-786	**63.7**	4.8	71.5	-3.0	31.4	-0.5	41.5	-6.6	96.6	43.6	134.5	-41.2	25.5	1.0	20.8	1.6
G35	1950	**-1193**	1350	-1426	**64.2**	**4.3**	76.8	**-10 3**	11.6	-7.6	36.8	-11.8	52.8	-9.6	120.2	-16.2	26.7	1.2	19.1	1.0
G36	1365	**-1596**	2625	-1536	52.9	**-3.5**	70.9	**-17 9**	24.6	6.1	33.9	-17.4	51.6	-9.5	109.2	-101	27.9	3.3	19.7	0.6
G37	1875	**-1260**	1875	-2663	**65.3**	**-3.6**	75.6	**3.0**	33.5	-0.6	41.6	-10.8	47.4	-53.3	85.5	-86.6	29.6	3.9	20.7	2.0
G38	2100	-748	2475	-244	**68.3**	10.7	84.0	-6.1	35.3	1.3	38.6	-10.8	92.0	30.6	172.3	10.9	26.1	3.1	20.2	0.5
G39	1920	**-946**	2400	-1676	**70.5**	18.4	61.4	-13 3	30.6	2.2	36.5	-13.9	67.8	20.8	70.5	-59.1	25.5	1.7	20.8	3.4
G40	1785	-1586	2550	-1319	58.1	-3.8	70.7	-13 9	24.7	1.8	41.3	-8.8	40.4	-29.2	147.4	33.1	26.1	0.8	20.0	0.3
G41	**2775**	237	2100	-2047	**64.5**	**3.8**	54.7	**-17 2**	45.2	8.8	42.5	-4.7	57.1	-22.6	122.3	-23.4	26.1	1.3	19.7	1.9
G42	1830	**-1225**	2250	-896	57.4	2.5	61.0	-8.9	20.2	-19.5	34.7	-16.8	30.6	-43.6	189.1	55.3	25.5	0.2	20.1	1.9
G43	**2280**	-161	2925	691	59.1	-9.6	62.2	-6.6	29.2	0.2	43.8	-3.4	81.3	40.8	102.3	33.1	25.7	2.5	19.1	0.8
G44	1650	-1351	1725	-1502	**68.8**	**6.5**	54.8	**-16 5**	37.7	8.3	40.7	-4.0	26.4	-51.3	184.8	18.0	26.4	2.9	19.6	1.5
G45	**2595**	229	3450	2491	**64.5**	2.3	65.9	-9.4	24.3	-0.8	36.7	-14.6	37.7	-33.3	202.7	96.1	27.0	3.4	19.6	1.6
G46	1800	-1158	1650	-1760	59.4	-17.1	60.2	-6.5	22.8	-6.5	32.8	-20.3	96.7	2.2	113.9	-56.3	27.3	3.9	20.9	2.6
G47	2085	-563	1950	-727	**66.8**	4.4	56.8	-1.6	25.2	-10.7	39.8	-7.7	64.5	20.7	80.0	-18.5	24.2	3.7	20.8	1.7
G48	2010	**-829**	2925	-1006	**67.7**	2.4	70.8	-2.9	29.6	-0.4	38.1	-10.4	75.5	14.7	113.3	33.1	26.8	3.9	20.1	2.1
G49	1590	-1158	2175	190	59.0	3.8	64.3	-6.8	30.4	-2.4	36.0	-8.6	102.6	-12.6	162.1	15.3	26.8	3.9	19.3	2.0
G50	**3525**	**2089**	1425	-2159	**68.2**	-2.5	66.4	0.4	29.6	1.0	43.9	0.9	25.5	-65.5	97.1	-30.0	25.6	4.2	19.3	2.2
G51	1200	**-930**	2625	678	58.3	4.7	56.2	-12.4	25.0	7.8	37.4	-6.2	52.0	-4.6	130.0	-11.4	25.4	3.2	18.9	-0.1
G52	1785	-40	2100	21	59.8	-13.5	58.3	-9.9	29.2	6.1	41.2	-6.5	66.1	19.0	163.9	23.0	29.7	3.9	20.4	3.0
G53	1950	**-242**	2115	-1037	**67.0**	8.6	66.1	-2.7	6.8	-32.0	25.2	-10.2	34.7	-42.1	155.2	6.8	26.5	2.3	20.8	2.2
G54	1305	**-1458**	1875	-2576	**64.6**	0.5	67.0	-25.7	33.1	1.1	42.9	-6.7	55.7	3.8	143.2	-4.1	30.4	2.4	21.1	3.7
G55	2100	-953	2250	-1416	**67.9**	0.7	64.3	-3.6	38.3	0.4	42.5	-7.7	85.8	-35.9	138.6	46.0	25.5	2.3	20.4	2.3
G56	**3000**	8.2	3105	462	**70.6**	4.9	80.2	2.2	38.2	2.0	39.2	-8.4	95.2	12.6	145.1	-17.1	22.8	2.1	20.2	2.2
G57	1545	-790	1950	-1779	**66.3**	-3.1	66.8	-14 1	44.5	9.8	44.2	-3.6	33.1	-47.1	161.9	-5.5	26.2	2.4	19.7	1.2

Geno	CB (kg/ha)				PHI (%)				LCC				SC (mmol m^{-2} s^{-1})				LT (°C)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G58	1800	-996	2250	-1079	**66.0**	-4.9	69.9	-11.4	23.0	-4.3	42.2	-7.9	71.2	27.9	97.6	-14.1	29.0	3.2	19.1	1.2
G59	**2625**	**613**	4050	1020	**66.0**	**-5.5**	73.0	**-4.6**	25.2	-3.6	41.0	-8.9	64.5	15.3	145.0	9.3	27.4	1.4	19.0	-0.3
G60	**2592**	**23**	2325	-621	**69.5**	**-3.6**	68.7	**-7.8**	40.3	1.5	44.4	-1.8	168.0	80.4	169.3	70.5	29.3	1.2	18.3	0.8
G61	1575	**-1246**	3375	1742	**68.2**	**3.5**	57.7	**-26 9**	32.7	-2.3	30.8	-17.5	100.7	13.7	74.8	-49.5	25.1	0.4	21.4	2.3
G62	1680	-435	1650	-339	**64.5**	-8.7	62.9	6.4	24.6	-3.0	33.7	-11.2	143.8	56.0	103.0	7.0	24.0	0.4	20.0	0.8
G63	1575	**-870**	2175	438	60.4	-5.0	58.1	-13.0	43.5	5.3	43.9	5.0	140.2	54.7	136.5	24.5	26.0	2.0	20.4	2.9
G64	**2250**	-1135	1725	-1059	58.2	-17.7	69.1	-9.5	36.8	-0.4	36.6	-17.7	72.7	-36.8	139.9	13.1	27.6	3.7	19.8	0.3
G65	1725	-946	2625	-808	55.0	**-12.4**	66.3	**-10 9**	19.1	-8.1	37.4	-12.7	86.9	-13.1	106.7	-12.6	26.4	1.4	20.0	1.2
G66	1725	**-239**	2190	-141	57.5	-3.8	61.8	-19.0	29.6	-4.3	41.3	-7.6	39.3	-36.9	139.8	-19.2	24.8	1.4	19.5	1.1
G67	1281	-585	1125	-1539	57.3	-14.7	83.0	-19 1	33.6	-3.4	35.5	-10.1	69.4	24.9	140.4	-18.4	25.1	0.9	21.8	2.6
G68	2175	330	1440	-882	66.3	**-2.5**	55.9	**-6.0**	32.2	-4.2	38.9	-4.3	69.5	28.2	175.8	19.8	24.0	1.1	20.7	2.1
G69	**2625**	-430	1695	-981	**65.4**	-0.4	66.1	-12 9	26.7	-1.0	39.0	-11.8	28.9	-57.0	140.1	-38.5	29.2	3.2	20.1	2.4
G70	**3315**	930	3165	2568	**66.3**	-1.6	73.3	2.4	33.9	8.5	42.6	1.1	102.3	72.9	104.2	22.0	28.2	0.9	20.3	1.9
G71	2145	-1266	2850	-1018	59.8	-8.0	68.7	-12 3	27.1	-2.5	39.3	-17.5	46.4	-9.8	139.1	-3.0	26.7	2.9	20.1	2.6
G72	1875	**-534**	3225	629	**65.0**	-3.0	68.2	-5.8	38.2	-5.1	42.2	-10.1	125.2	20.0	162.3	-26.8	27.7	5.5	19.9	2.1
G73	**3255**	2373	2850	-521	61.6	-7.7	52.3	-37 3	39.9	2.5	38.0	-13.3	74.3	-12.8	170.1	3.9	25.5	2.7	19.1	1.6
G74	1830	**130**	2835	191	50.0	-23.6	54.4	-23.8	43.6	9.5	37.7	-12.1	42.4	-21.8	119.7	-33.2	24.9	0.9	20.9	0.3
G75	1605	**-1014**	2565	938	57.1	-6.8	64.1	-12 2	31.7	6.7	41.2	-5.6	99.6	26.2	174.8	42.6	26.0	3.1	19.4	0.7
G76	1125	-1284	2400	-871	52.5	-16.4	50.7	-30.7	33.0	-2.9	41.2	-6.2	53.0	-3.6	128.9	3.7	25.3	2.0	20.3	2.3
G77	**2505**	**170**	3000	-439	**65.4**	-3.9	60.4	-17 2	42.7	4.4	46.9	-0.5	110.1	61.3	161.4	37.9	27.9	2.4	19.9	1.4
G78	2025	**-546**	3525	932	49.0	2.4	67.0	-12 9	38.4	-4.0	40.0	-4.7	84.5	21.8	140.9	20.8	26.2	2.9	21.3	3.0
G79	**3330**	625	3795	719	61.34	-8.5	56.8	-9.5	26.8	-2.2	43.2	-4.9	92.7	1.1	180.3	-9.9	27.0	3.8	20.9	1.8
G80	1665	-114	2265	-2833	57.7	-8.9	72.4	-10 9	33.4	0.2	46.5	-1.1	64.3	23.6	151.9	-14.9	27.2	3.3	19.3	1.9
G81	1530	-1165	1650	-2446	62.9	-5.7	79.1	-4.8	34.5	-1.8	38.9	-5.4	48.0	-40.0	136.5	-9.2	26.9	1.9	19.2	1.3
G82	1515	-1597	3825	-343	52.5	-11-9	67.8	-2.8	24.1	-2.9	39.2	-9.0	29.8	-43.1	119.5	0.1	29.4	4.0	18.8	0.9
G83	1620	**-611**	2880	-64	57.0	**-9.9**	63.3	**-5.2**	36.3	5.2	40.0	-4.6	70.2	32.3	138.5	28.4	25.7	0.0	18.6	0.7
G84	1725	**-1161**	1755	-2374	**64.6**	**-4.6**	60.4	**-25 8**	26.4	-7.1	31.0	-17.5	37.9	-30.9	121.0	-31.2	23.3	-0.4	20.7	3.2
G85	1830	**-844**	2085	-902	**75.4**	**9.0**	60.5	**-29.6**	34.6	-7.9	33.4	-12.6	78.4	-64.6	132.7	-11.5	25.8	4.5	19.8	1.5
G86	2145	-427	2640	-1213	**64.7**	11.3	84.0	5.2	30.4	-0.4	42.5	-4.8	58.9	15.1	136.5	-12.0	24.9	1.4	18.1	0.3
G87	**2400**	**-295**	1500	-1087	**67.7**	8.1	68.8	-2.9	39.2	-3.8	45.6	0.3	54.7	-17.8	178.2	12.1	27.9	4.2	19.3	1.8

Geno	CB (kg/ha)				PHI (%)				LCC				SC (mmol m^{-2} s^{-1})				LT (°C)			
	DS		NS		DS		NS		DS		NS		DS		NS		DS		NS	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G88	2175	-461	3450	-64	55.5	-13.3	68.8	-5.2	32.3	-6.0	33.7	-17.9	64.0	-3.1	138.6	-13.8	28.7	2.8	19.4	1.9
G89	2175	242	2700	-1046	59.2	**-5.6**	68.0	**-23 3**	43.1	0.3	45.6	0.4	126.8	25.1	103.5	-13.3	27.0	1.5	19.2	1.1
G90	**3150**	**-861**	2700	-1384	52.2	-29.6	63.6	-12 5	31.3	-13.1	32.7	-19.2	24.7	-57.4	179.0	20.1	27.4	0.0	20.4	3.8
G91	**2550**	-496	2325	-2094	63.3	2.5	69.6	-8.0	36.6	-3.5	41.8	-5.5	68.9	15.6	152.8	11.0	26.8	1.9	18.9	-0.5
G92	1689	-634	3525	-147	62.5	**3.8**	70.1	**-9.5**	37.3	2.2	40.9	-5.3	69.6	-13.6	110.4	26.6	27.3	2.8	20.5	2.5
G93	**3375**	323	2775	-97	**72.9**	6.4	65.8	-8.2	39.6	3.7	31.2	-14.6	77.4	43.7	155.7	16.9	23.3	0.5	20.8	1.7
G94	1140	-1363	2475	-223	54.2	-4.9	69.2	-25 9	33.8	-4.7	34.9	-9.8	66.5	-81.5	76.5	-71.6	26.2	3.2	19.9	-0.1
G95	**2471**	-465	2925	-594	**70.3**	10.0	76.1	-1.3	34.1	-3.5	40.7	-8.2	69.0	-7.4	156.5	20.1	26.6	3.1	21.7	2.8
G96	1419	**-1384**	2250	-1647	59.9	-4.5	63.5	-20.7	39.3	1.2	36.2	-15.8	32.0	-48.2	93.6	-66.7	29.9	2.4	21.4	2.6
G97	1725	-1230	2025	-1785	59.5	-11.8	66.7	-27 2	35.1	4.6	44.0	-5.3	61.7	-28.5	71.7	-45.5	26.5	2.2	21.5	3.2
G98	1560	**-964**	2925	-138	**64.1**	0.9	62.4	-21.6	29.3	1.0	42.4	-5.9	78.4	49.3	126.9	-79.5	27.8	3.6	22.6	3.7
G99	**2400**	**-346**	3225	-144	61.5	0.3	73.5	-6.8	29.7	-5.2	38.7	-8.6	59.5	-1.7	137.3	-37.5	24.2	2.9	19.5	-0.0
G100	**2400**	-830	2850	-15	**66.8**	7.9	67.6	-11 9	33.4	-0.2	40.8	-1.3	105.3	43.9	98.7	-10.5	25.4	0.9	20.1	1.0
G101	1425	**-1268**	2175	-1784	55.4	-16.9	47.5	-21 5	40.4	2.2	41.1	-1.8	65.7	-37.0	70.7	-24.6	28.0	2.4	19.3	1.1
G102	**2775**	**-274**	2550	-1533	58.3	-16.7	61.6	-15.7	37.3	-2.0	41.0	-1.9	99.9	-16.4	161.3	46.8	25.2	1.9	19.2	0.6
G103	**2400**	-1003	4575	-860	**64.2**	-0.7	72.3	-14.0	28.2	3.7	41.1	-6.1	87.5	-41.1	173.0	13.2	27.1	2.6	19.0	0.0
G104	**2409**	-736	2880	-1081	**74.7**	14.3	73.6	-13 1	39.1	0.4	45.4	-6.0	100.8	38.0	167.9	19.0	26.7	3.2	18.9	1.8
G105	**3705**	176	2925	-333	**69.8**	1.4	74.1	-9.6	39.9	4.8	39.7	-5.9	70.1	-41.1	146.2	1.5	26.8	2.5	19.4	-0.4
G106	**2355**	-920	2415	-1372	49.8	-11.2	52.1	-30 1	42.6	7.8	45.9	-0.7	76.0	-9.4	109.3	28.8	27.7	4.5	19.4	1.5
G107	1535	**-454**	2400	-1075	61.8	**-2.8**	65.7	**-17.4**	30.3	-12.7	31.5	-21.7	59.1	-15.1	82.1	-67.8	27.8	4.1	21.0	2.3
G108	**2400**	**-853**	2850	-1010	**64.1**	**-0.7**	73.9	**-16 1**	38.3	-0.3	34.6	-12.0	56.9	-0.5	158.5	-4.9	27.0	2.7	18.2	1.5
G109	1995	**-1024**	2100	-1983	**68.6**	**2.2**	64.6	**-19.0**	14.1	-26.4	25.5	-32.5	31.7	-51.4	108.7	-39.8	24.2	2.9	20.5	3.8
G110	**2070**	-1065	3225	-484	**63.7**	-7.6	74.3	-4.6	24.3	-5.0	41.1	-2.2	67.0	-17.9	145.1	-7.5	29.2	4.8	18.3	-0.1
Mean	2110		2403		61.9		65.0		23.1		39.6		26.6		135		26.3		19.6	
H^2 (%)	51		28		22		8		31		33		26		31		27		21	
LSD (5%)	1173		ns		12.3		20.6		13.1		9.4		28.7		32.5		4.1		ns	

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *LCC* leaf chlorophyll content, *CB* canopy biomass, *PHI* pod harvest index, *LT* leaf temperature, *SC* stomatal conductance, *DS* drought stressed, *NS* non-stressed, ns not significant, *LSD* least significance difference at 0.05, H^2 broad-sense heritability.

NB: Values in bold were above the breeding target and the respective genotype outperformed the standard check.

Appendix 5.5 Grain yield-based drought tolerance indices and predicted genotype values (Ĝ) and genotypic effects (ĝ) of 110 genotypes for agronomic traits evaluated under combined environments at Save valley experiment station in 2019 and 2020.

Geno	GYD (kg/ha)		NMPP		NSPP		DPM		SW (g)		GMP	%SYR	MR
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ			
G1	1804.0	-1800	35.3	22.4	148.5	70.4	104.7	0	20.8	0.6	1699	50.1	67
G2	1361.0	-1828	22.0	-26.6	72.5	-151.2	103.8	-2	25.8	7.0	1361	4.5	52
G3	1400.0	-1390	22.4	-22.5	77.4	-133.1	105.5	5	28.9	10.6	1377	-43.9	**40**
G4	1602.0	-922	23.1	-19.8	57.4	-144.4	105.5	6	30.9	8.3	1566	34.6	58
G5	1367.0	-1942	18.9	-24.6	49.8	-120.3	107.3	5	28.1	6.5	1339	33.4	72
G6	1459.0	-1689	20.3	-31.0	85.0	-145.5	104.3	0	20.5	-0.5	1443	25.7	58
G7	1569.0	-765	21.3	-11.1	86.8	-69.1	104.3	-2	25.7	1.8	1535	33.9	61
G8	1074.0	-2301	20.5	-32.0	78.3	-161.6	104.8	0	19.9	0.6	1056	30.5	81
G9	1241.0	-588	14.5	-21.3	28.3	-149.4	105.8	0	36.4	23.3	1233	18.9	64
G10	776.0	-1579	8.6	-20.6	17.3	-130.6	105.5	3	45.5	38.3	770	22.3	75
G11	1050.0	-1891	19.3	-28.3	77.4	-140.5	104.8	0	24.6	2.1	1044	-22.5	55
G12	1261.0	-1676	20.8	-24.0	99.3	-107.4	105.8	5	21.9	3.9	1258	-12.8	49
G13	1639.0	-1334	28.3	-17.6	101.9	-98.9	104.0	0	20.4	0.7	1633	15.2	**40**
G14	1691.0	-1273	24.5	-8.9	103.3	-60.7	105.8	5	22.3	1.0	1660	31.5	54
G15	1648.0	-961	14.6	-16.2	42.3	-106.4	104.3	0	42.1	25.4	1526	54.8	77
G16	1543.0	-1003	30.4	-8.1	105.5	-77.8	105.3	0	19.7	2.7	1496	-63.7	**29**
G17	1204.0	-1272	11.1	-17.2	26.0	-108.4	104.0	-2	43.3	26.9	1195	20.9	66
G18	1311.0	-1148	33.0	23.9	90.9	2.2	105.3	0	25.1	0.7	1226	52.2	92
G19	2520.0	-1066	26.8	-10.4	89.6	-91.2	106.0	0	23.5	5.5	2520	-0.4	**12**
G20	2028.0	257	22.5	-5.3	54.5	-108	105.0	0	40.3	33.1	2015	-23.9	**15**
G21	1502.0	-726	23.9	1.2	79.8	-35.3	106.0	6	22.7	5.8	1493	19.0	49
G22	798.0	-1433	20.8	-9.6	45.4	-103.3	104.8	-1	47.1	24.4	776	-59.5	54
G23	950.0	-1117	8.6	-23.4	25.9	-116.3	105.0	23	33.6	14.2	912	43.6	93
G24	1830.0	-1877	14.0	-22.1	61.0	-115.8	104.8	-1	21.6	1.9	1828	-7.5	**23**
G25	1341.0	-1286	21.4	-20.7	91.3	-103.1	105.8	3	23.0	2.4	1317	31.2	70
G26	1444.0	-1696	31.3	-19.1	102.3	-124.9	105.4	0	25.7	3.6	1430	24.7	62
G27	1520.0	-947	33.5	-9.4	94.1	-70.8	105.0	0	18.9	0.2	1508	21.9	50
G28	1498.0	-1423	27.8	-13.8	109.8	-88.3	105.0	0	21.6	2.8	1497	2.2	**40**
G29	2328.0	123	39.5	-2.6	135.9	-25.3	104.8	-2	22.9	4.9	2318	16.8	**21**
G30	2306.0	-756	40.5	1.9	131.5	5.6	104.6	-1	21.8	3.1	2305	1.4	**15**
G31	1378.0	-601	21.9	-7.1	55.1	-87.8	105.5	0	30.3	1.6	1393	2.3	49
G32	1419.0	-1659	33.5	-16.4	101.3	-97.0	106.3	3	20.7	4.0	1393	31.6	69
G33	967.0	-1536	19.8	-17.3	79.6	-86.5	106.5	2	19.7	1.8	951	30.0	82
G34	2226.0	-1096	33.0	-11.9	120.3	-72.5	106.8	0	20.0	2.0	2214	18.1	**24**
G35	1609.0	-1613	19.9	-17.8	78.9	-87.9	105.8	0	22.3	1.2	1544	-77.7	**27**
G36	1874.0	-1741	22.8	-20.9	98.0	-101.5	106.3	5	22.4	2.0	1682	61.2	71
G37	1313.0	-1649	22.5	-34.0	79.0	-159.6	105.8	-1	21.9	1.7	1195	58.5	95
G38	1687.0	-751	19.9	-14.8	92.4	-67.3	105.8	0	23.5	0.2	1672	23.1	**45**
G39	1678.0	1520	28.0	-19.9	109.9	-99.2	105.3	0	21.6	2.1	1656	27.4	52
G40	1733.0	-1395	20.8	-18.8	75.3	-99.0	105.3	0	23.1	4,8	1733	-3.5	**28**
G41	1381.0	-2022	28.3	-24.2	93.8	-119.3	106.0	5	21.9	0.0	1380	-7.3	**45**
G42	1948.0	-155	32.0	-3.0	81.3	-71.9	104.8	0	25.4	6.8	1928	24.7	**39**
G43	2359.0	255	28.9	6.1	115.3	25.0	106.0	0	23.2	6.7	2233	48.7	50

Geno	GYD (kg/ha)		NMPP		NSPP		DPM		SW (g)		GMP	%SYR	MR
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ			
G44	1456.0	-1709	16.0	-17.8	57.9	-91.3	106.3	3	25.9	5.4	1455	1.0	**41**
G45	1896.0	-323	32.3	8.6	111.5	29.5	104.8	1	20.8	1.7	1884	20.0	**35**
G46	1222.0	-1705	26.6	-9.9	93.4	-51.2	107.3	0	21.6	2.3	1205	28.1	74
G47	1733.0	-509	26.0	-4.9	94.9	-35.6	106.8	0	23.6	3.3	1726	16.5	**37**
G48	1978.0	-1164	29.3	-9.0	97.4	-71.9	106.3	0	22.6	3.0	1884	46.5	58
G49	1035.0	-1090	17.4	-15.9	37.6	-97.7	105.0	0	39.2	20.3	1033	-13.4	56
G50	1809.0	-1582	39.8	-14.9	114.9	-92.0	104.0	0	22.4	1.7	1767	-54.4	**21**
G51	1287.0	-401	11.6	-14.1	28.5	97.0	104.8	0	41.0	19.6	1230	45.2	86
G52	1833.0	230	18.3	-15.7	37.3	-77.2	104.5	0	44.1	29.5	1798	32.2	49
G53	2204.0	-447	29.4	-7.4	94.5	-51.0	104.5	-2	24.8	2.8	2189	-25.0	**10**
G54	1357.0	-2204	17.4	-30.7	67.3	-134.6	104.5	-1	26.1	-0.3	1268	52.5	91
G55	1639.0	-1462	24.4	-21.8	88.4	-93.1	106.0	0	21.6	3.5	1602	34.6	58
G56	2141.0	-290	32.9	9.4	153.5	27.7	105.3	0	24.7	1.6	2079	38.5	48
G57	1546.0	-1674	20.6	-21.2	88.4	-90.7	104.5	0	21.8	4.5	1479	45.1	71
G58	1687.0	-842	26.5	-15.2	102.3	-64.0	105.5	-1	18.8	0.9	1663	28.5	52
G59	2344.0	-100	39.9	6.4	173.6	60.6	105.5	0	19.9	3.1	2296	33.7	**38**
G60	1837.0	-872	28.8	-8.7	111.3	-43.2	106.3	3	41.5	3.0	1820	23.5	**39**
G61	2114.0	1351	25.8	22.1	115.0	91.6	104.8	0	22.2	6.8	1870	63.6	67
G62	969.0	-485	14.2	0.3	35.9	-66.2	104.5	-1	42.8	27.4	962	-25.5	54
G63	1446.0	444	14.4	-4.3	38.0	-57.5	105.3	5	40.7	31.3	1387	44.1	79
G64	1769.0	-857	30.0	-11.1	97.9	-65.3	105.0	-1	23.3	3.6	1745	28.0	48
G65	1404.0	-1079	26.5	-10.4	115.5	-36.4	104.9	0	28.6	6.8	1256	61.7	95
G66	1463.0	-978	20.4	-12.3	75.8	-36.8	104.5	0	24.3	5.6	1461	9.1	**45**
G67	724.0	-1211	18.9	-11.8	58.5	-82.2	106.5	3	22.1	1.4	690	46.1	95
G68	2052.0	126	18.8	-11.8	73.4	-61.0	105.5	0	22.0	6.3	2000	36.6	48
G69	1267.0	-1281	25.0	-2.2	82.3	-49.3	107.3	0	22.1	2.9	1266	0.6	53
G70	2652.0	1519	29.1	19.2	123.6	101.0	106.0	0	23.7	5.3	2571	39.3	**39**
G71	1956.0	-1499	29.0	-9.8	117.6	-68.9	106.3	0	23.9	3.4	1726	63.9	73
G72	2281.0	-86	30.4	8.3	145.4	73.6	104.5	-1	22.4	6.6	2049	61.1	62
G73	1472.0	-1451	35.0	12.3	78.0	-63.1	108.5	4	32.4	13.7	1468	13.8	**46**
G74	1385.0	-1358	19.4	-4.0	41.6	-79.4	107.5	3	36.3	17.0	1372	23.6	62
G75	1537.0	-701	25.8	10.8	62.8	-27.0	107.8	-1	30.3	7.7	1427	54.1	85
G76	1072.0	-1449	20.3	-4.7	50.4	-80.9	107.0	5	29.1	10.6	1042	38.2	88
G77	1481.0	-934	35.5	1.8	113.6	-35.7	105.0	0	19.5	0.8	1474	17.3	48
G78	2152.0	-18	33.3	9.2	109.6	11.6	104.5	-1	25.5	8.9	2128	25.5	**36**
G79	1811.0	-766	36.6	4.3	108.6	-41.8	107.8	2	25.0	8.3	1803	17.2	**34**
G80	1531.0	-1212	23.8	-6.2	92.3	-48.0	108.0	3	21.8	1.2	1474	42.4	70
G81	1561.0	-1552	21.1	-21.8	76.1	-95.4	105.3	-1	19.9	0.9	1477	48.9	74
G82	1889.0	-684	27.5	-15.8	108.8	-74.0	105.8	0	23.9	6.2	1676	63.1	75
G83	1122.0	-838	18.6	-13.7	70.5	-85.7	109.0	3	29.6	10.6	1065	47.8	93
G84	1367.0	-1854	18.0	-24.1	74.6	-125.9	107.0	2	21.8	-1.2	1364	-12.7	**44**
G85	1254.0	-1421	31.8	-15	107-9	-111.2	107.5	4	15.6	-2.6	1253	2.1	55
G86	2248.0	-1255	26.5	-21.8	112.6	-105.5	107.5	6	18.4	2.2	2227	23.5	**28**
G87	1122.0	-1219	29.8	-3.8	97.0	-62.1	106.5	0	19.3	3.5	1110	25.8	76
G88	2039.0	177	30.6	-1.7	143.6	3.3	106.0	0	23.0	3.1	1798	64.1	69
G89	2374.0	-517	31.1	-4.3	129.3	-19.6	106.3	3	22.3	3.5	2298	40.1	**12**
G90	2039.0	-1491	35.8	-8.1	113.0	-68.4	105.8	0	21.4	2.3	2031	15.3	**28**
G91	1865.0	-1867	28.8	-22.4	123.3	-112.3	108.0	8	21.3	2.2	1854	-24.3	**18**

Geno	GYD (kg/ha)		NMPP		NSPP		DPM		SW (g)		GMP	%SYR	MR
	$\hat{G}$	$\hat{g}$	$\hat{G}$	$\hat{g}$	$\hat{G}$	$\hat{g}$	$\hat{G}$	$\hat{g}$	$\hat{G}$	$\hat{g}$			
G92	2198.0	554	31.6	9.1	85.9	-56.7	106.8	0	29.5	7.4	2128	40.0	48
G93	2206.0	-11	32.3	-9.3	107.1	-47.9	106.3	0	25.8	4.5	2202	10.7	**21**
G94	1161.0	-989	23.3	-5.6	76.4	-76.0	108.0	5	25.4	0.4	949	73.1	106
G95	2619.0	-423	37.9	1.6	114.8	-28.3	109.0	7	26.3	4.2	2531	40.9	**42**
G96	1556.0	-1350	23.5	-11.4	91.0	-89.2	105.8	-1	17.3	-1.6	1543	22.8	49
G97	2235.0	-199	20.3	-18.6	90.9	-95.2	106.3	0	21.8	3.8	2033	58.7	61
G98	1780.0	-1239	30.3	6.6	81.1	-39.9	105.8	-1	18.5	3.0	1447	73.6	86
G99	2294.0	-504	30.9	-2.4	127.4	-14.8	106.8	5	20.0	1.2	2179	47.6	51
G100	1544.0	-502	28.1	-0.3	130.3	-9.0	107.0	5	24.4	2.1	1482	43.8	70
G101	1150.0	-2152	29.0	-13.9	98.4	-52.7	106.0	3	19.0	-0.6	1149	-7.8	52
G102	1406.0	-1498	37.1	-13.4	132.1	-78.5	105.8	-2	21.3	-2.7	1405	-0.8	**46**
G103	2526.0	-234	44.3	-9.1	179.0	-62.3	105.0	0	22.8	1.3	2389	49.0	48
G104	2267.0	-793	22.0	-20.5	71.6	-110.5	106.3	0	37.3	17.1	2199	38.9	**44**
G105	2776.0	124	35.4	-11.9	148.6	-37.0	105.9	-1	24.0	3.3	2771	10.7	**16**
G106	1131.0	-1347	36.8	-6.9	74.6	-114.3	109.5	6	21.3	1.0	1064	50.6	96
G107	1509.0	-454	19.1	-19.9	57.5	-115.1	105.5	-1	31.1	14.4	1470	36.7	66
G108	2154.0	-1093	36.0	-12.1	141.6	-76.8	106.0	0	20.1	1.3	2153	-6.2	**18**
G109	1561.0	-987	30.9	-21.4	129.1	-104	104.5	0	22.0	-1.7	1560	7.1	**40**
G110	2204.0	-1038	30.0	-14.4	122.6	-32.4	106.5	-1	20.7	2.0	2183	23.7	**30**
G109	1561.0	-987	30.9	-21.4	129.1	-104	104.5	0	22.0	-1.7	1560	7.1	**40**
G110	2204.0	-1038	30.0	-14.4	122.6	-32.4	106.5	-1	20.7	2.0	2183	23.7	**30**
Mean	1667.0		25.9		91.4		105.8		25.5		1617.2	22.8	
Reduction (%)	28.2		26.4		29.8		6.9		2.7				
H^2 (%)	34.5		44.9		50.9		27.9		68.5				
LSD (5%)	679.6		11.2		44.8		0.5		6.2				

Geno genotype, $\hat{G}$ predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], $\hat{g}$ = predicted genotypic effect of genotype, *GYD* seed yield, *NMPP* number of pods per plant, *NSPP* number of seeds per plant, *DPM* days to physiological maturity, *SW* 100 seed weight, *GMP* geometric mean productivity, *%SYR* percentage seed yield reduction, *MR* mean rank of a genotype across all the drought tolerance indices *LSD* least significance difference at 0.05, H^2 broad-sense heritability.

NB: Values in bold indicate that the respective genotype outperformed the standard check.

Appendix 5.6 Predicted genotype values (Ĝ) and genotypic effects (ĝ) of 110 genotypes for shoot and physiological traits evaluated under combined environments at Save valley experiment station in 2019 and 2020.

Geno	LCC		SC (mmol m^{-2} s^{-1})		LT (°C)		CB (kg/ha)		PHI (%)	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G1	38.3	0.8	88.8	20.8	22.7	-0.7	2865.0	980	61.8	-20.4
G2	18.9	-34.4	109.0	21.5	23.3	1.9	1560.0	-2586	64.6	-14.3
G3	32.4	-9.6	81.0	-2.7	22.5	0.3	2063.0	-1843	59.8	-20.5
G4	33.8	-5.4	92.5	0.5	22.6	-0.8	2175.0	-1426	57.0	-21.5
G5	32.6	-1.9	118.8	10.9	23.1	0.6	1727.0	-1941	62.9	-22.8
G6	31.6	-12.0	82.5	6.9	24.4	0.4	2077.0	-2700	56.5	-22.7
G7	36.7	-3.6	93.3	-6.5	24.1	2.3	2093.0	-560	64.0	-6.0
G8	30.4	-7.0	80.9	-16.1	21.6	1.7	2190.0	-2833	55.2	-25.5
G9	28.8	-6.5	59.2	-95.7	22.2	-1.2	1965.0	-826	62.8	-8.4
G10	35.7	-3.3	114.2	35.7	28.4	1.4	1572.0	-1760	54.1	-22.7
G11	28.6	-19.6	83.1	-3.8	25.5	1.2	1815.0	-2530	51.7	-33.7
G12	34.8	-8.4	60.1	-72.3	23.9	0.1	2288.0	-1881	69.0	-26.7
G13	34.9	-6.4	88.0	21.6	22.0	-1.0	2145.0	-1486	65.5	-19.9
G14	30.8	-5.4	61.2	-6.2	23.2	1.3	2512.0	-769	70.1	-14.2
G15	30.3	-9.2	106.4	-22.4	24.5	0.3	2033.0	-1254	57.4	-17.0
G16	36.6	-6.0	120.9	-20.3	23.9	-1.1	2513.0	-1143	58.4	-21.1
G17	41.4	-6.5	122.1	61.5	24.9	1.3	1688.0	-954	61.6	-21.2
G18	38.4	-8.1	78.5	-39.0	22.4	1.1	2640.0	1064	60.6	-28.4
G19	39.8	-2.8	106.0	-2.6	22.5	-2.0	2288.0	-1069	66.4	-23.4
G20	36.9	-4.0	160.7	58.8	23.6	1.5	2513.0	920	63.4	-16.2
G21	32.2	-9.7	42.1	-39.3	25.1	4.1	2025.0	445	72.1	-13.4
G22	30.0	-16 3	100.8	-21.1	24.5	2.5	1613.0	-428	56.9	-18.7
G23	29.3	-26 3	85.8	-29.4	24.2	2.4	1612.0	-240	59.4	-18.9
G24	38.4	-3.1	63.7	17.9	27.1	4.2	1545.0	-1478	65.1	-23.7
G25	29.3	-5.0	44.9	-99.3	24.3	1.6	1725.0	-993	55.8	-24.6
G26	35.1	-8.8	151.2	41.3	21.7	1.4	1875.0	-2004	57.7	-19.5
G27	39.4	-9.7	110.1	33.1	23.2	0.1	2400.0	-1110	60.7	-16.5
G28	31.2	-12 5	85.6	-27.0	22.7	0.9	1912.0	-1505	59.8	-20.9
G29	37.4	-13.0	113.5	44.9	24.6	-0.4	3525.0	22	66.6	-7.0
G30	37.8	-9.7	81.4	-8.5	24.1	1.7	2783.0	-54	63.6	-3.6
G31	34.7	-3.4	90.3	-18.7	24.7	2.0	2573.0	1498	56.6	-20.5
G32	38.8	-3.2	144.5	14.4	23.5	0.6	2588.0	-1536	63.1	-5.4
G33	29.5	-10 5	66.7	-16.8	23.4	0.0	1800.0	-1169	62.6	-17.8
G34	36.5	-6.6	115.6	-41.2	23.1	1.6	2588.0	-786	67.5	-3.0
G35	24.2	-11.8	86.5	-16.2	22.9	1.0	1650.0	-1426	70.4	-10.3
G36	29.3	-17.4	80.4	-100.6	23.8	0.6	1995.0	-1536	61.8	-17.9
G37	37.6	-10.8	66.5	-86.6	25.2	2.0	1875.0	-2663	70.3	3.0
G38	36.9	-10.8	132.2	10.9	23.1	0.5	2288.0	-244	76.1	-6.1
G39	33.6	-13 9	69.2	-59.1	23.1	3.4	2160.0	-1676	66.0	-13.3
G40	33.0	-8.8	93.9	33.1	23.0	0.3	2168.0	-1319	64.4	-13.9
G41	43.9	-4.7	89.7	-23.4	22.9	1.9	2438.0	-2047	59.7	-17.2
G42	27.5	-16.8	109.9	55.3	22.8	1.9	2040.0	-896	59.1	-8.9
G43	36.5	-3.4	91.8	33.1	22.4	0.8	2603.0	691	60.6	-6.6
G44	39.2	-4.0	105.6	18.0	23.0	1.5	1688.0	-1502	61.9	-16.5

Geno	LCC		SC (mmol m^{-2} s^{-1})		LT (°C)		CB (kg/ha)		PHI (%)	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G45	30.5	-14.6	120.2	96.1	23.3	1.6	3023.0	2491	65.2	-9.4
G46	27.8	-20 3	105.3	-56.3	24.1	2.6	1725.0	-1760	59.7	-6.5
G47	32.5	-7.7	72.3	-18.5	22.5	1.7	2018.0	-727	61.8	-1.7
G48	33.9	-10.4	94.4	33.1	23.4	2.1	2468.0	-1006	69.3	-2.9
G49	33.2	-8.6	132.4	15.3	23.0	2.0	1882.0	190	61.5	-6.8
G50	36.7	0.9	61.3	-30.0	22.5	2.2	2475.0	-2159	67.2	0.4
G51	31.2	-6.2	91.0	-11.4	22.1	-0.1	1913.0	678	57.3	-12.4
G52	35.2	-6.5	115.0	23.0	25.0	3.0	1943.0.0	21	59.0	-9.9
G53	16.0	-10 2	94.9	6.8	23.7	2.2	2032.0	-1037	66.6	-2.7
G54	38.0	-6.7	99.4	-4.1	25.7	3.7	1590.0	-2576	65.9	-25.7
G55	40.4	-7.7	112.2	46.0	22.9	2.3	2175.0	-1416	66.2	-3.6
G56	38.7	-8.4	120.2	-17.1	21.5	2.2	3053.0	462	75.5	2.2
G57	44.3	-3.6	97.5	-5.5	22.9	1.2	1748.0	-1779	66.6	-14.1
G58	32.6	-7.9	84.4	-14.1	24.0	1.2	2025.0	-1079	68.0	-11.4
G59	33.1	-8.9	104.8	9.3	23.2	-0.3	3338.0	1020	69.5	-4.6
G60	42.3	-1.8	168.7	70.5	22.3	0.8	2459.0	-621	69.1	-7.8
G61	31.8	-17 5	87.8	-49.5	23.2	2.3	2475.0	1742	63.1	-26.9
G62	29.2	-11 2	123.4	7.0	22.0	0.8	1665.0	-339	63.6	6.4
G63	43.7	5.0	138.4	24.5	23.2	2.9	1875.0	438	59.3	-13.0
G64	36.7	-17.7	106.3	13.1	23.7	0.3	1988.0	-1059	63.6	-9.5
G65	28.3	-12.7	96.8	-12.6	23.2	1.2	2175.0	-808	60.6	-10.9
G66	35.4	-7.6	89.6	-19.2	22.2	1.1	1958.0	-141	59.6	-19.0
G67	34.6	-10 1	104.9	-18.4	23.4	2.6	1203.0	-1539	70.2	-19.1
G68	35.5	-4.3	122.7	19.8	22.3	2.1	1807.0	-882	61.1	-6.0
G69	32.9	-11.8	84.5	-38.5	24.6	2.5	2160.0	-981	65.9	-12.9
G70	38.2	1.1	103.2	22.0	24.2	1.9	3240.0	2568	69.8	2.4
G71	33.2	-17 5	92.7	-3.0	23.4	2.6	2498.0	-1018	64.2	-12.3
G72	40.2	-10 1	143.8	-26.8	23.8	2.1	2550.0	629	66.6	-5.8
G73	39.0	-13 3	122.2	3.9	22.3	1.6	3053.0	-521	57.1	-37.3
G74	40.7	-12 1	81.0	-33.2	22.9	0.3	2332.0	191	52.2	-23.8
G75	36.4	-5.6	137.2	42.6	22.7	0.7	2085.0	938	60.5	-12.2
G76	37.1	-6.2	90.9	3.7	22.8	2.3	1763.0	-871	51.6	-30.7
G77	44.8	-0.5	135.7	37.9	23.9	1.4	2753.0	-439	63.0	-17.2
G78	39.2	-4.7	112.7	20.8	23.7	3.0	2775.0	932	57.9	-12.9
G79	35.0	-4.9	136.5	-9.9	24.0	1.8	3563.0	719	59.0	-9.5
G80	39.9	-1.1	108.1	-14.9	23.2	1.9	1965.0	-982	65.0	-10.9
G81	36.7	-5.4	92.3	-9.2	23.0	1.3	1590.0	-2446	70.9	-4.8
G82	31.6	-9.0	74.7	0.1	24.1	0.9	2670.0	-343	60.0	-2.8
G83	38.1	-4.6	104.4	28.4	22.2	0.7	2250.0	-64	60.0	-5.2
G84	28.7	-17 5	79.4	-31.2	22.0	3.2	1740.0	-2374	62.6	-25.8
G85	334	-12.6	105.6	-11.5	22.8	1.5	1958.0	-902	68.2	-29.6
G86	36.5	-4.7	97.7	-12.0	21.5	0.3	2393.0	-1213	74.2	5.2
G87	42.4	0.3	116.5	-12.1	23.6	1.8	1950.0	-1087	68.2	-2.9
G88	33.0	-17 9	101.3	-13.8	24.0	1.9	2812.0	-64	60.6	-5.2
G89	44.3	0.4	115.1	-13.3	23.1	1.1	2438.0	-1046	61.9	-23.3
G90	32.0	-19 2	101.8	20.1	23.9	3.8	2925.0	-1384	65.2	-12.5
G91	39.2	-5.5	110.8	11.0	22.9	-0.5	2438.0	-2094	59.7	-8.0
G92	39.1	-5.3	90.0	26.6	23.9	2.5	2607.0	-147	61.8	-9.5

Geno	LCC		SC (mmol m^{-2} s^{-1})		LT (°C)		CB (kg/ha)		PHI (%)	
	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ	Ĝ	ĝ
G93	35.4	-14.6	116.6	16.9	22.1	1.7	3075.0	-97	69.3	-8.2
G94	34.3	-9.8	71.5	-71.6	23.1	-0.1	1807.0	-223	61.5	-25.9
G95	37.4	-8.2	112.7	20.1	24.2	2.8	2698.0	-594	67.2	-1.3
G96	37.8	-15.8	62.8	-66.7	25.6	2.6	1834.0	-1647	57.3	-20.7
G97	39.5	-5.3	66.7	-45.5	24.0	3.2	1875.0	-1785	59.0	-27.2
G98	35.9	-5.9	102.7	-79.5	25.2	3.7	2243.0	-138	66.6	-21.6
G99	34.2	-8.6	98.4	-37.5	21.8	-0.0	2813.0	-144	65.9	-6.8
G100	37.1	-1.3	102	-10.5	22.8	1.0	2625.0	-15	66.2	-11.9
G101	40.7	-1.8	68.2	-24.6	23.7	1.1	1800.0	-1784	75.5	-21.5
G102	39.2	-1.9	130.6	46.8	22.2	0.6	2662.0	-1533	66.6	-15.7
G103	34.7	-6.1	130.2	13.2	23.1	0.0	3488.0	-860	68.0	-14.0
G104	42.3	-6.0	134.3	19.0	22.8	1.8	2644.0	-1081	69.5	-13.1
G105	39.8	-5.9	108.1	1.5	23.1	-0.4	3315.0	-333	69.1	-9.6
G106	44.3	-0.7	92.7	28.8	23.5	1.5	2385.0	-1372	63.1	-30.1
G107	30.9	-21.7	70.6	-67.8	24.4	2.3	1967.0	-1075	63.6	-17.4
G108	36.5	-12.0	107.7	-4.9	22.6	1.6	2625.0	-1010	59.3	-16.1
G109	19.8	-32 5	70.2	-39.8	22.4	3.8	2047.0	-1983	63.6	-19.0
G110	32.7	-2.2	106.1	-7.5	23.8	-0.1	2648.0	-484	60.6	-4.6
Mean	29.9		67.1		22.1		2257.0		63.4	
Reduction (%)	41.7		80.3		-34.2		12.0		4.8	
H^2 (%)	57.1		31.5		32.8		23.2		14.5	
LSD (5%)	8.04		21.6		2.4		1015.0		11.8	

Geno genotype, *Ĝ* predicted genotype value [û + ĝ + ĝe; general mean (û) summed to predicted genotypic effect of genotype (ĝ) and predicted genotype by environment interaction effect (ĝe) of genotype], *ĝ* predicted genotypic effect of genotype, *LCC* leaf chlorophyll content, *CB* canopy biomass, *PHI* pod harvest index, *LT* leaf temperature, *SC* stomatal conductance, *LSD* least significance difference at 0.05, H^2 broad-sense heritability.

NB: Values in bold were above the breeding target and the respective genotype outperformed the standard check.

Chapter 6 [1]Genetic analysis of grain yield and yield-attributing traits in navy bean (*Phaseolus vulgaris* L.) under drought and optimal environments

Abstract

Navy beans (*Phaseolus vulgaris* L.) are an important food and cash crop for export in the world. Knowledge of the genetic basis of navy bean performance under drought stress (DS) is important for planning appropriate breeding and selection strategies in DS environments. Eight parents and their twenty-eight F_2 progenies generated from an 8 x 8 half-diallel mating design were evaluated to determine combining ability effects and mode of gene action of grain yield (GYD) and yield attributing traits in navy bean under DS and non-stressed (NS) conditions. The experiments were conducted in two locations in a 6 x 6 square lattice design with two replications during the 2020 dry winter season. General and specific combining ability (GCA; SCA) effects were significant ($p < 0.05$) under both DS and NS for most traits indicating the importance of both additive and non-additive gene effects in the expression of the traits. Parents with best GCA for most of the studied traits were CZ113-13, G97, NAVY LINE-60, and G550 under NS, and ZABRA16575-73F22, G37, G97 and G550 under DS. Among these, only ZABRA16575-73F22 and NAVY LINE-60 were considered tolerant to DS because of their high values for drought tolerance index (DTI) and geometric mean productivity (GMP) and low values for percentage grain yield reduction (%GYR). The most promising progenies with high values for GYD and its component traits under DS, high values for DTI and GMP and low values for %GYR and DSI were CIM-NAV02-17-3 x ZABRA16575-73F22, CIM-NAV02-17-3 x G550, G37 x NAVY LINE-60 and NAVY LINE-60 x G550. There were significant ($p < 0.001$; $p < 0.05$) positive correlations for number of pods per plant (NPPP) and 100-seed weight (SW; g) with GYD under both DS and NS. Good general and specific combiners with desirable values of drought tolerance indices and high significant positive effects under DS should be used further in breeding for drought stress tolerance.

Keywords: Combining ability, drought tolerance, diallel analysis, yield components

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6.1 Introduction

Navy beans (*Phaseolus vulgaris* L.) are an important food and cash crop for export in the world. The average market shares of navy beans in China, Myanmar, Canada, USA, Argentina and Ethiopia is 26.7%, 18.4%, 10.9%, 10.4%, 9.4% and 2.4%, respectively (Gebeyehu, 2017). Between 2005 and 2012, the crop accounted for 41% of pulse production and export in Ethiopia (Gebeyehu, 2017). The US foreign food aid programs distribute navy beans either as dry or canned beans to selected developing countries, making it an important commodity in food aid programs (Siddiq and Uebersax, 2012). Despite its importance in human diets and the bean canning industry, average grain yields realised by smallholder farmers in Zimbabwe have remained relatively low (less than 700 kg/ha) (AGRITEX, 2016) against a yield potential of 3000 kg ha^{-1}. The large discrepancy in yield has been attributed to the different biotic and abiotic stresses, including drought stress (Rainy and Griffiths, 2005; Porch et al., 2007; Beebe et al., 2013; Katungi et al., 2017; Mutari et al., 2021).

The market segment for navy bean is very small. Those who do grow navy bean is normally under contract and with irrigation facilities (or around irrigation schemes) to facilitate bulk buying. Some of the navy bean farmers in Zimbabwe produce the crop under rain-fed conditions. All areas cultivated during the rainy season are prone to drought and most of the farmers have no capacity to supplement irrigation during periods of drought (Mutari et al., 2021). Moreover, the rainfall pattern fluctuates from season to season due to climate change, consequently exposing the crop to drought stress (intermittent or terminal) at some stage during growth. However, terminal drought stress, which affects the reproductive growth stage (flowering, pod formation and pod maturation) is more common than intermittent drought stress in Africa (Beebe et al., 2013), central America (Frahm et al., 2004; Beebe et al., 2013) and north eastern Brazil (Beebe et al., 2013). In Zimbabwe, the recent participatory rural appraisal study conducted by Mutari et al. (2021) in the main navy bean growing regions of Zimbabwe revealed that the crop experiences terminal drought stress during the reproductive stage of development.

In recent years, Zimbabwe and other countries in sub-Saharan Africa (SSA) have been receiving below normal rainfall totals due to climate change, resulting in significant decline of ground water. This has resulted in pumping restrictions in some of the irrigation schemes, in some cases causing terminal drought stress (Mutari et al., 2021). Furthermore, the frequent electricity or power cuts in Zimbabwe coupled with obsolete irrigation facilities affect the irrigation cycles (Mutari et al., 2021). Thus, navy bean farmers who produce the crop under

irrigated conditions still experience drought stress during the growing season. The above cited constraints coupled with high production costs associated with irrigation force farmers to produce the crop under rain fed conditions or seek cultivars that are tolerant to drought stress. Regrettably, there are no drought tolerant navy bean cultivars in Zimbabwe to match the drought scenarios experienced during the growing season (Mutari et al., 2021). As a result, in 2017, Crop Breeding Institute (CBI) in Zimbabwe initiated a navy bean breeding program targeting the development of cultivars that are tolerant to terminal drought stress.

Asadi et al. (2010), Assefa et al. (2013) and Assefa et al. (2017) reported that genetic variability for drought stress tolerance exists in navy beans implying that genetic improvement of this trait would be possible. However, when improving crops for drought tolerance, information on the genetic control of economic quantitative traits such as grain yield and the associated traits under drought stressed environments and the identification of good general and specific combiners are primary requirements (Chiipanthenga et al., 2021). Such information would assist the navy bean breeding programme at CBI in selecting an effective breeding and selection strategy to follow in breeding for improved drought tolerance, grain yield and yield-attributing traits. Regrettably, the combining ability estimates of the navy bean genotypes at CBI that were introduced from PABRA are not known despite their economic importance. Moreover, literature on combining ability and gene action controlling drought stress tolerance, grain yield and its components is scanty among navy bean lines in Zimbabwe and worldwide. Assefa et al. (2013) evaluated eight-one navy bean genotypes for their adaptation to drought stress and identified six genotypes that were tolerant to drought stress. Assefa et al. (2017) also evaluated thirty-five navy bean genotypes under drought stressed (DS) environments and identified eight genotypes that combined drought tolerance with good canning quality under DS environments. Regrettably, the combining ability estimates of the drought tolerant navy bean genotypes that were identified by Assefa et al. (2013, 2017) have not been determined, making it difficult for bean breeders to use the genotypes as donors in drought tolerance breeding programs.

Combining ability analysis assists bean breeders in the identification of the best cross combinations with high specific combing ability (SCA) and parental genotypes with high general combining ability (GCA), increasing the chances of selecting superior transgressive segregants in the subsequent segregating populations. It also provides information on the type of gene action governing the expression of different quantitative agronomic traits of interest. Evidence for the expression of grain yield and its components in beans under DS and non-

drought stressed (NS) environments is contradictory. Phiri (2015), using different market classes, reported the predominance of additive gene action over the non-additive gene action in controlling the number of pods per plant, number of days to 50% flowering, number of seeds per pod, and hundred seed weight except for grain yield under DS environments. Asadi et al. (2010), using navy beans, and Amongi et al. (2015), using different market classes, reported that drought tolerance is governed by both additive and non-additive genes with predominance of additive gene effects for grain yield, pod weight, number of seeds per pod and number of pods per plant. Senbetay and Tesfaye (2015) also observed the predominance of dominance effects for grain yield and its components under optimum conditions in navy beans. These differences further necessitate the need to conduct genetic analysis studies for germplasm to be used for specific breeding programs to elucidate the nature of gene action governing the inheritance of grain yield and yield related traits under drought stressed conditions.

The aims of this study were to: (i) determine the inheritance and mode of gene action governing the expression of grain yield and its components under DS environments, (ii) identify parents with superior GCA estimates under DS and NS conditions to be used as donor parents in the drought tolerance breeding program, and (iii) identify promising cross combinations with superior SCA estimates to be used in the development of drought tolerant navy bean cultivars. The specific objectives were to: (i) estimate the combining ability effects of parents and F_2 progenies under DS and NS conditions, (ii) identify superior combiners under DS and NS conditions, (iii) determine the mode of gene action controlling navy bean grain yield and its components, and (iv) determine association between grain yield and yield attributing traits under DS and NS conditions, in order to assess the feasibility of indirect selection for grain yield.

6.2 Materials and Methods

6.2.1 Plant materials

Eight parents of the navy bean market class comprising of three drought tolerant genotypes (ZABRA16575-73F22, NAVY LINE-60 and G550), three drought susceptible genotypes (CZ113-13, G6 and G97) and two moderately drought tolerant genotypes (CIM-NAV02-17-3 and G37) were selected for genetic studies (Table 6.1). The eight parents were selected during an earlier field-based drought evaluation trial by the national bean breeding programme at CBI, Harare, Zimbabwe (unpublished work). The parents had different drought tolerance index (DTI) ranging from 0.13 (G6) to NAVY LINE-60 (0.69) (Table 6.1).

Table 6.1 Description of selected characteristics of the eight parents used in the study.

Parent	Code	SW	DTI	Reaction to drought stress	Other characteristics
CZ113-13	G1	24	0.16	Susceptible	Tolerant to pod shattering
CIM-NAV02-17-3	G2	25	0.44	Moderately tolerant	Tolerant to diseases of economic importance
ZABRA16575-73F22	G3	24	0.65	Tolerant	Tolerant to diseases of economic importance
G37	G4	22	0.48	Moderately tolerant	Early maturing and high grain yield potential under optimum conditions
G6	G5	20	0.13	Susceptible	High grain yield potential under optimum conditions
NAVY LINE-60	G6	23	0.69	Tolerant	High grain yield potential drought stress
G97	G7	22	0.19	Susceptible	High grain yield potential under optimum conditions
G550	G8	25	0.63	Tolerant	Early maturing

Canning Quality Traits

Parent	Code	HC	WDW	PWDW	Uniformity	Clumping	Splitting
CZ113-13	G1	1.81	245	63.4	7.0	5.0	5.0
CIM-NAV02-17-3	G2	1.90	275	61.3	7.0	7.0	7.0
ZABRA16575-73F22	G3	1.80	263	68.8	7.0	4.0	5.0
G37	G4	1.85	248	60.2	5.0	4.0	5.0
G6	G5	1.92	243	61.5	7.0	4.0	5.0
NAVY LINE-60	G6	1.83	278	71.4	7.0	6.0	6.0
G97	G7	1.81	242	62.1	7.0	4.0	5.0
G550	G8	1.83	241	60.8	5.0	3.0	3.0

HC hydration coefficient, *SW* 100-seed weight (g), *DTI* drought tolerance index, *WDW* washed drained weight (g), *PWDW* percentage washed drained weight (%)
Note – canning quality traits are scored as follows; clumping (1 indicates very much clumping and 7 very little clumping), splits (1 indicates very broken and 7 very intact), uniformity (1 indicates very variable and 7 indicate very uniform) (Balasubramanian et al., 2000). Optimum HC for navy bean processors range between 1.8-2.0 (Balasubramanian et al., 2000). A WDW of 240-280 grams for a navy bean sample equivalent to 90 g of initial solids is desired by navy bean processors (Mutari et al., 2021b). The desired PWDW is 60% (Balasubramanian et al., 2000).

Also, the moderately drought tolerant and susceptible genotypes possessed desirable characteristics including good canning quality traits (Table 6.1). This was done to increase the chances of selecting superior progenies which combine drought tolerance with good agronomic traits and canning quality profiles. The 100 seed weight (100 SW; g) canning quality profiles and other desirable characteristics of the parental genotypes are outlined in Table 6.1. All the genotypes were obtained from the Alliance of Bioversity International and International Center of Tropical Agriculture (ABC) in Malawi.

6.2.2 Experimental sites

Controlled biparental crosses were conducted at CBI and field experiments were conducted at Chiredzi research station (CRS) and Chisumbanje experiment station (CES) in Zimbabwe. The details of the study locations (CRS and CES) are presented in Table 4.1 under section 4.2.1 in Chapter 4. The soil micronutrient profiles for CRS and CES and weather conditions that were recorded during the study period are summarized in Appendix 6.1. Notably, no rainfall was recorded during the duration of the field experiment.

6.2.3 Development of progenies

Artificial hybridizations were conducted between July 2019 and November 2019. At flowering, the parents were cross pollinated inside a glasshouse using an 8*8 half diallel mating design, method II (with parents and excluding reciprocals) and model I (fixed genotypes/fixed effect assumption). The number of single crosses attempted were equal to [p(p-1)/2], where p is the number of parental lines used. Emasculations and pollinations were conducted following the artificial hybridization procedure of Makunde (2007). A total of ten crosses were conducted for each cross combination. The twenty-eight F_1 crosses, along with eight parents, were left to self-pollinate in a glasshouse from January 2020 to April 2020 to produce sufficient seed for genetic analysis at the F_2 generation in replicated field trials.

6.2.4 Field evaluation of parents and F_2 progenies

Eight parents and twenty-eight F_2 progenies were evaluated under DS and NS (control) environments in a 6*6 square lattice design with two replications during the dry season between May 2020 to August 2020. Each F_2 progeny and parent was planted in four row plots, 3 m long and 0.45 m wide. Intra-row spacing was 0.20 m. Both the NS and DS experimental plots were established adjacent to each other in the same field separated by a 30 m wide buffer zone to avoid water seepage between the NS and DS treatments. Sprinkler irrigation system was used at CRS, while furrow irrigation was used at CES. The irrigation scheduling in both treatments

was as described in section 5.2.3 under Chapter 5. Briefly, the DS experiments at both CRS and CES received a total of 6 irrigations, amounting to 240 mm and 248 mm respectively. A total of 10 irrigations were applied to the NS treatments at CRS (400 mm) and CES (415 mm).

6.2.5 Data collection

The data for number of days from planting to 50% flowering (DFW, defined as the number of days when 50% of the plants in a plot have one open flower), number of days from planting to physiological maturity (DPM, defined as the number of days when 90% of the pods lose their green pigmentation), and number of days of seed fill (DSF = DPM - DFW) were recorded on plot basis from the two middle rows of each plot excluding the boarder plants on the ends of each row. At physiological maturity, the number of pods per plant (NPPP) and number of seeds per pod (NSP) were averaged from ten randomly selected plants per plot. Grain yield (GYD) data was determined in grams from the weight of seeds harvested from ten plants per plot. After recording GYD, 100-seed weight (SW) was determined in grams from the weight of 100 seeds selected randomly from the GYD seed lot. A beam balance weighing scale was used to measure GYD and the weight of 100 seeds.

6.2.6 Statistical analyses

The collected data were subjected to analysis of variance (ANOVA) per environment and also across environment (combined ANOVA) using the Breeding Management Systems (BMS) statistical analysis software version 18 (The Integrated Breeding Platform's BMS, 2021). Bartlett's test of homogeneity of error variance across the two locations was conducted for all traits (Bartlett, 1947). The means were separated using the Least Significant Difference (LSD). In the combined ANOVA a mixed linear model was followed, the F_2 progeny and parents were considered as fixed effects and the environment, blocks and replications were considered as random effects. Pearson's correlation analysis was performed using Genstat 18th edition (Payne et al., 2018) to determine the degree of trait association within separate moisture treatments. The GCA and SCA effects were determined separately per environment according to Griffing's (1956a) method II, model I using the analysis of genetic designs in R software, version 3.0 (Rodriguez et al., 2015). The fixed model for combining ability analysis was as follows:

$$Y_{ijk} = \mu + g_i + g_j + S_{ij} + \mathrm{rk} + e_{ijk} \quad (1)$$

where Y_{ijk} is the mean phenotypic value of a character measured on cross i x j in *k*th replication, μ is the general/population mean effect, g_i and g_j are the GCA effects of i^{th} and j^{th} parental

genotypes, respectively, S*ij* is the SCA effect of *i* x *j* crosses, rk is the replication effect and e_{ijk} is the environmental effect associated with the ijk^{th} individual observation (Griffing, 1956a; Dabholkar, 1992). The significance of variance due to GCA and SCA effects was tested using 't' test. To make inferences on the type of gene action involved in the expression of GYD and yield components, the relative importance of GCA and SCA was determined using Baker's ratio (Baker, 1978) as follows:

$$\text{Baker's ratio} = \frac{2MS_{GCA}}{2MS_{GCA}+MS_{SCA}} \quad (2)$$

where MS_{GCA} = mean square for GCA, and MS_{SCA} = mean square for SCA. The GCA: SCA ratio was estimated by dividing GCA with SCA using the sum of squares of the respective trait. In addition to the direct measurements, drought indices were calculated from the primary data. Drought intensity index (DII) at each location, percentage GYD reduction (% GYR) due to DS, drought susceptibility index (DSI), geometric mean productivity (GMP) and drought tolerance index (DTI) of each entry were calculated according to Fischer and Maurer (1978). In this study, genetic variance components (additive and dominance) were not calculated. The genetic variance components can only be estimated if the random effects statistical model II (the selected parents represent a random sample from a population in linkage equilibrium) is used (Griffing, 1956b; Hallauer and Miranda, 1981; Sughroue, 1995, Sughroue and Hallauer, 1997). In this study, a fixed effects statistical model I was used in which the parents were purposively/deliberately selected based on performance (response to drought stress, good canning quality and desirable agronomic traits), thus only genetic effects and not genetic variances were estimated.

6.3 Results

6.3.1 Analysis of variance for grain yield and yield components under drought stressed and non-stressed environments

The mean square values and significant tests for the seven traits of 28 F_2 progenies and 8 parents evaluated across two water regimes and two locations are presented in Table 6.2. Under the NS treatment, genotype (G) and location (L) effects on DFW, DPM, GYD, NPPP and NSP of the parents and progenies were significant.

Table 6.2 Analysis of variance for grain yield and yield components for eight parents and twenty-eight F_2 progenies evaluated under drought stressed and non-stressed environments at Chiredzi research station and Chisumbanje experiment station in 2020.

		Non-stressed environments						
		Mean square and significance						
Source of variation	df	DFW (days)	DPM (days)	DSF (days)	GYD (g)	NPPP	NSP	SW (g)
Location (L)	1	308.69***	223.34***	6.89	1061673.00***	1277.57***	25.00***	1.23
Rep(L)	2	43.70*	36.20*	3.97	52774.00*	94.64	1.69	157.48
Block(L*Rep)	20	82.45***	59.17***	4.96	146616.00*	145.49	4.78***	89.06
Genotype (G)	35	110.64***	99.37***	4.73	105628.00*	163.52*	5.02***	206.42***
G*L	35	8.05	6.87	1.90	44313.00	32.08	4.18***	38.28
Residual	50	12.28	9.32	4.39	69067.00	88.83	1.36	62.75
		Drought stressed environments						
		Mean square and significance						
Source of variation	df	DFW (days)	DPM (days)	DSF (days)	GYD (g)	NPPP	NSP	SW (g)
Location (L)	1	58.78	90.78*	289.95***	276234.00***	2629.40***	24.04***	101.34
Rep(L)	2	217.12***	701.62***	141.69**	416.00	207.90	11.58***	62.34
Block(L*Rep)	20	68.12***	62.70***	41.34	52789.00**	382.00**	4.23**	105.27***
Genotype (G)	35	80.92***	74.57***	35.17	58310.00***	337.40**	3.50**	232.06***
G*L	35	13.30	20.35	16.33	2877.00	86.30	1.28	26.60
Residual	50	14.84	21.09	28.71	23679.00	147.80	1.89	35.64

DFW days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of seeds per pod, *GYD* grain yield, *SW* 100 seed weight, *Rep(L)* replications nested in locations, *Block(L*Rep)* incomplete block within a location, *G*L* genotype by location interaction, *Df* degrees of freedom, * $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$.

However, the genotype interaction with location (G*L) effect was only significant for NSP. Under the DS treatment, the mean square for genotypes was only significant for DFW ($p < 0.001$), DPM ($p < 0.001$), GYD ($p < 0.01$), NPPP ($p < 0.01$), NSP ($p < 0.01$) and SW ($p < 0.00$) while location (L) effect was significant ($p < 0.001$; $p < 0.05$) for all traits except for DFW and SW. However, their interaction (G*L) effect was not significant for all the studied traits (Table 6.2).

6.3.2 Mean performance of genotypes under drought stressed and non-stressed environments

The means of parental genotypes and F_2 progenies with respect to GYD and its components are presented in Table 6.3 and Appendix 6.2. Generally, the average performance values of all the parents and F_2 progenies for all the traits under DS were lower than the mean performance of all the parents and F_2 progenies under NS conditions due to drought stress. For instance, DPM decreased from 98.78 to 92.33 in the NS and DS experiments, respectively. A decrease in NPPP from 24.45 to 18.80 in the NS and DS experiments, respectively was observed. Grain yield also decreased from 2125 g under NS conditions to 1116 g under DS conditions. Under DS, the best performing progeny (G6 X G8) with respect to GYD, SW and DPM ranked seventh in terms of NPPP (29.50), however, this was not significantly different from the NPPP of the top performer with 37.00 (G1 X G5).

This progeny also ranked second and third best with respect to GYD (2616 g) and SW (32.75 g), however, these were not significantly different from the GYD (2580 g; G4 X G8) and SW (41.50 g; G3 X G8) of the top performers. The progeny G4 X G8 ranked second best in SW under both DS (48.25 g) and NS (40.25 g), however, the SW was not significantly different from the SW of the top performers. Among the parents under DS, the best performing genotypes with respect to GYD, NPPP, NSP and SW were G3, G6, G7, and G8. Under NS, the parent G8 ranked best for DPM, GYD, and SW and second for GYD under DS. Generally, the parents G3, G7, G4, and G8 were the top performing genotypes in terms of NSP, GYD, SW and NPPP under NS. The drought tolerance indices for the F_2 progenies and parents based on mean GYD are presented in Table 6.3 and Appendix 6.2. During this study, drought stress severity was moderate at both CRS (DII = 0.47) and CES (DII = 0.48). Across both locations, DII was 0.48. Of the test materials evaluated, the progeny G4 X G5 was one of the least affected by DS based on its low DSI value (0.65) and its low %GYR between NS and DS environments (31.29%). G6, G1 X G8, G1 X G7, G2 X G3, G2 X G4, G2 X G7, G2 X G8 and G4 X G5 also had low DSI values and %GYR.

Table 6.3 Grain yield based drought tolerance indices, mean values for grain yield (grams per 10 plants) and yield attributing traits of three key parents (based on drought tolerance and grain yield performance performance of their progenies under drought stress) and their F_2 progenies evaluated under drought stressed and non-stressed conditions across two locations in Zimbabwe.

Genotype	DFW (days)		DPM (days)		DSF (days)		NPPP	
	DS	NS	DS	NS	DS	NS	DS	NS
Parent								
G3	56.50^{a-d}	57.75^{a-e}	85.75^{ab}	92.25^{a-e}	29.25^{a-e}	34.50^{a-d}	9.50^{a-d}	27.00^{a-h}
G4	58.75^{a-g}	59.00^{a-g}	86.00^{ab}	93.75^{a-g}	27.25^{a-e}	34.75^{a-e}	11.50^{a-e}	2012^{a-f}
G8	58.25^{a-f}	53.25^{ab}	84.25^{a}	89.50^{a}	26.00^{a-c}	36.25^{de}	15.00^{a-f}	22.38^{a-g}
F_2 Progenies								
G1 X G3	63.92^{d-I}	70.21^{k-o}	92.42^{a-g}	104.17^{k-o}	28.50^{a-e}	33.96^{a-d}	22.00^{a-f}	25.94^{a-h}
G1 X G4	64.00^{d-I}	65.25^{g-m}	88.50^{a-e}	97.75^{e-j}	24.50^{a}	32.50^{ab}	15.75^{a-f}	20.50^{a-f}
G1 X G8	64.50^{e-I}	63.25^{e-j}	88.75^{a-e}	98.50^{f-k}	24.25^{a}	35.25^{a-e}	16.50^{a-f}	26.12^{a-h}
G2 X G3	57.50^{a-e}	60.50^{c-h}	88.75^{a-e}	93.00^{a-f}	31.25^{a-e}	32.50^{ab}	18.00^{a-f}	37.88^{gh}
G2 X G4	62.50^{c-k}	61.75^{d-i}	93.50^{b-g}	96.25^{b-i}	31.00^{a-e}	34.50^{a-d}	14.00^{a-f}	25.00^{a-h}
G2 X G8	63.75^{d-I}	65.50^{g-m}	89.75^{a-e}	98.50^{f-k}	26.00^{a-c}	33.00^{a-c}	24.00^{a-f}	31.38^{d-h}
G3 X G4	56.75^{a-d}	58.50^{a-f}	88.25^{a-e}	91.75^{a-d}	31.50^{a-e}	33.25^{a-d}	8.00^{a-c}	14.50^{a-c}
G3 X G5	65.75^{f-m}	69.00^{j-o}	95.50^{c-i}	102.75^{j-m}	29.75^{a-e}	33.75^{a-d}	33.00^{ef}	28.50^{c-h}
G3 X G6	61.92^{c-k}	61.50^{d-i}	92.33^{a-f}	95.08^{a-h}	30.67^{a-e}	34.08^{a-d}	10.50^{a-e}	19.83^{a-f}
G3 X G7	62.25^{c-k}	64.75^{f-m}	92.75^{a-g}	100.50^{h-I}	30.50^{a-e}	35.75^{c-e}	36.00^{f}	30.00^{c-h}
G3 X G8	55.00^{a-c}	52.75^{a}	86.75^{a-c}	90.50^{ab}	31.75^{a-e}	37.75^{e}	31.50^{d-f}	29.25^{c-h}
G4 X G5	60.75^{b-j}	62.75^{e-j}	93.25^{b-g}	96.50^{c-i}	32.50^{a-e}	33.75^{a-d}	12.75^{a-e}	39.12^{h}
G4 X G6	60.17^{a-i}	60.08^{c-h}	88.42^{a-e}	95.17^{a-h}	28.50^{a-e}	35.58^{b-e}	23.92^{a-f}	27.87^{b-h}
G4 X G7	57.50^{a-e}	63.75^{e-k}	93.75^{b-g}	98.50^{f-k}	36.25^{e}	34.75^{a-e}	14.50^{a-f}	15.25^{a-d}
G4 X G8	53.25^{a}	54.50^{a-c}	88.50^{a-e}	90.75^{a-c}	35.25^{d-e}	36.25^{de}	36.25^{f}	36.12^{f-h}
G5 X G8	66.00^{g-m}	67.50^{i-m}	95.00^{c-h}	101.50^{i-m}	29.00^{a-e}	34.00^{a-d}	7.75^{a-c}	11.62^{ab}
G6 X G8	54.25^{ab}	55.50^{a-d}	86.75^{a-c}	91.00^{a-d}	32.50^{a-e}	35.50^{b-e}	29.50^{b-f}	24.88^{a-h}
G7 X G8	62.50^{c-k}	62.75^{e-j}	89.50^{a-e}	97.75^{e-j}	27.00^{a-d}	35.00^{a-e}	24.00^{a-f}	26.25^{a-h}
Mean	62.67	64.33	92.33	98.78	29.68	34.48	18.80	24.45
SED	3.11	2.79	3.56	2.44	3.64	1.28	9.34	6.57
LSD (5%)	6.17	5.52	7.05	4.83	7.22	2.53	18.52	13.02

Table 6.3 (Continued).

Genotype	NSP		GYD (g)		SW (g)		% GYR	DTI	DSI	GMP
	DS	NS	DS	NS	DS	NS				
Parent										
G3	7.00^{b-d}	7.50^{a-d}	1153.00^{b-j}	2010.00^{a-d}	15.75^{a-c}	25.50^{a-f}	42.62	0.57	0.89	1522
G4	6.00^{a-c}	7.25^{a-d}	1071.00^{a-g}	2051.00^{a-d}	26.50^{d-h}	41.00^{h}	47.79	0.52	0.99	1482
G8	6.25^{a-c}	6.50^{a-d}	1188.00^{c-j}	2362.00^{b-f}	28.00^{e-h}	30.25^{d-h}	49.71	0.50	1.04	1675
F_2 Progenies										
G1 X G3	6.46^{a-c}	6.42^{a-d}	1040.00^{a-f}	2129.00^{a-e}	14.83^{a-c}	21.00^{a-f}	51.16	0.49	1.07	1488
G1 X G4	6.75^{a-d}	6.75^{a-d}	956.00^{a-c}	2116.00^{a-d}	15.50^{a-c}	17.25^{a-d}	54.79	0.48	1.14	1422
G1 X G8	6.75^{a-d}	6.75^{a-d}	1243.00^{e-k}	2122.00^{a-e}	20.75^{a-g}	25.75^{a-f}	41.45	0.59	0.86	1624
G2 X G3	9.25^{d}	11.25^{e}	1300.00^{g-k}	2018.00^{a-d}	18.50^{a-e}	23.50^{a-f}	35.56	0.64	0.74	1619
G2 X G4	6.50^{a-c}	7.25^{a-d}	1241.00^{e-k}	2060.00^{a-d}	18.75^{a-e}	20.75^{a-f}	39.73	0.60	0.83	1599
G2 X G8	7.00^{b-d}	6.75^{a-d}	1373.00^{j-k}	2240.00^{a-f}	23.50^{c-h}	23.50^{a-f}	38.71	0.61	0.81	1754
G3 X G4	6.00^{a-c}	7.00^{a-d}	1082.00^{a-h}	1982.00^{a-c}	22.25^{b-h}	21.50^{a-f}	45.42	0.55	0.95	1465
G3 X G5	8.00^{cd}	8.00^{b-d}	1024.00^{a-f}	2115.00^{a-d}	19.50^{a-f}	18.50^{a-d}	51.60	0.48	1.10	1471
G3 X G6	6.83^{a-d}	7.67^{a-d}	1092.00^{a-i}	2000.00^{a-d}	22.08^{b-h}	19.83^{a-e}	45.44	0.55	0.95	1478
G3 X G7	7 25^{b-d}	7.75^{a-d}	1117.00^{a-i}	2293.00^{a-f}	17.75^{a-d}	16.00^{ab}	51.29	0.49	1.07	1600
G3 X G8	5.75^{a-c}	6.25^{a-d}	1187.00^{c-j}	2375.00^{c-f}	28.75^{f-h}	41.50^{h}	50.04	0.50	1.04	1679
G4 X G5	6 50^{a-c}	6.50^{a-d}	1326.00^{i-k}	1930.00^{a-c}	19.50^{a-f}	17.50^{a-d}	31.29	0.69	0.65	1600
G4 X G6	7.08^{b-d}	8.25^{cd}	1170.00^{c-j}	2236.00^{a-f}	30.83^{h}	28.08^{b-g}	47.68	0.52	0.99	1617
G4 X G7	6 50^{a-c}	7.50^{a-d}	994.00^{a-d}	2062.00^{a-d}	29.25^{gh}	22.00^{a-f}	51.83	0.48	1.08	1431
G4 X G8	6 50^{a-c}	7.25^{a-d}	1256.00^{f-k}	2580.00^{ef}	48.25^{i}	40.25^{gh}	51.31	0.49	1.07	1800
G5 X G8	5.00^{ab}	5.50^{a-c}	924.00^{ab}	1892.00^{ab}	14.45^{a-c}	20.50^{a-f}	51.15	0.49	1.07	1322
G6 X G8	5.00^{ab}	5.00^{a}	1428.00^{k}	2616.00^{f}	50.25^{i}	32.75^{e-h}	45.43	0.55	0.95	1932
G7 X G8	7 50^{b-d}	7.50^{a-d}	1077.00^{a-h}	2462.00^{d-f}	22.50^{b-h}	26.00^{a-f}	56.26	0.44	1.17	1629
Mean	6.41	6.79	1116.00	2125.00	21.64	23.98	47.32	0.53	0.99	1538
SED	1.09	1.19	99.50	189.00	3.97	5.61				
LSD (5%)	2 16	2.36	197.30	374.70	7.87	11.13				

DFW days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of seeds per pod, *GYD* grain yield, *SW* 100 seed weight, *DS* drought stressed environments, *NS* non-stressed environments, *GYR* percentage grain yield reduction, *DTI* drought tolerance index, *DSI* drought susceptibility index, *GMP* geometric mean productivity, *SED* standard error of differences, *LSD* least significant difference at 0.05, * $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$. Means in a column followed by the same letter(s) are not significantly different at $P \geq 0.05$ under DS and NS conditions.

Geometric mean productivity showed that G4 X G8 and G6 X G8 performed better under both NS and DS environments followed by G2 X G8. Overall, based on DTI, GMP, %GYR and DSI, 2 parents (G3 and G6) and 6 F_2 progenies (G1 X G8, G2 X G3, G2 X G7, G2 X G8, G4 X G5 and G6 X G8) were considered tolerant to drought stress because of their high values for DTI and GMP and low values for %GYR and DSI.

6.3.3 Combining ability analysis of F_2 progenies and their parents for grain yield and yield attributing traits under drought stressed and non-stressed conditions

Analysis of variance on combining ability revealed significant ($p < 0.05$) mean square of GCA effects on DFW, DPM, DSF and SW under both DS and NS conditions (Table 6.4). Grain yield had significant ($p < 0.05$) GCA effects only under NS and DS conditions respectively, while NPPP and NSP had non-significant ($p > 0.05$) GCA effects under both test conditions. Mean squares due to SCA effects were only significant ($p < 0.05$) for DFW, DPM, NPPP, GYD, and SW under both test conditions. Genotypes and SCA significantly ($p < 0.01$) interacted with location under both environments with respect to PH, and NSP had highly significant ($p < 0.001$) location x GCA (L x GCA) and location x SCA (L x SCA) interactions under NS conditions. On the other hand, GCA significantly ($p < 0.05$) interacted with location under DS environment with respect to DFW. Under NS, all the Baker's ratios for the characters studied were more than 0.5 but less than unity. In addition, under NS, the estimate of GCA variance was relatively greater than that of SCA for all the studied traits except for PH, and NPPP. However, under DS environments, all the Baker's genetic ratios for the studied traits were more than 0.5 except for NPPP. Furthermore, under DS, the estimate of GCA: SCA ratio was relatively greater (more than 1) than that of SCA for all traits except for PH, NPPP and NSP.

6.3.4 General combining ability effects of parental genotypes for grain yield and yield attributing traits under drought stressed environment

Estimates of the GCA effects for the eight parents under DS conditions are presented in Table 6.5. Parents which combine significant, low, and negative GCA effects for DFW, DSF, and DPM with significant, positive, and high GCA effects for GYD are considered desirable under DS environments. On the other hand, parents that exhibit significant and positive GCA effects for NPPP, NSP, GYD, and SW are preferred for improving these traits under DS conditions.

Table 6.4 Analysis of variance, combining ability effects, general combining ability:specific combining ability ratio and Baker's ratio for grain yield and yield-attributing traits under drought stressed and non-stressed environments across two locations in Zimbabwe.

		Mean squares						
Source of Variation	*df*	DFW	DPM	DSF (days)	NPPP	NSP	GYD (g)	SW (g)
Drought stressed environments								
Location (Loc)	1	20.70	66.81	289.94***	1104.96**	15.23**	175603.60 **	101.33
Replication (Loc)	2	76.48***	516.30	141.69**	87.35	7.34***	264.69	62.34
Genotype (G)	35	86.07***	90.76***	44.79*	347.31***	3.52***	65374.65 ***	279.08***
GCA	7	293.59***	275.78***	64.07*	175.93	3.47	100339.70	672.53**
SCA	28	47.86***	51.10**	39.97	430.28***	3.84*	63208.22 ***	180.72***
Loc X G	35	13.32	19.80	22.20	86.78***	1.72	2671.10	26.37
Loc X GCA	7	28.02*	29.07	14.23	87.46	2.56	3329.16	40.25
Loc X SCA	28	12.15	19.10	24.19	94.26	1.81	2557.36	22.90
Residual	50	14.87	20.22	24.58	146.25	1.88	23072.69	32.14
GCA:SCA		6.13	5.36	1.60	0.41	0.90	1.59	3.72
Baker's ratio		0.92	0.92	0.76	0.45	0.64	0.76	0.88
Non-stressed environments								
Location (Loc)	1	107.30**	86.28**	6.89	693.34**	9.21*	945854.17***	0.67
Replication (Loc)	2	15.19*	13.98*	3.97	51.36*	0.62	47016.58***	85.92***
Genotype (G)	35	120.83***	107.45***	6.16***	164.38***	5.17	142123.88***	196.74***
GCA	7	477.54***	387.76***	10.80*	105.23	6.06	334959.49*	374.95*
SCA	28	55.53***	51.94***	5.00**	198.81***	5.43	100419.46*	166.06***
Loc X G	35	6.96	6.33	1.73	30.53	4.22***	50336.72	41.13
Loc X GCA	7	10.15	9.69	0.76	19.48	5.61	64448.15	40.43
Loc X SCA	28	7.17	6.23	1.97	36.17	4.82***	47985.91	46.81
Residual	50	12.41	9.41	3.92	86.35	1.38	65394.42	62.12
GCA:SCA		8.60	7.47	2.16	0.53	1.12	3.34	2.26
Baker's ratio	1	0.95	0.94	0.81	0.51	0.69	0.87	0.82

DFW days to flowering *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of seed per pod, *GYD* grain yield, *SW* 100 seed weight, *df* degrees of freedom, *GCA* general combining ability, *SCA* specific combining ability, * $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$.

Table 6.5 General combining ability estimates of parents for grain yield and yield-attributing traits under drought-stressed and non-stressed conditions.

Parents	DPM (days)		DSF (days)		NPPP		NSP	
	DS	NS	DS	NS	DS	NS	DS	NS
G1	2.76***	4.41***	-2.06**	-0.66*	2.56	2.88*	-0.06	-0.27
G2	1.42*	0.72	1.04	-0.73**	-3.52*	-2.32*	-0.03	-0.11
G3	-2.29**	-2.66***	0.53	-0.03	1.18	1.16	0.60**	0.71***
G4	-2.47***	-3.56***	0.69	-0.03	-1.20	-0.30	0.02	0.41*
G5	1.31*	2.04***	-0.86	0.17	-2.03	-1.14	-0.42*	-0.41*
G6	3.35***	2.43***	1.86**	0.13	-0.09	-0.24	-0.10	-0.04
G7	-0.30	0.80*	-0.26	0.27	1.30	-1.00	0.16	0.06
G8	-3.77***	-4.18***	-0.94	0.89**	1.79	0.96	-0.17	-0.35*
Parents	GYD (g)		SW (g)		DFW			
	DS	NS	DS	NS	DS	NS		
G1	-32.16	12.35	-4.60***	-0.68	4.28***	5.06***		
G2	-15.28	-89.19*	-3.93***	-1.04	0.81	1.44**		
G3	1.60	-19.02	-1.96**	-0.23	-2.56***	-2.58***		
G4	12.56	-5.24	4.25***	3.32***	-3.26***	-3.41***		
G5	-79.10**	-118.37**	-2.04*	-3.69**	2.11***	1.93***		
G6	55.80**	21.84	2.34**	-1.02	1.37*	2.29***		
G7	-22.49	9.08	-1.03	-2.39*	0.22	0.58		
G8	79.09**	188.55***	6.97***	5.71***	-2.97***	-5.32***		

See footnote in Table 6.1 for genotype codes. *DFW* days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of seeds per pod, *GYD* grain yield, *SW* 100 seed weight, *DS* drought stressed environments, *NS* non-stressed environments, * $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$.

Significant ($p < 0.01$) positive and desirable GCA effects for GYD were observed on G6 and G8, while G3 had significant ($p < 0.01$) positive GCA effects for NSP. Notably, G8 had the highest positive, desirable and significant ($p < 0.01$) GCA effects for GYD under drought stressed conditions, followed by G6. Thus, G8 and G6 were the best combiners for GYD under DS. Significant ($p < 0.05$) and negative GCA effects for GYD, NSP, SW, and DPM were observed on parent G5 under DS. G6 was a high general combiner for DSF, G3 for NSP, G1 for NPPP, PH and DFW.

6.3.5 General combining ability effects of parental genotypes for grain yield and yield attributing traits under non-drought stressed environment

Estimates of the GCA effects for the eight parents under NS conditions are presented in Table 6.5. The parent G8 was the best general combiner for GYD as revealed by its significant ($p < 0.001$), positive and high GCA effects, followed by G6. Therefore, both G8 and G6 would be good general combiners for grain yield under DS and NS conditions. On the other hand, significant ($p < 0.05$) and negative GCA effects for GYD were observed on parents G2 and G5. G4 and G8 were high general combiners for SW with significant ($p < 0.05$) positive GCA effects, and G4 for NSP with significant ($p < 0.05$) positive GCA effects.

6.3.6 Specific combining ability estimates for grain yield and yield attributing traits under drought stressed conditions

The estimates of SCA of 28 F_2 families for GYD and its components are presented in Table 6.6 and Appendix 6.3. Four crosses, namely G3 X G5, G3 X G7, G4 X G8, and G1 X G5 exhibited significant ($p < 0.05$) and positive SCA effects for NPPP under DS conditions. On the other hand, four crosses, namely G4 X G5, G2 X G8, G2 X G3, and G6 X G8 showed significant ($p < 0.05$) and positive SCA effects for GYD. However, significant ($p < 0.05$) and negative SCA effects on GYD were exhibited by G2 X G6 and G5 X G8. For DPM, significant ($p < 0.05$) negative SCA effects were exhibited by G1 X G4, G1 X G7, G4 X G6, G5 X G7, and G6 X G8. Thus, parent combination G6 X G8 combined significant ($p < 0.05$), negative and positive SCA effects for DPM and GYD respectively.

6.3.7 Specific combining ability estimates for grain yield and yield attributing traits under non-drought stressed conditions

Higher positive and significant SCA values were considered desirable for GYD and its components under NS environments (Table 6.6).

Table 6.6 Specific combining ability effects of top ten and bottom five yielding crosses for grain yield (g/10 plants) and yield-attributing traits under drought stressed and non-stressed conditions.

Cross	DFW (days)		DPM (days)		DSF (days)		NPPP		NSP	
	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
SCA effects of 10 top yielding crosses under drought stress										
G1 X G5	-2.98	-2.79	0.63	-1.48	3.74	1 52	16.16**	7.10	1.41*	1.30*
G1 X G7	-5.00**	-6.70***	-7.10**	-7.25***	-2.36	-0.33	-17.31**	2.41	0.77	0.98
G1 X G8	-0.34	-0.56	-2.62	-0.23	-2.43	0 54	-10.12	-0.31	0.59	0.77
G2 X G3	-2.91	-2.69	-2.77	-3.74	0.00	-1.22	0.20	13.87**	2.23***	3.53***
G2 X G4	2.81	-0.56	2.18	0.44	-0.41	0.78	0.08	3.29	-0.02	-0.12
G2 X G7	-0.96	-1.34	-3.02	-1.92	-1.96	-0.51	-6.27	-2.06	-0.25	-1.78**
G2 X G8	3.52*	5.53**	-0.38	3.84**	-3.78	-1.64	5.78	7.91	0.76	0.16
G4 X G5	-0.67	-0.70	2.08	-1.42	2.99	-0.87	-2.85	15.59***	0.64	0.07
G4 X G8	-4.68*	-2.91	2.03	-1.83	5.82*	0 90	19.71***	9.77*	0.37	0.52
G6 X G8	-6.43***	-5.82***	-5.02*	-5.72***	1.90	-0.01	6.00	-0.17	-1.20	-1.49**

Cross	GYD (g)		SW (g)	
	DS	NS	DS	NS
SCA effects of 10 top yielding crosses under drought stress				
G1 XG5	53.80	183.80	2.73	6.08
G1 X G7	61.34	-233.66*	-1.77	-0.82
G1 X G8	103.94	-209.77	-3.26	-3.60
G2 X G3	184.80**	0.56	2.75	1.80
G2 X G4	122.83	26.25	-3.22	-4.81
G2 X G7	112.69	-111.97	2.32	-1.40
G2 X G8	189.94**	13.16	-1.18	-5.78
G4 X G5	284.61***	-72.69	-4.36	-7.92*
G4 X G8	33.02	278.69*	15.39***	7.71*
G6 X G8	175.22*	278.50*	19.30***	4.29

Table 6.6 (Continued).

Cross	DFW (days)		DPM (days)		DSF (days)		NPPP		NSP	
	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
SCA effects of 5 bottom yielding crosses under drought stress										
G1 X G4	-1.62	-1.67	-4.32*	-2.78	-3.81	-1.29	-2.68	-4.65	0.39	0.14
G2 X G5	1.50	3.29*	3.52	2.55	2.14	-0.91	-7.23	-4.15	-0.81	-0.70
G2 X G6	-3.07	-1.75	-0.89	-2.80*	2.43	-1.13	-7.03	-3.27	0.84	2.08***
G4 X G7	-1.66	2.76	4.42*	2.63	6.14*	0.03	-3.58	-8.80*	-0.06	0.28
G5 X G8	2.42	5.00**	4.70*	3.65**	1.11	-1.54	-8.40	-13.06**	-0.76	-0.49

Cross	GYD (g)		SW (g)	
	DS	NS	DS	NS
SCA effects of 5 bottom yielding crosses under drought stress				
G1 X G4	-126.36	-13 30	-5.80*	-8.50*
G2 X G5	-112.34	-17 36	0.57	1.91
G2 X G6	-266.16***	-138.08	-8.30**	-3.96
G4 X G7	-112.98	-66 33	4.38	-3.41
G5 X G8	-202.83**	-296.91*	-12 12***	-4.42

See footnote in Table 6.1 for genotype codes. *DS* drought stressed environments, *NS* non-stressed environments, *DFW* days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of pods per pod, *GYD* grain yield, *SW* 100 seed weight, * $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$.

The parent combination G4 X G5 showed non-significant ($p > 0.05$) and negative SCA estimates for GYD under NS despite exhibiting significant SCA estimates for GYD under DS conditions. In addition, significant ($p < 0.05$) and negative SCA effects on GYD were exhibited by crosses G1 X G7 and G5 X G8. Two crosses, namely G4 X G8 and G6 X G8 showed significant ($p < 0.05$) and positive SCA effects for GYD, and SW. Other good combiners with significant ($p < 0.05$) SCA effects for SW under NS conditions were G3 X G8 and G5 X G7. Good specific combiners for NSP were G1 X G5, G2 X G3 and G2 X G6. For NPPP, significant ($p < 0.05$) and positive SCA effects were exhibited by the crosses G2 X G3, G4 X G5, and G4 X G8. Crosses G2 X G8, G3 X G5, G3 X G7, G5 X G6 and G5 X G8 showed significant ($p < 0.05$) and positive SCA for DPM. On the other hand, significant ($p < 0.05$) and negative SCA effects for DPM were exhibited by the crosses G1 X G7, G2 X G6, G5 X G7 and G6 X G8.

6.3.8 Association of grain yield with yield attributing traits under drought stressed and optimal environments

Results of correlation coefficients among different traits under DS and NS conditions are presented in Table 6.7. Most of the correlations observed ranged from weak to strong. Significant and positive correlations were observed for NPPP ($r = 0.19$, $p < 0.05$), and SW ($r = 0.36$, $p < 0.001$) with GYD under DS conditions. In addition, the NPPP was significantly and positively correlated with NSP ($r = 0.17$, $p < 0.05$) and SW ($r = 0.17$, $p < 0.05$) under DS conditions. Under NS conditions, significant and positive correlations were observed for DPM ($r = 0.96$), NPPP ($r = 0.33$) and SW ($r = 0.29$) with grain yield. In addition, the NPPP was significantly ($p < 0.001$) and positively correlated with NSP ($r = 0.32$) under NS conditions.

6.3.9 Association among the four environments based on grain yield

Results of correlation coefficients among the four environments based on GYD are presented in Table 6.7. Generally, high, positive and significant correlation values were observed for GYD within water regimes (DS and NS) such as CRS under DS vs CES under DS ($r = 0.93$, $p < 0.001$) and CRS under NS vs CES under NS ($r = 0.42$, $p < 0.001$). In contrast, low and positive correlation values were observed across water regimes between GYD in the NS environments and GYD in the DS environments.

Table 6.7 Pearson's correlation coefficients for pairwise comparison of nine traits among twenty-eight families and eight parents under drought stressed and non-stressed environments in Zimbabwe.

Under drought stressed environments							
Trait	DF	DPM	DSF	GYD	NPPP	NSP	SW
DF	1						
DPM	0.65***	1					
DSF	-0.33***	0.51***	1				
GYD	-0.19*	-0.16*	0.01	1			
NPPP	0.05	-0.05	-0.11	0.19*	1		
NSP	-0.13	-0.16	-0.05	-0.01	0.17*	1	
SW	-0.37***	-0.20**	0.17*	0.36***	0.17*	-0.05	1
Under non-stressed environments							
Trait	DF	DPM	DSF	GYD	NPPP	NSP	SW
DF	1						
DPM	0.96***	1					
DSF	-0.44	-0.17	1				
GYD	-0.26	-0.19	0.29	1			
NPPP	-0.07	-0.08	-0.01	0.33***	1		
NSP	-0.13	-0.16*	-0.05	0.10	0.32***	1	
SW	-0.31***	-0.27***	0.23***	0.29***	0.14	-0.03	1

Among the four environments						
Trait			GYD			
	WR		DS		NS	
		Location	CRS	CES	CRS	CES
GYD	DS	CRS	1	0.93***	0.17	0.23*
		CES		1	0.11	0.26*
	NS	CRS			1	0.42***
		CES				1

WR water regime, *DS* drought stressed, *NS* non-stressed, *CRS* chiredzi research station, *CES* chisumbanje experiment station, *DFW* days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of pods per pod, *GYD* grain yield, *SW* 100 seed weight, * $P < 0.05$ and *** $P < 0.001$.

6.4 Discussion

The total amount of water (irrigation plus rainfall) received by the bean crop at both locations in the DS experiments was less than 300 mm. This was below 350 – 500 mm required by the bean crop for growth and development during the life cycle of the crop (Darkwa et al., 2016). As such, the DS experiments experienced moderate drought stress, which corresponds to the DII of 0.48. The moderate DII of 0.48 was sufficient to discriminate the F_2 progenies and parents, as revealed by their differential response for GYD and yield-attributing traits. The

significant mean squares of genotypes observed in most of the traits under DS environments indicate the presence of wide genetic variability for drought tolerance among the parents and their progenies. This, therefore provides an opportunity to bean breeders to identify drought tolerant genotypes with desirable traits, which address the needs and preferences of farmers and processors. Several studies have previously reported such genetic variability for drought stress tolerance among parents and progenies in dry beans (Makunde et al., 2007; Asadi et al., 2010; Habibi, 2011; Amongi et al., 2015; Phiri, 2015).

The parents G3 and G6 and their progenies performed consistently well under DS environments with respect to NSP, GYD, SW, NPPP, SW, %GYR, DTI, DSI and GMP. This indicates that the aforementioned genotypes might have genetic factors conferring tolerance to drought stress and are therefore likely to perform well in areas that are prone to drought stress. In self-pollinating crops such as navy bean, which have a lesser theoretical magnitude of heterosis, breeding programs should put more attention on additive gene effects that are fixable. Both additive and non-additive gene effects were important in the expression of traits under both environments as signified by the significant GCA and SCA effects for most of the studied traits. Traits such as DFW, DPM, DSF, and SW were influenced by additive gene action as shown by the existence of significant mean squares of GCA effects under both test environments. On the other hand, the significant mean squares of SCA observed under both test environments for traits such as DFW, DPM, NPPP, GYD, and SW indicate that non-additive gene action was also important in accounting for the expression of the aforementioned traits. This implies that artificial selection of these characters for further genetic improvement could be possible through artificial hybridization and recurrent selection methods (Owusu et al., 2017). The observed non-significant GCA and SCA effects for NSP under NS environments suggest that both traits were influenced by epistatic gene effects. These findings are consistent with those by Goncalves et al. (2015) who observed non-significant SCA effects for NSP in an F_2 dry beans population under NS conditions.

The significant interaction of genotypes, GCA and SCA with location for some of the traits indicates that different gene combinations, alleles and genes may be present for developing improved cultivars of navy bean that are adapted to drought stress. For instance, “G1” exhibited positive and negative GCA effects for GYD under NS and DS environments respectively; thus, the gene/s influencing the expression of GYD under optimal conditions in “G1” did not contribute to drought stress tolerance. Conversely, the parent “G3” had positive (tolerant to

drought stress) and negative (poorly adapted to optimal conditions) GCA effects under DS and optimal environments. Similar findings were reported by Rainey and Griffiths (2005) in snap beans under high and low temperature environments and Chiipanthenga et al. (2021) in soybean (*Glycine max* L.) under DS and NS environments. Therefore, there is need to evaluate and select F_2 progenies independently (separately) across contrasting water regimes in order to identify superior and stable F_2 progenies that are tolerant to drought stress. The GCA x Loc interaction effects were not significant for all the traits except for DFW (under DS) while SCA x Loc interaction effects were not significant for all the traits except for NSP (under NS) which was an indication of consistent expression of the studied traits across environments. These findings corroborate with the findings of Nkhata et al. (2021) who reported non-significant mean squares of GCA x Loc interaction effects for DFW, DPM, NPPP, and GYD under optimal conditions in dry beans.

Several studies (Mwije et al., 2014; Nayak et al., 2018; Nkhata et al., 2021; Chiipanthenga et al., 2021) suggest the predominance of additive gene effects in the expression of a trait when Baker's ratio is more than 0.5. In the present study, Baker's ratio was greater than 0.5 for all characters under DS, NS and across all environments except for NPPP (under DS), coupled with higher estimates of GCA variance (more than 1) over SCA for all the traits except for NPPP under DS and NS environments, respectively. This suggests that both additive and non-additive gene action were important, with a preponderance of additive gene action in controlling most of the studied traits under DS, NS and across environments. Therefore, early generation selection for all the studied traits may be effective except for NPPP. The present results agree with previous studies by Asadi et al. (2010) and Amongi et al. (2015) who observed the preponderance of additive gene action in the expression of GYD, pod weight and NPPP in dry beans under drought stressed conditions. Contrary to the current findings, Iqbal et al. (2012) and Senbetay and Tesfaye (2015) observed the predominance of non-additive gene action for the expression of GYD, and NPPP in dry beans under optimal environments. Differences in the genetic backgrounds of the parents used and the environments under which the experiments were conducted by the different researchers could be the reasons for the disparities in results with respect to the genetic control of certain traits. These conflicting results by several authors confirm that both additive and non-additive genes contribute to the expression of grain yield and its components in navy bean under DS and NS environments. This necessitates the need to harness both additive and non-additive types of genes through the population plant breeding approach (bi-parental mating) followed by reciprocal recurrent

selection, backcross, pedigree method of selection and single seed descent in early filial generations of navy beans (Nayak et al., 2018).

Parental genotypes G3, G4, and G8 which consistently exhibited significant, positive, and high GCA effects for GYD and its attributing traits in a desirable direction under both environments are good general combiners. This suggests that they could possibly pass on the favourable alleles to their offspring during breeding which may result in transgressive segregants in subsequent segregating populations (Dholariya et al., 2014; Goncalves et al., 2015; Fasahat et al., 2016; Chiipanthenga et al., 2021). Furthermore, G3, G4, and G8 exhibited significant and negative GCA effects for DFW and DPM, indicating that they could also be useful in breeding for earliness in drought prone regions. Therefore, G3, G4, and G8 could be useful in navy bean breeding programs to improve GYD and its components under both DS and NS environments. Parental genotypes such as G1, G7, and G8 showed higher GCA effects on GYD under optimal conditions than under DS conditions suggesting that the ability of genotypes to combine well depends on action, interaction, and linkage relationships of genes (Sofi et al., 2006). This highlights that superior GCA effects of genotypes under optimal conditions indicates their relative superiority under NS but does not necessarily indicate their ability to combine well with other genotypes under DS environments.

Under all the testing conditions, no single parent had high significant GCA effects for all the studied traits. Nevertheless, genetic recombination and gene pyramiding can be enhanced through several cycles of artificial hybridization and selection among the parental genotypes and their progenies to fix transgressive segregants (Joshi and Nayak, 2010). Romanus et al. (2008) also suggested the use of various cross-combinations (double crosses, three-way crosses, and four-way crosses) other than single crosses in order to enhance genetic recombination. Mutation breeding through mutation induction and backcrossing breeding can also be used to enhance genetic recombination. The significant, positive, and high SCA effects for GYD observed under DS environments for cross-combinations G2 X G3, G2 X G8, G4 X G5, and G6 X G8 was an indication of transfer of favourable alleles for improved GYD performance from the parents to the progenies. Such crosses may result in transgressive segregants that could be selected for DS environments. Thus, these crosses represent potential breeding material to further select for improved GYD and yield attributing traits under DS and NS environments. The superior performance of these crosses may be attributed to the involvement of additive x dominance (high/low - G2 X G8; G4 X G5; G6 X G8), and additive

x additive (high/high - G4 X G8) type of gene action interactions for expression of GYD and its components. According to Masood et al. (2014), breeding for improved grain yield and yield components should target superior cross-combinations with significant, positive and high SCA effects involving good combiner parents (high GCA x high GCA) or at least one parent with high and significant GCA effects in the desired direction to increase the chances of selecting transgressive segregants of a fixable nature. In studies by Iqbal et al. (2012) on dry beans, most of the superior cross-combinations under optimal environments involved high GCA x low GCA, average GCA x low GCA, high GCA x average GCA and average GCA x average GCA general combiners.

Over dominance, wide genetic base and complimentary epistatic gene effects (non-allelic interaction) at heterozygous loci could be attributed to the superiority of progenies from parents with low GCA effects (Girase and Deshmukh, 2000; Nayak et al., 2018). Similar findings were observed by Goncalves-Vidigal et al. (2008) and Senbetay and Tesfaye (2015) who reported that parental genotypes with unfavourable GCA effects resulted in superior hybrids in dry beans under optimal conditions. These findings imply that parental genotypes should not be discarded from the breeding pipeline based on only unfavourable and negative GCA estimates. Interestingly, some of the parents with high and positive GCA effects for some of the traits produced progenies with unfavourable negative SCA effects under both DS and NS environments. Similar findings were reported by Mwije et al. (2014) and Musembi et al. (2015) in sweet potato (*Ipomea batatas L*. Lam.) and Chiipanthenga et al. (2021) in soybean. These findings could be attributed to the lack of genetic complementation between genes of the parents involved and the presence of modifier genes which may act in combination resulting in large phenotypic variability. This suggests that high GCA effects of the parental genotypes indicate their relative superiority but does not necessarily mean that crossing of parental genotypes with high GCA effects will result in progenies with significant, positive, and high SCA effects.

The significant positive correlations that were observed between GYD and NPPP and NSPP under DS and NS environments suggest that these traits can be improved simultaneously. Therefore, GYD improvement in navy bean under both DS and NS environments can be achieved through both direct and indirect selection for NPPP and NSPP. Similar findings were reported by Romanus et al. (2008) in cowpeas with respect to DF, DSF, and DPM under optimal conditions. The significant, high and positive correlations that were observed between GYD within the same water regime (DS or NS) indicated that the entries that performed well

under DS or NS at CES also performed well under DS or NS at CRS respectively. On the other hand, the weak positive correlation values that were observed between GYD in NS environments and GYD in DS environments suggest that indirect selection of the F_2 progenies and parents for DS environments based on their performance on NS environments is unlikely. This also indicates the existence of a strong genotype by environment interaction across water regimes. These findings suggest that it is a challenge for bean breeders to obtain entries with good performance under both water regimes. This concurs with Annicchiarico (2002) who reported that it is practically impossible for crop breeders to pyramid genes responsible for superior GYD response in all environments into a single genotype. Therefore, the performance of F_2 progenies and parents under DS conditions may not be a good reflection of their performance under NS conditions *vis-a-vis*.

6.5 Conclusions and recommendations

There is potential for breeding progenies with superior GYD performance under NS and less GYD reduction under DS environments in Zimbabwe. Both additive and non-additive gene effects were important in the inheritance of GYD and its attributing traits with preponderance of additive gene action under both test environments. This implies that there is need to incorporate breeding schemes that exploit both additive and non-additive genes in navy bean breeding. Parents ZABRA16575-73F22, G37, G97, and G550 were the best combiners for GYD and its components under DS. Among these, only ZABRA16575-73F22 was considered tolerant to drought stress because of its high values for DTI and GMP and low values for %GYR and DSI. Therefore, ZABRA16575-73F22 could be utilized in navy bean improvement programs to form base populations with improved tolerance to drought. The best performing specific combiners with consistent high values for most of the studied traits under both environments were CIM-NAV02-17-3 x ZABRA16575-73F22, CIM-NAV02-17-3 x G550, G37 x G6, G37 x G550, and NAVY LINE-60 x G550. These cross-combinations involved at least one parent with high and significant GCA effects in the desired direction. Among these, CIM-NAV02-17-3 x ZABRA16575-73F22, CIM-NAV02-17-3 x G550, G37 x G6 and NAVY LINE-60 x G550 were considered tolerant to drought stress because of their high values for DTI and GMP and low values for %GYR and DSI. Thus, potential genotypes with improved tolerance to drought can be selected from these promising crosses for further evaluation before release. Weak and positive correlation values were observed across the water regimes. The implication is that in order to select entries with superior GYD performance under DS and NS environments, these entries need to be identified under DS and NS conditions respectively. The

significant and positive correlations of GYD with NPPP, and SW suggest the feasibility of indirect selection for GYD through secondary traits. Grain yield, NPPP, and SW were identified as best selection criteria for utilization in navy bean breeding. Breeding for superior grain yield under DS should involve high GCA x high GCA or high GCA x low GCA parental combinations. High GCA effects of the parental genotypes indicate their relative superiority but do not necessarily mean that crossing of parental genotypes with high GCA effects will result in progenies with significant, positive, and high SCA effects. The parents which had significant and poor GCA estimates as well as produced inferior cross combinations are undesirable for the genetic improvement of these traits since they are likely to have low gene frequencies for the respective traits. Such kind of parents should be discarded from the breeding pipeline. However, the parents with poor GCA estimates which produced superior cross-combinations must be retained in the breeding pipeline. Parental genotypes should not be discarded from the breeding pipeline based on only unfavourable and negative GCA estimates. The best F_2 progenies should be evaluated further through the single seed descent method to rapidly advance the progenies to homozygosity, after which selection for canning quality and GYD can be initiated.

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Appendix 6.1 Soil micronutrient profiles and monthly weather data during the field trials at Chiredzi research station and Chisumbanje experiment station, from May to August 2020.

Weather parameters								
	CRS				CES			
Month	May	June	July	August	May	June	July	August
Tmax (°C)	30.00	26.30	28.00	32.10	30.10	27.30	29.40	30.20
Tmin (°C)	10.00	9.50	8.00	12.60	11.60	10.90	15.70	14.40
RHmax (%)	74.00	85.00	67.00	91.00	67.00	78.00	69.00	84.00
RHmin (%)	42.00	57.00	44.00	23.00	47.00	61.00	50.00	27.00
Total Rainfall (mm)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

Soil micronutrient profiles		
Parameter	CRS	CES
pH (Calcium Chloride)	6.20	5.50
OM (%)	2.10	1.30
N (ppm)	19.0	11.0
P (ppm)	73.0	78.0
Ca (mg/100g)	8.40	9.20
Mg (mg/100g)	5.80	6.40
K (mg/100g)	0.32	0.25
Zn (ppm)	1.96	0.46
Fe (ppm)	7.38	5.83

CRS chiredzi experiment station, *CES* chisumbanje experiment station, *Tmax* average maximum temperature, *Tmin* average minimum temperature, *RHmax* average maximum relative humidity, *RHmin* average minimum relative humidity, *OM* organic matter, *N* nitrogen, *P* phosphorus, *Ca* calcium, *Mg* magnesium, *K* potassium, *Zn* zinc, *Fe* iron.

Appendix 6.2 Grain yield-based drought tolerance indices, mean values for grain yield (grams) and yield attributing traits of F_2 progenies and their parents evaluated under drought stressed and non-stressed conditions across two locations in Zimbabwe.

Genotype	DFW (days)		DPM (days)		DSF (days)		NPPP	
	DS	NS	DS	NS	DS	NS	DS	NS
Parent								
G1	75.25^{n}	77.75^{p}	103.50^{i}	110.00^{p}	28.25^{a-e}	32.25^{a}	21.00^{a-f}	27.75^{b-h}
G2	60.75^{b-j}	65.25^{f-m}	95.50^{c-i}	100.00^{h-I}	34.75^{c-e}	34.75^{a-e}	14.25^{a-f}	11.00^{a}
G3	56.50^{a-d}	57.75^{a-e}	85.75^{ab}	92.25^{a-e}	29.25^{a-e}	34.50^{a-d}	9.50^{a-d}	27.00^{a-h}
G4	58.75^{a-g}	59.00^{a-g}	86.00^{ab}	93.75^{a-g}	27.25^{a-e}	34.75^{a-e}	11.50^{a-e}	2012^{a-f}
G5	66.00^{g-m}	64.75^{f-m}	90.25^{a-f}	100.25^{h-I}	24.25^{a}	35.50^{b-e}	7.50^{a-c}	18.25^{a-e}
G6	70.75^{I-n}	75.00^{n-p}	103.00^{hi}	109.00^{n-p}	32.25^{a-e}	34.00^{a-d}	6.00^{a}	23.12^{a-h}
G7	67.00^{i-m}	68.75^{j-n}	94.50^{b-g}	103.75^{k-o}	27.50^{a-e}	35.00^{a-e}	31.50^{d-f}	20.12^{a-f}
G8	58.25^{a-f}	53.25^{ab}	84.25^{a}	89.50^{a}	26.00^{a-c}	36.25^{de}	15.00^{a-f}	22.38^{a-g}
F_2 Progenies								
G1 X G2	72.75^{m-n}	70.75^{I-o}	97.00^{e-i}	105.00^{I-p}	24.25^{a}	34.25^{a-d}	26.50^{a-f}	25.62^{a-h}
G1 X G3	63.92^{d-I}	70.21^{k-o}	92.42^{a-g}	104.17^{k-o}	28.50^{a-e}	33.96^{a-d}	22.00^{a-f}	25.94^{a-h}
G1 X G4	64.00^{d-I}	65.25^{g-m}	88.50^{a-e}	97.75^{e-j}	24.50^{a}	32.50^{ab}	15.75^{a-f}	20.50^{a-f}
G1 X G5	66.50^{h-m}	68.00^{i-m}	97.00^{e-i}	103.50^{j-n}	30.50^{a-e}	35.50^{b-e}	37.00^{f}	32.62^{e-h}
G1 X G6	68.00^{j-m}	75.25^{op}	101.00^{g-1}	109.25^{op}	33.00^{a-e}	34.00^{a-d}	30.50^{c-f}	26.12^{a-h}
G1 X G7	62.50^{c-k}	63.00^{e-j}	87.50^{a-d}	96.75^{d-i}	25.00^{ab}	33.75^{a-d}	6.50^{ab}	26.12^{a-h}
G1 X G8	64.50^{e-I}	63.25^{e-j}	88.75^{a-e}	98.50^{f-k}	24.25^{a}	35.25^{a-e}	16.50^{a-f}	26.12^{a-h}
G2 X G3	57.50^{a-e}	60.50^{c-h}	88.75^{a-e}	93.00^{a-f}	31.25^{a-e}	32.50^{ab}	18.00^{a-f}	37.88^{gh}
G2 X G4	62.50^{c-k}	61.75^{d-i}	93.50^{b-g}	96.25^{b-i}	31.00^{a-e}	34.50^{a-d}	14.00^{a-f}	25.00^{a-h}
G2 X G5	66.50^{h-m}	71.25^{m-o}	98.50^{f-1}	104.25^{k-o}	32.00^{a-e}	33.00^{a-c}	7.00^{ab}	15.62^{a-d}
G2 X G6	61.25^{b-j}	66.25^{h-m}	96.25^{d-i}	99.00^{g-k}	35.00^{c-e}	32.75^{a-c}	8.00^{a-c}	18.50^{a-e}
G2 X G7	62.00^{c-k}	64.25^{e-I}	90.50^{a-f}	97.75^{e-j}	28.50^{a-e}	33.50^{a-d}	9.50^{a-d}	20.62^{a-f}
G2 X G8	63.75^{d-I}	65.50^{g-m}	89.75^{a-e}	98.50^{f-k}	26.00^{a-c}	33.00^{a-c}	24.00^{a-f}	31.38^{d-h}
G3 X G4	56.75^{a-d}	58.50^{a-f}	88.25^{a-e}	91.75^{a-d}	31.50^{a-e}	33.25^{a-d}	8.00^{a-c}	14.50^{a-c}
G3 X G5	65.75^{f-m}	69.00^{j-o}	95.50^{c-i}	102.75^{j-m}	29.75^{a-e}	33.75^{a-d}	33.00^{ef}	28.50^{c-h}
G3 X G6	61.92^{c-k}	61.50^{d-i}	92.33^{a-f}	95.08^{a-h}	30.67^{a-e}	34.08^{a-d}	10.50^{a-e}	19.83^{a-f}
G3 X G7	62.25^{c-k}	64.75^{f-m}	92.75^{a-g}	100.50^{h-I}	30.50^{a-e}	35.75^{c-e}	36.00^{f}	30.00^{c-h}

Genotype	DFW (days)		DPM (days)		DSF (days)		NPPP	
	DS	NS	DS	NS	DS	NS	DS	NS
G3 X G8	55.00^{a-c}	52.75^{a}	86.75^{a-c}	90.50^{ab}	31.75^{a-e}	37.75^{e}	31.50^{d-f}	29.25^{c-h}
G4 X G5	60.75^{b-j}	62.75^{e-j}	93.25^{b-g}	96.50^{c-i}	32.50^{a-e}	33.75^{a-d}	12.75^{a-e}	39.12^{h}
G4 X G6	60.17^{a-i}	60.08^{c-h}	88.42^{a-e}	95.17^{a-h}	28.50^{a-e}	35.58^{b-e}	23.92^{a-f}	27.87^{b-h}
G4 X G7	57.50^{a-e}	63.75^{e-k}	93.75^{b-g}	98.50^{f-k}	36.25^{e}	34.75^{a-e}	14.50^{a-f}	15.25^{a-d}
G4 X G8	53.25^{a}	54.50^{a-c}	88.50^{a-e}	90.75^{a-c}	35.25^{d-e}	36.25^{de}	36.25^{f}	36.12^{f-h}
G5 X G6	69.00^{k-n}	70.25^{k-o}	96.75^{e-i}	106.50^{m-p}	27.75^{a-e}	36.25^{de}	28.00^{a-f}	22.12^{a-g}
G5 X G7	59.00^{a-h}	59.25^{b-g}	87.50^{a-d}	94.00^{a-g}	28.50^{a-e}	34.75^{a-e}	7.00^{ab}	23.00^{a-h}
G5 X G8	66.00^{g-m}	67.50^{i-m}	95.00^{c-h}	101.50^{i-m}	29.00^{a-e}	34.00^{a-d}	7.75^{a-c}	11.62^{ab}
G6 X G7	63.00^{d-k}	66.25^{h-m}	96.75^{e-i}	101.75^{i-m}	33.75^{b-e}	35.50^{b-e}	22.25^{a-f}	30.12^{c-h}
G6 X G8	54.25^{ab}	55.50^{a-d}	86.75^{a-c}	91.00^{a-d}	32.50^{a-e}	35.50^{b-e}	29.50^{b-f}	24.88^{a-h}
G7 X G8	62.50^{c-k}	62.75^{e-j}	89.50^{a-e}	97.75^{e-j}	27.00^{a-d}	35.00^{a-e}	24.00^{a-f}	26.25^{a-h}
Mean	62.67	64.33	92.33	98.78	29.68	34.48	18.80	24.45
SED	3.11	2.79	3.56	2.44	3.64	1.28	9.34	6.57
LSD 0.05	6.17	5.52	7.05	4.83	7.22	2.53	18.52	13.02

Appendix 6.2 (Continued).

Genotype	NSP		GYD (g)		SW (g)		% GYR	DTI	DSI	GMP
	DS	NS	DS	NS	DS	NS				
Parent										
G1	5.25^{ab}	5.75^{a-c}	1081.00^{a-h}	2160.00^{a-e}	18.50^{a-e}	28.00^{b-g}	49.94	0.50	1.04	1528
G2	5.00^{ab}	5.25^{ab}	1000.00^{a-e}	1958.00^{a-c}	16.25^{a-c}	33.75^{f-h}	48.90	0.51	1.02	1399
G3	7.00^{b-d}	7.50^{a-d}	1153.00^{b-j}	2010.00^{a-d}	15.75^{a-c}	25.50^{a-f}	42.62	0.57	0.89	1522
G4	6.00^{a-c}	7.25^{a-d}	1071.00^{a-g}	2051.00^{a-d}	26.50^{d-h}	41.00^{h}	47.79	0.52	0.99	1482
G5	5.50^{a-c}	6.00^{a-c}	958.00^{a-c}	1879.00^{a}	21.25^{a-g}	15.50^{ab}	49.02	0.51	1.02	1341
G6	6.00^{a-c}	5.50	1317.00^{h-k}	1965.00^{a-c}	24.00^{c-h}	22.75^{a-f}	32.98	0.67	0.69	1609
G7	6.75^{a-d}	7.25^{a-d}	1091.00^{a-i}	2218.00^{a-f}	15.50^{a-c}	21.00^{a-f}	50.82	0.49	1.06	1555
G8	6.25^{a-c}	6.50^{a-d}	1188.00^{c-j}	2362.00^{b-f}	28.00^{e-h}	30.25^{d-h}	49.71	0.50	1.04	1675
F_2 Progenies										
G1 X G2	6.25^{a-c}	5.50^{a-c}	979.00^{a-d}	2259.00^{a-f}	15.25^{a-c}	14.00^{a}	56.65	0.43	1.18	1487
G1 X G3	6.46^{a-c}	6.42^{a-d}	1040.00^{a-f}	2129.00^{a-e}	14.83^{a-c}	21.00^{a-f}	51.16	0.49	1.07	1488
G1 X G4	6.75^{a-d}	6.75^{a-d}	956.00^{a-c}	2116.00^{a-d}	15.50^{a-c}	17.25^{a-d}	54.79	0.48	1.14	1422
G1 X G5	7.25^{b-d}	7.25^{a-d}	1050.00^{a-f}	2206.00^{a-f}	17.75^{a-d}	22.50^{a-f}	52.39	0.48	1.09	1522
G1 X G6	6.00^{a-c}	6.25^{a-d}	1118.00^{a-i}	2189.00^{a-f}	13.50^{ab}	24.50^{a-f}	48.91	0.51	1.02	1565
G1 X G7	7.25^{b-d}	7.00^{a-d}	1086.00^{a-i}	1918.00^{a-c}	14.25^{a-c}	21.50^{a-f}	43.40	0.57	0.90	1443
G1 X G8	6.75^{a-d}	6.75^{a-d}	1243.00^{e-k}	2122.00^{a-e}	20.75^{a-g}	25.75^{a-f}	41.45	0.59	0.86	1624
G2 X G3	9.25^{d}	11.25^{e}	1300.00^{g-k}	2018.00^{a-d}	18.50^{a-e}	23.50^{a-f}	35.56	0.64	0.74	1619
G2 X G4	6.50^{a-c}	7.25^{a-d}	1241.00^{e-k}	2060.00^{a-d}	18.75^{a-e}	20.75^{a-f}	39.73	0.60	0.83	1599
G2 X G5	5.25^{ab}	5.50^{a-c}	893.00^{a}	1902.00^{ab}	16.25^{a-c}	21.75^{a-f}	53.04	0.47	1.11	1304
G2 X G6	7.25^{b-d}	9.00^{de}	896.00^{a}	1922.00^{a-c}	11.75^{a}	17.25^{a-d}	53.41	0.47	1.11	1312
G2 X G7	6.25^{a-c}	5.25^{ab}	1210.00^{d-k}	1932.00^{a-c}	19.00^{a-e}	19.25^{a-e}	37.37	0.63	0.78	1529
G2 X G8	7.00^{b-d}	6.75^{a-d}	1373.00^{j-k}	2240.00^{a-f}	23.50^{c-h}	23.50^{a-f}	38.71	0.61	0.81	1754
G3 X G4	6.00^{a-c}	7.00^{a-d}	1082.00^{a-h}	1982.00^{a-c}	22.25^{b-h}	21.50^{a-f}	45.42	0.55	0.95	1465
G3 X G5	8.00^{cd}	8.00^{b-d}	1024.00^{a-f}	2115.00^{a-d}	19.50^{a-f}	18.50^{a-d}	51.60	0.48	1.10	1471
G3 X G6	6.83^{a-d}	7.67^{a-d}	1092.00^{a-i}	2000.00^{a-d}	22.08^{b-h}	19.83^{a-e}	45.44	0.55	0.95	1478
G3 X G7	7.25^{b-d}	7.75^{a-d}	1117.00^{a-i}	2293.00^{a-f}	17.75^{a-d}	16.00^{ab}	51.29	0.49	1.07	1600
G3 X G8	5.75^{a-c}	6.25^{a-d}	1187.00^{c-j}	2375.00^{c-f}	28.75^{f-h}	41.50^{h}	50.04	0.50	1.04	1679
G4 X G5	6.50^{a-c}	6.50^{a-d}	1326.00^{i-k}	1930.00^{a-c}	19.50^{a-f}	17.50^{a-d}	31.29	0.69	0.65	1600

Genotype	NSP		GYD (g)		SW (g)		% GYR	DTI	DSI	GMP
	DS	NS	DS	NS	DS	NS				
G4 X G6	7.08^{b-d}	8.25^{cd}	1170.00^{c-j}	2236.00^{a-f}	30.83^{h}	28.08^{b-g}	47.68	0.52	0.99	1617
G4 X G7	6.50^{a-c}	7.50^{a-d}	994.00^{a-d}	2062.00^{a-d}	29.25^{gh}	22.00^{a-f}	51.83	0.48	1.08	1431
G4 X G8	6.50^{a-c}	7.25^{a-d}	1256.00^{f-k}	2580.00^{ef}	48.25^{i}	40.25^{gh}	51.31	0.49	1.07	1800
G5 X G6	6.00^{a-c}	6.25^{a-d}	1104.00^{a-i}	2228.00^{a-f}	17.75^{a-d}	16.25^{a-c}	50.44	0.50	1.05	1568
G5 X G7	4.25^{a}	5.50^{a-c}	988.00^{a-d}	1912.00^{a-c}	26.75^{d-h}	30.00^{c-h}	48.34	0.52	1.01	1375
G5 X G8	5.00^{ab}	5.50^{a-c}	924.00^{ab}	1892.00^{ab}	14.45^{a-c}	20.50^{a-f}	51.15	0.49	1.07	1322
G6 X G7	6.75^{a-d}	6.75^{a-d}	1162.00^{b-j}	2212.00^{a-f}	24.00^{c-h}	19.25^{a-e}	47.47	0.53	0.99	1603
G6 X G8	5.00^{ab}	5.00^{a}	1428.00^{k}	2616.00^{f}	50.25^{i}	32.75^{e-h}	45.43	0.55	0.95	1932
G7 X G8	7.50^{b-d}	7.50^{a-d}	1077.00^{a-h}	2462.00^{d-f}	22.50^{b-h}	26.00^{a-f}	56.26	0.44	1.17	1629
Mean	6.41	6.79	1116.00	2125.00	21.64	23.98	47.32	0.53	0.99	1538
SED	1.09	1.19	99.50	189.00	3.97	5.61				
LSD (5%)	2.16	2.36	197.30	374.70	7.87	11.13				

See footnote in Table 6.1 for genotype codes. *DFW* days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of seeds per pod, *NSPP* number of seeds per plant, *GYD* grain yield, *SW* 100 seed weight, *DS* drought stressed environments, *NS* non-stressed environments, *%GYR* percentage grain yield reduction, *DTI* drought tolerance index, *DSI* drought susceptibility index, *GMP* geometric mean productivity, *SED* standard error of differences, *LSD* least significant difference at 0.05, $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$. Means in a column followed by the same letter(s) are not significantly different at $P \geq 0.05$ under DS and NS conditions.

Appendix 6.3 Specific combining ability effects of crosses for grain yield and yield-attributing traits under drought stressed and non-stressed conditions.

Cross	DFW (days)		DPM (days)		DSF (days)		NPPP		NSP	
	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
G1 X G2	4.58*	0.45	0.53	1.34	-4.41	1.17	7.16	1.29	0.02	-0.75
G1 X G3	-1.48	1.93	-0.69	2.59	0.35	0.17	1.35	-2.06	-0.61	-0.98
G1 X G4	-1.62	-1.67	-4.32	-2.78	-3.81	-1.29	-2.68	-4.65	0.39	0.14
G1 X G5	-2.98	-2.79	0.63	-1.48	3.74	1.52	16.16**	7.10	1.41*	1.30*
G1 X G6	-2.25	2.64	2.35	2.73	3.53	0.05	10.95	0.91	-0.25	0.09
G1 X G7	-5.00**	-6.70***	-7.10**	-7.25***	-2.36	-0.33	-17.31**	2.41	0.77	0.98
G1 X G8	-0.34	-0.56	-2.62	-0.23	-2.43	0.54	-10.12	-0.31	0.59	0.77
G2 X G3	-2.91	-2.69	-2.77	-3.74	0.00	-1.22	0.20	13.87**	2.23***	3.53***
G2 X G4	2.81	-0.56	2.18	0.44	-0.41	0.78	0.08	3.29	-0.02	-0.12
G2 X G5	1.50	3.29*	3.52	2.55	2.14	-0.91	-7.23	-4.15	-0.81	-0.70
G2 X G6	-3.07	-1.75	-0.89	-2.80*	2.43	-1.13	-7.03	-3.27	0.84	2.08***

Cross	GYD (g)		SW (g)	
	DS	NS	DS	NS
G1 X G2	-81.02	207.87	2.13	-8.06*
G1 X G3	-53.20	16.68	-0.25	-0.38
G1 X G4	-126.36	-13.30	-5.80*	-8.50*
G1 XG5	53.80	183.80	2.73	6.08
G1 X G6	-7.60	33.12	-5.88*	3.10
G1 X G7	61.34	-233.66*	-1.77	-0.82
G1 X G8	103.94	-209.77	-3.26	-3.60
G2 X G3	184.80**	0.56	2.75	1.80
G2 X G4	122.83	26.25	-3.22	-4.81
G2 X G5	-112.34	-17.36	0.57	1.91
G2 X G6	-266.16***	-138.08	-8.30**	-3.96

Appendix 6.3 (Continued)

Cross	DFW (days)		DPM (days)		DSF (days)		NPPP		NSP	
	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
G2 X G7	-0.96	-1.34	-3.02	-1.92	-1.96	-0.51	-6.27	-2.06	-0.25	-1.78**
G2 X G8	3.52*	5.53**	-0.38	3.84**	-3.78	-1.64	5.78	7.91	0.76	0.16
G3 X G4	0.65	0.97	0.63	-0.16	0.60	-1.18	-8.47	-11.53*	-1.07	-1.16*
G3 X G5	4.25*	6.07***	4.07	5.21***	0.40	-0.87	15.86**	2.47	1.45*	0.62
G3 X G6	0.48	-2.82	-1.18	-3.83**	-1.40	-0.50	-8.28	-7.15	0.05	0.20
G3 X G7	1.50	1.81	2.78	3.23*	0.55	1.03	12.36*	4.13	0.22	0.17
G3 X G8	-1.30	-3.45*	0.70	-1.16	2.48	2.41**	8.69	1.62	-1.08	-1.03
G4 X G5	-0.67	-0.70	2.08	-1.42	2.99	-0.87	-2.85	15.59***	0.64	0.07
G4 X G6	-0.42	-2.37	-4.61*	-2.01	-3.72	0.99	6.80	3.90	0.72	1.06
G4 X G7	-1.66	2.76	4.42*	2.63	6.14*	0.03	-3.58	-8.80*	-0.06	0.28
G4 X G8	-4.68*	-2.91	2.03	-1.83	5.82*	0.90	19.71***	9.77*	0.37	0.52

Cross	GYD (g)		SW (g)	
	DS	NS	DS	NS
G2 X G7	112.69	-111.97	2.32	-1.40
G2 X G8	189.94**	13.16	-1.18	-5.78
G3 X G4	-59.51	-120.08	-1.68	-5.98
G3 X G5	-33.83	128.32	1.85	-1.67
G3 XG6	-95.00	-128.87	0.07	-3.41
G3 X G7	16.63	175.27	-0.90	-6.10
G3 X G8	-27.15	82.01	2.10	12.78**
G4 X G5	284.61***	-72.69	-4.36	-7.92*
G4 X G6	-10.03	94.43	2.60	1.92
G4 X G7	-112.98	-66.33	4.38	-3.41
G4 X G8	33.02	278.69*	15.39***	7.71*

Appendix 6.3 (Continued)

Cross	DFW (days)		DPM (days)		DSF (days)		NPPP		NSP	
	DS	NS	DS	NS	DS	NS	DS	NS	DS	NS
G5 X G6	2.68	1.35	-0.28	2.92*	-2.92	1.47	10.86	-0.63	0 20	0.19
G5 X G7	-5.81**	-6.84***	-5.66**	-7.14***	-0.05	-0.16	-10.69	0.63	-1.93**	-0.98
G5 X G8	2.42	5.00**	4.70*	3.65**	1.11	-1.54	-8.40	-13.06**	-0.76	-0.49
G6 X G7	-0.34	-0.96	1.74	-0.25	2.48	0.62	1.56	7.80	0 23	0.22
G6 X G8	-6.43***	-5.82***	-5.02*	-5.72***	1.90	-0.01	6.00	-0.17	-1.20	-1.49**
G7 X G8	2.97	3.13	1.39	2.66	-1.48	-0.64	-0.89	1.97	1.05	0.91

Cross	GYD (g)		SW (g)	
	DS	NS	DS	NS
G5 X G6	24.11	197.76	-4.20	-4.22
G5 XG7	-22.08	-103.43	8.17**	12.21**
G5 X G8	-202.83**	-296.91*	-12 12***	-4.42
G6 X G7	24.62	55.86	1.05	-2.18
G6 X G8	175.22*	278.50*	19.30***	4.29
G7 X G8	-96.99	137.76	-5.08	-1.09

See footnote in Table 6.1 for genotype codes. *DS* drought stressed environments, *NS* non-stressed environments, *DFW* days to flowering, *DPM* days to physiological maturity, *DSF* days to seed fill, *NPPP* number of pods per plant, *NSP* number of pods per pod, *GYD* grain yield, *SW* 100 seed weight, $P < 0.05$; ** $P < 0.01$ and *** $P < 0.001$.

Chapter 7 Identification of genomic regions of dry beans (*Phaseolus vulgaris* L.) associated with agronomic and physiological traits under drought stressed and non-stressed conditions using genome-wide association study

Abstract

Understanding the genetic basis of traits of economic importance under drought stress (DS) and non-stressed (NS) conditions is important in enhancing genetic gains in dry beans (*Phaseolus vulgaris* L., 2*n* = 2x = 22). The objectives of the study were to (i) identify markers in dry beans significantly associated with agronomic and physiological traits for drought tolerance and (ii) identify drought-related putative candidate genes within the mapped genomic regions. An andean and middle-american diversity panel (AMDP) comprising 185 genotypes were screened in the field under DS and NS conditions for two successive seasons (2019 and 2020). The AMDP was phenotyped for days to 50% flowering (DFW), plant height (PH), days to physiological maturity (DPM), grain yield (GYD), 100-seed weight (SW), leaf temperature (LT), leaf chlorophyll content (LCC) and stomatal conductance (SC). Principal component and association analysis were conducted using the filtered 9370 Diversity Arrays Technology sequencing (DArTseq) markers. The mean PH, GYD, SW, DPM, LCC and SC of the AMDP was reduced by 12.1, 29.6, 10.3, 12.6, 28.5 and 62.0%, respectively under DS. Population structure analysis revealed two sub-populations corresponding to the andean and middle-american gene pools. Overall, 68 significant ($p < 10^{-03}$) marker-trait associations (MTAs) and 22 putative candidate genes were detected across both DS and NS conditions. Most of the identified genes had known biological functions related to regulating the response to drought stress, growth and development under water deficit. The findings provide new insights into the genetic architecture of drought stress tolerance in common bean at the reproductive stage. The findings also provide potential candidate SNPs and putative genes that can be utilized in gene discovery and marker-assisted breeding for drought tolerance after validation.

Keywords: common bean (*Phaseolus vulgaris* L.), Diversity Arrays Technology, genome wide association study, andean, middle-american, drought stress, population structure

7.1 Introduction

Common bean was subjected to two parallel domestication events on the American continent, resulting in two different primary gene pools namely the andean and the middle-american (Sauer, 1993; Keller et al., 2022). The andean gene pool originated from the Andes mountains of South America and consists of medium (25-40 grams per 100 seeds) or large (≥ 40 grams per 100 seeds) seeded genotypes (Singh et al., 1991). On the other hand, the middle-american gene pool is native to Central America and Mexico, and comprises of small seeded genotypes (≤ 25 grams per 100 seeds). According to Bitocchi et al. (2013), there is more genetic variation within the middle-american gene pool compared to the andean gene pool.

Common beans are notably sensitive to climatic and environmental variations. This is aggravated by the fact that most bean growing regions in the world experience different production constraints including intermittent and terminal drought stress which adversely affect grain yield (Katungi et al., 2009; Beebe, 2012). As reported by Katungi et al. (2010), 73% of common bean production in SSA occurs in environments which experience moderate to severe drought stress. Beebe et al. (2013), Hoyos-Villegas et al. (2017) and Valdisser et al. (2020) reiterated that drought stress is the most important grain yield-limiting abiotic factor of dry beans worldwide. It is predicted from various climate models that the duration and frequency of droughts are expected to increase in Sub-Saharan Africa (SSA) (Kotir, 2011). Drought stress reduces stomatal conductance, total chlorophyll content, leaf expansion, number of days to physiological maturity, seed yield and biomass, number of pods and seeds per plant, seed size and harvest index (Tar'an et al., 2002; Barrios et al., 2005; Beebe et al., 2008; Beebe et al., 2010; Darkwa et al., 2016). According to Asfaw et al. (2012), severe drought stress can result in grain yield losses of up to 80%. In Zimbabwe, grain yield reductions of more than 50% were reported by Mutari et al. (2022) under terminal drought stress.

As reported by Mutari et al. (2021), bean farmers in Zimbabwe have been using different mitigation strategies to minimize grain yield losses due to terminal drought stress. These strategies include soil mulching, ridging, cultivating the soil to retain more moisture and reducing the area under the bean crop. However, host plant resistance is a more sustainable, environmentally friendly technology for managing drought stress in common beans compared to the multiple cultural practices. For this reason, most dry beans breeding programs aim to introduce drought tolerance into new cultivars to address the needs and preferences of smallholder farmers in the face of climate change (Builes et al., 2011). Understanding the

underlying genetic architecture of agronomic and physiological traits under drought stress (DS) and non-stressed (NS) conditions is a fundamental prerequisite for the genetic improvement of these traits in common beans using MAS. Thus, dissecting the genetic basis of multiple polygenic traits of economic importance such as drought tolerance with respect to the genomic regions and/or genes involved and their effects is important to improve genetic gains in breeding for superior grain yield in dry beans under DS and NS environments. This can be accomplished through complementary approaches such as genome wide association studies (GWAS) and genomic prediction models (Keller et al., 2022). Genome wide association study is a powerful tool for characterizing the genetic basis of quantitative traits, and identifying multiple candidate genes (marker alleles) associated with variation in quantitative traits (marker-trait associations; MTA) of interest in crop species using high density DNA markers at high level of genetic resolution (Ingvarsson and Street, 2011; Huang et al., 2012; Li et al., 2013, Li et al., 2014; Dramadri et al., 2019).

Genome wide association study has been successfully used to detect MTAs and quantitative trait loci (QTLs) in dry beans. Several QTLs associated with disease and insect pest tolerance have been identified in dry beans (Perseguini et al., 2016; Tigist et al., 2019; Nkhata et al., 2021; Zia et al., 2022). Similarly, MTAs were identified for drought tolerance traits in dry beans (Mukeshimana et al., 2014; Trapp et al., 2015; Briñez et al., 2017; Hoyos-Villegas et al., 2017; Valdisser et al., 2020). Also, MTAs were identified for nutritional composition-related traits (Katuuramu et al., 2018; Keller et al., 2022), symbiotic nitrogen fixation (Kamfwa et al., 2015a), cooking time (Cichy et al., 2015b) and photosynthetic traits (Makunde, 2013; Dramadri et al., 2019) in dry beans. Genomic regions governing agronomic traits in drought stressed (DS) and high yield potential environments were also identified in dry beans (Schmutz et al., 2014; Moghaddam et al., 2016; Hoyos-Villegas et al., 2017; Dramadri et al., 2019; Keller et al., 2022). Even though several significant MTAs were identified in previous GWAS studies for agronomic traits in DS environments, the use of very low thresholds ($-\log_{10}$ *p*-value ≥ 3.0) in most of the studies in determining significant MTAs might have resulted in many false positives. In addition, despite the fact that several QTLs/MTAs associated with agronomic traits have been identified in dry beans, further genetic studies are required using different genetic backgrounds to reach a saturation point. Moreover, most of the reported putative genes for agronomic and physiological traits were detected under yield potential environments.

Additionally, some of the previous mapping studies (Tar'an et al., 2002; Blair et al., 2006; Wright and Kelly, 2011; Checa and Blair, 2012; Mukeshimana et al., 2014; Hoyos-Villegas et

al., 2017) conducted on agronomic and physiological traits used a small population size and a limited number of molecular markers. This resulted in QTL with low resolution or poor estimation of marker effects, making it difficult to make inferences on putative candidate genes correlated with the identified QTL. Moreover, some of the identified QTLs explained low total genetic variance (Asfaw et al., 2012), and were sometimes not stable across environments due to genotype by environment interaction (GEI) (Trapp et al., 2015). Thus, their potential for MAS in developing genotypes that are tolerant to drought stress was inconclusive. Therefore, additional studies are required to dissect the genetic basis of agronomic and physiological traits in dry beans under DS and optimal environments for increased genetic gains. The objectives of this study were: (i) to identify single nucleotide polymorphism (SNP) markers significantly associated with agronomic and physiological traits for drought tolerance and; (ii) to identify drought-related putative candidate genes associated with traits within the mapped genomic regions.

7.2 Materials and Methods

7.2.1 Description of the study location

The field experiments (drought stress; DS and non-stressed; NS) were conducted at the screening site for drought stress tolerance located at Save valley experiment station (SVES), Zimbabwe. The experiments were carried out during the 2019 and 2020 dry winter seasons (April - July). Save valley experiment station is characterised by clay soils and is located in the drier lowveld region of Zimbabwe where dry beans are commercially produced during the dry winter season (Table 7.1). The research station receives an average annual rainfall of 450 mm that is usually distributed between the months of December and April. In both seasons, no precipitation was received during the trial evaluation period. Historically, SVES presents few rainfall occurrences during the dry winter season (Mutari et al., 2022). Daily temperatures (°C) and relative humidity (%) were recorded with a digital weather station (Table 7.1) during the growing seasons. More details on the agro-ecological characteristics of SVES are outlined in Table 7.1.

7.2.1 Germplasm

A total of 185 dry beans genotypes constituted the andean and middle-american diversity panel (AMDP). The AMDP comprised of landrace collections (25), released cultivars (18) and elite breeding lines (142) of different market classes such as sugars, calimas, small whites, large whites and large red kidneys (Appendix 7.1).

Table 7.1 Geographic information, monthly weather conditions and soil characteristics during the growing seasons at Save valley experiment station, Zimbabwe (April to July, 2019 and 2020).

Parameter		2019 dry season				2020 dry season			
		April	May	June	July	April	May	June	July
Temperature (^{o}C)	Max	33.00	29.00	28.00	30.00	31.00	28.50	27.00	32.00
	Min	9.00	9.50	10.00	12.00	11.50	8.00	8.5.00	12.50
Relative Humidity (%)	Max	82.00	95.00	69.00	91.00	74.00	85.00	69.00	71.00
	Min	42.00	56.00	44.00	25.00	46.00	59.00	50.00	30.00
Total Rainfall (mm)		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Soil type		Clay				Clay			
Latitude		$20^{0}32$`S				$20^{0}43$'S			
Longitude		$33^{0}09$`E				$33^{0}03$'E			
Altitude (m.a.s.l)		452				449			

masl meters above sea level, *mm* millimetres, *ppm* parts per million, *Max* maximum, *Min* minimum.

The genotypes were sourced from public and private breeding institutions located in different geographic regions. These included the Alliance of Bioversity International and International Center for Tropical Agriculture (ABC) in Colombia (87), ABC in Malawi (67), ABC in Uganda (18), Ethiopian Institute of Agricultural Research (EIAR) in Ethiopia (3), Crop Breeding Institute in Zimbabwe (6) and Seed-Co, also in Zimbabwe (4) (Appendix 7.1).

7.2.2 Field phenotyping of the diversity panel

7.2.2.1 Experimental design, irrigation scheduling and trial management

The AMDP was evaluated side by side under DS and NS treatment conditions. In both seasons, the genotypes in both DS and NS treatments were established in a 5 x 37 alpha lattice design with two replications. The seepage of water from the NS treatment to the DS treatment was minimized by maintaining a 30 m buffer zone between the two treatments. Each genotype was hand planted in four-row plots of 3 m in length, and an inter-row spacing of 0.45 m. Compound D (N = 7%, P = 14%, K = 7%) was applied at planting at a rate of 300 kg/ha. Ammonium nitrate (34.5% N) was applied in both DS and NS treatments as a top-dressing fertilizer thirty days after emergence at a rate of 100 kg/ha. An overhead sprinkler irrigation system was used to irrigate both DS and NS treatments during both seasons of evaluation. The irrigation cycles in both DS and NS treatments were as described by Mutari et al. (2022). In both seasons,

recommended agronomic practices were followed for the management and control of pests such as diseases, insects and weeds.

7.2.2.2 Collection of data on agronomic and physiological traits

At flowering, the number of days from planting to 50% flowering (DFW) were recorded in both treatments. The DFW was recorded when 50% of the plants in a plot had at least one or more open flowers. At mid-pod filling, leaf temperature (LT; ℃), stomatal conductance (SC; mmol m^{-2} s^{-1}) and leaf chlorophyll (LCC) content were collected on all genotypes in both DS and NS treatments. The LT and SC data were recorded from the surface of the uppermost fully expanded young leaf between 11:00 am to 14:00 pm using a FLUKE precision infrared thermometer (Everest Interscience, Tucson, AZ, USA) and a hand-held leaf porometer (Decagon Devices®, Pullman, WA, USA), respectively. Three readings were collected on three different randomly chosen plants from each plot per replicate in both the DS and NS treatments. The three measurements were averaged to obtain one final reading per plot. Phenotyping for LT and SC was done for an average of six days on clear, sunny days with minimal wind. Regarding the LCC, this was measured using a soil and plant analysis development (SPAD) chlorophyll meter (SPAD-502*Plus*, Konica-Minolta, Osaka, Japan) on two fully developed leaves of three plants in each plot. Then, the average value was calculated.

At physiological maturity, the following traits were recorded from the two inner rows from every plot for every genotype in both treatments and seasons: plant height (PH; cm), days from planting to physiological maturity (DPM), grain yield (GYD; kg/ha) and 100-seed weight (SW; g). Plant height which was averaged from three plants per plot was measured from the base of the plant (soil surface) to the top node bearing at least one dry pod with seed. The DPM were recorded as the average number of days from planting to when 95% of pods in a plot lost their green colour. Grain yield was recorded from the two middle rows in each plot using a weighing scale, and converted to kilograms per hectare (kg/ha) at 12.5% moisture basis. The SW was determined using a beam balance weighing scale by measuring the weight of 100 seeds that had been selected randomly from each plot harvest.

7.2.3 Statistical analysis of phenotypic data

Before conducting analysis of variance, normality tests were conducted in Genstat® Discovery 18th Edition (Payne et al., 2018) using residuals of the agronomic and physiological traits. The agronomic and physiological traits were analysed in Genstat® Discovery 18th Edition (Payne et al., 2018) using mixed models from which the best linear unbiased predictors (BLUPs) were

obtained. The BLUPs were estimated for the studied traits to minimize the environmental and seasonal effects. The BLUPs for each entry were estimated through individual environment (DS or NS) analysis, and by combined analysis (across water regimes). In the first step of analysis (single-environment analysis), the phenotypic data of each individual environment were analysed using a mixed linear model (MLM). In this model, blocks and genotypes were treated as random effects, and replications were considered as fixed effects. Genotype effects were declared to be random to enable the calculation of BLUPs and broad-sense heritability (H^2). The MLM presented below was fitted:

$$Y_{ijl} = \mu + g_i + r_j + b_{lj} + e_{ijl} \quad (1)$$

where Y_{jkl} = is the phenotypic observation of the genotype i in replicate j in block l within replicate j, μ = grand mean effect, g_i = random effect associated with genotype i, r_j = fixed effect associated with replicate j, b_{lj} = random effect associated with block l nested within replicate j, and e_{ijl} = residual effect associated with observation ijl. For a combined or multi-environment analysis, a MLM was used. In this model, blocks nested within replications, replicates nested within environments, genotypes and their interactions with environments (GEI) were considered as random effects. Environments, defined as year x water regime combination were considered as fixed effects. The MLM presented below was fitted:

$$Y_{ijkl} = \mu + G_i + E_j + R_{k(j)} + B_{l(jk)} + GE_{ij} + e_{ijkl} \quad (2)$$

where Y_{ijkl} = effect of genotype i in environment j and kth replication within environment j and Ith block nested within replicate k and environment j, μ = grand mean, G_i = random effect of the ith genotype, E_j = fixed effect of the jth environment, $R_{k(j)}$ = random effect associated with the replicate k nested within environment j, $B_{l(jk)}$ = random effect of block l nested within environment j and replicate k, GE_{ij} = random effect of the interaction between genotype i and environment j, and e_{ijkl} = random error associated with observation $ijkl$. The analysis was performed using the Restricted Maximum Likelihood (REML) method implemented in GenStat 18th edition (Payne et al., 2018). Broad-sense heritability estimates for the agronomic and physiological traits were calculated following the formula proposed by Cullis et al. (2006);

$$H^2 = 1 - \frac{\bar{v}BLUP}{2\sigma_G^2} \quad (3)$$

where σ_G^2 = genetic variance due to genotype and v̄BLUP = mean variance of a difference of two best linear unbiased predictions of genotypic effects. The REML analysis enabled the computation of BLUPs, v̄BLUP and genetic variance for each trait. Heritability was classified as low when less than 30 %, moderate when between 30-60 % and high when more 60 % (Johnson et al., 1955). Drought intensity index (DII) at the location, percentage GYD reduction

(%GYR) due to DS, drought susceptibility index (DSI), geometric mean productivity (GMP) and drought tolerance index (DTI) of each entry were calculated as described by Mutari et al. (2022). A ranking method was used to select superior drought tolerant genotypes by calculating the mean rank of each genotype across all the studied indices.

7.2.4 Genotyping of the diversity panel

Genomic DNA of the 185 genotypes was extracted from young leaves of 2-week old bean plants following the plant DNA extraction protocol for Diversity Arrays Technology (DArT; DArT, 2014). A NanoDrop Spectrophotometer (ND-8000, NanoDrop Technologies, Inc.) was used to determine the concentration of the DNA. Agarose gel (1% agarose gel) electrophoresis was used to evaluate the quality of the DNA. The DNA from the samples used in this study were genotyped using the Diversity Arrays Technology Sequencing (DArTseq) protocol using a set of 24,450 silico DArT markers. The DArT markers used were evenly distributed across all the 11 chromosomes of common bean. Genotyping by sequencing (GBS) was done at the Biosciences Eastern and Central Africa (BecA) Hub of the International Livestock Research Institute (BecA-ILRI) in Kenya. The silico DArTs used had polymorphic information content (PIC) values ranging from 0.01 to 0.50, reproducibility values of 1.00, and the proportion of missing data per marker was 7% (mean call rate of 93%, ranging from 81 to 100%). The entire data set of SNP markers was filtered in TASSEL v5.2 (Bradbury et al., 2007) to remove SNP loci with unknown physical positions on the common bean genome, monomorphic SNPs, and SNP markers with more than 20% missing data and minor allele frequency (MAF) of less than 5% (<0.05) threshold (Qin et al., 2016; Valdisser et al., 2020; Nkhata et al., 2021). A final total of 9370 (38%) DArTseq-derived SNPs distributed across the 11 chromosomes were retained after filtering for use in association analysis and population structure analysis via principal component analysis (PCA).

7.2.5 Inference of population structure

The genotypic data was imputed for missing alleles of SNPs on the KDCompute online sever (*https://kdcompute.igs-africa.org/kdcompute/*) using the optimal imputation algorithm to increase the power of the study. KDCompute was also used to graphically visualize the distribution of SNPs across the common bean genome. The population genetic structure was determined based on the Bayesian model-based clustering approach using the Bayesian inference program in STRUCTURE software version 2.3.4 (Pritchard et al., 2010). A subset of additionally filtered SNP markers (4095) at or near Hardy-Weinberg equilibrium ($r^2 < 0.8$) and

that covered the entire genome were used in population structure analysis with STRUCTURE (Cichy et al., 2015a; Hoyos-Villegas et al., 2017; Valdisser et al., 2020). This was done to reduce the background and admixture linkage disequilibrium (LD) owing to linked loci (Pritchard et al., 2010).

Settings for the STRUCTURE program were set as follows to derive the population structure: a burn-in period length of 10,000, and after burn-in, 10,000 Markov Chain-Monte Carlo (MCMC) repetitions. The number of sub-populations or clusters (K) was set from 1 to 10, with ten independent runs for each *K* (Kamfwa et al., 2015b; Cichy et al., 2015b; Tigist et al., 2019). The best K-value explaining the population structure was inferred using the Delta *K* (ΔK) method in Evanno et al. (2005) implemented in the on-line tool structure harvester software (Earl and vonHoldt, 2012). Genotypes with ancestry probability/coefficient ≥ 0.90 (≥ 90%) (pure genotypes) for the andean sub-population were allocated to the andean gene pool (Cichy et al., 2015a; Ojwang et al., 2021) (Appendix 7.1). On the other hand, genotypes with ancestry probability ≥ 0.90 for the Mesoamerican sub-population were allocated to the middle-american gene pool. Those with ancestry probability < 0.90 were considered as admixed (Ojwang et al., 2021). The clustering of the AMDP was further assessed and visualized in a 3D scatter plot using PCA in prcomp R 3.0 function (Price et al., 2006).

7.2.6 Marker-trait association tests and linkage disequilibrium analyses

The filtered 9370 SNPs and the adjusted trait means (BLUPs) for each of the environments (DS and NS) were used as input data in marker-trait association (MTA) analysis. The more conservative compressed mixed linear model (CMLM) procedure in the genome association and prediction integrated tool (GAPIT) (v3) program of R software was used to determine the MTAs following the *Q* + *K* model according to Lipka et al. (2012). *Phaseolus vulgaris* is characterised by a strong genetic structure necessitating the need to use the Q + K model (Raggi et al., 2019). The CMLM incorporated both the population structure (*Q*; fixed effect) and kinship (*K*; random effect) matrices as covariates to correct the population structure, increase statistical power of the analysis and minimize false positives (spurious MTAs) (Price et al., 2006; Qin et al., 2016; Liu et al., 2019). The K matrix was included in the association analysis to correct for cryptic relatedness within the AMDP (Kamfwa et al., 2015a; Qin et al., 2016). The threshold for significant MTA was set at $p < 0.001$ and false discovery rate (FDR) of 5% to reduce the risk of false MTAs.

The Manhattan plots drawn using the CMplot package in R 3.5.3 were used to visualise the significant MTAs for each environment. The p-values were plotted as $-\log_{10}(p)$ to generate the Quantile-Quantile (Q-Q) and Manhattan plots using the CMplot package in R package (Yin, 2016). The Q-Q plots were produced from the observed and expected logarithm of the odds (LOD) scores for each trait. The LD Heatmap package in R 3.0 was used to generate the LD Heatmaps for the significant markers of each trait (Shin et al., 2006; R. Core Team, 2016). Alleles with positive additive effects resulting in higher values of GYD, SZ and LCC were described as "superior alleles" under both DS and NS conditions, whereas alleles resulting in decreased GYD, SZ, and LCC were "inferior alleles". On the other hand, alleles with negative effects resulting in lower values of DFW, DPM, LT and SC were considered to be "superior alleles" under DS conditions. The Jbrowse feature on Phytozome v13 was used to browse the *P. vulgaris* G19833 v2.1 reference genome sequence (Schmutz et al., 2014) to gain insight into potential putative candidate genes associated with significant SNPs for each trait. The functional annotation of the gene was checked on Phytozome v13 website (http://phytozome.net) to postulate the role of the gene in the control of a target trait.

7.2.7 Putative candidate gene prediction

Plausible candidate genes were identified based on the window size of 200 kb (maximum ± 100 kb) on either side (upstream and downstream) of the significant marker (Blair et al., 2018; Raggi et al., 2019). The window size of 200 kb is the average LD (Blair et al., 2018; Raggi et al., 2019). A gene was considered a potential candidate using the following criteria: (i) if the gene contained a significant SNP or the gene contained a SNP that was in LD with a significant SNP (Kamfwa et al., 2015b), and (ii) if the gene had a known role related to regulating drought stress response, plant growth and development under water deficit based on gene ontology term descriptions in Phytozome v13. For the positional candidate genes that did not have adequate functional annotation information on Phytozome v13, the sequence data of the significant SNP was used against NCBI database using the basic local alignment search tool for nucleotide (BLASTn; https://blast.ncbi.nlm.nih.gov/smartblast/smartBlast.cgi).

7.3 Results

7.3.1 Phenotypic variability for agronomic and physiological traits under two water regimes

The descriptive statistics and H^2 estimates for the agronomic and physiological traits under DS and NS environments are shown in Table 7.2. Residual maximum likelihood analysis revealed

highly significant ($p < 0.001$) genotypic main effects on all the studied traits under both DS and NS environments supporting the use of the AMDP for GWAS purposes. Overall, phenotypic variability was observed among the genotypes for DFW, LCC, LT, SC, PH, DPM, GYD and SW under DS and NS conditions. High H^2 estimates (0.83 - 0.97) were observed for all the studied traits under DS, except for SC ($H^2 = 0.32$), LT ($H^2 = 0.46$), and LCC ($H^2 = 0.54$). Under NS conditions, high H^2 estimates (0.88 – 0.98) were observed for all the traits except for LCC ($H^2 = 0.14$), SC ($H^2 = 0.33$), and LT ($H^2 = 0.42$).

In general, the observed H^2 estimates under both environments revealed that much of the observed phenotypic variation was due to the genetic component, supporting the suitability of the AMDP for GWAS studies. Grain yield was highest under NS (1016 kg/ha; $H^2 = 0.88$), and lower under DS (715 kg/ha; $H^2 = 0.92$). The SW also varied among the environments at 34.98 g/100 seeds ($H^2 = 0.97$), and 31.39 g/100 seeds ($H^2 = 0.97$) under NS and DS, respectively. The AMDP had a shorter duration (lower values) under DS (DPM = 90.97 days), compared to NS (DPM = 104.10 days). The same trend was observed for PH, LCC, and SC. On the other hand, LT was lower (19.75 ℃) under NS environments, compared to DS environments (25.22 ℃). Under DS, GYD ranged from 39.4 kg/ha to 2134 kg/ha, and exhibited a narrower range than in NS where GYD ranged from 55.0 kg/ha to 2586 kg/ha. As indicated in Table 7.2, the coefficient of variation (CV) ranged from 3.71% (DPM) to 36.57% (GYD) under DS conditions and from 2.55% (DPM) to 35.93% (SC) under NS conditions. Low standard deviations (SD) were observed for LT and LCC under both environments. Combined GYD data over two seasons across environments revealed that the highest yielding genotype was G184 (DAB91 – 2223 kg/ha) followed by G176 (DAB302 – 2098 kg/ha) and G147 (CIM-SUG07-ALS-S1-3 - 2080 kg/ha) (Table 7.3).

Table 7.2 Phenotypic summary statistics, coefficient of variation and broad-sense heritability of the measured traits for all the 185 dry beans genotypes based on the best liner unbiased prediction (BLUP) value grown under drought stressed and non-stressed conditions.

Traits	Treatment												
	Drought stressed						Non-stressed						AC
	Average	SD	Range	Wald statistic (genotype)	CV (%)	H^2	Average	SD	Range	Wald statistic (genotype)	CV (%)	H^2	H^2
DFW	43.32	7 11	32-60	139.64***	5.58	0.96	41.28	5.69	32.50-60.00	95.66***	5.32	0.98	0.94
DPM	90.97	8.40	71.50-106	187.89***	3.71	0.85	104.10	9.31	83.50-120 20	210.74***	2.55	0.94	0.93
GYD	715.40	457.80	39.4-2134	600772.00***	36.57	0.92	1016.00	555.00	55.00-2586.00	797047.00***	33.68	0.88	0.92
SW	31.39	11.61	14.25-60.00	420.66***	16.91	0.97	34.98	12.27	16.75-65.00	463.60***	12.45	0.97	0.98
PH	50.05	16.75	25.25-102.2	963.70***	28.13	0.83	56.97	18.46	28.5-125.00	1145.90***	22.53	0.92	0.88
LCC	31.12	3.80	18.17-44.15	53.51***	16.62	0.54	43.55	4.46	33.10-62.43	78.08***	16.21	0.14	0.35
LT	25.22	2 59	16.85-30.95	29.29***	9.42	0.46	19.76	1.15	17.23-24 90	4.78***	7.12	0.42	0.37
SC	96.66	13.97	59.38-141.4	760.10***	18.90	0.32	254.50	75.69	64.00-465.00	23883.00***	35.93	0.33	0.24

AC across environments (drought stressed and non-stressed), *SD* standard deviation of the trait means, *CV* coefficient of variation, H^2 broad-sense heritability, *DFW* days to flowering, *DPM* days to physiological maturity, *GYD* grain yield (kg/ha), *SW* 100 seed weight (g), *PH* plant height (cm), *LCC* leaf chlorophyll content, *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), * $P < 0.05$; ** $P < 0.01$ and, *** $P < 0.001$.

Table 7.3 Drought tolerance indices and predicted genotype values for grain yield (across environments) of top 20 drought tolerant genotypes.

Genotype	Gene pool	GYD (kg/ha)	DSI	GMP	DTI	%GYR	Mean rank
G184	Andean	2222.7	0.16	2205.3	4.74	4.69	25.5
G176	Andean	2097.5	0.35	2084.0	4.25	10.60	29.9
G147	Andean	2080.1	1.26	1995.6	4.03	37.83	66.3
G146	Andean	2067.4	1.18	1994.5	4.02	35.49	61.5
G158	Admixed	2017.1	-0.01	1979.5	3.82	-0.26	24.5
G135	Andean	1968.7	-0.37	1956.9	3.75	-11.17	19.8
G101	Andean	1964.8	1.32	1890.6	3.78	39.72	69.3
G138	Andean	1846.8	0.22	1826.1	3.25	6.50	31.0
G180	Andean	1838.9	0.09	1789.6	3.13	2.57	29.5
G162	Andean	1828.7	0.57	1814.3	3.20	16.97	40.5
G124	Andean	1815.0	-0.03	1805.5	3.19	-0.78	26.0
G173	Andean	1792.6	0.68	1780.4	3.07	20.40	46.0
G115	Andean	1788.9	0.40	1765.4	3.04	11.87	35.5
G150	Andean	1758.8	0.40	1750.8	2.98	12.03	36.5
G127	Andean	1750.0	-0.02	1733.0	2.94	-0.73	29.0
G159	Andean	1743.3	1.12	1694.7	2.90	33.67	65.3
G113	Andean	1683.8	1.76	1548.0	2.35	52.77	91.5
G125	Andean	1628.2	-0.25	1590.2	2.49	-7.39	26.8
G181	Andean	1614.1	1.03	1585.2	2.44	31.00	64.5
G104	Andean	1608.8	0.58	1601.1	2.49	17.37	45.3

GYD grain yield, *DSI* drought susceptibility index, *GMP* geometric mean productivity, *DTI* drought tolerance index, *%GYR* percent grain yield reduction. **NB**: Mean rank is the mean rank of a genotype across all the drought tolerance indices. Admixed includes genotypes that are 10 to 90% andean or middle-american according to the structure analysis results.

The drought tolerance indices for the 185 genotypes based on mean GYD are summarised in Table 7.3 (top 20 drought tolerant genotypes) and Appendix 7.2 (all study genotypes). The severity of DS at SVES across the 2 seasons of evaluation was moderate (DII of 0.30). Among the evaluated genotypes, G158 (SWEET WILLIAM/DAB287), G135 (DAB539), G124 (DAB487), G127 (CIM-SUG07-ALS-2), G125 (CIM-RM09-ALS-BSM-12), G138 (CZ104-72) and G184 are some of the genotypes that were less sensitive to DS based on their low DSI, %GYR and overall mean ranks across the indices. These genotypes had DSI values ranging from -0.37 (G135) to 0.16 (G184) and %GYR ranging from -11.17 (G135) to 4.69 (G184). In summary, all the top 20 drought tolerant genotypes were members of the andean gene pool, except for G158 which is an admixture (Table 7.3).

7.3.2 Population structure analysis

The STRUCTURE analysis results and Evanno test (ΔK) revealed the presence of two major sub-populations (highest ΔK value occurred at $K = 2$) within the AMDP of dry beans (Figures 7.1A, B). The two sub-populations correspond to the andean and middle-american domesticated gene pools. The minimum ancestry or membership coefficient to a particular cluster was 0.63 (Figure 7.1B and Appendix 7.1). Most of the genotypes (90) clustered within the middle-american gene pool (Figure 7.1B). Seventy-six genotypes clustered within the andean gene pool (Figure 7.1B and Appendix 7.1). On the other hand, 19 were andean-middle american admixed genotypes of the two gene pools (10 to 90% andean or middle-american). The admixed genotypes included SMC16, SMC21, NUA674, NUA59-4, G75, DAB115, DAB63, DAB142, DAB477, CIM-RM02-36-1, CIM-RM09-ALS-BSM-11, CIM-RM02-134-1, Sweet William, ZABRA16575-60F22, GLP585/MLB49-89A-3, RWR2154, SAB792, NAVY LINE 22, and CIM-SUG07-ALS-S1-3 (Appendix 7.1).

The genetic structure result of the AMDP was verified with the PCA based on SNP marker data and is illustrated by a 3D scatter plot (Figure 7.1C). The first principal component (PC) accounted for more than 55% of the observed genotypic variability in the AMDP, while the second and third PCs separately accounted for less than 5% of the overall genetic variance in the AMDP (Figure 7.1D). The PCA also divided the genotypes into two distinct clusters (andean and middle-american sub-populations) as were found with STRUCTURE output (Figure 7.1C). Furthermore, the andean-middle-american admixed genotypes (positioned between the two groups) were isolated from the andean and middle-american sub-groups by PCA (Figure 7.1C).

7.3.3 Analysis of marker-trait associations under drought stressed conditions

The significant MTAs and their respective statistical parameters for agronomic and physiological traits are summarised in Table 7.4. In this study, the threshold for significant MTA was set at $p < 0.001$ to reduce the risk of false MTAs. Under DS conditions, 29 significant MTAs were identified for six traits (excluding DPM and LCC) with $p < 10^{-03}$. The associations are shown in Figure 7.2. The quantile-quantile (QQ) plots for the studied traits revealed that the expected and observed probability values were normally distributed (Appendix 7.3). The highest number of significant MTAs were observed on *P. vulgaris* (*Pv*) chromosome *Pv11* (28%), followed by *Pv8* (17%), with the least on chromosomes *Pv6* and *Pv4*, both with 3%.

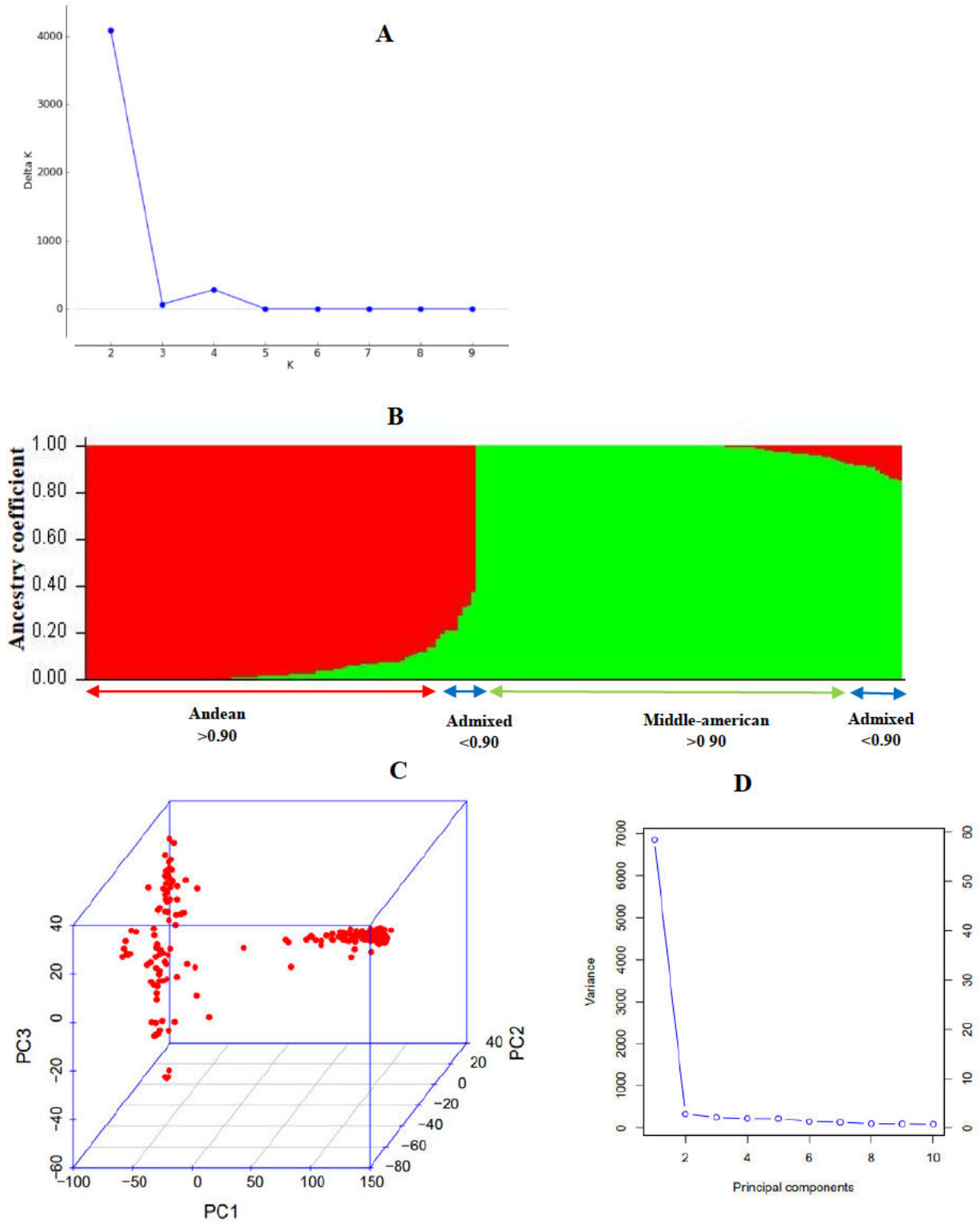

Figure 7.1 Population structure of 185 andean and middle-american diversity panel (AMDP) from different models: **(A)** The ΔK determined by the Evanno method showing the stratification of the 185 AMDP into two main sub-populations. The cluster with the largest ΔK ($K = 2$) was used to determine the number of sub-populations in the AMDP of dry beans and the existence of two-sub-populations was inferred; **(B)** Population structure of 185 AMDP of dry beans genotypes based on 4095 SNP markers ($K = 2$ gives the best separation) as determined from STRUCTURE analysis. Red and green represents andean and middle-american sub-populations, respectively; **(C)** Three dimensional principal component analysis (PCA) scatter plot illustrating the population structure of 185 AMDP of dry beans genotypes based on 9370 SNP markers; **(D)** Screen plot showing the percentage of variation explained by the different principal components.

Table 7.4 Single nucleotide polymorphism (SNP) markers associated with agronomic and physiological traits in dry beans genotypes under drought stress conditions.

Phenotype	SNP name	Ch	SNP position on genome (bp)	MAF	Allele	Effect of allele	-log10 (*P*) value	R^2	Candidate gene
LT	100106140	06	14389438	0.25	A/C	1.34	0.000	0.23	
	100065202	08	52504423	0.12	G/A	-1.43	0.000	0.22	
DFW	100132383	03	47240686	0.04	A/G	3.76	0.000	0.70	
	3381050	02	25978891	0.03	C/T	3.85	0.000	0.70	*Phvul.002G122100*
	8204238	10	42089084	0.06	A/G	2.78	0.000	0.70	
	8212194	10	42105474	0.04	A/T	3.54	0.000	0.69	
GYD	3384334	11	2362591	0.10	A/G	-176.67	0.000	0.44	
	3381526	11	2362591	0.09	A/G	-174.56	0.000	0.44	
	3382688	04	45231105	0.09	G/A	202.90	0.000	0.43	*Phvul.004G150500*
	100061855	11	40802478	0.42	T/G	138.98	0.000	0.43	
PH	100101387	05	34925013	0.03	G/A	17.82	0.000	0.32	
	8198531	07	9701750	0.04	G/A	-16.03	0.000	0.31	
	100060987	01	42938094	0.04	G/A	15.57	0.000	0.31	*Phvul.001G172300*
	100181735	08	22152034	0.23	G/A	7.57	0.000	0.30	*Phvul.008G133100*
	3379684	07	5239949	0.22	T/A	-5.62	0.000	0.30	
	16650827	07	51719432	0.09	T/C	-8.41	0.000	0.30	
	3380814	11	11934462	0.11	C/T	7.15	0.000	0.30	
	100119463	08	6003908	0.03	G/A	15.56	0.000	0.30	*Phvul.008G065700*
	8196298	11	12212674	0.12	T/G	-0.67	0.000	0.30	
	3379078	08	7823952	0.02	C/G	17.75	0.000	0.30	*Phvul.008G080600*
	3377272	11	9410740	0.16	T/C	-6.15	0.000	0.29	
	3379350	11	43494132	0.16	C/T	6.35	0.000	0.29	
	100063156	10	7307165	0.44	T/C	4.85	0.000	0.29	
	3379405	05	4782514	0.24	G/A	-7.80	0.000	0.29	
	3377900	11	9691109	0.14	T/A	-6.02	0.000	0.29	
SW	16647170	08	36620996	0.11	T/C	4.46	0.000	0.66	
	3383047	03	50229319	0.33	G/A	-2.41	0.000	0.65	*Phvul.003G263200*
SC	3380850	01	50427390	0.08	T/C	-10.79	0.000	0.10	*Phvul.001G254100*
	3381030	02	33669423	0.04	G/A	-10.33	0.000	0.08	

CH chromosome, *DFW* days to flowering, *GYD* grain yield (kg/ha), *SW* 100 seed weight (g), *PH* plant height (cm), *LT* leaf temperature (°C), *SC* stomatal conductance (mmol m^{-2} s^{-1}), *SNP* single nucleotide polymorphism, *MAF* minor allele frequency, R^2 proportion of the total phenotypic variation explained by the significant SNP marker after fitting the other model effects, $-\log_{10}(P)$ *p* value of the association.

No significant associations for DPM and LCC were identified under DS conditions in this study. The highest number of significant MTAs were identified for PH (15), and the SNPs were distributed across six different chromosomes (*Pv1*, *Pv5*, *Pv7*, *Pv8*, *Pv10*, and *Pv11*). Additionally, the allele effect of these SNPs ranged from -16.03 cm (SNP 8198531) to 17.82 cm (SNP 100101387).

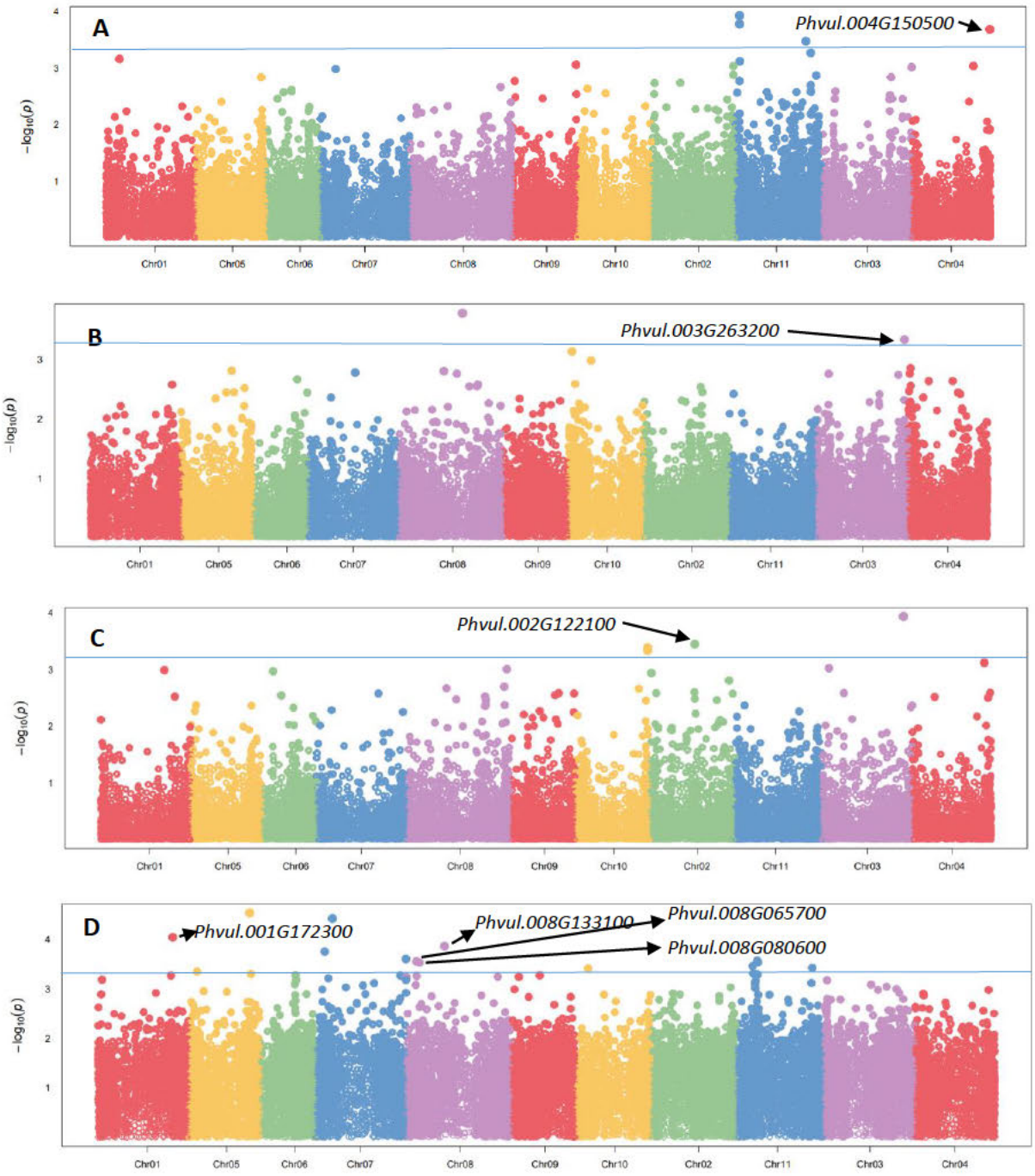

Figure 7.2 Manhattan plots indicating the significant marker-trait associations, their p-values and candidate genes for agronomic and physiological traits in 185 dry beans genotypes evaluated under drought stressed conditions: **(A)** Grain yield, **(B)** Seed size, **(C)** Days to 50% flowering, **(D)** Plant height, **(E)** Leaf temperature, **(F)** Stomatal conductance. *Chr represents Chromosome, x-axis represents the physical map locations of the SNPs on each chromosome and the y-axis (–log base$_{10}$ p-values) represents the degree to which a SNP is associated with a trait. The blue horizontal significant line represents FDR adjusted $p < 0.001$.

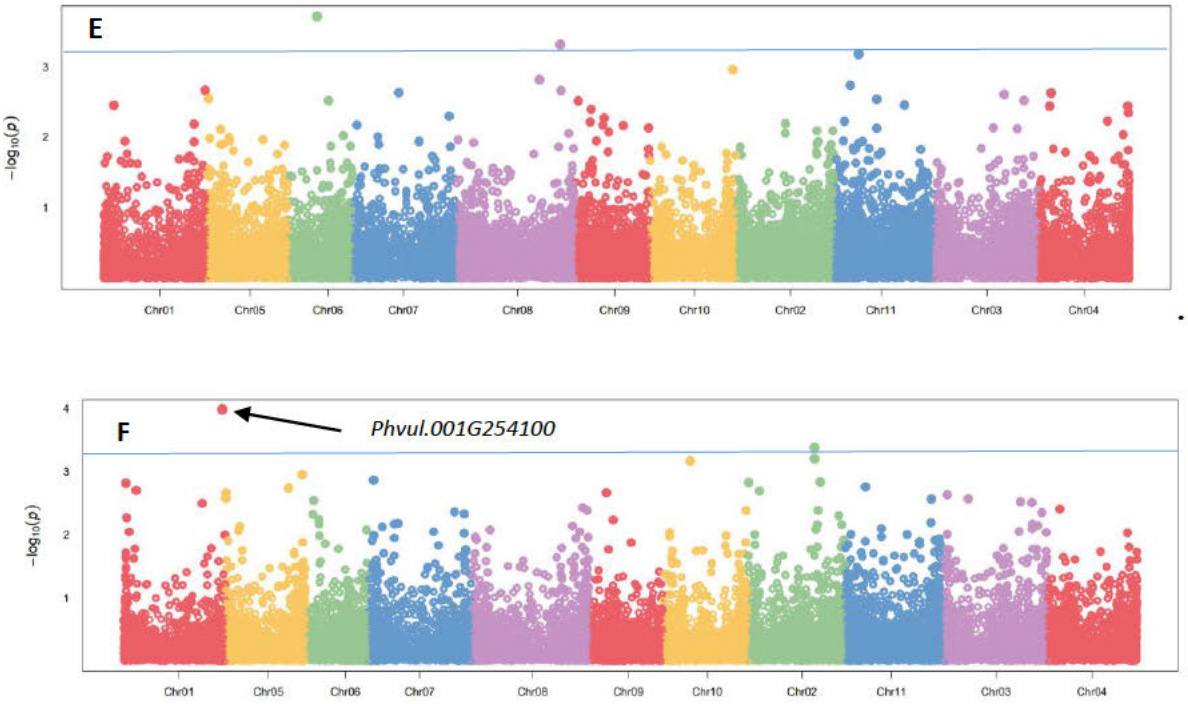

Figure 7.2 (Continued).

Four SNPs (SNPs 2362591, 2362591, 45231105, and 40802478) that had a significant association with GYD were also identified, and these were located on chromosomes *Pv4* and *Pv11*, with allele effect ranging from -174.56 kg/ha (SNP 3381526) to 202.90 kg/ha (SNP 3382688). Notably, 75% of the SNPs that were significantly associated with GYD were located on chromosome *Pv11*. The sum of the SNPs with a significant positive effect on GYD was 341,88 kg/ha and -351,23 kg/ha for all the SNPs with a significant negative effect on GYD (Table 7.4). For SW, two SNPs that were significantly associated with this trait were identified on chromosomes *Pv03* and *Pv08*, with allelic effects ranging from -2.41 g per 100 seeds (SNP 3383047) to 4.46 g per 100 seeds (SNP 16647170).

Regarding physiological traits, SNPs were identified that had a significant association with LT distributed across two chromosomes (*Pv6* and *Pv8*), with allele effect ranging from -1.23°C (SNP 100065202) to 1.34°C (SNP 100106140). Notably, two SNPs on chromosomes *Pv1* and *Pv2* were significantly associated with SC, with allele effect ranging from -10.79 mmol m^{-2} s^{-1} (SNP 3380850) to -10.33 mmol m^{-2} s^{-1} (SNP 3381030). Common regions associated with multiple traits on chromosomes were not identified under DS environments in this study. Markers explained 0.08 – 0.10, 0.22 – 0.23, 0.29 – 0.32, 0.43 – 0.44, 0.65 – 0.66 and 0.69 – 0.70 of the total phenotypic variability (R^2) for SC, LT, PH, GYD, SW and DFW, respectively.

Overall, the R^2 varied from 0.08 (SC: SNP 3381030) to 0.70 (DFW: SNPs 100132383, 3381050 and 8204238).

7.3.4 Analysis of marker-trait associations under non-stressed environments

The significant MTAs and their respective statistical parameters for agronomic and physiological traits are summarised in Table 7.5. Under NS conditions, 39 significant MTAs were detected for six traits (excluding SW and SC) with $p < 10^{-03}$. The associations are shown in Figure 7.3. The quantile-quantile (QQ) plots for the studied traits revealed that the expected and observed probability values were normally distributed (Appendix 7.4). The highest number of significant MTAs were observed on *Pv11* (15%), followed by chromosomes *Pv3* and *Pv4* (both with 18%), with the least on *Pv2* and *Pv10* (both with 3%). No significant markers for SW and SC were detected under NS conditions in this study. The highest number of significant MTAs were observed on PH (14), with markers accounting for 0.39 – 0.40 of the total traits variations. Additionally, the allele effect of these SNPs ranged from -10.46 cm (SNP 13121517) to 9.30 cm (SNP 13121517). Interestingly, 38% of the markers that were significantly associated with PH were located on chromosome 11. For DFW, a total of 12 significant associations were identified, with markers explaining 0.45 – 0.46 of the observed traits variations. Additionally, the significant SNPs for DFW were located on chromosomes *Pv1*, *Pv3*, *Pv4*, *Pv5*, *Pv6*, *Pv7* and *Pv11*, with allele effect ranging from -2.27 days (SNP 100175933) to 2.23 days (SNP 100175934).

Notably, one SNP (SNP 100124606) on chromosome *Pv01* was significantly associated with GYD, with a large positive allelic effect of 199.11 kg/ha. In addition, this SNP had a MAF of 0.17 in the population. Regarding physiological traits, SNPs were identified that have a significant association with LCC distributed across two chromosomes (*Pv6* and *Pv8*), with positive allele effects ranging from 1.90 (SNP 100167635) to 2.18 (SNP 8198945). For LT, nine significant associations were detected, with markers accounting for 0.08 – 0.15 of the traits variations. The significant SNPs for LT were located on chromosomes *Pv1*, *Pv3*, *Pv4*, *Pv5* and *Pv8*, with allele effect ranging from -0.71℃ (SNP 100102687) to 0.80℃ (SNP 100070187). Additionally, the sum of the SNPs with a significant positive effect on LT was 2.88℃ and -2.46℃ for all the SNPs with a significant negative effect. A locus (SNP 100117381) on chromosome *Pv02* explained the highest proportion of the phenotypic variation (0.70) among the studied traits and was associated with DPM. In addition, SNP 100117381 had a MAF of 0.18 in the population and a large positive effect (2.90 days) on DPM.

Table 7.5 Single nucleotide polymorphism (SNP) markers associated with agronomic and physiological traits in dry beans genotypes under non- stressed conditions.

Phenotype	SNP name	Ch	SNP position on genome (bp)	MAF	Allele	Effect of allele	-log10 (*P*) value	R^2	Candidate gene
DFW	3372129	04	43770691	0.20	C/T	1.85	0.000	0.46	
	3368616	01	48386869	0.29	C/G	2.19	0.000	0.46	
	8212932	04	43742237	0.35	C/A	-1.39	0.000	0.46	
	3379964	03	48424846	0.37	C/T	-1.61	0.000	0.46	
	100175933	06	31464277	0.27	A/G	-2.27	0.000	0.46	
	100175934	06	31464277	0.27	A/T	2.23	0.000	0.45	
	16647096	03	19481003	0.28	A/C	1.49	0.000	0.45	
	3378741	03	1178534	0.38	A/C	1.56	0.000	0.45	*Phvul.003G011400*
	100140152	04	43939513	0.32	A/G	1.67	0.000	0.45	*Phvul.004G037700*
	3374827	11	47036209	0.34	T/G	1.63	0.000	0.45	*Phvul.011G166300*
	3381380	05	1315962	0.27	T/C	-2.05	0.000	0.45	
	100122216	07	23590138	0.39	A/T	1.79	0.000	0.45	*Phvul.007G144000*
DPM	100117381	02	24161867	0.18	A/T	2.90	0.000	0.70	*Phvul.002G112700*
GYD	100124606	01	32783904	0.17	T/A	199.11	0.000	0.50	
LCC	8198945	06	30370228	0.16	T/C	2.18	0.000	0.12	*Phvul.006G209700*
	100167635	08	44516286	0.32	T/G	1.90	0.000	0.11	*Phvul.008G163600*
PH	3383709	11	23343020	0.28	A/G	7.30	0.000	0.41	
	100123206	03	41669536	0.27	G/T	9.02	0.000	0.40	*Phvul.003G192800*
	13121517	11	5699564	0.08	C/T	9.30	0.000	0.40	
	100164602	03	32040779	0.43	A/C	-4.72	0.000	0.40	
	100065600	11	38863980	0.27	C/G	-8.10	0.000	0.40	
	100181804	07	37529193	0.42	G/T	-4.77	0.000	0.40	*Phvul.007G253400*
	100124008	03	36956076	0.38	T/C	5.98	0.000	0.40	
	100101486	04	38236692	0.37	T/C	4.92	0.000	0.39	
	100073620	11	42969050	0.35	C/T	-7.00	0.000	0.39	*Phvul.011G152000*
	100068647	01	39765027	0.38	T/G	5.76	0.000	0.39	
	3382850	10	40091053	0.39	A/G	4.52	0.000	0.39	
	13121517	11	5699564	0.06	T/C	-10.46	0.000	0.39	
	3379157	06	30312046	0.44	T/C	-4.39	0.000	0.39	*Phvul.006G208800*
	13121469	01	44975217	0.49	C/A	5.29	0.000	0.39	*Phvul.001G190800*
LT	100101691	03	18922335	0.28	G/A	-0.56	0.000	0.08	
	100070187	04	12643816	0.21	A/G	0.80	0.000	0.15	
	100061661	01	19177470	0.16	T/A	0.69	0.000	0.09	
	100071816	04	33722284	0.45	A/G	0.39	0.000	0.08	
	100100644	08	26794110	0.21	A/C	0.54	0.000	0.08	
	100102687	04	7507744	0.14	G/A	-0.61	0.000	0.08	*Phvul.004G055500*
	100120897	08	20306142	0.06	C/A	-0.71	0.000	0.08	
	100167520	05	23720983	0.36	C/G	0.46	0.000	0.08	
	100161682	05	18689401	0.17	G/A	-0.58	0.000	0.08	*Phvul.005G077500*

Ch chromosome, *DFW* days to flowering, *DPM* days to physiological maturity, *GYD* grain yield (kg/ha), *PH* plant height (cm), *LCC* leaf chlorophyll content, *LT* leaf temperature (°C), *SNP* single nucleotide polymorphism, *MAF* minor allele frequency, R^2 proportion of the total phenotypic variation explained by the significant SNP marker after fitting the other model effects, $-\log_{10}(P)$ *p* value of the association.

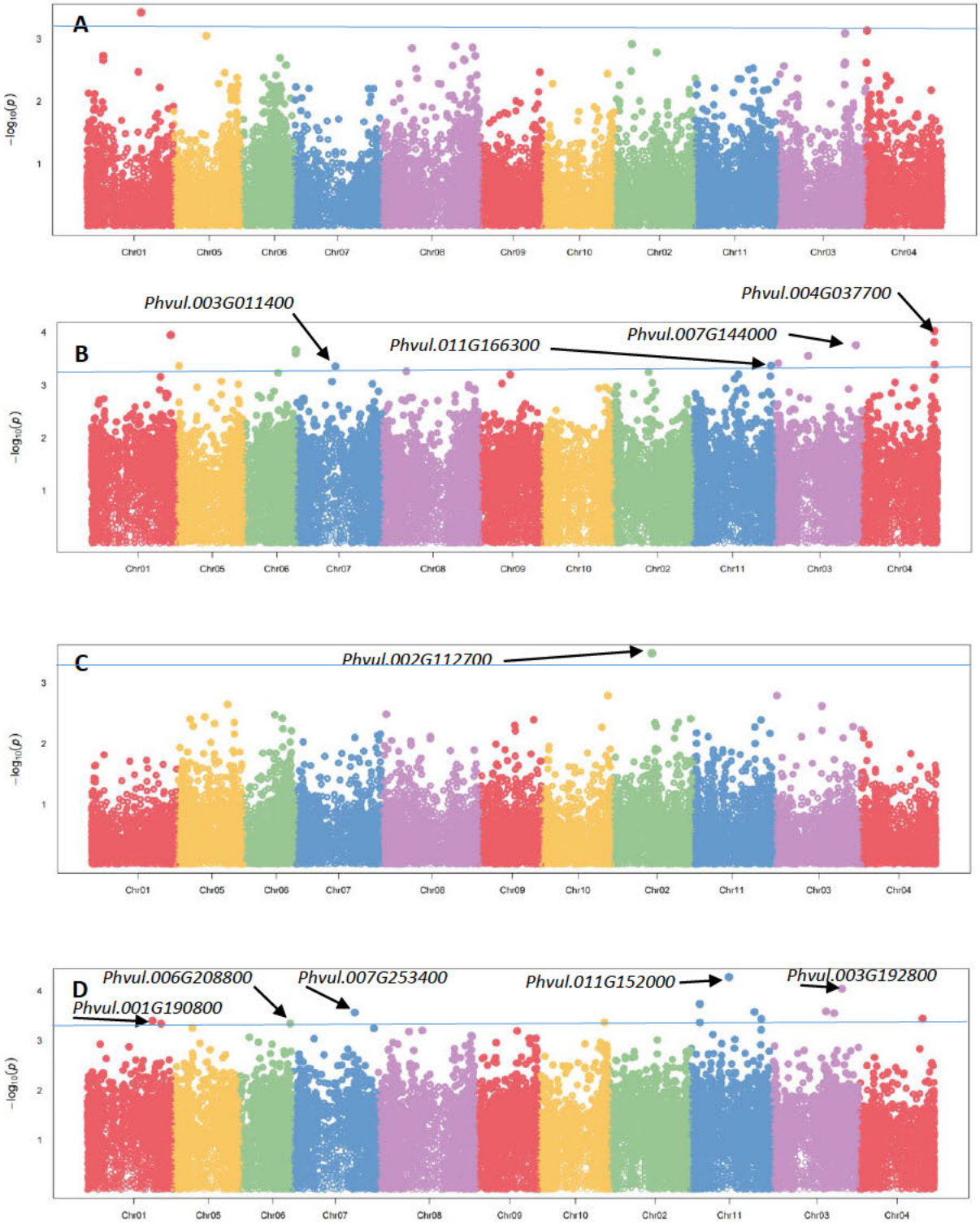

Figure 7.3 Manhattan plots showing significant marker-trait associations, their p-values and candidate genes for agronomic and physiological traits under non-stressed conditions: **(A)** Grain Yield, **(B)** Days to 50% flowering, **(C)** Days to physiological maturity, **(D)** Plant height, **(E)** Leaf chlorophyll content, **(F)** Leaf temperature. *Chr represents Chromosome, x-axis represents the physical map locations of the SNPs and the y-axis (–log base$_{10}$ p-values) represents the degree to which a SNP is associated with a trait. The blue horizontal significant line represents the FDR adjusted $p < 0.001$.

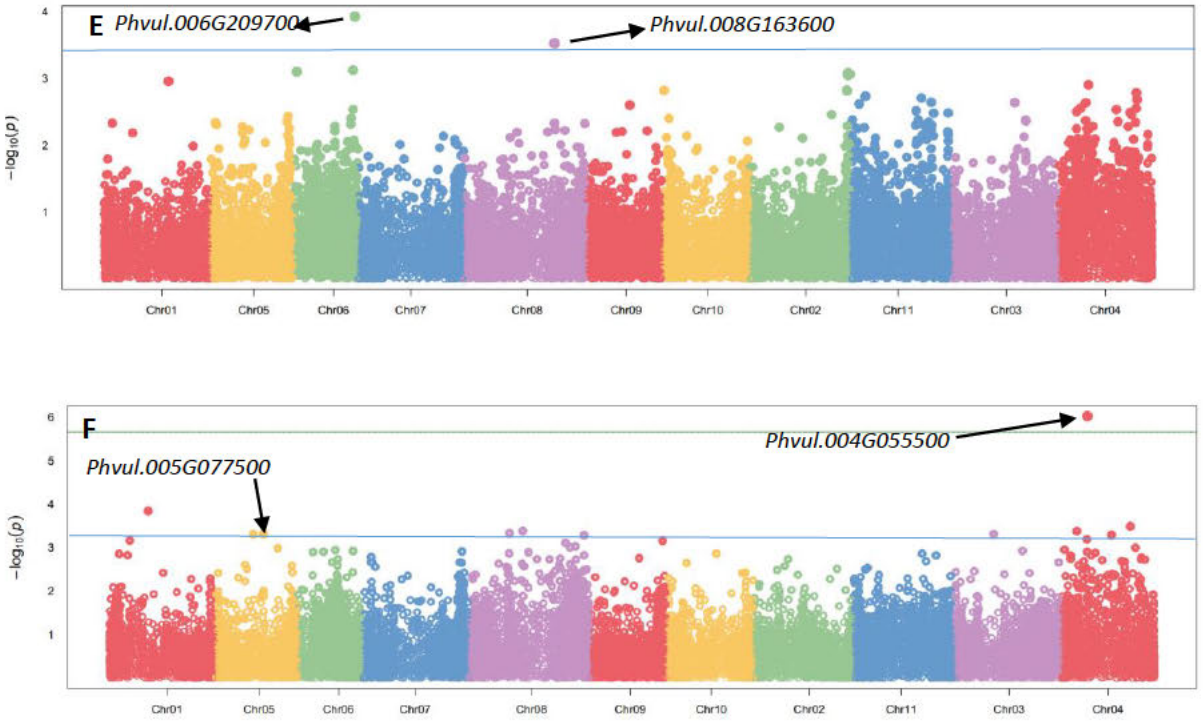

Figure 7.3 (Continued)

On the other hand, nine significant SNPs for LT on chromosomes *Pv3*, *Pv4*, *Pv8* and *Pv5* explained the least proportion of the observed phenotypic variation (0.08) among the studied traits. Common regions associated with multiple traits on chromosomes were not identified under NS environments. Overall, R^2 varied from 0.08 (LT – SNPs 100101691, 100071816, 100100644, 100102687, 100102687, 100167520 and 100161682) to 0.70 (DPM - SNP 100117381) (Table 7.5).

7.3.5 Gene annotation

7.3.5.1 Drought stressed environments

A total of eight potential candidate genes (DFW - 1; GYD - 1; PH - 4; SW - 1; SC - 1) were identified under DS environments (Table 7.4 and Figure 7.2). The candidate genes for DFW (*Phvul.002G122100*), SC (*Phvul.001G254100*), SW (*Phvul.003G263200*) and GYD (*Phvul.004G150500*) were identified on chromosomes *Pv02*, *Pv01*, *Pv03* and *Pv04*, respectively (Table 7.4). These genes had diverse putative functions ranging from RNA recognition motif or RNP domain functions (DFW), NADPH dehydrogenase/NADPH diaphosare activity (SW), helicase activity and CCCH zinc finger protein domain functions (SC) to Phosphoethanolamine N-methyltransferese activity (GYD), respectively. On the other hand, the candidate genes for PH were identified on chromosomes *Pv01* (*Phvul.001G172300*) and *Pv08* (*Phvul.008G133100*; *Phvul.008G065700*; *Phvul.008G080600*) (Table 7.4). These

genes had diverse putative functions ranging from calcium transporting ATPase 1 activity, peptidyl prolyl cis trans isomerase activity, acyl-coenzyme A thiosterase activity to centrosomal protein nuf function, respectively.

7.3.5.2 Non-stressed environments

A total of fourteen potential candidate genes (DFW - 4; DPM - 1; LCC - 2; PH - 5; LT - 2) were identified under NS environments (Table 7.5 and Figure 7.3). The candidate genes for DFW were identified on chromosomes *Pv03* (*Phvul.003G011400*), *Pv04* (*Phvul.004G037700*), *Pv07* (*Phvul.007G144000*) and *Pv11* (*Phvul.0011G166300*), whereas the candidate gene for DPM was identified on chromosome *Pv02* (*Phvul.002G112700*) (Table 7.5). Candidate genes for DFW had diverse putative functions related to SORTING NEXIN-13, transcription factor TCP 13, U6 SNRNA-associated SM LIKE PROTEIN LSM4 and NHL domain containing protein. On the other hand, the candidate gene for DPM had a putative function related to the activity of thiol disulphide oxidoreductase. Chromosomes *Pv4* and *Pv5* harboured the two candidate genes for LT namely *Phvul.004G055500 and Phvul.005G077500,* respectively (Table 7.5). These genes had diverse putative functions related to the mitochondrial transcription termination factor family protein and leucine rich repeat protein associated with apoptosis in muscle tissue, respectively.

The genes *Phvul.006G209700* and *Phvul.008G163600* for LCC were identified on chromosomes *Pv06* and *Pv08*, respectively. These genes had diverse putative functions, such as premnaspirodiene oxygenase or hyoscymus muticus premnaspirodiene oxygenase activity and nucleoside triphosphate hydrolases activity, respectively. On the other hand, the candidate genes for PH were identified on chromosomes *Pv01* (*Phvul.001G190800*), *Pv03* (*Phvul.00G192800*), *Pv06* (*Phvul.006G208800*), *Pv07* (*Phvul.007G253400*), and *Pv11* (*Phvul.011G152000*) (Table 7.5). These genes also had diverse putative functions, such as f-box-like domain superfamily functions, protein NRT1 or PTR family related functions, phosphatidylserine decarboxylase activity, typa-like translation elongation factor svrs-related functions, and inactive g-type lectin s-receptor like serine or threonine protein kinase activity, respectively.

7.3.6 Linkage disequilibrium analysis using significant SNP markers

The analysis of LD using SNP markers is shown in Figure 7.4. A high and extensive LD was observed for the common bean genome, which is expected in self-pollinated crops such as common bean. The results show that the overall LD decay across the genome of 185 common

bean genotypes was 30 bp, at a cut–off of r^2 = 0.4. Generally, there was a slow decay of LD throughout the common bean genome, and the LD extended to several mega-bases as shown in Figure 7.4. The population structure usually affects the extent of LD decay.

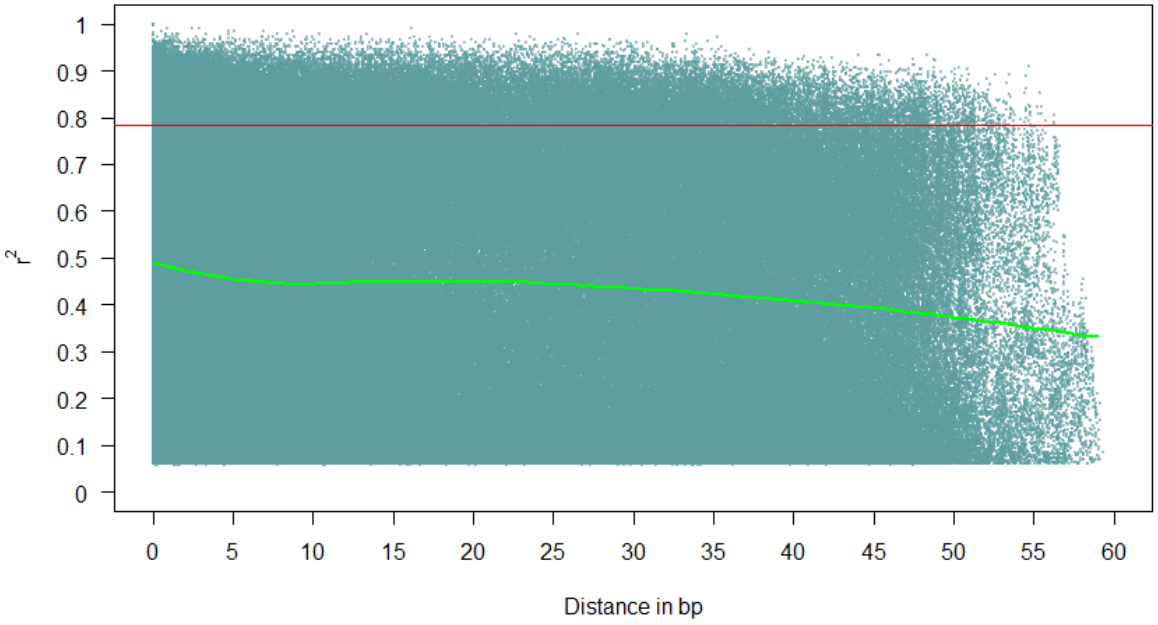

Figure 7.4 Linkage disequilibrium (LD, r^2) decay plot in genome of dry beans based on 9370 single nucleotide polymorphisms (SNPs) in 185 diverse genotypes.

7.4 Discussion

7.4.1 Phenotypic variability for agronomic and physiological traits

The low to moderate H^2 estimates observed for SC, LT and LCC under DS and NS conditions imply that these physiological traits might be influenced by a number of genes (polygenic inheritance) and the production environment. Therefore, direct selection for SC, LT and LCC under DS and NS conditions could be a challenge to dry beans breeders. On the other hand, the high H^2 estimates (97%) for seed size observed under DS and NS environments reflect the predominance of additive gene action (genetic control of this trait) across environments. The current findings agree with Assefa et al. (2013) and Hoyos-Villegas et al. (2017) who reported H^2 estimates of 77 and 93.4%, respectively under NS conditions. In this study, drought stress reduced PH, GYD, SW, DPM, LCC and SC by 12.1, 29.6, 10.3, 12.6, 28.5 and 62.0%, respectively, highlighting the detrimental effect of drought stress under field conditions. These findings corroborate previous reports by Assefa et al. (2013), Darkwa et al. (2016), Assefa et al. (2017), and Mathobo et al. (2017) in common bean. Mathobo et al. (2017) reported reductions of 48 and 39% in SC and LCC, respectively under DS conditions. Darkwa et al. (2016), using navy beans, reported reductions of 10.7, 14.8, 12.7 and 26.1% in SW, PH, DPM

and LCC under DS conditions. Assefa et al. (2013), using navy beans, also reported reductions of 12% and 17.6% in SW and DPM, respectively under DS conditions.

Crop plants close their stomata when exposed to drought stress to minimize excessive water loss and avoid dehydration. However, the closing of stomata reduces stomatal conductance, and also affects cooling mechanisms resulting in increased leaf or canopy temperature. Therefore, in this study, drought stress increased LT by 21.6%. Drought stress also reduced GYD by 30%, close to the GYD reductions reported by Darkwa et al. (2016) (30%) and Mutari et al. (2022) (28%) in dry beans drought tolerance screening trials. Breeding for enhanced GYD under both DS and NS environments is one of the greatest challenges faced by dry beans breeders (Valdisser et al., 2020). Therefore, one of the most important contribution of this study was to indicate drought tolerant genotypes (DAB91, DAB302, AFR703, CIM-SUG07-ALS-51-3, DAB487, DAB287, CIM-RM09-ALS-BSM-12 and DAB539) with consistent outstanding and stable GYD performance under both DS and NS environments.

Terminal drought stress is an important factor limiting common bean productivity in the SSA region. Therefore, the identification and subsequent release of drought tolerant genotypes will positively impact on socio-economic, food and nutrition security in SSA. These genotypes could also serve as important genetic resources in drought tolerance breeding programs to improve released cultivars. Both DAB287 and AFR703 were released in Zimbabwe as Sweet William and Gloxinia, respectively. Among the drought tolerant genotypes with superior GYD performance under water deficit conditions, most of the top 20 genotypes were of the andean gene pool, coded as drought andean (DAB lines) (Table 7.3 and Appendix 7.2). Notably, all the DAB lines evaluated in this study were developed for improved tolerance to drought by the Alliance of Bioversity International and International Center for Tropical Agriculture in Colombia (Chirwa, personal communication, April 2018[1]). The current observation suggests that progress in improving drought tolerance in the middle-american gene pool has been limited compared to the andean gene pool. The current findings agree with Assefa et al. (2017) who reported that progress in improving drought tolerance in navy beans (middle-american gene pool) worldwide has been limited compared to the other commercial classes of small seeded middle-american beans.

[1] Regional dry bean breeder at the Alliance of Bioversity International and International Center of Tropical Agriculture, Malawi

7.4.2 Population structure and linkage disequilibrium analysis

The AMDP was delineated into two distinct major sub-populations based on the genotypes' genetic ancestry, and this corresponded to the andean and middle-american gene pools (Figures 7.1B, C). This is expected considering that the domestication of dry beans on the American continent in two main centers of origin (andean and middle-american regions of America) resulted in two major and diverse gene pools (Blair et al., 2006; Beebe, 2020). Cichy et al. (2015a, 2015b), Raggi et al. (2019), Tigist et al. (2019), Nkhata et al. (2021), Ojwang et al. (2021), Keller et al. (2022) and Liu et al. (2022) also observed two sub-populations (andean and middle-american gene pools) in their GWAS studies. A number of the identified andean-middle-american admixed genotypes carrying genomic regions from both gene pools are released cultivars in Rwanda (RWR2154), Malawi (NUA59-4), Zimbabwe (SMC16, NUA674, and Sweet William) and Eswatini (NUA674) (Crop Breeding Institute, 2017, 2018, 2019; Kondwakwenda et al., 2022). Further, most of the admixed genotypes have commercial seed types, are biofortified (RWR2154, SMC16, SMC21, NUA674 and NUA59-4) and drought tolerant (Sweet William, DAB115, DAB63, DAB142 and DAB477).

Singh (1995), Beebe et al. (2008, 2013) and Beebe (2020) reported that interracial hybridizations between races or sister species (*Phaseolus coccineus*, *Phaseolus acutifolius* and *Phaseolus dumosus*) of *Phaseolus vulgaris* have been widely used in dry beans improvement programs when breeding for enhanced grain yield, micronutrient density and drought tolerance. For example, the biofortified admixed genotype NUA674 is a product of an inter-gene pool cross between AND277 (andean gene pool) and G21242 (andean-middle-american inter-gene pool landrace) made at the Alliance of Bioversity International and International Center of Tropical Agriculture (ABC) in Colombia (Crop Breeding Institute, 2018). Islam et al. (2004) and Beebe (2020), also reported that one of the parents to NUA674, G21242 (source of high seed iron in biofortification breeding programs) is a product of andean–middle-american inter-gene pool hybridization, validating the current findings. Therefore, the current observation suggests that most of the admixed genotypes identified in this study resulted from deliberate breeding efforts (inter-gene pool hybridizations) to introgress genes for enhanced grain yield, drought tolerance and micronutrient density. Similar findings were reported by Hoyos-Villegas et al. (2017) and Tigist et al. (2019) in common bean.

The biofortified and drought tolerant admixed genotypes identified in this study may be used as a bridge to transfer favourable alleles for micronutrient density and drought tolerance into either the andean or middle-american seed types. The extent and structure of LD decay in the

study germplasm usually determines the resolution of GWAS. The slow decay of LD observed in this study is expected in self-pollinating crop species, such as common bean because of the loss of recombination, which results in a homozygous genetic background. According to Vos et al. (2017), recombination events in crops with a homozygous genetic background are ineffective to cause LD decay, resulting in extended (large) and slow decay of LD. The slow decay of LD, and the large extent of LD observed in this study corroborates previous reports in dry beans (Perseguini et al., 2016; Liu et al., 2022).

7.4.3 Marker-trait association

In dry beans, it is important to enhance drought stress tolerance by identifying genotypes with high grain yield potential under water deficit conditions, and by introgressing desirable alleles conferring drought tolerance. The mean call rate (93%) and reproducibility (100%) of the silico DArTs used in this study were consistent with previous reports (Valdisser et al., 2020; Nkhata et al., 2021), thus demonstrating the reliability and high quality of this set of silico DArTs. A higher number of significant MTAs were detected under NS conditions, corroborating previous reports in bread wheat (*Triticum aestivum* L.) (Mwadzingeni et al., 2017; El Gataa et al., 2021) and dry beans (Valdisser et al., 2020). The observed trend could be due to the fact that drought tolerance is a complex polygenic trait which is highly influenced by the production environment, resulting in unpredictable performance of genotypes [genotype-by-environment interaction (GEI)] under different environments (DS and NS).

Even though a smaller number of significant MTA was observed under DS compared to the NS condition, novel genomic regions associated with key agronomic and physiological traits were detected under DS conditions. Notably, no significant SNPs for all the studied agronomic and physiological traits were consistent across DS and NS treatments. Similar findings were reported in wheat (Mwadzingeni et al., 2017 – plant height and spike length) and dry beans (Valdisser et al., 2020 – grain yield) under DS and NS treatments. The observed trend suggests that some markers may influence the expression of phenotypic traits differently under DS and NS environments. Furthermore, the GEI could have confounded the identification of significant SNPs that are consistent across DS and NS treatments. The highest number of significant SNPs were identified for PH. Similar findings were reported by Sukumaran et al. (2018) who observed 30 significant MTAs for PH in durum wheat (*Triticum turgidum* L. ssp. *durum*). Some of the SNPs identified in this study were located on genomic regions that had been previously reported to be harbouring genes and QTLs for the studied traits. For example, in this study, chromosomes *Pv01*, *Pv03, Pv04, Pv06* and *Pv07* harboured 1 SNP, 4 SNPs, 3 SNPs, 2 SNPs

and 1 SNP, respectively that were significantly associated with DFW under optimal conditions. These results are consistent with Dramadri et al. (2019), Nkhata et al. (2021) and Keller et al. (2022). Dramadri et al. (2019) identified 2 QTLs that were associated with DFW on *Pv03* under DS and NS conditions.

Nkhata et al. (2021) identified 2 and 5 SNPs that were significantly associated with DFW on *Pv03* and *Pv06*, respectively under NS conditions. Furthermore, Keller et al. (2022) identified 6 SNPs, 1 SNP and 1 SNP that were significantly associated with DFW on *Pv01*, *Pv04* and *Pv07*, respectively under optimal conditions. These findings suggest that the aforementioned QTL regions are stable across different environments and genetic backgrounds. In addition, these findings also suggest that chromosomes *Pv01, Pv03, Pv04, Pv06* and *Pv07* harbour genes for controlling flowering. In this study, only one marker (SNP 1667170) was significantly associated with SW on chromosome *Pv08* under DS conditions. These results are in accordance with Moghaddam et al. (2016), and Valdisser et al. (2020) who identified significant MTAs for SW on chromosome *Pv*8 under DS and NS environments, suggesting that this QTL is stable across different environments and genetic backgrounds. On the contrary, several significant MTAs for SW were previously identified under DS on chromosome *Pv01*, (Trapp et al., 2015), chromosome *Pv03* (Mukeshimana et al., 2014), chromosome *Pv09* (Hoyos-Villegas et al., 2017), and chromosomes *Pv2* to *Pv4* and *Pv6* to *Pv11* (Valdisser et al., 2020). Thus, the detection of significant MTAs for SW on different chromosomes and locations indicates high genetic diversity in common bean with respect to genomic regions associated with SW under drought stress.

In this study, the identified SNPs that were significantly associated with GYD under DS were located on chromosomes *Pv04* (SNP 3382688) and *Pv11* (SNP 3384334 and SNP 3381526). Similarly, Dramadri et al. (2019) identified significant QTL signals for GYD and yield components on chromosomes *Pv01*, *Pv02*, *Pv03*, *Pv04*, *Pv06*, and *Pv11* under DS conditions. Dramadrid et al. (2021) identified significant SNPs that were significiantly associated with GYD on chromosomes *Pv06* and *Pv06* under DS conditions. Oladzad et al. (2019) also identified SNPs that were significantly associated with GYD, placed on chromosomes *Pv03*, *Pv08*, and *Pv11* under heat stress. Furthermore, Valdisser et al. (2020) found 25 QTLs that were associated with GYD on chromosomes *Pv02, Pv03, Pv04, Pv08, Pv09* and *Pv11* under NS conditions, in agreement with the current findings. These findings suggest that chromosomes *Pv04* and *Pv11* harbour genes for controlling GYD. The identification of SNPs associated with GYD, under drought stress, would significantly contribute to the development

of molecular tools for MAS and identification of genes of interest for edition. The proportion of the total phenotypic variation (R^2) explained by the significant SNP markers for LCC and LT was generally low (0.11 – 0.12 for LCC under NS and 0.08 – 0.15 for LT under NS). Therefore, to account for the missing variation, it might be worthwhile to complement the SNP-based GWAS by haplotype-based GWAS (N'Diaye et al., 2017).

7.4.4 Candidate genes

7.4.4.1 Drought stressed

The functional annotation revealed that the candidate gene for SC, *Phvul.001G254100* on chromosome *Pv01* encodes the CCCH zinc finger family protein which plays an important function in response of plants to biotic and abiotic stresses (Pi et al., 2018; Han et al., 2020, 2021; Ai et al., 2022). This functional gene also plays an important role in physiological and plant developmental processes (Ai et al., 2022). Similar findings were reported in *Brassica rapa* (Pi et al., 2018), common bean (Valdisser et al., 2020) and Barley (*Hordeum vulgare* L.) (Ai et al., 2022). Wang et al. (2015), Seong et al. (2020) and Selvaraj et al. (2020) reported that several types of CCCH zinc finger family genes such as $O_sC_3H_{10}$, $O_sC_3H_{47}$, and $OsTZF_5$ are involved in the regulation of tolerance to drought stress in rice (*Oryza Sativa* L.). According to Lin et al. (2011), the CCCH zinc finger protein gene confers drought tolerance in plants by regulating the opening and closing of stomata. They further reiterated that genotypes that are tolerant to drought stress have abnormal and lower stomatal conductance under drought stressed conditions. In this study, the marker SNP 3380850 for the gene *Phvul.001G254100* which confers tolerance to drought stress exhibited negative allelic effects (-10.79 $mmol\ m^{-2}\ s^{-1}$) on SC.

The functional annotation revealed that the candidate gene for DFW, *Phvul.002G122100* on chromosome *Pv02* encodes an RNA-recognition motif protein, which plays a comprehensive biological function (critical modulators) in abiotic stress (drought, heat flooding, cold and high salinity) responding processes in plants (Muthusamy et al., 2021). Zhou et al. (2014) observed that the RNA-recognition motif gene "OsCBP20" from rice confers abiotic stress tolerance in *escherichia coli*. Therefore, the candidate gene *Phvul.002G122100* identified in this study may play a protective role under DS conditions. Candidate genes such as *Phvul.003G263200* (*Pv08*) for SW which encodes for NADPH dehydrogenase plays an important role in mechanisms which protect plants against nitro-oxidative stresses generated by biotic and abiotic stresses such as drought, low temperature, heat, and salinity (Corpas and Barroso, 2014). Under DS,

the seed is significantly affected by oxidative damages, and oxidative damages are minimized by the activity of NADPH dehydrogenase (Berny Mier y Teran et al., 2019).

The candidate gene for GYD, *Phvul.004G150500* on chromosome *Pv04*, encodes the enzyme, phosphoethanolamine N-methyltransferese in plants. This catalytic enzyme plays an important role in the response of plants to abiotic stresses such as drought and salt tolerance by catalysing the methylation of phosphoethanolamine to phosphocholine (Wang et al., 2021). Studies conducted by Wang et al. (2021) in transgenic tobacco revealed that phosphoethanolamine N-methyltransferese improved the drought tolerance of transgenic tobacco. Notably, the marker (SNP 3382688) for this candidate gene *Phvul.004G150500* had large positive allelic effects (202.90 kg/ha) on GYD. The candidate gene for PH, *Phvul.001G172300* encodes the calcium transporting ATPase, which plays an important role in growth and development processes, opening and closing of stomata, hormonal signalling, and regulation of responses to biotic and abiotic stresses in plants (Singh et al., 2014). In summary, these results further confirmed that the identified putative potential candidate genes were associated with drought stress tolerance of dry beans. Therefore, the putative candidate genes identified in the current AMDP under DS conditions are important genetic resources. The candidate genes could be utilized in drought tolerance breeding programs by creating and introgressing new genetic variability into commercial cultivars.

7.4.4.2 Non-stressed conditions

The functional annotation revealed that the candidate gene for PH "*Phvul.011G152000*" on chromosome *Pv11* encodes the threonine protein kinase, which is associated with enhanced tolerance to biotic and abiotic stresses in plants (Valdisser et al., 2020). Similar results were reported in dry beans by Valdisser et al. (2020). In rice, kinase causes dwarfism by reducing plant height (Zhang et al., 2012). Similarly, in this study, the marker SNP 100073620 for the gene "*Phvul.001G152000*" exhibited negative allelic effects (-7.00 cm) on PH. According to Zhang et al. (2012), kinases also has an impact on grain yield. The candidate gene *Phvul.004G037700* which was found on chromosome *Pv04* in association with DFW encodes transcription factor TCP_{13}. The transcription factor families are strongly involved in abiotic and biotic stress responses, including zinc-finger, dehydration-responsive element-binding (DREB), and basic helix-loop-helix (bHLH) families which regulate plant growth in leaves and roots under water deficit conditions (Urano et al., 2022). Studies conducted by Urano et al. (2022) in *Arabidopsis thaliana* revealed that TCP_{13} induces changes in leaf (leaf rolling and reduced leaf growth) and root morphology (enhanced root growth). This results in enhanced

tolerance to dehydration stress under osmotic stress. The candidate gene *Phvul.004G055500* which was found in association with LT on chromosome *Pv04* encodes mitochondrial transcription termination factor family protein. According to Kim et al. (2012), the mitochondrial transcription termination factor family protein enhances thermo-tolerance in *Arabidopsis*.

7.5 Conclusions

This study contributes many significant MTAs in common bean for agronomic and physiological traits under DS and NS environments. The present study identified a total of 68 SNPs that were significantly ($p < 10^{-03}$) associated with key agronomic and physiological traits under DS and NS conditions. The highest number of significant MTAs were observed on chromosome *Pv11* in both environments. For the two environments (DS and NS), no common SNPs for the studied traits were detected. Overall, twenty-two potential candidate genes were identified across environments. Most of the identified genes had known biological functions related to regulating drought stress response, and growth and development under drought stress. The information generated from this study provides insights into the genetic basis of agronomic and physiological traits under DS and NS conditions, and lays the foundation for future validation studies of drought tolerance genes in dry beans. Thus, the significant MTAs identified in this study should be explored and validated further to estimate their effects using segregating populations and in different genetic backgrounds before utilization in gene discovery and marker-assisted breeding for drought tolerance. Furthermore, functional characterization and the application of gene knockout to the identified putative candidate genes would further confirm their roles in regulating drought stress response, and growth and development under DS and NS conditions. More powerful statistical genetics tools such as genomic prediction models would be needed to identify minor genes that are associated with agronomic and physiological traits. The admixed genotypes identified in this study offer potential as genetic resources in drought tolerance and biofortification breeding programs, especially within the sugar, red mottled and navy bean market classes.

7.6 References

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Appendix 7.1 List of common bean genotypes used in the study, their sources and structure membership coefficient (K2) for K = 2.

Status	Genotype	Code	Genepool	K2	Source
Cultivar	PROTEA	G1	M	0.00 – 1.00	CBI Zimbabwe
Cultivar	SMC16	G2	ADM	0.14 – 0.86	CBI Zimbabwe
Breeding line	RAZ 42	G3	M	0.01 – 0.99	CBI Zimbabwe
Landrace	BIOFORT SMALL SEEDED 15	G4	M	0.00 – 1.00	CBI Zimbabwe
Breeding line	SAA12	G5	A	1.00 – 0.00	CBI Zimbabwe
Breeding line	SAA2	G6	A	0.99 – 0.01	CBI Zimbabwe
Breeding line	NAE80	G7	M	0.00 – 1.00	ABC Colombia
Breeding line	NAE13	G8	M	0.00 – 1.00	ABC Colombia
Breeding line	ZABRA16575-73F22	G9	M	0.00 – 1.00	ABC Colombia
Breeding line	SAA18	G10	A	0.99 – 0.01	ABC Colombia
Breeding line	ZABR-16576-20F22	G11	M	0.00 – 1.00	ABC Colombia
Breeding line	G48	G12	M	0.00 – 1.00	ABC Colombia
Landrace	CZ108-52	G13	M	0.08 – 0.92	ABC Colombia
Breeding line	SMC21	G14	ADM	0.12 – 0.88	ABC Colombia
Breeding line	RAZ11	G15	M	0.01 – 0.99	ABC Colombia
Landrace	SWAT-10 (SELIAM 10)	G16	M	0.00 – 1.00	ABC Colombia
Breeding line	SAA1	G17	A	0.99 – 0.01	ABC Colombia
Breeding line	RAZ-36	G18	M	0.00 – 1.00	ABC Colombia
Breeding line	SAB-662	G19	M	0.03 – 0.97	ABC Colombia
Breeding line	NAVY LINE-48	G20	M	0.00 – 1.00	ABC Colombia
Breeding line	CIM-NAV02-17-3	G21	M	0.00 – 1.00	ABC Colombia
Breeding line	G738	G22	M	0.00 – 1.00	ABC Colombia
Breeding line	G49	G23	M	0.00 – 1.00	ABC Colombia
Landrace	CZ108-53	G24	M	0.03 – 0.97	ABC Colombia
Landrace	RWR2154	G25	ADM	0.14 – 0.86	ABC Colombia
Landrace	CAB 2	G26	M	0.06 – 0.94	ABC Colombia
Landrace	SWAT-12 (SELIAM-11)	G27	M	0.00 – 1.00	ABC Colombia
Breeding line	G54	G28	M	0.00 – 1.00	ABC Colombia
Breeding line	ZABRA16575-57F22	G29	M	0.01 – 0.99	ABC Colombia
Breeding line	ZABRA16575-26F22	G30	M	0.00 – 1.00	ABC Colombia
Breeding line	G30	G31	M	0.00 – 1.00	ABC Colombia
Breeding line	NAVY LINE-60	G32	M	0.00 – 1.00	ABC Colombia
Breeding line	SAA17	G33	A	1.00 – 0.00	ABC Colombia
Breeding line	NAVY19	G34	M	0.00 – 1.00	ABC Colombia
Breeding line	G70	G35	M	0.00 – 1.00	ABC Colombia
Breeding line	SMB31	G36	M	0.03 – 0.97	ABC Colombia
Cultivar	SMC17	G37	M	0.09 – 0.91	ABC Colombia
Breeding line	G53	G38	M	0.00 – 1.00	ABC Colombia
Landrace	R02/1	G39	M	0.09 – 0.92	ABC Colombia
Breeding line	G14	G40	M	0.00 – 1.00	ABC Colombia
Breeding line	DAB562	G41	A	0.92 – 0.08	ABC Colombia
Breeding line	NAE24	G42	M	0.00 – 1.00	ABC Colombia
Breeding line	ICABUNSIxSXB405/9C-1C-1C-3	G43	M	0.00 – 1.00	ABC Colombia
Breeding line	G99	G44	M	0.00 – 1.00	ABC Colombia
Breeding line	SAA7	G45	A	1.00 – 0.00	ABC Colombia
Cultivar	UBR(92)25	G46	M	0.00 – 1.00	ABC Colombia
Breeding line	G40	G47	M	0.00 – 1.00	ABC Colombia
Breeding line	NAE60	G48	M	0.04 – 0.96	ABC Colombia
Landrace	Michigan Pea Bean	G49	M	0.02 – 0.98	ABC Colombia
Landrace	Chore	G50	M	0.03 – 0.97	ABC Colombia
Landrace	BASABEER	G51	M	0.09 – 0.91	ABC Colombia
Cultivar	AWASH-1	G52	M	0.00 – 1.00	ABC Colombia
Breeding line	ICA BUNSIxSXB405-1C-1C	G53	M	0.00 – 1.00	ABC Colombia
Landrace	NAIN DEKYONDO	G54	M	0.00 – 1.00	ABC Colombia
Breeding line	ZABRA16575-51F22	G55	M	0.00 – 1.00	ABC Colombia

Status	Genotype	Code	Genepool	K2	Source
Breeding line	G6	G56	M	0.00 – 1.00	ABC Colombia
Breeding line	NAVY46	G57	M	0.05 – 0.95	ABC Colombia
Breeding line	G16	G58	M	0.04 – 0.96	ABC Colombia
Breeding line	G37	G59	M	0.00 – 1.00	ABC Colombia
Breeding line	NAE19	G60	M	0.00 – 1.00	ABC Colombia
Landrace	Chercher	G61	M	0.04 – 0.96	ABC Colombia
Landrace	Argene	G62	M	0.00 – 1.00	ABC Colombia
Landrace	SIRAJ	G63	M	0.08 – 0.92	ABC Colombia
Breeding line	NAE40	G64	M	0.00 – 1.00	ABC Colombia
Breeding line	G550	G65	A	0.96 – 0.04	ABC Colombia
Landrace	CZ108-27	G66	M	0.00 – 1.00	ABC Colombia
Breeding line	NAE70	G67	M	0.00 – 1.00	ABC Colombia
Breeding line	G24	G68	M	0.00 – 1.00	ABC Colombia
Breeding line	G90	G69	M	0.00 – 1.00	ABC Colombia
Breeding line	SAA19	G70	A	0.98 – 0.02	ABC Colombia
Breeding line	G34	G71	M	0.00 – 1.00	ABC Colombia
Breeding line	NAE87	G72	M	0.00 – 1.00	ABC Colombia
Cultivar	AWASH MELKA	G73	M	0.00 – 1.00	ABC Colombia
Landrace	NAZARETHE2	G74	M	0.03 – 0.97	ABC Colombia
Landrace	SAB792	G75	ADM	0.86 – 0.14	ABC Colombia
Landrace	CZ113-13	G76	A	0.95 – 0.05	ABC Colombia
Breeding line	SAB793	G77	A	0.93 – 0.07	ABC Colombia
Breeding line	ICA BUNSIxSXB405/3C-1C-1C-8	G78	M	0.00 – 1.00	ABC Colombia
Breeding line	NAVY LINE 22	G79	ADM	0.15 – 0.85	ABC Colombia
Breeding line	G100	G80	M	0.00 – 1.00	ABC Colombia
Breeding line	SAB791	G81	A	0.88 – 0.12	ABC Colombia
Breeding line	G27	G82	M	0.00 – 1.00	ABC Colombia
Breeding line	NAE78	G83	M	0.00 – 1.00	ABC Colombia
Cultivar	AWASH 2	G84	M	0.00 – 1.00	ABC Colombia
Landrace	SWAT-09 (SELIAM 9)	G85	M	0.00 – 1.00	ABC Colombia
Breeding line	ZABRA16573-25F22	G86	M	0.00 – 1.00	ABC Colombia
Breeding line	ICABUNSIxSXB405/4C-1C-1C-8	G87	M	0.00 – 1.00	ABC Colombia
Breeding line	RAZ-44	G88	M	0.03 – 0.97	ABC Colombia
Breeding line	G32	G89	M	0.00 – 1.00	ABC Colombia
Breeding line	CIM-NAV02-35-1	G90	M	0.05 – 0.95	ABC Colombia
Cultivar	CANPSULA	G91	M	0.00 – 1.00	ABC Colombia
Breeding line	CIM-NAV02-10-1	G92	M	0.04 – 0.96	ABC Colombia
Breeding line	CIM-DWRF-CLIM01-1-1	G93	M	0.00 – 1.00	ABC Malawi
Landrace	MUTWAKIL	G94	M	0.08 – 0.92	ABC Malawi
Breeding line	MAB89	G95	A	0.98 – 0.02	ABC Malawi
Breeding line	CIM-RM02-71-1	G96	A	0.96 – 0.04	ABC Malawi
Cultivar	G97 (Seed-co)	G97	A	0.92 – 0.08	ABC Malawi
Breeding line	ZABRA16575-86F22	G98	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB363	G99	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB367	G100	A	0.97 – 0.03	ABC Malawi
Breeding line	DAB482	G101	A	0.99 – 0.01	ABC Malawi
Cultivar	Sweet Violet	G102	A	0.98 – 0.02	ABC Malawi
Landrace	CZ104-65	G103	A	0.98 – 0.02	ABC Malawi
Breeding line	DAB210	G104	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB470	G105	M	0.00 – 1.00	ABC Malawi
Breeding line	G19	G106	A	0.98 – 0.02	ABC Malawi
Breeding line	VTTT926/9-6	G107	A	0.94 – 0.06	ABC Malawi
Breeding line	DAB142	G108	ADM	0.89 – 0.11	ABC Malawi
Cultivar	NUA674	G109	ADM	0.11 – 0.89	ABC Malawi
Landrace	Waju	G110	A	0.96 – 0.04	ABC Malawi
Breeding line	DAB447	G111	A	0.93 – 0.07	ABC Malawi
Breeding line	DAB62	G112	A	0.93 – 0.07	ABC Malawi
Cultivar	Gloria	G113	A	1.00 – 0.00	ABC Malawi
Breeding line	CIM-RM09-ALS-BSM-11	G114	ADM	0.82 – 0.18	ABC Malawi

Status	Genotype	Code	Genepool	K2	Source
Landrace	CZ104-11	G115	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB133	G116	M	0.07 – 0.93	ABC Malawi
Breeding line	G22	G117	A	1.00 – 0.00	ABC Malawi
Breeding line	CIM-RM00-321LN02	G118	A	0.99 – 0.01	ABC Malawi
Breeding line	VTTT925/2-5-2-2	G119	A	0.93 – 0.07	ABC Malawi
Breeding line	CIM-CBB-FeZn08-21-2	G120	M	0.00 – 1.00	ABC Malawi
Breeding line	ZABRA16573-78F22	G121	A	1.00 – 0.00	ABC Malawi
Breeding line	CIM-RM09-ALS-BSM-1	G122	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB361	G123	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB487	G124	A	1.00 – 0.00	ABC Malawi
Breeding line	CIM-RM09-ALS-BSM-12	G125	A	1.00 – 0.00	ABC Malawi
Breeding line	CIM-RM09-ALS-BSM-14	G126	A	0.95 – 0.05	ABC Malawi
Breeding line	CIM-SUG07-ALS-2	G127	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB224	G128	M	0.00 – 1.00	ABC Malawi
Breeding line	G75	G129	ADM	0.68 – 0.32	ABC Malawi
Breeding line	DAB115	G130	ADM	0.86 – 0.14	ABC Malawi
Breeding line	DAB296	G131	M	0.02 – 0.98	ABC Malawi
Breeding line	RAZ-34	G132	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB355	G133	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB368	G134	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB539	G135	A	0.99 – 0.01	ABC Malawi
Breeding line	DAB63	G136	ADM	0.69 – 0.31	ABC Malawi
Breeding line	DAB477	G137	ADM	0.79 – 0.21	ABC Malawi
Breeding line	CZ104-72	G138	A	1.00 – 0.00	ABC Malawi
Breeding line	CZ113-15	G139	M	0.00 – 1.00	ABC Malawi
Breeding line	G97	G140	A	1.00 – 0.00	ABC Malawi
Breeding line	CIM-RM02-36-1	G141	ADM	0.13 – 0.88	ABC Malawi
Breeding line	RCB234	G142	A	0.98 – 0.02	ABC Malawi
Breeding line	NUA59-4	G143	ADM	0.73 – 0.27	ABC Malawi
Breeding line	NAVY LINE-47	G144	A	1.00 – 0.00	ABC Malawi
Landrace	RWR222	G145	A	0.93 – 0.07	ABC Malawi
Cultivar	AFR703	G146	A	0.98 – 0.02	ABC Malawi
Breeding line	CIM-SUG07-ALS-S1-3	G147	A	0.98 – 0.02	ABC Malawi
Breeding line	CIM-RM-03-03-45	G148	A	0.94 – 0.06	ABC Malawi
Breeding line	DAB523	G149	A	0.92 – 0.08	ABC Malawi
Breeding line	CIM-DRHT-SUG-S5-3	G150	A	0.96 – 0.04	ABC Malawi
Breeding line	CIM-RK05-ALS-39	G151	M	0.00 – 1.00	ABC Malawi
Breeding line	ICN BunsixSxB405/7C-1C-1C-5	G152	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB124	G153	A	0.96 – 0.04	ABC Malawi
Breeding line	CIM-RM02-134-1	G154	ADM	0.79 – 0.21	ABC Malawi
Breeding line	NUA735-2	G155	M	0.02 – 0.98	ABC Malawi
Breeding line	NAVY LINE-52	G156	A	1.00 – 0.00	ABC Malawi
Breeding line	DCIM-RM09-ALSBSM-	G157	A	1.00 – 0.00	ABC Malawi
Cultivar	Sweet William	G158	ADM	0.88 – 0.12	ABC Malawi
Cultivar	G159 (Seed-Co)	G159	A	1.00 – 0.00	ABC Malawi
Breeding line	DAB299	G160	A	0.98 – 0.02	ABC Uganda
Breeding line	DAB378	G161	A	1.00 – 0.00	ABC Uganda
Breeding line	DAB150	G162	A	0.90 – 0.10	ABC Uganda
Breeding line	DAB112	G163	M	0.00 – 1.00	ABC Uganda
Breeding line	ZABRA16575-60F22	G164	ADM	0.79 – 0.21	ABC Uganda
Breeding line	DAB143	G165	M	0.00 – 1.00	ABC Uganda
Cultivar	G166 (Seed-Co)	G166	M	0.00 – 1.00	ABC Uganda
Breeding line	NAVY LINE-54	G167	A	1.00 – 0.00	ABC Uganda
Breeding line	DAB410	G168	A	1.00 – 0.00	ABC Uganda
Cultivar	Cherry	G169	A	0.93 – 0.07	ABC Uganda
Breeding line	CIM-SUG05-01-02	G170	A	0.90 – 0.10	ABC Uganda
Breeding line	DAB360	G171	A	1.00 – 0.00	ABC Uganda
Breeding line	KG27-8	G172	A	1.00 – 0.00	ABC Uganda
Breeding line	CZ104-61	G173	A	0.98 – 0.02	ABC Uganda

Status	Genotype	Code	Genepool	K2	Source
*957410	CIM-RM00-104	G174	M	0.08 – 0.92	ABC Uganda
Breeding line	ZABRA16574-37F22	G175	A	1.00 – 0.00	ABC Uganda
Breeding line	DAB302	G176	A	0.97 – 0.03	ABC Uganda
Cultivar	G177 (Seed-co)	G177	M	0.02 – 0.98	ABC Uganda
Breeding line	CIM-NAV08-1	G178	A	0.93 – 0.07	ABC Colombia
Breeding line	GLP585/MLB49-89A-3	G179	ADM	0.80 – 0.20	EIAR Ethiopia
Breeding line	DAB78	G180	A	1.00 – 0.00	EIAR Ethiopia
Breeding line	DAB61	G181	A	0.98 – 0.02	EIAR Ethiopia
Breeding line	CIM-SUG07-ALS-S1-3	G182	ADM	0.63 – 0.37	ABC Malawi
Breeding line	CIM-SUG02-14-3	G183	A	0.94 – 0.06	ABC Malawi
Breeding line	DAB91	G184	A	0.99 – 0.01	ABC Malawi
Breeding line	DAB433	G185	A	1.00 – 0.00	ABC Malawi

K2 structure membership coefficient/ancestry probability, *ADM* admixed, *M* middle-american, *A* andean, *CBI* crop breeding institute, *ABC* alliance of bioversity international and international center for tropical agriculture, *EIAR* ethiopian institute of agricultural research. Admixed includes genotypes that are 10 to 90% andean or middle-american according to the structure analysis results.

Appendix 7.2 Drought tolerance indices and predicted genotype values for grain yield (across environments) of the 185 andean-middle-american diversity panel.

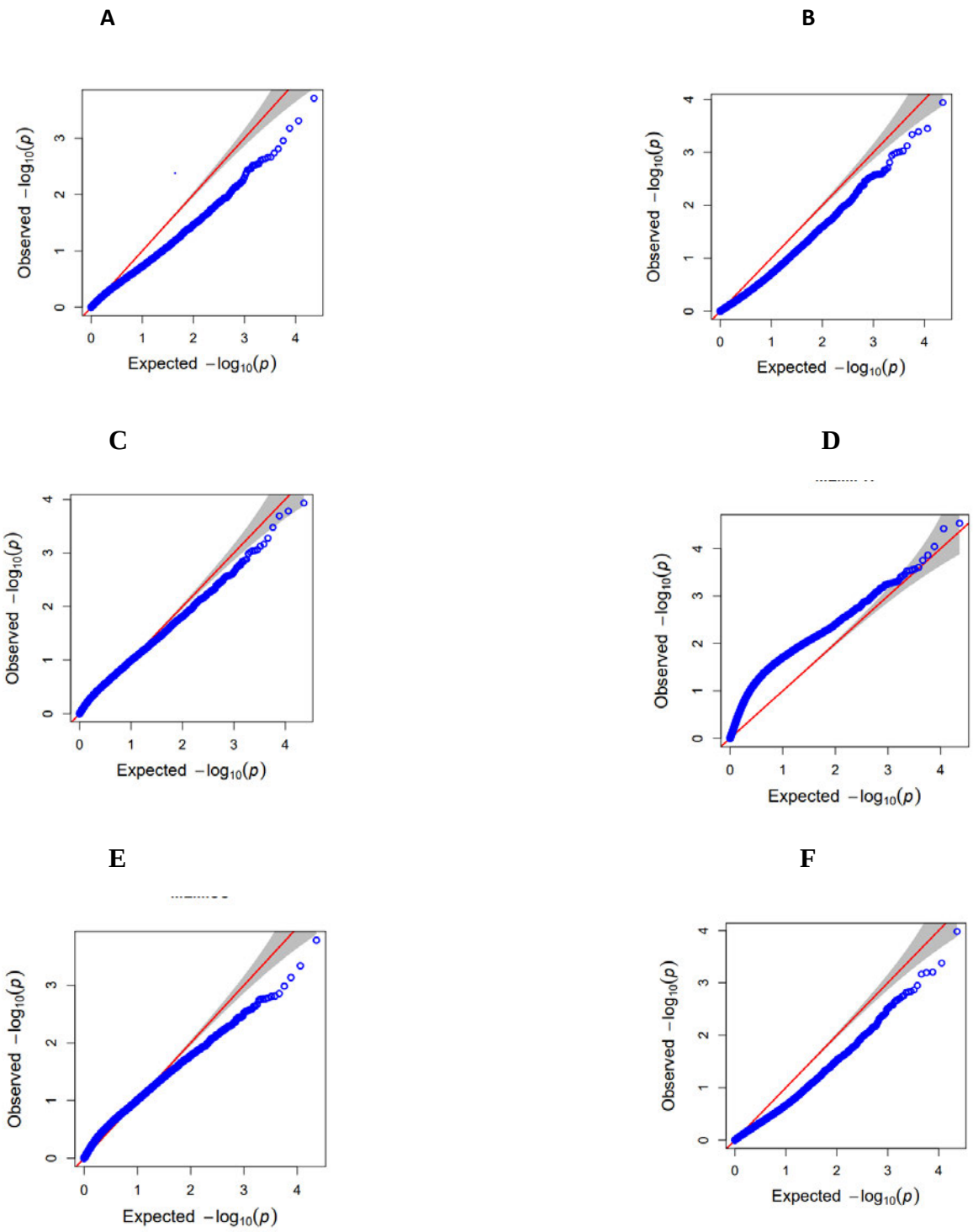
Genotype	Gene pool	GYD (kg/ha)	DSI	GMP	DTI	%GYR	Mean rank
G1	M	242.6	1.84	167.5	0.03	55.07	172.5
G2	ADM	400.9	1.73	349.9	0.12	51.96	162.5
G3	M	570.8	-2.41	557.2	0.35	-72.21	61.8
G4	M	1191.4	1.50	1132.7	1.50	44.96	89.8
G5	A	483.1	-1.74	426.7	0.20	-52.34	83.3
G6	A	508.3	0.50	503.3	0.26	15.11	99.0
G7	M	586.3	-2.12	570.8	0.35	-63.69	61.5
G8	M	506.0	-2.95	481.9	0.24	-88.46	73.8
G9	M	765.3	1.54	722.0	0.53	46.23	116.0
G10	A	488.4	-0.75	485.0	0.23	-22.57	84.0
G11	M	424.1	2.34	356.4	0.14	70.26	171.5
G12	M	160.9	2.26	134.2	0.02	67.90	180.5
G13	M	612.5	1.74	569.4	0.33	52.24	136.8
G14	ADM	305.3	-1.64	279.8	0.08	-49.34	95.5
G15	M	519.4	0.47	515.2	0.31	14.01	92.3
G16	M	842.6	-2.90	704.1	0.65	-86.87	45.0
G17	A	507.4	0.53	500.1	0.24	15.75	102.3
G18	M	549.3	-0.22	530.8	0.28	-6.63	79.5
G19	M	585.2	1.25	543.9	0.30	37.39	122.5
G20	M	676.2	1.98	607.8	0.40	59.43	135.0
G21	M	555.8	1.19	526.2	0.27	35.78	123.5
G22	M	548.4	0.90	539.8	0.30	27.02	106.8
G23	M	506.7	0.44	505.1	0.25	13.06	96.3
G24	M	553.7	1.11	522.0	0.28	33.34	118.8
G25	ADM	391.9	0.97	373.6	0.14	29.12	131.3
G26	M	350.5	0.89	343.7	0.14	26.55	128.8
G27	M	813.3	-7.68	733.1	0.63	-230.5	42.0
G28	M	560.0	0.68	554.2	0.30	20.37	97.5
G29	M	535.0	2.00	472.8	0.23	60.13	156.5
G30	M	751.2	1.58	703.6	0.49	47.46	120.3
G31	M	873.8	1.09	833.3	0.69	32.82	90.0
G32	M	781.3	2.06	619.1	0.38	61.83	137.8
G33	A	253.7	-0.89	236.4	0.06	-26.7	101.0
G34	M	558.6	0.05	545.0	0.30	1.560	82.0
G35	M	170.8	0.72	157.7	0.03	21.75	131.0
G36	M	365.5	1.24	347.0	0.12	37.10	146.5
G37	M	294.2	1.56	280.7	0.09	46.82	160.3
G38	M	619.7	0.51	615.3	0.40	15.35	85.0
G39	M	1015.4	0.78	936.6	1.09	23.39	68.8
G40	M	541.7	0.53	536.3	0.29	15.88	96.0
G41	A	541.9	0.82	508.5	0.25	24.67	109.8
G42	M	482.6	0.01	478.9	0.24	0.26	92.8
G43	M	600.7	-0.6	585.7	0.38	-17.93	68.8
G44	M	499.5	-0.25	490.9	0.23	-7.47	86.5
G45	A	294.4	1.12	287.6	0.10	33.55	142.5
G46	M	380.1	0.96	341.9	0.12	28.84	134.8
G47	M	60.6	-0.54	58.8	0.01	-16.3	107.5
G48	M	407.2	2.13	352.1	0.13	63.80	169.8
G49	M	47.2	0.42	45.4	0.00	12.50	122.5
G50	M	466.0	-1.74	443.9	0.21	-52.25	81.5
G51	M	796.3	1.64	748.1	0.56	49.35	120.8
G52	M	513.4	0.94	505.8	0.25	28.19	115.0
G53	M	554.2	0.80	541.6	0.29	24.01	104.0
G54	M	426.9	-0.03	426.1	0.19	-0.80	97.5
G55	M	480.8	1.34	464.8	0.21	40.20	139.8

Genotype	Gene pool	GYD (kg/ha)	DSI	GMP	DTI	%GYR	Mean rank
G56	M	497.2	-5.52	467.5	0.24	-165.70	73.8
G57	M	547.9	-0.92	530.6	0.28	-27.55	73.8
G58	M	528.5	1.21	508.9	0.25	36.44	126.0
G59	M	534.7	1.80	497.1	0.24	53.87	150.0
G60	M	474.8	0.79	428.1	0.19	23.66	120.0
G61	M	613.7	1.56	581.0	0.33	46.75	129.5
G62	M	1109.6	0.30	1071.9	1.18	9.11	52.5
G63	M	504.6	2.26	362.8	0.14	67.92	170.0
G64	M	661.8	-1.19	648.7	0.42	-35.73	58.8
G65	A	389.1	1.13	364.7	0.13	33.83	138.8
G66	M	533.8	1.61	473.8	0.22	48.36	148.3
G67	M	604.6	-0.03	587.0	0.36	-0.96	73.5
G68	M	678.5	1.00	658.1	0.43	29.87	100.5
G69	M	295.8	1.48	252.1	0.07	44.41	156.5
G70	A	399.1	0.79	387.8	0.15	23.56	122.0
G71	M	221.5	-3.29	154.0	0.03	-98.74	95.0
G72	M	467.8	0.80	453.5	0.20	23.97	118.5
G73	M	920.1	1.51	859.3	0.74	45.30	103.0
G74	M	356.5	3.04	190.3	0.04	91.16	181.5
G75	ADM	511.3	-1.38	499.9	0.25	-41.49	76.5
G76	A	476.9	0.25	474.6	0.25	7.61	96.5
G77	A	243.3	1.55	213.4	0.05	46.42	161.0
G78	M	618.7	-0.92	605.3	0.37	-27.55	64.8
G79	ADM	781.3	-0.20	777.0	0.60	-5.90	59.3
G80	M	542.6	-0.78	534.9	0.28	-23.34	74.5
G81	A	464.1	1.36	440.8	0.19	40.71	142.8
G82	M	325.2	2.94	183.3	0.04	88.11	181.5
G83	M	511.1	1.56	472.4	0.23	46.73	145.8
G84	M	627.8	-0.03	626.4	0.39	-1.04	69.3
G85	M	796.3	1.52	438.3	0.22	45.70	145.0
G86	M	666.7	1.59	623.3	0.38	47.59	126.3
G87	M	921.8	-0.62	901.5	0.81	-18.54	44.5
G88	M	489.4	1.59	437.1	0.19	47.75	152.0
G89	M	594.4	0.00	592.9	0.35	0.03	76.8
G90	M	368.1	0.64	364.5	0.13	19.29	119.8
G91	M	786.8	1.12	770.7	0.59	33.67	98.5
G92	M	875.0	1.19	846.9	0.70	35.67	94.3
G93	M	743.1	1.72	693.3	0.48	51.53	125.0
G94	M	1203.7	1.19	1115.1	1.33	35.77	82.3
G95	A	900.9	2.07	778.8	0.63	62.17	125.3
G96	A	1040.7	-0.90	1017.1	1.04	-27.05	38.3
G97	A	781.5	1.16	763.5	0.57	34.80	100.5
G98	A	854.9	1.26	814.3	0.67	37.71	99.5
G99	A	1465.0	0.17	1457.3	2.17	5.21	38.5
G100	A	1158.8	1.64	1089.6	1.24	49.29	100.8
G101	A	1964.8	1.32	1890.6	3.78	39.72	69.3
G102	A	717.3	1.56	633.3	0.44	46.68	121.8
G103	A	1463.0	0.94	1442.6	2.02	28.09	63.3
G104	A	1608.8	0.58	1601.1	2.49	17.37	45.3
G105	M	709.3	1.54	649.3	0.58	46.17	116.8
G106	A	719.1	-1.65	680.1	0.54	-49.45	53.5
G107	A	936.8	1.88	831.0	0.71	56.39	117.5
G108	ADM	1131.9	-1.44	1105.1	1.19	-43.32	32.0
G109	ADM	697.2	2.11	504.7	0.32	63.31	148.5
G110	A	921.3	1.43	796.2	0.71	42.92	104.0
G111	A	1229.6	0.48	1193.8	1.40	14.53	53.0
G112	A	1050.3	0.96	1024.2	1.04	28.90	76.3
G113	A	1683.8	1.76	1548.0	2.35	52.77	91.5

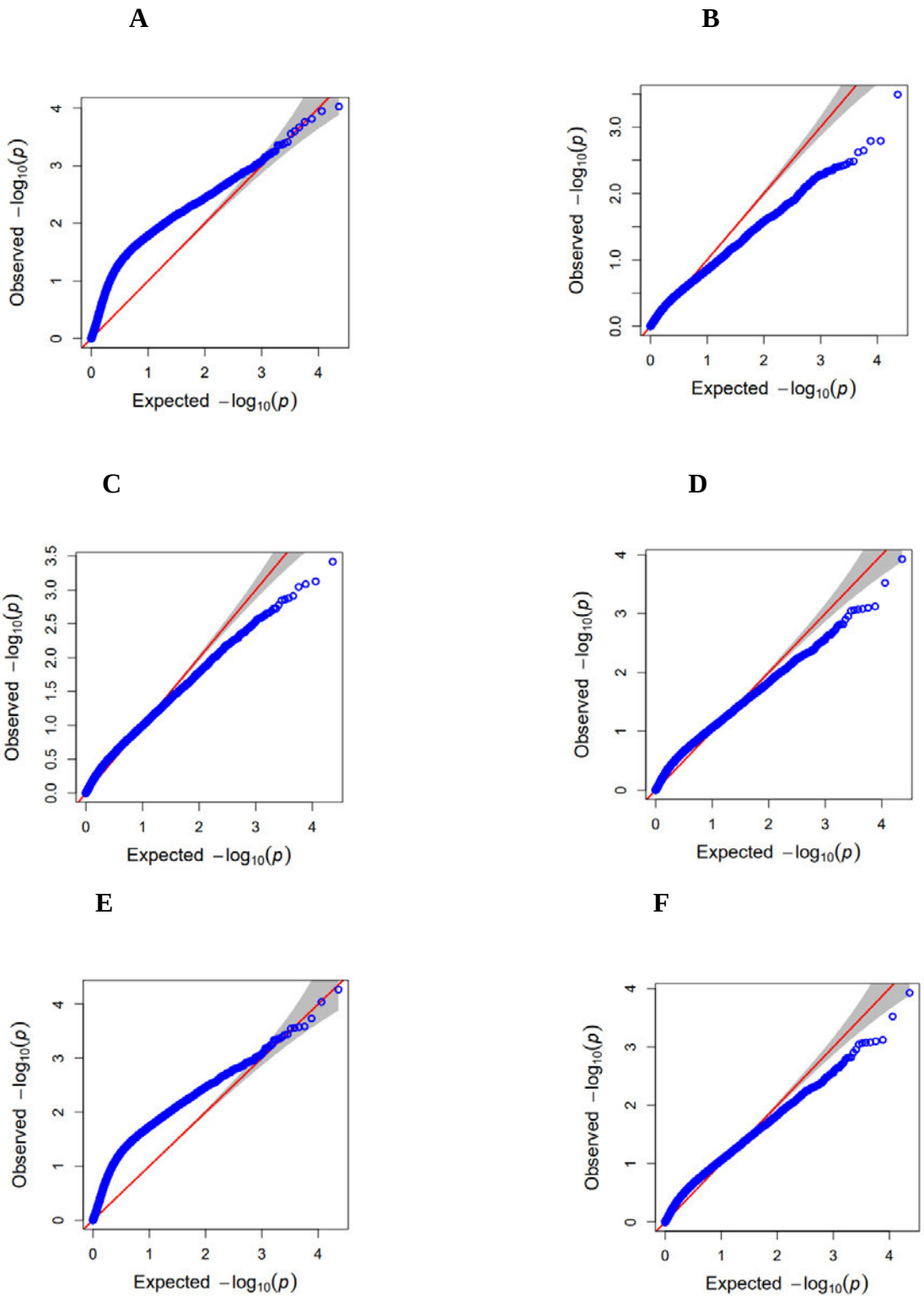
Genotype	Gene pool	GYD (kg/ha)	DSI	GMP	DTI	%GYR	Mean rank
G114	ADM	1560.6	1.18	1518.9	2.28	35.28	70.5
G115	A	1788.9	0.40	1765.4	3.04	11.87	35.5
G116	M	796.3	-0.50	785.4	0.62	-15.14	55.0
G117	A	1260.8	-1.12	678.9	0.62	-33.59	54.3
G118	A	952.8	0.50	940.3	0.86	14.88	62.8
G119	A	1180.1	0.85	1132.7	1.32	25.56	67.0
G120	M	626.2	-0.03	624.6	0.38	-0.93	70.5
G121	A	1114.2	0.47	972.7	0.96	13.98	59.5
G122	A	1354.2	0.65	1329.0	1.86	19.59	55.0
G123	A	1228.1	0.97	1207.1	1.42	28.95	70.0
G124	A	1815.0	-0.03	1805.5	3.19	-0.78	26.0
G125	A	1628.2	-0.25	1590.2	2.49	-7.39	26.8
G126	A	1416.7	1.22	1370.7	1.83	36.52	78.8
G127	A	1750.0	-0.02	1733.0	2.94	-0.73	29.0
G128	M	808.3	2.21	556.3	0.46	66.16	140.8
G129	ADM	853.4	2.42	418.1	0.21	72.67	167.8
G130	ADM	987.3	0.20	970.9	0.92	6.09	54.3
G131	M	1222.5	0.59	1195.3	1.40	17.63	56.8
G132	A	433.6	2.15	313.5	0.11	64.64	173.5
G133	A	1219.3	0.76	1195.1	1.40	22.91	61.3
G134	A	892.6	0.91	873.8	0.74	27.41	79.5
G135	A	1968.7	-0.37	1956.9	3.75	-11.17	19.8
G136	ADM	1448.6	0.61	1440.5	2.01	18.26	52.0
G137	ADM	1411.6	0.79	1395.5	1.89	23.56	57.5
G138	A	1846.8	0.22	1826.1	3.25	6.50	31.0
G139	M	833.1	1.63	756.6	0.57	49.03	119.5
G140	A	986.1	1.74	912.1	1.02	52.23	108.3
G141	ADM	1023.4	-1.31	993.1	0.96	-39.23	37.3
G142	A	810.9	0.21	793.7	0.63	6.30	64.0
G143	ADM	645.8	1.02	621.7	0.38	30.51	105.3
G144	A	671.3	1.77	627.8	0.62	52.98	126.3
G145	A	1184.6	1.34	1091.1	1.18	40.32	90.5
G146	A	2067.4	1.18	1994.5	4.02	35.49	61.5
G147	A	2080.1	1.26	1995.6	4.03	37.83	66.3
G148	A	1418.1	1.00	1394.2	1.89	30.01	68.5
G149	A	1607.9	0.48	1595.1	2.47	14.42	42.0
G150	A	1758.8	0.40	1750.8	2.98	12.03	36.5
G151	M	841.9	1.48	788.3	0.62	44.47	108.0
G152	A	416.7	2.33	319.3	0.13	69.76	173.8
G153	A	1017.4	0.75	1009.0	1.00	22.46	67.8
G154	ADM	882.4	0.58	878.4	0.76	17.32	67.8
G155	M	446.8	0.46	434.0	0.19	13.75	107.5
G156	A	905.9	-4.73	824.5	0.72	-141.87	37.0
G157	A	1308.0	1.38	1243.9	1.53	41.44	85.5
G158	ADM	2017.1	-0.01	1979.5	3.82	-0.26	24.5
G159	A	1743.3	1.12	1694.7	2.90	33.67	65.3
G160	A	1246.8	0.92	1196.4	1.40	27.49	66.8
G161	A	1195.4	0.85	1156.5	1.31	25.42	67.0
G162	A	1828.7	0.57	1814.3	3.20	16.97	40.5
G163	M	997.7	1.98	784.0	0.61	59.50	124.5
G164	ADM	518.5	-9.82	389.3	0.17	-294.46	79.5
G165	M	761.6	1.65	720.3	0.54	49.49	122.5
G166	M	815.3	0.93	804.5	0.63	27.82	85.3
G167	A	620.4	-12.98	495.4	0.28	-389.46	66.3
G168	A	1207.9	1.84	1083.4	1.24	55.10	106.5
G169	A	629.4	1.26	599.1	0.35	37.76	118.5
G170	A	1599.5	1.31	1543.2	2.34	39.22	76.5
G171	A	1497.2	0.15	1490.2	2.17	4.63	37.0

Genotype	Gene pool	GYD (kg/ha)	DSI	GMP	DTI	%GYR	Mean rank
G172	A	1367.6	1.08	1287.0	1.63	32.45	72.0
G173	A	1792.6	0.68	1780.4	3.07	20.40	46.0
G174	M	982.4	-6.11	900.2	0.90	-183.33	31.8
G175	A	407.4	-2.00	315.7	0.12	-59.87	91.5
G176	A	2097.5	0.35	2084.0	4.25	10.60	29.5
G177	M	813.4	0.92	802.7	0.63	27.70	85.3
G178	A	887.3	-4.17	855.8	1.03	-125.00	33.0
G179	ADM	1148.8	2.35	875.1	0.75	70.37	122.5
G180	A	1838.9	0.09	1789.6	3.13	2.57	29.5
G181	A	1614.1	1.03	1585.2	2.44	31.00	64.5
G182	ADM	1415.3	1.21	1373.5	1.84	36.21	77.5
G183	A	1540.3	0.97	1513.3	2.23	29.22	64.5
G184	A	2222.7	0.16	2205.3	4.74	4.69	25.5
G185	A	776.2	2.01	701.7	0.79	60.15	123.3

GYD grain yield, *DSI* drought susceptibility index, *GMP* geometric mean productivity, *DTI* drought tolerance index, *%GYR* percent grain yield reduction, *ADM* admixed, *M* middle-american, *A* andean. **NB**: Admixed includes genotypes that are 10 to 90% andean or middle-american according to the structure analysis results. Mean rank is the mean rank of a genotype across all the drought tolerance indices.



Appendix 7.3 Quantile –Quantile (QQ) plots of the p- values observed and the expected from the genome-wide association study under drought stressed conditions: (**A)** Leaf temperature, (**B)** Days to 50% flowering, (**C)** Grain yield, (**D)** Plant height, (**E)** Seed size, (**F)** Stomatal conductance.



Appendix 7.4 Quantile –Quantile (QQ) plots of the p- values observed and the expected from the genome-wide association study under non-stressed conditions: (**A)** Days to 50% flowering, (**B)** Days to physiological maturity, (**C)** Grain yield, (**D)** Leaf chlorophyll content, (**E)** Plant height, (**F)** Leaf temperature.

Chapter 8 General discussion and implications of the study

8.1 Introduction

This study aimed at closing some of the gaps that exist in navy bean breeding in Zimbabwe to assist breeders in making comprehensive and informed decisions regarding development of new product profiles for the crop. The lack of biofortified navy bean cultivars has forced some of the bean processors in Zimbabwe to establish production lines for micronutrient dense dry beans cultivars of other market classes which generally do not have good canning-quality attributes. This necessitated the need to develop and identify navy bean genotypes that combine drought tolerance with superior canning and nutritional quality traits. The current study, therefore, sought (i) to identify farmers' perceived production and marketing constraints, preferred traits and cultivars of navy bean, and strategies used to mitigate drought and heat stress in the South East Lowveld region of Zimbabwe, (ii) to evaluate the adaptability and stability of navy bean genotypes for grain yield and nutritional quality traits (Fe and Zn) across multiple locations in Zimbabwe, (iii) to investigate the impact of drought stress on agronomic and shoot traits, canning and nutritional quality traits of navy beans, and identify drought tolerant genotypes with superior canning and nutritional quality, (iv) to determine combining ability effects and mode of gene action of grain yield and yield-attributing traits in navy bean under drought stressed and non-stressed environments and select best combiners for effective breeding and (v) to quantify genome-wide marker-trait association of agronomic and physiological traits in dry beans under non-stressed and drought-stressed conditions and to identify candidate markers for marker-assisted selection.

The study identified farmer-preferred traits and marketing and production constraints that should be considered by the breeding programme in Zimbabwe during the development of improved cultivars. Stable high yielding genotypes that are drought tolerant and possess desirable micronutrient density, superior canning and nutritional quality were also identified. Good general and specific combiners with desirable values of drought tolerance indices and high significant positive effects under drought stress were also identified, including molecular markers that have potential to be used for marker-assisted breeding for drought tolerance.

8.2 Recommendations and implications of research findings to navy bean breeding for improved drought tolerance, superior canning and nutritional quality

8.2.1 Farmers' perceptions of navy bean (*Phaseolus vulgaris* L.) production constraints, preferred traits, farming systems and their implications on bean breeding: A case study from south east lowveld region of Zimbabwe

Improving seed size, pod shattering tolerance, fungal disease tolerance, drought tolerance, and heat tolerance of the cultivar "Zimbabwe White Bean" predominantly grown in the Lowveld region without compromising on its short maturity duration, short cooking time, and sweet taste would potentially have a large impact on farmers' livelihoods in the study areas. These findings imply that bean breeders should employ participatory plant breeding strategies and conventional approaches to improve existing navy bean cultivars. Therefore, navy bean improvement programs in Zimbabwe should consider and integrate the farmer-preferred traits and marketing and production constraints during the development of improved cultivars. Where navy bean breeding cannot incorporate all the preferred traits, the key attributes should be included in particular cultivars, making sure that maturity duration is short and there is no grain yield sacrifice since both are essential traits for farmers.

8.2.2 Genotype x environment interaction and stability analyses of grain yield and micronutrient (Fe and Zn) concentrations in navy bean (*Phaseolus vulgaris* L.) genotypes under varied production environments

There is a need to pyramid high grain yield and nutritional quality traits into a single genetic background considering that the best performing genotypes for grain yield, iron, and zinc were different. The gamete selection technique is highly recommended to combine the traits into a single genetic background. Most importantly, bean breeders could probably aim to develop genotypes that combine micronutrient density with "acceptable grain yield potential" taking into consideration the 'dilution effects'. The genotypes which combined high grain yield stability and desirable seed iron and zinc concentrations above breeding targets of 90 and 40 ppm, respectively should be used as parents for crossing with other cultivars to improve micronutrient density and grain yield stability. On the other hand, the genotypes ZABRA16575-26F22, ICA BUNSIxSXB405/4C-1C-1C-8 and NAE13 which combined specific adaptation and high grain yield with desirable micronutrient density could be recommended for deployment in their respective mega-environments. However, before their deployment, there is a need to evaluate their preference among different stakeholders such as

farmers, traders, bean processors, and consumers. Furthermore, these genotypes should be subjected to on-farm multi-environment testing, bioavailability studies, and confirmatory micronutrient analysis using the Inductively Coupled Plasma Atomic Emission Spectrometry (ICP-AES).

8.2.3 Drought stress impact on agronomic and shoot traits, canning and nutritional quality of navy beans (*Phaseolus vulgaris* L.)

The identified genotypes for use as parents in breeding for drought tolerance, superior canning and nutritional quality under drought stressed conditions require further study to understand the mechanism behind the observed 'no or minimal' impact of drought stress on their grain yield, shoot traits, canning and nutritional quality. Considering that the superior genotypes identified in this study did not combine most of the studied traits, the use of the gamete selection technique to simultaneously combine multiple traits into a single genetic background is recommended. The significant associations observed in this study between seed iron and zinc imply that both traits can be improved simultaneously. The selected navy bean genotypes; ZABRA16575-86F22 and CIM-NAV08-1 which combined high grain yield with acceptable canning and nutritional quality under drought stressed and non-stressed environments are valuable genetic resources for drought tolerance, canning and nutritional quality breeding in the near future. However, these genotypes should undergo confirmatory canning and nutritional quality analysis using the industrial canning protocol and ICP-AES analytical technique, respectively. The high broad-sense heritability (H^2) estimates (> 90%) obtained for all the studied canning quality traits under drought stressed environments imply that genetic gains for these traits are likely to increase under drought stressed environments. Furthermore, the observed high H^2 estimates for canning quality traits, seed iron and zinc contents under drought stressed environments implies greater opportunity for selection of micronutrient dense navy bean genotypes that also exhibit superior canning quality attributes. In this study, it was not feasible to phenotype for canning quality under both drought stressed and non-stressed environments due to high costs associated with canning quality analysis. This implies that, there is need to fast-track the development and validation of molecular markers that are associated with canning quality parameters.

8.2.4 Genetic analysis of grain yield and yield-attributing traits in navy bean (*Phaseolus vulgaris* L.) under drought and optimal environments

The importance of both additive and non-additive gene effects in the inheritance of grain yield and its attributing traits under both test environments imply that there is need to incorporate breeding schemes that exploit both additive and non-additive genes in navy bean breeding. ZABRA16575-73F22 could be utilized in navy bean improvement programs (recurrent selection) to form base populations with improved tolerance to drought considering that it exhibited high values for drought tolerance index and geometric mean productivity and low values for percentage grain yield reduction and drought susceptibility index. The best performing specific combiners which consistently had high values for most of the studied traits under both environments should be evaluated further through the single seed descent method to rapidly advance the progenies to homozygosity, after which selection for canning quality and grain yield can be initiated. Breeding for superior grain yield under drought stressed conditions should involve high general combining ability x high general combining ability or high general combining ability x low general combining ability parental combinations. The parents which had significant and poor general combining ability estimates as well as produced inferior cross combinations are undesirable for the genetic improvement of these traits and should be discarded from the breeding pipeline. However, the parents with poor general combining ability estimates which produced superior cross-combinations must be retained in the breeding pipeline.

8.2.5 Identification of genomic regions of dry beans (*Phaseolus vulgaris* L.) associated with agronomic and physiological traits under drought stressed and non-stressed conditions using genome-wide association study

The identified significant marker-trait associations should be explored and validated further using segregating populations and in different genetic backgrounds before utilization in marker-assisted breeding for drought tolerance. Furthermore, functional characterization and the application of gene knockout to the identified putative candidate genes would further confirm their roles in regulating drought stress response, and growth and development under drought stressed and non-stressed conditions. All the identified drought tolerant genotypes (DAB91, DAB302, AFR703, CIM-SUG07-ALS-51-3, DAB487, DAB287, CIM-RM09-ALS-BSM-12 and DAB539) could be utilized in drought tolerance breeding programs (recurrent selection) to form base populations with improved tolerance to drought stress. More powerful statistical genetics tools such as genomic prediction models would be needed to identify minor

genes that are associated with agronomic and physiological traits. The proportion of the total phenotypic variation (R^2) explained by the significant single nucleotide polymorphism (SNP) markers for leaf chlorophyll content and leaf temperature was generally low (0.11 – 0.12 for leaf chlorophyll content under non-stressed conditions and 0.08 – 0.15 for leaf temperature under non-stressed conditions). Therefore, to account for the missing variation, it might be worthwhile to complement the single nucleotide polymorphism-based genome wide association study by haplotype-based genome wide association study.