# APPLICATION OF BACTERIAL BIOFLOCCULANTS FOR WASTEWATER AND RIVER WATER TREATMENT

Simphiwe P. Buthelezi

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As the candidate's supervisor, I have approved this dissertation for submission.

Signed:	Name:	Date:
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For my parents: Mr and Mrs E. Buthelezi

This MSc study was carried out in the School of Biochemistry, Genetics, Microbiology and Plant Pathology, University of KwaZulu-Natal, Westville Campus, under the supervision of Professor B Pillay.

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Simphiwe Promise Buthelezi (Candidate)

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#### ABSTRACT

Dyes are often recalcitrant organic molecules that produce a colour change and contribute to the organic load and toxicity of textile industrial wastewater. Untreated effluent from such sources is harmful to aquatic life in the rivers and lakes due to reduced light penetration and the presence of highly toxic metal complex dyes. The use of alum as flocculant/coagulant in wastewater treatment is not encouraged as it induces Alzheimer's disease in humans and results in the production of large amounts of sludge. Therefore, the development of safe and biodegradable flocculating agents that will minimize environmental and health risks may be considered as an important issue in wastewater treatment. Bioflocculants are extracellular polymers synthesized by living cells. In this study, bacterial bioflocculants were assessed for their ability to remove dyes from textile wastewater as well as reducing the microbial load in untreated river water. The bacteria were isolated from a wastewater treatment plant and identified using standard biochemical tests as well as the analysis of their 16S rDNA gene sequences. Six bacterial isolates were identified viz. Staphylococcus aureus, Pseudomonas plecoglossicida, Pseudomonas pseudoalcaligenes, Exiguobacterium acetylicum, Bacillus subtilis, and Klebsiella terrigena. The flocculating activities of the bioflocculants produced by these isolates were characterized. The effect of temperature, pH, cations and bioflocculant concentration on the removal of dyes, kaolin clay and microbial load was also determined. The amount of bioflocculants produced by the bacterial isolates ranged between 5 and 27.66 g/l. According to the findings of the present study, bacterial bioflocculants were composed of carbohydrates, proteins, uronic acid, and hexosamine in varying quantities. The bioflocculants were effective to varying degrees in removing the dyes in aqueous solution, in particular whale dye, medi-blue, fawn dye and mixed dyes, with a decolourization efficiency ranging between 20-99.9%. Decolourization efficiency was influenced by the bioflocculant concentration, pH, temperature, and cations. The bacterial bioflocculants were also capable of reducing both the kaolin clay and the microbial load from river water. The flocculating activity ranged between 2.395–3.709  $\mathrm{OD}^{\text{-1}}$  while up to 70.84% of kaolin clay and 99% of the microbial load from the river water was removed. The efficiency of kaolin clay flocculation increased with higher concentration of bacterial bioflocculants. The optimum pH for the flocculating activity was observed between 6 and 9. The best flocculating activity was observed at  $28^{\circ}$ C. Divalent cations such as Mg<sup>2+</sup> and Mn<sup>2+</sup> improved the flocculation while salts such as K<sub>2</sub>HPO<sub>4</sub>, CH<sub>2</sub>COONa, and Na<sub>2</sub>CO<sub>3</sub> did not. The findings of this study strongly suggest that microbial bioflocculants could provide a promising alternative to replace or supplement the physical and chemical treatment processes of river water and textile industry effluent.

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#### **CHAPTER ONE**

#### **INTRODUCTION AND LITERATURE REVIEW**

A great number of industries such as textile, paper and pulp, printing, iron-steel, coke, petroleum, pesticide, paint, solvent, pharmaceutics, wood preserving chemicals, consume large volumes of water and organic based chemicals. These chemicals show a vast difference in chemical composition, molecular weight, and toxicity. Effluents from these industries may also contain undesired quantities of these pollutants and need to be treated (Aksu, 2005).

## 1.1 MICROBIAL PROCESSES FOR THE DECOLOURIZATION OF TEXTILE EFFLUENTS

The most common textile-processing set-up (Fig. 1.1) for the decolourization of textile effluents consists of desizing, scouring, bleaching, mercerising, and dyeing processes (Dos Santos et al., 2007). Sizing is the first preparation step, which involves the addition of sizing agents such as starch, polyvinyl alcohol (PAVE) and carboxymethyl cellulose. These agents provide strength to the fibres and minimize breakage. Desizing is employed next, to remove sizing materials prior to weaving. Scouring removes impurities from the fibres by using alkali solution (commonly sodium hydroxide) to breakdown natural oils, fats, waxes and surfactants, as well as to emulsify and suspend impurities in the scouring bath. Bleaching is the step used to remove unwanted colour from the fibres by using chemicals such as sodium hypochlorite and hydrogen peroxide. Bleaching is followed by mercerising which is a continuous chemical process used to increase dye-ability, lustre, and fibre appearance. In this step, a concentrated alkaline solution is applied and an acid solution washes the fibres before the dyeing step. Finally, dyeing is the process of adding colour to the fibres, which normally requires large volumes of water not only in the dye bath, but also during the rinsing step. Depending on the dyeing process, many chemicals like metals, salts, surfactants, organic processing assistants, sulphide and formaldehyde, may be added to improve dye adsorption onto the fibres. Figure 1.1 shows some potential pollutants from cotton processing operations in which the desiring/scouring and dye bath/rinsing wastewaters are mainly composed of organic pollutants and colour-causing pollutants, respectively (Dos Santos *et al.*, 2006; 2007).



Fig. 1.1: Scheme of operations involved in textile cotton industry and the main pollutants from each step (Dos Santos *et al.*, 2007).

Synthetic dyestuffs are a group of organic pollutants, which are used extensively in textile, paper, printing industries, and dye houses. It has been reported that there are over 100 000 commercially available dyes with a production of over  $7 \times 10^5$  metric tonnes per year (Clarke and Anliker, 1980). Effluents from dyeing industries constitute one of the most problematic wastewaters because of their high chemical and biological oxygen demands. It has been recognized that the public perception of water quality is greatly influenced by colour. Colour is the first contaminant recognized in wastewater. The presence of very small amounts of dyes in water (less than 1 ppm for some dyes) is highly visible and undesirable (Banat *et al.*, 1996; Robinson *et al.*, 2001). Dyes may significantly affect photosynthetic activity in aquatic life due to reduced light penetration and may be toxic to some aquatic life due to the presence of aromatics, metals, and chlorides, in them. Dyes usually have a synthetic origin and complex aromatic molecular structures, which make them more stable and more difficult to biodegrade (Clarke and Anliker, 1980; Mishra and Tripathy, 1993; Banat *et al.*, 1996; Fu and Viraraghavan, 2001; Robinson *et al.*, 2001).

#### 1.1.1 Classification of dyes

Dyes are classified as follows: anionic-direct, acid, and reactive dyes; cationicbasic dyes; and non-ionic disperse dyes. The chromophores in anionic and non-ionic dyes are mostly azo groups or anthraquinone types. The reductive cleavage of azo linkages is responsible for the formation of toxic amines in the effluent (Mishra and Tripathy, 1993; Fu and Viraraghavan, 2001). Anthraquinone-based dyes are more resistant to degradation due to their fused aromatic structures and thus remain coloured for a longer time in the wastewater. Reactive dyes are typically azo-based chromophores combined with different types of reactive groups e.g., vinyl sulfone, chlorotriazine, trichloropyrimidine, difluorochloropyrimidine. They differ from all other classes of dyes in that they bind to the textile fibres such as cotton through the covalent bonds. They are widely used in textile industries because of their favourable characteristics such as bright colour, waterfast, simple application techniques with low energy consumption. Water-soluble reactive and acid dyes are the most problematic, as they tend to pass through conventional treatment systems unaffected. Hence, their removal is also of great importance (Hu, 1992; Juang *et al.*, 1997; Moran *et al.*, 1997; Karcher *et al.*, 1999; Aksu and Tezer, 2000; Sumathi and Manju, 2000; Robinson *et al.*, 2001; O'Mahony *et al.*, 2002).

Basic dyes have high brilliance and intensity of colours and are highly visible even in a very low concentration (Clarke and Anliker, 1980; Banat et al., 1996; Mittal and Gupta, 1996; Fu and Viraraghavan, 2001; Chu and Chen, 2002; Fu and Viraraghavan, 2002). Metal complex dyes are mostly based on chromium, which is carcinogenic (Gupta et al., 1990; Mishra and Tripathy, 1993). Disperse dyes do not ionize in an aqueous medium and some disperse dyes have also been shown to have a tendency to bioaccumulate (Baughman and Perenich, 1988; Srivastava and Prakash, 1991). Due to the chemical stability and low biodegradability of these dyes, conventional biological wastewater treatment systems are inefficient in treating dye wastewater. Physical or chemical treatment processes are usually employed to treat dye wastewater. These include chemical coagulation/flocculation, ozonation, oxidation, ion exchange, irradiation, precipitation, and adsorption. Some of these techniques are effective, but have their limitations. These include: excess amount of chemical usage, or accumulation of concentrated sludge with obvious disposal problems; expensive plant requirements or operational costs; lack of effective colour reduction; and sensitivity to a variable wastewater input (McKay and Poots, 1980; El-Geundi, 1991; Juang et al., 1997; Lambert et al., 1997; Low and Lee, 1997; Ramakrishna and Viraraghavan, 1997; Slokar and Le-Marechal, 1997; Ho and McKay, 1999; Lee et al., 1999; Morais et al., 1999; Otero et al., 2003).

In recent years, a number of studies have focused on some microorganisms, which are able to biodegrade or bioaccumulate azo dyes in wastewaters (Dhodapkar *et al.*, 2006). A wide variety of microorganisms including bacteria, fungi, and algae are capable of decolourizing a wide range of dyes via anaerobic, aerobic, and sequential anaerobic– aerobic treatment processes. Cytoplasmic azo reductases play an important role in the anaerobic biodegradation of azo dyes to produce colourless aromatic amines although complete mineralization is difficult and the resulting aromatic amines may be toxic and carcinogenic. These amines are resistant to further anaerobic mineralization. Fortunately, once the xenobiotic azo component of the dye molecule has been removed, the resultant amino compounds are good substrates for aerobic biodegradation suggesting a choice of a sequential anaerobic–aerobic system for wastewater treatment (Razo-Flores *et al.*, 1997; Fu and Viraraghavan, 2001; Manu and Chaudhari, 2001). A number of aerobic biological processes for the removal of dyes from textile effluents exist. This includes decolourization through liquid fermentations by white-rot fungi (such as *Phanerochaete chrysosporium, Trametes versicolor, Coriolus versicolor*); bacterial cultures (such as *Pseudomonas* strains, mixed bacterial cultures, *Bacillus subtilis*) and yeasts (such as *Klyveromyces marxianus, Candida zeylanoides*). Biochemical oxidation suffers from significant limitations since more dyestuffs found in the commercial market have been intentionally designed to be resistant to aerobic microbial degradation (Pearce *et al.*, 2003).

Reactive azo dyes are electron deficient in nature and this property makes them less susceptible to oxidative catabolism (Banat et al., 1996). Research has shown that the efficiency of biological treatment systems are greatly influenced by the operational parameters, the composition of textile wastewater and the structure and substituents of dye molecule. The level of aeration, temperature, pH, and redox potential of the system are the variables that can be optimized to produce the maximum rate of dye reduction. The ability of microorganisms to reduce dyes from wastewater depends on the classes of dyes used (acidic, basic, direct, disperse, metal-complex, and reactive). The composition of textile wastewater varies and can include organics, nutrients, salts, sulphur compounds and toxicants as well as colour. Therefore, the inhibitory effect of any of these compounds on the dye reduction process should be investigated (Glenn and Gold, 1983; Knapp and Newby, 1999; Kapdan et al., 2000; Meehan et al., 2000; Fu and Viraraghavan, 2001; Manu and Chaudhari, 2001; Ramalho et al., 2002). Another biological treatment method is bioaccumulation. Bioaccumulation is defined as the accumulation of pollutants by actively growing cells by metabolism; temperatureindependent; and metabolism-dependent mechanism steps. Although bioaccumulations of dyes by yeasts were accomplished, significant practical limitations exist. These include the inhibition of cell growth at high dye concentrations and requirement of metabolic energy externally provided (Dönmez, 2002; Aksu, 2003). Therefore, there is a need to find alternative treatment methods that are effective in removing dyes from large volumes of effluents and are low in cost, such as biosorption or bioflocculation.

### **1.2 THE NEED FOR WASTEWATER TREATMENT**

Matter in water may be broadly classified according to its origin as inorganic mineral matter or organic carbonaceous material. Substances producing turbidity are often inorganic, while those causing taste, odour, and colour are generally organic compounds. The particles producing turbidity may be further classified according to their size, which may range from molecular dimensions of 50 microns or larger. The fraction greater than 1 micron in diameter is generally referred to as silt and will settle out on standing. The smaller particles, which are classified as colloidal, will remain suspended for very long time. Most attention has therefore been directed towards the use of coagulation for removal of colloidal material, although this process also removes the larger particles (Jones, 1998). It is important to keep our water clean because of our environment and health. Some of the reasons include:

- Fisheries; clean water is critical to plants and animals that live in water. This is important to the fishing industry, sport fishing enthusiasts, and future generations;
- Wildlife habitat, rivers and ocean waters teem with life that depends on shoreline, beaches, and marshes. They are critical habitats for hundreds of species of fish and other aquatic life. Migratory water birds use the areas for resting and feeding;
- Recreation and quality of life; water is a great playground for us all. The scenic and recreational values of our waters are reasons many people choose to live where they do. Visitors are drawn to water activities such as swimming, fishing, boating, and picnicking; and
- Health concern; water may carry disease if not properly cleaned. Since we live, work and play so close to water, harmful bacteria have to be removed to make water safe (Cowan and Talaro, 2006).

#### **1.3 WATER SOURCES AND QUALITY**

Water is usually withdrawn for drinking and household purposes from the following sources (Navin *et al.*, 2006):

- Ground water (springs, infiltration galleries, and wells)
- Surface water (rivers, lakes, ponds, streams, impounded reservoirs, and stored rainwater).

Ground water is one of the nation's most important natural resources. Ground water provides drinking water for more than one-half of the nation's population and is the sole source of drinking water for many rural communities and some large cities. In 1990, ground water accounted for 39% of the public water supply for cities and towns and 96% for self-supplied systems for domestic use (Twarakavi and Kaluarachchi, 2006). It is also the source of much of the water used for irrigation. Ground water is a major contributor to flow in many streams and rivers and has a strong influence on river and wetland habitats for plants and animals. Ground water withdrawal in the USA in 1995 was estimated to be approximately 77 billion gallons per day, which is about 8% of the used 1 trillion gallons per day of natural recharge to the ground water system of the USA (Navin *et al.*, 2006; Twarakavi and Kaluarachchi, 2006).

If groundwater is conveniently located and in sufficient quantities it should be used, as it is less polluted compared with surface water. Groundwater may be aerobic or anaerobic depending on the environmental conditions where it is located. The anaerobic groundwater often contains  $CO_2$ , which makes it corrosive. The removal of  $CO_2$  as well as provision of oxygen can be facilitated by aeration. Chlorination also removes  $CO_2$ . Some ground water contains excessive amounts of Fe, Mn, hardness, and/or fluoride (Decker and Long, 1992).

The surface waters are generally more polluted than groundwater due to their exposure to the environment. They may require more treatment steps than ground water.

The typical impurities may include turbidity, colour, algae, floating debris, bacteria, and other microorganisms, in addition to the constituents of ground water. Surface water in general contains physical, chemical, and biological impurities (such as clay, sand, colloids, minerals, colour, odour, taste, and microorganisms). Rivers have been used by man since the dawn of civilization as a source of water, for food, for transport, as a source of power to drive machinery, and a means of disposing of waste (Vigneswaran and Visvanathan, 1995). Thus river water requires adequate treatment steps so that it can be suitable for domestic purposes. Figure 1.2 is an illustration of the water cycle.



**Fig. 1.2:** The water cycle (http://www.usgcrp.gov/usgcrp/images/ocp2003/WaterCycle optimized.jpg).

The majority of water supplies require treatment to make them suitable for use in domestic and industrial applications. Although appearance, taste, and odour are useful indicators of the quality of drinking water, suitability in terms of public is determined by microbiological, physical, chemical, and radiological characteristics. Of these, the most important is microbiological quality. In addition, a number of chemical contaminants (both organic and inorganic) are found in water. These may lead to health problems. Therefore, detailed analyses of water are warranted (Vigneswaran and Visvanathan, 1995). The drinking water thus should be; free from pathogenic (disease causing) organisms; clear (i.e., low turbidity, little colour); not saline (salty); free from offensive taste or smell; and free from compounds that may have adverse effects on human health (harmful in the long term) (Vigneswaran and Visvanathan, 1995).

### **1.4 WASTEWATER TREATMENT PROCESSES**

The major aim of wastewater treatment is to remove as much of the suspended solids as possible before the remaining water, called effluent, is discharged back to the environment. As solid material decays, it uses up oxygen, which is needed by the plants and animals living in the water. Conventional wastewater treatment process involves primary, secondary, and tertiary treatment (Prescott *et al.*, 1996; Nester *et al.*, 2001).

#### **1.4.1 Primary treatment**

Primary treatment involves aerating (stirring up) the wastewater, in order to replenish oxygen back in. Primary treatment can remove 20 to 30% of the BOD, which is present in particulate form and about 60% of suspended solids from wastewater. In this treatment, particulate material is removed by screening, precipitation of small particles, and settling in basins or tanks. The resulting solid material is called sludge. This treatment of physical removal of settleable solids (primary treatment) and secondary treatment (biological transformation of dissolved organic matter to microbial biomass and carbon dioxide) is shown together with final clarifiers. The final clarifiers separate the

newly formed microbial biomass (sewage sludge) from the processed water stream, which can be returned to the receiving body of water (Prescott *et al.*, 1996).

#### 1.4.2 Secondary treatment

Secondary treatment is used after primary treatment for the biological removal of dissolved organic matter. This process removes about 90 to 95% of the BOD and many bacterial pathogens and more than 90% of suspended solids. Several approaches involving similar microbial activities can be used for secondary treatment to biologically remove dissolved organic matter. Under aerobic conditions, dissolved organic matter is transformed into additional microbial biomass plus carbon dioxide (Ford, 1993). When these processes occur with lower oxygen levels or with a microbial community too young or too old, unsatisfactory floc formation and settling can occur. The result is a bulking sludge, caused by massive development of filamentous bacteria such as *Sphaerotilus* and *thiothrix*, together with many poorly characterized filamentous organisms. These important filamentous bacteria form flocs that do not settle well and have effluent quality problems (Prescott *et al.*, 1996).

An aerobic activated sludge process is a biological method of wastewater treatment that is performed by a variable and mixed community of microorganisms in an aerobic aquatic environment. These microorganisms derive energy from carbonaceous organic matter in aerated wastewater for the production of new cells in a process known as synthesis. Simultaneously energy is released through the conversion of this organic matter into compounds that contain lower energy, such as carbon dioxide and water, in a process called respiration. A variable number of microorganisms in the system obtain energy by converting ammonia nitrogen to nitrate nitrogen in a process termed nitrification. In this consortium of microorganisms, the biological component of the process is known collectively as activated sludge. The overall goal of the activated-sludge process is to remove substances that have a demand for oxygen from the system (Huang and Shui, 1996).

After the bacteria and fungi in sewage treatment have used certain nutrients, they serve as food for ciliates, protozoa, nematodes, and other forms of life. The end result is a small increase in the mass of organisms present in a given amount of treated sewage and a large decrease in the amount of biodegradable organic material (Bitton, 1994). The increased microbial biomass in the sewage is removed to the digester; a portion is left behind as inoculum to act on a new load of waste material. Within the sewage digester, anaerobic organisms act on the solids remaining in sewage after its aerobic treatment. The digester provides anaerobic conversion of organic to inorganic matter and removes water from the sewage so that a minimum of solid matter remains in it. Various populations act sequentially. In the sewage digester, the anaerobic methane-forming organisms can perform their role of converting the simple organic acids in sewage into the useful end product methane ( $CH_4$ ). Many sewage treatment plants are equipped to use their own methane, thereby avoiding the cost of other sources of energy to run their equipment (Nester *et al.*, 2001). Figure 1.3 illustrates the processes involved for the production of methane on small scale.



Fig. 1.3: Production of methane on a small scale (Nester et al., 2001).

Pathogenic bacteria are generally removed from sewage during secondary treatment, but disease-producing viruses may survive. Pathogens account for only a small proportion of the total number of bacteria in faeces, and they are diluted by the water in sewage. During the secondary treatment of sewage, these pathogens must compete for nutrients with a huge mass of bacteria that have been adapted to grow best at the temperature and conditions provided. As a result, most pathogenic bacteria are overgrown and are eliminated by their competitors (Huang and Shui, 1996). Animal viruses lack appropriate host cells in sewage and replicate there, although they may survive for long periods. If large quantities of virus particles are present in raw sewage, some may be recovered after secondary treatment. Although sewage effluents are often chlorinated before being discharged into receiving waters, chlorine treatment at this stage does not inactivate viruses. The virus particles are commonly enclosed within small clumps of effluent materials where they are protected from the chlorine. Because viruses do adhere to large particles, they can be removed along with other solid materials (Huang and Shui, 1996; Nester *et al.*, 2001).

#### **1.4.3 Tertiary treatment**

Tertiary treatment purifies wastewater more than is possible with primary and secondary treatments. The goal is to remove such pollutants as nonbiodegradable organic matter e.g. polychlorinated biphenyls, heavy metals, and minerals (Prescott *et al.*, 1996). Tertiary treatment provides a final stage to raise the effluent quality to the standard required before it is discharged to the receiving environment (sea, river, lake, and ground). The large quantities of phosphates or nitrites remaining in sewage after secondary treatment may increase the growth of microorganism, which gradually deplete the oxygen and thus threaten other forms of aquatic life. The tertiary treatment of sewage, to remove nitrates and phosphates, can greatly alleviate this problem (Cowan *et al.*, 1995).

In some designs for the tertiary treatment of sewage, chemical precipitation of phosphates has been combined with biological removal of nitrates. Certain bacteria (particularly species of *Pseudomonas* and *Bacillus*) can completely reduce nitrates ( $NO_3^-$ ) to  $N_2$  (denitrification). The  $N_2$  gas is inert, non-toxic, and easily removed. More than one tertiary treatment process may be used at any treatment plant. If disinfection is practiced, it is always the final process. It is also called "effluent polishing" (Nester *et al.*, 2001). Figure 1.4 is an illustration of the major steps in modern sewage treatment plant.



Fig. 1.4: Major steps involved in modern sewage treatment plants (http://web.deu.edu.tr/atiksu/toprak/summary4.html).

# 1.5 TECHNOLOGIES AVAILABLE FOR COLOUR REMOVAL FROM EFFLUENTS

There are several reported technologies for the removal of dyes from effluents (Table 1.1). The technologies can be divided into three categories: biological, chemical and physical (Robinson *et al.*, 2001). Many of these conventional methods for treating dye wastewater have not been widely applied on a large scale in the textile and paper industries because of the high cost and disposal problems (Ghoreishi and Haghighi, 2003). At the present time, there is no single process capable of adequate treatment, mainly due to the complex nature of the effluents (Marco *et al.*, 1997; Pereira *et al.*, 2003). In practice, a combination of different processes is often used to achieve the desired water quality in the most economical way. Research is ongoing and in the areas

of combined adsorption-biological treatments in order to improve the biodegradation of dyestuffs and minimize the sludge production (Pearce *et al.*, 2003).

	Technology	Advantages	Disadvantages
Conventional treatment	Coagulation Flocculation	Simple, economically	High sludge production,
processes		feasible	handling and disposal
			problems
	Biodegradation	Economically attractive,	Slow process, necessary to
		publicly acceptable	create an optimal
		treatment	favourable environment,
			maintenance and nutrition
			requirements
	Adsorption on activated	The most effective	Ineffective against disperse
	carbons	adsorbent, great, capacity,	and vat dyes, the
		produce a high-quality	regeneration is expensive
		treated effluent	and results in loss of the
			adsorbent, non-destructive
			process
Established recovery	Membrane separations	Removes all dye types,	High pressures, expensive,
processes		produce a high-quality	incapable of treating large
		treated effluent	volumes
	Ion-exchange	No loss of sorbet on	Economic constraints, not
		regeneration, effective	effective for disperse dyes
	Oxidation	Rapid and efficient process	High energy cost,
			chemicals required
Emerging removal	Advanced oxidation	No sludge production, little	Economically unfeasible,
processes	process	or no consumption of	formation of by-products,
		chemicals, efficiency for	technical constraints
		recalcitrant dyes	
	Selective bioadsorbents	Economically attractive,	Requires chemical
		regeneration is not	modification, non-
		necessary, high selectivity	destructive process
	Biomass	Low operating cost, good	Slow process, performance
		efficiency and selectivity,	depends on some external
		no toxic effect on	factors (pH, salts)
		microorganisms	

Table 1.1: Principal existing and emerging processes for dye removal (Robinson et al., 2001)
#### **1.5.1 Biological treatments**

Biological treatment is often the most economical alternative compared to physical and chemical processes. Biodegradation methods such as fungal decolourization, microbial degradation, adsorption by (living or dead) microbial biomass and bioremediation systems are commonly applied to the treatment of industrial effluents because many microorganisms such as bacteria, yeasts, algae and fungi are able to accumulate and degrade different pollutants (Fu and Viraraghavan, 2001; McMullan *et al.*, 2001). However, their application is often restricted because of technical constraints. Biological treatment requires a large land area and is constrained by sensitivity toward diurnal variation as well as toxicity of some chemicals, and less flexibility in design and operation (Bhattacharyya and Sarma, 2003). Biological treatment is incapable of obtaining satisfactory colour elimination with current conventional biodegradation processes (Robinson *et al.*, 2001). Moreover, although many organic molecules are degraded, many others are recalcitrant due to their complex chemical structure and synthetic organic origin. In particular, due to their xenobiotic nature, azo dyes are not totally degraded (Ravi-Kumar *et al.*, 1998).

#### **1.5.2 Chemical treatments**

Chemical methods include coagulation or flocculation combined with flotation and filtration, precipitation–flocculation with  $Fe(II)/Ca(OH)_2$ , electroflotation, electrokinetic coagulation, conventional oxidation methods by oxidizing agents (ozone), irradiation or electrochemical processes. These chemical techniques are often expensive, and although the dyes are removed, accumulation of concentrated sludge creates a disposal problem. There is also the possibility that a secondary pollution problem may arise because of excessive chemical use. Recently, other emerging techniques, known as advanced oxidation processes, which are based on the generation of very powerful oxidizing agents such as hydroxyl radicals, have been applied with success for pollutant degradation. Although these methods are efficient for the treatment of waters contaminated with pollutants, they are costly and commercially unattractive. The high electrical energy demand and the consumption of chemical reagents are common problems (Crini, 2006).

#### **1.5.3 Physical treatments**

Different physical methods are also widely used, such as membrane-filtration processes (nanofiltration, reverse osmosis, electrodialysis) and adsorption techniques. The major disadvantage of the membrane processes is that they have a limited lifetime before membrane fouling occurs. The cost of periodic membrane replacement must thus be included in any analysis for their economic viability. In accordance with the literature, liquid-phase adsorption is one of the most popular methods for the removal of pollutants from wastewater. Proper design of the adsorption process may produce a high-quality treated effluent. This process provides an attractive alternative for the treatment of contaminated waters, especially if the sorbent is inexpensive and does not require an additional pre-treatment step before its application (Dabrowski, 2001).

Adsorption is a well known equilibrium separation process and an effective method for water decontamination applications. Adsorption has been found to be superior to other techniques for water re-use in terms of initial cost, flexibility and simplicity of design, ease of operation and insensitivity to toxic pollutants. Adsorption also does not result in the formation of harmful substances (Dabrowski, 2001).

#### **1.6 MECHANISM OF COLOUR REMOVAL BY BACTERIA**

The simplest mechanism of colour removal by whole bacterial cells is that of the adsorption of the dye onto the biomass (Bras *et al.*, 2001). However, this mechanism is similar to many other physical adsorption mechanisms for the removal of colour. It is not suitable for long-term treatment and during adsorption; the dye is concentrated onto the biomass, which will become saturated with time. The dye-adsorbent composition must also be disposed off. Bio-association between the dye and the bacterial cells tends to be

the first step in the biological reduction of azo dyes, which is a destructive treatment technology (Southern, 1995).

Biodegradation processes may be anaerobic, aerobic or involve a combination of both. In the reaction between bacterial cells and azo dyes, there are significant differences between the physiology of microorganisms grown under aerobic and anaerobic conditions. For aerobic bacteria to be significant in the reductive process, the bacteria must be specifically adapted. This adaptation involves long-term aerobic growth in continuous culture in the presence of a very simple azo compound. The bacteria synthesise an azoreductase specific for this compound, which, under controlled conditions, can reductively cleave the azo group in the presence of oxygen. In contrast, bacterial reduction under anaerobic conditions is relatively unspecific with regard to the azo compounds involved, and is, therefore, of more use for the removal of colour in azo dye wastewater (Stolz, 2001).

It is thought that, as most azo dyes have sulphonate substituent groups and a high molecular weight, they are unlikely to pass through cell membranes. Therefore, the reducing activity referred to above is not dependant on the intracellular uptake of the dye (Robinson *et al.*, 2002). This was shown by Russ *et al.* (2000), who also suggested that bacterial membranes are almost impermeable to flavin-containing cofactors and, therefore, restrict the transfer of reduction equivalents by flavins from the cytoplasm to the sulphonated azo dyes. Thus, a mechanism other than reduction by reduced flavins formed by cytoplasmic flavin-dependent azoreductases might be responsible for sulphonated azo dye reduction in bacterial cells with intact cell membranes (Russ *et al.*, 2000).

One such mechanism involves the electron transport-linked reduction of azo dyes in the extra-cellular environment. To achieve this, bacteria must establish a link between their intracellular electron transport systems and the high molecular weight, azo dye molecules. For such a link to be established, the electron transport components must be localised in the outer membrane of the bacterial cells (in the case of gram-negative bacteria), where they can make direct contact with either the azo dye substrate or a redox mediator at the cell surface (Myers and Myers, 1992). In addition, low molecular weight redox mediator compounds can act as electron shuttles between the azo dye and an NADH (nicotinamide adenine dinucleotide)-dependent azo reductase that is situated in the outer membrane. These mediator compounds are either formed during the metabolism of certain substrates by the bacteria or they may be added externally (Gingell and Walker, 1971).

The addition of synthetic redox mediators such as anthraquinone sulphonates, even at very low concentrations, will facilitate the non-enzymatic reduction of the azo dyes in the extra-cellular environment (Plumb *et al.*, 2001; Yoo *et al.*, 2001). However, if the extra-cellular environment is aerobic, this reduction mechanism would be inhibited by oxygen, due to the preferential oxidation of the reduced redox mediator by oxygen rather than by the azo dye. Membrane-bound azo reductase activity, mediated by redox compounds, is different from the soluble cytoplasmic azo reductase that is responsible for the reduction of non-sulphonated dyes that permeate through the cell membrane. Their results show that a thiol-specific inhibitor almost completely inactivates the membrane-bound azo reductase. Therefore, the membrane-bound and the cytoplasmic azo reductases are two different enzyme systems (Kudlich *et al.*, 1997).

Figure 1.5 illustrates a proposed mechanism for the redox-mediator-dependent reduction of azo dyes using whole bacterial cells, under anaerobic conditions. Although the final reduction of the azo dyes in the cell supernatants is a dominantly chemical redox reaction, the redox mediators depend on cytoplasmic reducing enzymes to supply electrons (Yoo *et al.*, 2001). It is also possible that this chemical redox reaction works in conjunction with a direct enzymatic reaction involving an azo reductase, which may be a dehydrogenase enzyme that is synthesized throughout the cytoplasm and secreted without accumulation inside the cell (Bragger *et al.*, 1997).



Fig. 1.5: Proposed mechanism for reduction of azo dyes by whole bacterial cells (Keck *et al.*, 1997).

A study into the kinetics of anaerobic colour removal indicated that the transfer, rather than the production of reduced redox mediators was the rate-limiting step in the reduction of azo dyes. The reduction rate was also governed by the redox potential of the dyes and the redox mediators. In the same study, it was found that amino quinone compounds that are formed during the reduction of certain azo dyes were involved in autocatalysis and contributed substantially to the reduction process (Van der Zee *et al.*, 2000). Another possible mechanism for colour removal involves the reduction of the azo bond by reduced inorganic compounds, such as Fe<sup>2+</sup> or H<sub>2</sub>S that are formed as the end product of certain anaerobic bacterial metabolic reactions (Kudlich *et al.*, 1997).

In summary, it is probable that there are at least two mechanisms for the decolourization of azo dyes in bacterial systems:

- Direct electron transfer to azo dyes as terminal electron acceptors via enzymes during bacterial catabolism, connected to ATP-generation (energy conservation); and
- Reduction of azo dyes by the end products of bacterial catabolism not linked to ATP-generation.

Organics or inorganics may be involved in both mechanisms by acting as electron shuttles between the reducing equivalents and the azo dyes (Yoo *et al.*, 2000).

#### 1.6.1 Colour removal using whole bacterial cells

Alternative approaches to colour removal, utilizing microbial biocatalysts to reduce the dyes that are present in the effluent, offer potential advantages over physiochemical processes. In particular, the ability of whole bacterial cells to metabolise azo dyes has been extensively investigated (Pearce et al., 2003). Under aerobic conditions, azo dyes are not readily metabolized (Robinson et al., 2001). However, under anaerobic conditions, many bacteria reduce the highly electrophilic azo bond in the dye molecule, reportedly by the activity of low specificity cytoplasmic azo reductases, to produce colourless aromatic amines. These amines are resistant to further anaerobic mineralization and can be toxic or mutagenic to animals. Fortunately, once the xenobiotic azo component of the dye molecule has been removed, the resultant amino compounds are good substrates for aerobic biodegradation. According to Lourenco et al. (2000), if a sequential anaerobic-aerobic system is employed for wastewater treatment, the amines can be mineralised under aerobic conditions by a hydroxylation pathway involving a ring opening mechanism. Degradation of dyes in coloured wastewater involves the use of whole cells rather than isolated enzymes. This approach is advantageous because of the high costs associated with enzyme purification. In addition, degradation is often associated with a number of enzymes working sequentially (Pearce et al., 2003).

#### 1.6.2 Colour removal using mixed bacterial cultures

Degradation of xenobiotics such as azo dyes is often carried out by mixed cultures (Knackmuss, 1996; Pearce *et al.*, 2003). Pearce *et al.* (2003) have reported that a higher degree of biodegradation and mineralization can be expected when co-metabolic activities within a microbial community complement each other. Knackmuss (1996) gives an example of this using the degradation of naphthalene sulphonates by a two-species culture. *Sphingomonas* strain BN6 was able to degrade naphthalene-2-sulphonate, a building block of azo dyes, into salicylate ion equivalents. The salicylate ion cannot be further degraded and is toxic to strain BN6. Therefore, naphthalene-2-sulphonate can only be degraded completely in the presence of a complementary organism that is capable of degrading the salicylate ion (Knackmuss, 1996). In addition, it can be difficult to isolate a single bacterial strain from dye-containing wastewater samples and, in some instances, long term adaptation procedures are necessary before the isolate is capable of using the azo dye as a respiratory substrate (Pearce *et al.*, 2003).

#### **1.6.3** Colour removal using single bacterial cultures

The advantages of mixed cultures are apparent as some microbial consortia can collectively carry out biodegradation tasks that no individual pure strain can undertake successfully (Nigam *et al.*, 1996). In addition, mixed culture studies may be more comparable to practical situations. However, mixed cultures only provide an average macroscopic view of what is happening in the system and results are not easily reproduced, making thorough, effective interpretation difficult. For these reasons, a substantial amount of research on the subject of colour removal has been employed using single bacterial cultures. The use of a pure culture system ensures that the data are reproducible and that the interpretation of experimental observations is easier (Chang and Lin, 2000).

## 1.7 NOVEL AND ESTABLISHED APPLICATIONS OF MICROBIAL POLYSACCHARIDES

Flocculation in microbial systems was first reported by Louis Pasteur 1876 (cited by Salehizadeh and Shojaosadati, 2001) for the yeast *Levure casseeuse*. Two years later, this phenomenon was observed in bacterial cultures (Salehizadeh and Shojaosadati, 2001). Butterfield (1935) isolated *Zoogloea*-forming bacteria from activated sludge in 1935. Later, bioflocculation was investigated extensively and a correlation was established between the accumulation of extracellular biopolymeric flocculants (EBFs) and cell aggregation (McKinney, 1956; Tenny and Stumm 1965). Many EBF-producing microorganisms including bacteria, fungi, yeast, and algae have since been isolated from soil and wastewater (Bar-or and Shilo, 1987; Bender *et al.*, 1989; Huang, 1990; Kakii *et al.*, 1990; Morgan *et al.*, 1990; Fumio, 1991; Hantula and Bamford, 1991a, b; Dube, 1992; Guirand, 1992; Sousa *et al.*, 1992; Kim, 1993; Seo, 1993; Kurane *et al.*, 1995; Yokoi *et al.*, 1995; Suh *et al.*, 1997; Salehizadeh *et al.*, 1998; Tong *et al.*, 1999; Misra, 2002).

Many microorganisms synthesize exopolysaccharides (EPS) or EBFs, which either remain attached to the cell surface or are found in the extracellular medium in the form of amorphous slime. In the natural environments in which the microorganisms are found, such polymers may either be associated with virulence, as in the case of plant or animal pathogens, with plant microbial interactions or even protect the microbial cell against desiccation or attack by bacteriophages and protozoa. In both natural and manmade environments, the EPS play a major structural role in 'biofilms', the normal habitat of many microbial communities, in which varying numbers of prokaryotic and eukaryotic microorganisms grow while attached to solid-liquid interfaces (Yokoi *et al.*, 1995; Salehizadeh *et al.*, 1998). Several such microbial polysaccharides are now widely accepted products of biotechnology, while others are in various stages of development. The uses of such polymers vary widely; some are employed because of their unique or superior physical properties relative to traditional plant polysaccharides. In this category are xanthans, from *Xanthomonas campestris* pv. *campestris* and gellan (Gelrite) from *Sphingomonas paucimobilis* strains (Fig. 1.6). These two polysaccharides have found various food and non-food applications. Xanthan is, in many ways, the 'benchmark' product, having received food approval many years ago and being a relatively inexpensive product because of the high conversion of 60-70% substrate to polymer (Sutherland, 1995).

Other microbial polysaccharides are more expensive to produce, some markedly so. The microbial products always have to compete against other natural or synthetic polymers, which may be inferior in their physical or ecological properties but are much cheaper to produce and market. Alteration of the chemical properties of the original exopolysaccharide may also greatly enhance their value and extend their range of applications, as exemplified by the dextran-derived Sephadex products (Sutherland, 1998).



# Fig. 1.6: (a) The structure of the exopolysaccharide from Xanthomonas campestris pv campestris (xanthan). (b) The structure of gellan from Sphingomonas paucimobilis (Sutherland, 1998).

Although a better understanding of the relationships that exist between structure and function have been ascertained, it is still difficult to predict which microbial polymers will be worth developing. Many initial reports in the literature have proved overoptimistic. On the other hand, two products have proved to be valuable, i.e. bacterial cellulose and hyaluronic acid, despite the fact that both were already available from nonbacterial sources. Another example of biological properties that have led to a polysaccharide application can be found in the range of fungal 1.4- $\beta$ -D-glucans, which have proved to be potent immune-system modulators, a property that is still poorly understood (Sutherland, 1990).

#### 1.7.1 β-D Glucan

#### **1.7.1.1 Bacterial cellulose**

Two groups of  $\beta$ -D-glucans are of biotechnological interest. Bacterial cellulose is perhaps the more surprising, given the universal availability and cheapness, of plant cellulose. In contrast to its role in the wall of plants, cellulose is produced as an exopolysaccharide by Acetobacter xylinum and others, mainly Gram-negative bacterial species. It is excreted into the medium where it rapidly aggregates as microfibrils, yielding a surface pellicle. Fermenter design and the degree of aeration are important factors in optimizing yield. Bacterial cellulose is essentially a high-value speciality chemical with specific applications and usage. Some are produced commercially as a source of highly pure polymer in the so-called cellulose-I form (60% Ia: 40% IB), free from lignin and other noncellulosic material. The fibrils form a unique ribbon 3-8 nm thick and approximately 100 nm wide, which differ in morphology from other native celluloses (Fig. 1.6). Bacterial cellulose also forms the basis for high-quality acousticdiaphragm membranes, in which the distribution of the fibrils containing a parallel orientation of the glucan chains yield fibres possessing high tensile strengths. Bacterial cellulose can also be used as a binder for ceramic powders and minerals and as a thickener for adhesives (Yoshinaga et al., 1997).

#### 1.7.1.2 (1 $\rightarrow$ 3) $\beta\text{-D-}$ glucans from bacteria and fungi

Several bacteria, including *Agrobacterium* and *Rhizobium* species, can each produce several EPS under appropriate physiological conditions. One of these is curdlan, a neutral gel forming  $1.3-\beta$  -D-glucan of relatively low molecular weight

(approximately 74 000 g/mol). Curdlan is formed in the stationary phase following depletion of nitrogen and is insoluble in cold water but can be dissolved in hot water or in dimethylsulphoxide. Curdlan forms a weak gel on heating above 55°C followed by cooling. Further heating to 80-100°C increases the gel strength and produces a firm, resilient gel, while autoclaving at 120°C converts the molecular structure to a triple helix. The gel formed by this high-temperature treatment no longer melts when heated and, unlike the similar alginate gels, is independent of the presence of divalent cations. The gels are intermediate in properties between the high elasticity of gelatine and the brittleness of agar. Those formed at higher temperature do not melt below 140°C. They are very susceptible to shrinkage and syneresis but resistant to degradation by most  $\beta$ -D-glucanases (Vossoughl and Buller, 1991).

#### 1.7.2 Pullulan

Aureobasidium pullulans synthesizes a  $\alpha$ -D-glucan in which maltotriose and a small number of maltotetraose units (1.4-  $\alpha$  -linked) are coupled through 1.6  $\alpha$  -bonds to form an essentially linear polymer. The molecular mass is between  $10^3$  and 3 x  $10^6$  and is dependent on the physiological conditions and the culture strain used (Wiley *et al.*, 1993). Pullulan is not degraded by most amylases, but specific pullulanase enzymes (isolated from sources including Enterobacter aerogenes) can be used to hydrolyze the polysaccharide to its component maltotriose (and maltotetraose) units and thus provide a useful means of preparing these oligosaccharides. Similar products are formed by several other fungal species including Tremella mesenterica and Cyttaria harioti. Pullulan is highly water soluble, forming viscous solutions that are stable in the presence of most cations, but does not form gels. Esterification can be used both to increase its range of physical properties and to reduce its susceptibility to enzyme attack. A proposed use of pullulan is to form oil-resistant, water-soluble films with low oxygen permeability. This novel packaging material assists in flavour retention and maintains the fresh appearance of foods, which can then be cooked directly. Solutions of the polymer can also be used to form odourless and tasteless coating directly onto food. These applications have apparently been made in Japan, but usage of the polymer in other countries appears to be limited (Nguyen *et al.*, 1988).

#### **1.7.3 Gellan and related polysaccharides**

In its native form gellan carries O-acetyl and glyceryl substituents on a linear polymer of 500 kDa that is composed of tetrasaccharide repeat units (Fig. 1.6). The acyl groups inhibit crystallization of localized regions of the gellan chains and weak elastic thermoreversible gels are formed. Deacylation causes extensive intermolecular association, and strong, brittle gels form with various cations. Control of the degree of acylation of the polymer yields a range of gel textures with properties similar in some respects to agar, alginate or carrageenan gels. Gellan forms thermoreversible gels and concentrations as low as 0.75% provides high gel strength. Marketed as Kelcogelm or Gelrite, gellan has approval in the USA and the EU for food use as a gelling, stabilizing, and suspending agent for a wide range of foods, either on its own or in combination with other hydrocolloids. The gels give good flavour release and are stable over the wide pH range found in food products. As a replacement for agar, Gelrite can be incorporated into microbiological and cell-culture media. It may even lead to some growth enhancement when compared with agar-based bacterial culture media. The high clarity of the gels may have distinct advantages, as may the lower concentration required to provide gels of equivalent strength (Pollock, 1993).

#### 1.7.4 Xanthan

Xanthan, from *Xanthomonas campestris*, is a major commercial biopolymer. Production from several commercial sources probably exceeds 20 000 tonnes per annum. Alternate glucose residues of a cellulose backbone carry the side-chains composed of Dmannose and D-glucuronic acid (Fig. 1.6). Mutants, different *X. campestris* pathovars and different nutrient conditions yield a range of polysaccharides that conform to the same general structure but differ in the completeness of carbohydrate side chains and extent of acylation. Many of the rheological properties of xanthan derive from the double-helical ordered conformation adopted in solution. The trisaccharide side chains align with the cellulosic backbone, stabilizing the conformation by noncovalent interactions. Several strains of *A. xylinum* also yield xanthan-like polysaccharides (acetans). One product has a cellulosic main chain together with a pentasaccharide side chain on alternate main-chain sugars (Jansson *et al.*, 1993).

Solutions of xanthan are highly pseudoplastic, rapidly regain viscosity on removal of shear stress and show very good suspending properties; they show high viscosity at low shear rates. The polysaccharide is incorporated into foods to alter the rheological properties of the water present, and has found applications that take advantage of many of its physical properties (Table 1.2). In many foodstuffs, xanthan possesses further useful attributes, including rapid flavour release, good 'mouthfeel' and compatibility with other food ingredients such as proteins, lipids and polysaccharides [most foodstuff already contain polysaccharides such as starch or pectin in addition to proteins and lipids, and any added polymer such as xanthan should be compatible with them] (Jansson *et al.*, 1993).

#### **1.8 SCOPE OF THIS STUDY**

Various flocculants such as inorganic flocculants, organic high-polymer flocculants and naturally occurring flocculants have been used in wastewater treatment, dredging, and industrial downstream processes. Although organic high-polymer flocculants such as polyacrylamide are frequently used because they are inexpensive and highly effective, some of them are not easily degraded in nature and some of the monomers derived from synthetic polymers are harmful to the human body. In recent years, to solve these environmental problems, use of microbial flocculants has been anticipated due to their biodegradability and the harmlessness of their degradation intermediates to the environment (Yokoi *et al.*, 1995).

	Use	Polymer
<b>Biological properties:</b>	Antitumour agents	β-D-Glucans
	Eye and joint surgery	Hyaluronic acid
		(Streptococcus EPS)
	Heparin analogues	Escherichia coli K5 EPS
	Wound dressings	Bacterial cellulose
Chemical properties:	Enzyme substrates	<i>Escherichia coli</i> K4 and K5 EPS
	Oligosaccharide preparation	Curdlan, pullulan, scleroglucan
Physical properties:	Foods thixotropic paints	Xanthan
Emulsions stabilization	Acoustic membranes	Bacterial cellulose
Fibre strength	Food coatings	Pullulan
Film formation	Water clarification, ore	Various
Flocculant	extraction	
	Beer, fire-fighting fluids	Xanthan
Foam stabilization	Cell and enzyme technology	Gellan
Gelling agents	Foods	Curdlan, gellan
	Oil recovery (blockage of permeable zones)	Curdlan, xanthan
Hydrating agent	Cosmetics pharmaceuticals	Hyaluronic acid
Inhibitor of crystal formation	Frozen foods, pastilles and	Xanthan
, , , , , , , , , , , , , , , , , , ,	sugar syrups	
Shear thinning and viscosity control	Oil-drilling 'muds'	Xanthan
Suspending agent	Food	Xanthan
superioning agent	Paper coatings	Various
	Agrochemical pesticides and	Xanthan
	sprays	
Viscosity control	Jet printing	Xanthan
-		

**Table 1.2:** Established applications of microbial exopolysaccharides (Sutherland, 1998)

Colour pollution in aquatic environments is an escalating problem, despite the fact that there has been substantial research into the modification of the dyeing process to improve the level of affinity/fixation of the dyestuffs onto the substrate. The recalcitrant nature of modern synthetic dyes has led to the imposition of strict environmental regulations. The need for a cost-effective process to remove colour from wastewater produced by the textile industries has been recognised and several strategies have been investigated (Willmott *et al.*, 1998).

Chlorine is widely used in the treatment of water for both industrial and domestic purposes. Chlorination of water results in formation of an array of disinfection by-products (DBPs). Trihalomethanes (THMs) are the most common volatile DBPs and haloacetic acids (HAAs) are the major non-volatile DBPs. Other DBPs, such as, haloacetonitriles (HANs), chloropicrine and chlorinated furanones, are usually present at lower concentrations. Health effects of exposures to DBPs include various cancers and reproductive health effects, including spontaneous abortions, stillbirths, congenital malformations and retarded fetal development (Egorov *et al.*, 2003). Therefore, the development of safe and biodegradable flocculant agents that will minimize the environmental and health risk is of paramount importance in various industries. Hence, the current study will focus on investigating the role of bacterial bioflocculants in the reduction and removal of microbial load and textile industrial effluents.

#### **1.8.1** Hypotheses to be tested

It is hypothesized that bacterial bioflocculants can significantly reduce the microbial load in river water as well as remove a variety of dyes and chemicals from textile industrial effluents.

#### **1.8.2 Objectives**

- a. To isolate and characterize the properties of the bioflocculants from bacteria.
- b. To evaluate the efficacy of the bacterial bioflocculant on decreasing the microbial load of river water and compare the findings to alum.
- c. To evaluate the ability of the bacterial bioflocculants to remove dyes and chemicals from the industrial effluents.

#### 1.8.3 Key questions

a. Do all bacterial strains found in wastewater produce extracellular polysaccharides?b. What is the chemical composition and properties of these bacterial bioflocculants?

- c. What are the factors that influence bioflocculation?
- d. Can these bioflocculants be used as an alternative to alum?
- e. Can these bacterial bioflocculants remove dyes from textile industrial effluents?

#### **CHAPTER TWO**

## PRODUCTION AND CHARACTERIZATION OF BACTERIAL BIOFLOCCULANTS

#### **2.1 INTRODUCTION**

Microbial extracellular polysaccharides (EPS) or extracellular biopolymeric flocculants (EBFs) are either associated with, and often covalently bound to, the cell surface in the form of capsules, or secreted into the environment in the form of slime. They are referred to as capsular (CPS) or slime (EPS) exopolysaccharides, respectively. Cell wall polysaccharides (WPS) are another type that, in contrast to EPS, are not released into the medium and are associated with the cell envelope, and may again be either covalently bound to the peptidoglycan layer or loosely associated with it. The lack of economical production limits their use and consequently they represent a small fraction of today's biopolymer market. Efficient production and reduction in recovery costs requires knowledge of biosynthesis and adoption of appropriate bioprocess technologies (De Vuyst *et al.*, 2001).

Understanding and controlling the important environmental variables affecting polymer synthesis can be advantageous in the design of an economic process. The basic carbohydrate structure of most exopolysaccharides does not change with growth conditions, but the content of groups attached to the basic carbohydrate structure, can vary widely and may have a dramatic effect on the properties of the polymer and hence their effectiveness in various applications (Lopez *et al.*, 2003). For the production of these biopolymer flocculants, sugars such as glucose, fructose or sucrose (Takagi and Kodowaki, 1985; Kurane *et al.*, 1986b; Kurane and Nohata, 1991; Toeda and Kurane, 1991), casein, L-glutamate or citrate are usually required as the main substrate(s).

Polysaccharides, which constitute the outermost layer of cells, are thought to mediate interaction between cells or the adherence of cells to surfaces. Some polysaccharides are liberated outside of the cell, and some are bound to the cell envelope, but under certain physiological conditions, extracellular polysaccharide molecules may remain bound and associated with the cell surface without detectable membrane anchoring. The function of the extracellular polysaccharide in flocculation and adhesion is an important theme as is the function of envelope bound polysaccharides (Nakata and Kurane, 1999).

Bioflocculants are essentially polymers produced by microorganisms during growth, with their flocculating activities being dependent on the characteristics of the flocculants. Most bioflocculants are reported to comprise of polysaccharides and proteins. For example, *Bacillus subtillis* (Yokoi *et al.*, 1996a ), *Bacillus licheniformis* (Shih *et al.*, 2001), *Paecilomyces* sp. (Shubo *et al.*, 2005) and *Nocardia amarae* YK1 (Takeda *et al.*, 1992) produce proteinaceous bioflocculants. *Alcaligenes latus* KT201 (Toeda and Kurane, 1991) and *Enterobacter* sp. (Yokoi *et al.*, 1997) produce polysaccharide bioflocculants, while glycoprotein bioflocculants are produced by *Arcuadendron* sp. TS-4 (Lee *et al.*, 1995).

In proteinaceous bioflocculants, the amino and carboxyl groups are the effective groups for flocculation, and their molecular weights are usually low (Kurane *et al.*, 1994a). In contrast, polysaccharide bioflocculants have high molecular weights and many functional groups (Kurane *et al.*, 1991). The molecular weight of most bioflocculants reported in the literature is in the range of  $10^5$  to  $2.5 \times 10^6$  Da (Salehizadeh and Shojaosadati, 2001). The components and structures of bioflocculants are complex, with different organisms producing various bioflocculants with diverse properties. The bridging mechanism was found to play an important role in flocculating organic particles in wastewater and yeast cells using the bioflocculants produced by *Bacillus mucilaginosus* and *Aspergillus sojae* (Deng *et al.*, 2003). Charge neutralization occurs when the flocculant is oppositely charged compared to the particles. As most bioflocculants and particles are negatively charged, charge neutralization seldom occurs in the bioflocculation process. Compared with conventional chemical and synthetic flocculants, which are relatively well developed, and their flocculating mechanisms

(including bridging and charge neutralization) well understood, the flocculating mechanisms of bioflocculants still needs to be investigated (Zouboulis *et al.*, 2004).

Many microorganisms secrete EBFs in the culture broth. Bioflocculation resulting from synthesis and secretion of EBFs by microorganisms has been well known in activated sludge (Salehizadeh and Shojaosadati, 2001). Generally, soil and activated sludge samples are the best sources for isolating EBF-producing microorganisms. *Rhodococcus erythropolis* was isolated from activated sludge using phthalic acid assimilation as an indicator (Kurane and Matsuyama, 1994).

Many factors influence the production of EBFs and the bioflocculation process. These include genotypic, physiological and environmental aspects. The environmental aspects involve physical, chemical and biological factors. The carbon and nitrogen concentration (C/N ratio), culture pH, temperature, and agitation speed used in the fermentor need to be optimized for efficient production (Salehizadeh and Shojaosadati, 2001). This optimization is essential because productivity and distribution of EBFs depend on the culture conditions. The pH of the culture medium can influence the production of EBFs. For example, in one case, the localization of the flocculant on the cell's surface of Aspergillus sojae at pH 6 was greater than at pH 8. In the case of C. xerosis, the flocculant was produced at relatively low pH whereas the optimum pH for production of EBF by A. sojae was in the alkaline range. Temperature is another physical factor that affects the production of EBFs. The best production of EBFs by A. sojae was obtained within the temperature range of 30–34°C. The interaction between different microorganisms in a mixed culture is another biological parameter that can have a positive effect on aggregation of cells and the production of EBFs (Nakamura et al., 1976c). By adjusting the growth conditions, the adsorption of the flocculant F-1 on the cell's surface could be raised by 5% of the concentration in the filtrate (Nakamura et al., 1976c).

The importance of carbon and nitrogen sources and the C/N ratio has been emphasized for EBFs production (Nakamura *et al.*, 1976c; Kurane *et al.*, 1994a). The

addition of sugars to the medium reduced the pH of the culture broth and inhibited the accumulation of the flocculant. Ethanol is also a good carbon source for flocculant production on an industrial scale (Nakata and Kurane, 1999). The canning factories wastes and spillage from distilleries are alternative inexpensive carbon sources. Urea, ammonium sulphate, yeast extract, and casamino acids are good nitrogen sources for EBF production and growth of *R. erythropolis* (Tong *et al.*, 1999).

The application potential of EBF is determined by their physical and rheological properties. Factors influencing these properties are molecular mass, stiffness of the polymer, presence of side chains, and presence of nonsaccharide components, such as organic (e.g., acetyl, pyruvyl, or succinyl groups) or inorganic (e.g., sulphate or phosphate groups) substituents. Genetic engineering may be applied as a tool to direct the EPS synthesis and introduce desired properties by altering the composition or chain length. This requires a proper understanding of the genetics and biochemistry of EPS biosynthesis (Van-Kranenburg *et al.*, 1999).

Inorganic and organic synthetic polymer flocculants are frequently used in water and wastewater treatment because they are economical and highly effective. However, their use often gives rise to environmental and health problems in that some of them are not readily biodegradable and some of their degraded monomers, such as acrylamide, are neurotoxic and even strong human carcinogens. Residual alum concentration in treated water can also impose health problems apart from the production of high amount of sludge (Letterman and Driscoll, 1988). There is also a problem of reaction of alum with natural alkalinity present in water leading to a reduction of pH and a low efficiency in coagulation of cold waters (Degremont, 1989 – cited by Ndabigengesere and Narasiah, 1998). Thus, the development of safe biodegradable flocculants that will minimize environmental and health risks is urgently required (Shih *et al.*, 2001). Hence, the objective of this chapter were to isolate and identify bacteria capable of bioflocculant production; to quantify the amount of flocculant produced by the bacteria; and to characterize the properties of the bioflocculants produced by these bacteria isolated from the wastewater treatment plant.

#### **2.2 MATERIALS AND METHODS**

#### 2.2.1 Isolation and identification of bioflocculant producing bacteria

## 2.2.1.1 Isolation and biochemical characterization of the bacterial isolates

Microorganisms were isolated from the effluent samples collected from various points at the Northern Wastewater Treatment Plant, Durban, including; activated sludge (aerobic), activated sludge (anaerobic), digested sludge, and effluent clarifier. Pure cultures were obtained by using four way streaks on nutrient agar and dilution methods (Prescott *et al.*, 1996). Bacterial isolates were maintained on YMPG agar. Bacterial strains were identified and characterized using standard biochemical tests with reference to Bergey's Manual of Systematic Bacteriology (Peter *et al.*, 1986; Garrity, 2005) and the API Kit (Biomerieux).

## 2.2.1.2 DNA isolation and 16S rDNA gene amplification and sequencing

Total genomic DNA was isolated from LB-grown cells using QIAamp DNA Miniprep Kit (Qiagen) following manufacture's instructions, and used directly as the template for PCR amplification. The 16S rDNA of the bacterial isolates were amplified with the oligonucleotide primers: 63f (5'–CAGGCCTAACACATGCAAGTC-3') and 1387r (5'–GGGCGG(A/T)GTGTACAAGGC-3') [numbering based on the *E. coli* 16S rRNA gene (Brosius *et al.*, 1978)] described by Marchesi *et al.* (1998). The amplification reaction mixture contained standard *Taq* amplification buffer, 100  $\mu$ M (each) deoxyribonucleotide triphosphate, 0.5  $\mu$ M (each) primer, 100 ng of genomic DNA and 2.5 U of *Taq* DNA polymerase in a 50  $\mu$ l reaction volume. The cycling parameters were 94°C for 2 min followed by 30 cycles of denaturation at 92°C for 30 s, annealing at 55°C for 30 s, and elongation at 75°C for 45 s, with a final elongation step of 75°C for 5 min. The PCR products obtained above were visualized in 1% agarose by horizontal

electrophoresis at 80 V for 2 hrs. The agarose gels were stained in 0.5  $\mu$ g/ml ethidium bromide solution for 15 min and fluorescent bands visualized under a UV transilluminator (UVP Inc.). The PCR products were sent to Inqaba Biotech for sequencing. Similarity searches in DNA data bases were performed using BLAST analysis (Pubmed).

#### 2.2.2 Measurement of bioflocculant production

Microorganisms were cultivated in 250 ml Erlenmeyer flasks containing 30 ml YMPG medium for 20 hrs at 28°C on a rotary shaker at 220 rpm. A 0.7 ml aliquot was added into a 500 ml Erlenmeyer flask containing 70 ml of production medium (0.5% yeast extract, 0.5% polypeptone, 2% ethanol, 1% glycerol, 0.05% K<sub>2</sub>HPO<sub>4</sub>, 0.05% MgSO<sub>4</sub>.7H<sub>2</sub>O, 0.2% NaCl, and 0.2% CaCO<sub>3</sub>). The flasks were incubated for 3 days at 28°C before determining the amount of bioflocculant produced by the ethanol precipitation method (Kurane *et al.*, 1994a).

#### **2.2.3 Bioflocculant purification**

In order to purify the biopolymer flocculant, the viscous culture broth was diluted with an equal volume of distilled water and centrifuged at  $2800 \times g$  for 30 min to remove cell pellets. Two volumes of cold ethanol (4°C) was added to the supernatant and the crude bioflocculant precipitate was dried in a dessicator overnight. Thereafter, the crude bioflocculant was dissolved in distilled water and 2% (w/v) cetylpyridinium chloride solution (CPC) was added until no more insoluble CPC-bioflocculants complex were formed. After several hours, the precipitate collected by centrifugal separation of the CPC-bioflocculants complex was dissolved in saline solution [0.85% (w/v) NaCl], washed with cold ethanol three times and lyophilized (Salehizadeh and Shojaosadati, 2002).

#### 2.2.4 Analysis of the bioflocculants

### 2.2.4.1 Determination of carbohydrate, protein, uronic acid, and amino sugar content of the purified bioflocculants

The total sugar content of the purified bioflocculants was determined by the phenol-sulphuric acid method (Chaplin, 1994). The Folin-Lowry method was used to measure the total protein content of the bioflocculants (Plummer, 1978). Aromatic amino acids and  $\alpha$ -amino acids were determined by xanthoprotein and ninhydrin reactions (Plummer, 1978). Amino sugars were determined by the Elson-Morgan method (Chaplin, 1994). The carbazol method was used to measure uronic acid (Chaplin, 1994). Full description of the methodology and data sets obtained are given in Appendix B.

#### **2.3 RESULTS**

#### **2.3.1 Bacterial isolation and identification**

Of the thirty bioflocculant producing bacteria initially isolated from the wastewater treatment plant, only six were selected on the basis of the amount of bioflocculant produced (the highest, intermediate and the lowest producers) were used in subsequent experiments. The biochemical tests and the API Kit (Appendix A Table 6.1) were used to tentatively identify the organisms up to the genus level, and then confirmed by the analysis of their 16S rRNA gene sequences. Figure 2.1 shows the amplicons of 16S rDNA genes of the bacterial isolates. The analysis of the gene sequences (shown in Appendix A) identified the bacterial isolates as indicated in Table 2.1

Isolate code	Identification
A22	Staphylococcus aureus
A14	Pseudomonas plecoglossicida
A17	Pseudomonas pseudoalcaligenes
D1	Exiguobacterium acetylicum
E1	Bacillus subtilis
R2	Klebsiella terrigena

**Table 2.1:** Identity of bacterial isolates based on 16S rDNA sequencing data (Appendix A)



**Fig. 2.1:** PCR products after amplification of the 16S rDNA sequences of the bacterial isolates. Lanes 1–6: E1; A17; D1; A22; R2; A14; and lane 7: Molecular weight marker VI (Roche Biochemicals).

#### 2.3.2 Measurement of bioflocculant production

Temperature was maintained at  $28^{\circ}$ C for the production of bacterial polysaccharides (Fig. 2.2). The bacterial isolates produced bioflocculants in varying amounts, ranging from 6.33 to 27.66 g/l, with isolate R2 being the highest producer and isolate E1 the lowest producer.



Fig. 2.2: Bioflocculant produced by the bacterial isolates

# 2.3.3 Purification and analysis of the composition of the bacterial bioflocculants

The standard curves for carbohydrate (CHO), protein, uronic acid, and amino sugars (hexosamine), from which the values below were derived, are shown in Appendix B.

#### 2.3.3.1 Carbohydrate and protein

Bioflocculants from all the bacterial isolates were composed of both CHO and proteins in varying quantities (Fig. 2.3). The flocculants of isolates R2, A22 and A14 had more carbohydrate than protein. Isolates A17 and D1 had approximately similar concentration of CHO and protein in their bioflocculants. Isolate E1 had 45% carbohydrates and 55% proteins.



Fig. 2.3: Carbohydrate and protein content of the bacterial bioflocculants.

#### 2.3.3.2 Uronic acid and Amino sugars

The uronic acid content of the bacterial bioflocculants is shown in Fig. 2.4. All the bacterial bioflocculants were composed of uronic acid in varying quantities. Isolate R2 (45.5 mM) had more uronic acid compared to the other isolates. Isolates E1, A17, A14, A22, and D1 had similar concentration of uronic acid (25.5 mM). The amino sugar content of the bioflocculants is depicted in Fig. 2.5. Isolate A17 contained the highest concentrations of hexosamine (amino sugars) followed by isolate E1. Isolate R2 and A14

had the same concentration of amino sugars and only isolate D1 lacked the presence of hexosamine.



Fig. 2.4: Uronic acid content of the bacterial bioflocculants.



Fig. 2.5: Amino sugar content of the bacterial bioflocculants.

#### 2.4 DISCUSSION

In this study the YMPG medium which contained yeast extract, polypeptone, glycerol, and ethanol were used as substrates for the production of bacterial bioflocculants. Yeast extract was a very good organic nitrogen source for the production of bioflocculants (Fig. 2.2). Nataka and Kurane (1999) indicated that polypeptone and yeast extract were good nitrogen sources for the production of EPS by *Klebsiella pneumoniae* H12. Kurane *et al.* (1994a) determined ethanol to be the cheapest substrate for bioflocculant production. According to Nakamura *et al.* (1976c) and Kurane *et al.* (1994a) the production of EPS by *A. sojae* was enhanced when casein, yeast extract, polypeptone, and some amino acids (e.g. glutamic acid and alanine) were added to the medium.

The six bacterial isolates investigated in this study produced extracellular polysaccharide/bioflocculants in varying quantities (Fig. 2.2). Isolate R2 (K. terrigena) produced 27.66 g/l while the production by D1 (E. acetylicum) was 10.167 g/l. The lowest producer was isolate E1 (B. subtilis) which produced only 6.33 g/l. Salehizadeh and Shojaosadati (2002) reported that 1.36 g/l of crude bioflocculant was produced by Bacillus firmus. This amount is much lower than that produced by B. subtilis in this study. In a similar study done by Shih et al. (2001), 14 g/l of crude bioflocculant was produced by *Bacillus licheniformis* CCRC 12826 which was higher than that produced by isolate B. subtilis. Only 3 g of bacterial bioflocculant was produced by K. pneumoniae H12 in a study done by Nakata and Kurane (1999). The amount produced by this bacterium is lower than that produced by isolate R2 (K. terrigena). This may be due to the fact that different species of *Klebsiella* were used. Zouboulis *et al.* (2004) reported on the production of bioflocculant by the bacterium *Rhizomonas* sp.; and have shown that only 2 g of bioflocculant were produced. Amongst the five genera used in the present study (Table 2.1) only four have been extensively studied previously, namely, Bacillus sp. (Kim, 1993; Yokoi et al., 1995, 1996a; Suh et al., 1997; Salehizadeh et al., 2000); Pseudomonas sp. (Tago and Aida 1977); Klebsiella sp. (Dermlim et al., 1999) and *Staphylococcus* sp. (Nakamura *et al.*, 1976b). Currently there are no reports regarding the production of bioflocculants by *E. acetylicum*.

According to the findings of the present study, bacterial bioflocculants were composed of carbohydrates, proteins, uronic acid, and hexosamine. Isolate R2 and A22 had 99% carbohydrate and 1% protein while isolate D1 and A17 had 40% carbohydrate and 60% protein in their bioflocculants (Fig. 2.3). In a study done by Fujita *et al.* (2000) on the characterization of a bioflocculant produced by *Citrobacter* TKF04 from acetic and propionic acids, the total sugar content of the bioflocculant was 10% and no proteins were detected. A similar study was carried out by Salehizadeh and Shojaosadati (2002) on the isolation and characterization of bioflocculant produced by *B. firmus*. The bioflocculant was composed of 87% total sugar, 38% uronic acid and no proteins were detected (Fig. 2.4). Shubo *et al.* (2005) indicated that bioflocculant produced by *Aspergillus parasiticus* had 76.3% sugar content and a 21.6% protein. In general, bacterial bioflocculants contain proteins in minute quantities. Higgins (1995) reported that extracellular proteins in the floc are associated with improvements in settling and dewatering properties.

To date, many studies on the microbial production of flocculating substances have been reported. Microbiologically-produced bioflocculants are generally high molecularweight polymers, and have been identified or presumed to be proteins (Takeda *et al.*, 1991; Takeda *et al.*, 1992), glycoproteins (Kurane *et al.*, 1986b), polysaccharides (Kurane and Nohata, 1991; Toeda and Kurane, 1991), glycolipids (Kurane *et al.*, 1994a), cellulose (Napoli *et al.*, 1975), DNA (Sakka and Takahashi, 1981) or complex heteropolymers (Nakamura *et al.*, 1976a). The primary structure of proteins and polysaccharides describes the arrangement of the different building blocks, amino acids and monosaccharides, respectively, along the polymer chain. The possible structural variability due to available units and connecting patterns is estimated to be about three orders of magnitude larger for polysaccharides than for proteins (Sletmoen *et al.*, 2003).

In this study, all the bacterial bioflocculants were composed of uronic acid in varying quantities. Isolate R2 had the highest concentration of uronic acid [45.3 mM] (Fig. 2.4) compared to the other bacterial isolates. Nakata and Kurane (1999) showed that the bioflocculant produced by K. pneumoniae was composed of only 10% uronic acid. This amount was very low when compared to that produced by isolate R2 (K. terrigena) in the current study. Salehizadeh et al. (2000) analyzed the composition of the bioflocculant produced by *Bacillus* sp As 101, and indicated that it was composed of only 11.4% uronic acid, this amount was lower than that produce by *B. subtilis* (25%) in this study. Uronic acids appear to be the most universal and specific indicators of extracellular polymers that are used by the invertebrates in feeding nets, faecal pelletization, or feeding tube structures in the benthic environment and of the polymers that protect and regulate the ionic traffic at the surface of the bacteria. These polymers are important in the stabilization of marine sediments. The uronic acid content of the extracellular polymers can be measured by the formation of the ester and the reduction of the carboxylic acid moiety to an alcohol. This process eliminates the problems of resistance to hydrolysis and of quantitative recovery in separation from the neutral carbohydrates (Fazio et al., 1982). They are also found in the polysaccharide polymers of higher plant cell walls, in gram-positive microbes under conditions of phosphate limitation (Elwood and Tempest, 1972), and in some gram-negative microbial lipopolysaccharides. Polymers containing uronic acid are resistant to quantitative hydrolysis, and the uronic acid, once released, form lactones irreproducibly and are difficult to separate from the neutral sugars. Uronic acids are often estimated by their acid catalyzed decarboxylation under controlled conditions (Kiss, 1974). The known microbial exopolysaccharides contain D-glucuronic acid, D-galacturonic acid, Dmannuronic acid, and L-gulonic acid (Dudman, 1977).

Amino sugars are important structural components of bacterial cell walls, and neutral carbohydrates make up a basic unit of plant cells (Cheng and Kaplan, 2003). Five of the six bacterial bioflocculants used in this study were composed of hexosamine or amino sugars in very low concentrations except for isolate D1, which is *E. acetylicum*. The small yield might be due to the unstability of the amino sugar or the presence of

some reducing substance other than amino sugar in the bioflocculant. This finding is consistent with that done by Nakata and Kurane (1999); who showed that no hexosamine was detected in the bioflocculant produced by *K. pneumoniae* H12. Generally, amino sugars are present in very small quantities in bacterial cell walls. Fujita *et al.* (2000) reported that bioflocculant produced by *Citrobacter* sp. TKF04 was composed of 29.4% of hexosamine. In this study, bacterial bioflocculants were produced and characterized. They were found to be composed of carbohydrate, protein, uronic acid, and hexosamine in varying quantities.

#### **CHAPTER THREE**

#### **COAGULATION-FLOCCULATION BY MICROBIAL BIOFLOCCULANTS**

#### **3.1 INTRODUCTION**

Historically, the term "coagulation" and "flocculation" have been used indiscriminately to describe the process of removal of turbidity from water. There is however a clear distinction between the two terms. The term "coagulation" comes from the Latin *coagulare*, meaning to drive together (Faust and Aly, 1998; Nester et al., 2001). This process describes the effect produced by the addition of chemicals to a colloidal dispersion resulting in particle destabilization by a reduction of the forces tending to keep the particles apart. Colloidal particles have a net negative surface charge. The size of colloids (0.001 to 1  $\mu$ m) is such that the attractive forces between particles are considerably less than the repelling forces of the electrical charge. Under these stable conditions, particle growth does not occur, and Brownian motion keeps the particles in suspension. Operationally, coagulation is achieved by adding appropriate chemicals, which causes particles to stick together when contact is made. Rapid mixing is important at this stage to obtain uniform dispersion of the chemical and to increase the opportunity for particle-to-particle contact. The entire process occurs in a very short time, probably less than a second, and initially results in particles submicroscopic in size (Cohen et al., 1972; Prescott et al., 1996). The settling velocities of finely divided and colloidal particles under gravity alone are so small that ordinary sedimentation is not practical. It is therefore necessary to use procedures, which agglomerate the small particles into larger aggregates, which then have the settling velocities required for various applications. Formation of larger particles from smaller ones is also required for their removal by filtration (Nester et al., 2001).

The second stage of the formation of settleable particles from destabilized colloidal-sized particles is termed flocculation. This term also has its derivation from Latin, *flocculare*, meaning to form a floc, which visually resembles a tuft of wool or

highly fibrous porous structure. In contrast to coagulation, where the primary force is electrostatic, flocculation occurs by a chemical bridging of physical enmeshment mechanism. Flocculation is operationally obtained by gentle and prolonged mixing which converts the submicroscopic coagulated particles into discrete, visible, suspended particles. At this stage, the particles are large enough to settle rapidly under gravity and may be removed from suspension by filtration. The more usual practice has been to physically separate the unit processes into coagulation-flocculation, sedimentation, and filtration (Cohen *et al.*, 1972; Faust and Aly, 1998).

The chemical coagulation of turbid water or naturally coloured surface water involves the interaction of particulates and/or colloids with a destabilizing agent. The essential purpose of coagulation is to aggregate these particles into larger sizes that will settle quickly within an hour or two and/or will be filtered by sand or other media. This aggregation process is also called destabilization of colloidal systems. Colloids are characterized by their size and by the mechanism by which they are stabilized in water. Another characteristic of colloids is their affinity for the solvent in which stabilization occurs. This is a process of salvation. Lyophilic is the general term given to colloids "loving" the solvent. In water, this becomes hydrophilic, and such colloids are stabilized by the formation of adherent thick layers of oriented water molecules around the particle. Lyophobic is the general term given to colloids are stabilized by an electrostatic repulsion between the particles arising from ions that are attracted to the surface from bulk solution or dissolved out of the solid's surface (Bitton, 1994).

Recently there has been a large increase in the utilization of synthetic organic polymers in the treatment of water and wastewaters as coagulants or aids to coagulation. Optimum treatment is frequently obtained with anionic and polymeric destabilization of negatively charged particles. It is obvious that an electrostatic mechanism is not the only means of destabilization. A bridging theory was proposed by La-Mer and Healy (1963) to account for the destabilization of colloidal systems by high molecular weight organic polymers. Adsorption of the polymer on specific sites of the colloid plays an important role in the bridging theory. This theory resembles the binder theory proposed for alum precipitation and coagulation. In order for a polymer molecule to be an effective destabilizer, it must contain constituents that can interact with sites on the colloidal particle (Singh *et al.*, 2000).

A number of methods and/or chemicals are used either as aids to coagulation or as the primary coagulant. Polyelectrolytes are mostly synthetic organic compounds of highmolecular weight. They are polymers composed of a chain of monomers. In turn, these monomers are varied frequently within a given polymer, which results in compounds with different molecular weights. These polymers are linear or branched. If the monomer contains an ionisable group, such as carboxyl, amino, or sulfonic, then the polymer is called a polyelectrolyte. There are cationic, anionic, or ampholytic (has both positive and negative) groups which, of course, depends on the nature of the functional groups within the monomer. Non-ionic polymers are those compounds without any ionisable groups. These polymers and polyelectrolyte are able to flocculate colloidal particles due to adsorption. In most cases, the bonding mechanism between a functional group on the polymer and a site on a colloid's surface is quite specific. In addition, molecular weight and degree of branching of the polymer play a mechanistic role in their ability to flocculate (Bitton, 1994; Faust and Aly, 1998).

The rate of flocculation is determined by the collision frequency induced by the relative motion. Because Brownian movement causes this, it is called perikinetic flocculation. That which is caused by velocity gradients is called orthokinetic flocculation. If there is no surface, repulsion between the particles, then every collision leads to aggregation and the process is called rapid flocculation. If a significant repulsion exists, then only a fraction of the collisions results in aggregation. This is called slow flocculation. The floc blanket clarifier provides a special case of orthokinetic flocculation. In addition to the fluidized bed giving rise to velocity gradients, the fluidized particles are participating in the process of agglomeration. If particles are settling at different velocities, then the faster settling particles may collide with slower settling particles, leading to aggregation. The aggregates will then settle faster due to

their increased mass, and possibly experience further collisions and aggregations (Yan *et al.*, 2004).

Compared with present understanding of floc formation through perikinetic and orthokinetic mechanisms, understanding of floc breakup in agitated systems is qualitative and speculative, despite research efforts (Faust and Aly, 1998; Nester *et al.*, 2001). Proper characterization of floc disruption is an important problem since it is well documented that break-up can appreciably affect the performance of solid-liquid separation processes downstream. Floc break-up in dilute agitated suspensions is governed by the interaction of individual flocs with fluid forces. Depending on its constituent materials, a floc can be viewed roughly as an aggregate of primary micro particles that are bound together to form a matrix possessing a substantial fraction of fluid within its framework. The size and compactness of the matrix, size, and shape of the microparticles contribute to floc structure and the ability to withstand disruption by fluid forces. This also includes the number and strength of bonds that the microparticle contacts (DiTerlizzi and Fall, 1994; Singh *et al.*, 2000).

The biopolymers in activated sludge flocs appear to affect the physico-chemical properties associated with the flocs such as floc density, floc particle size, specific surface area, charge density, bound water content, and hydrophobicity. These physicochemical floc characteristics express themselves among other things as activated sludge settling and dewatering properties. Research indicates that an increase in floc density and floc particle size increases settling velocity. The theoretical basis for improved settling through an increase in floc density and floc particle size is presented in Stokes Law. An increase in floc density results in improved dewatering properties through a decrease in bound water associated with the flocs (Eriksson and Alm, 1991). Calcium may create denser sludge flocs through a decrease in bound water associated with the floc is also an indicator of the maximum dryness that can be achieved in the sludge cake by mechanical means (Foster, 1983).

A variety of flocculants, including inorganic flocculants (polyaluminium chloride and aluminium sulphate), organic flocculants (polyacrylamide, polyethylene imine), and natural flocculants or bioflocculants (gelatin, chitosan guar gum and microbial flocculants) have been widely used for tap water production, wastewater treatment, dredging, downstream processing, fermentation, and in the food industry (Zouboulis *et al.*, 2004, Crini, 2006).

Kaolin's are white raw materials, their essential constituent being fine grained white clay which are amenable for beneficiation that make them ideal for an assortment of industrial applications. Kaolin deposits can be classified into two types, primary (residual) and secondary (sedimentary) (Prasad et al., 1991). Kaolin or china clay is a versatile industrial mineral and one of the highest value additions is achieved when it is beneficiated to pigment grade suitable for paper and paint industries. In kaolin, minor quantities of transition elements such as iron, titanium, and manganese are generally present as ancillary minerals, which adversely affect its optical properties (Chandrasekhar and Ramaswamy, 2006). The valence state of the ion and atomic position in the structure depend on the conditions of formation of the mineral (Muller et al., 1995). Extensive research has been carried out on the nature of iron impurities in kaolin, which leads to the conclusion that iron is present as a part of the kaolinite or ancillary mineral structure i.e., "structural iron" or as separate iron minerals such as oxides, hydroxides, oxy-hydroxides, sulphides and carbonates i.e., free iron. Clay particles are strongly anisotropic and exhibit faces and edges, which are very different in surface area and in chemical behaviour. The explanation for dispersion of clay minerals suspensions in water is usually done by considering that the surfaces are electrically charged. Kaolin clay has been widely used as a test sample or material for flocculation because of its characteristics (Konan et al., 2006). Therefore, the objective of this chapter was to evaluate the ability of the bacterial bioflocculants to flocculate kaolin clay and determine the effects of temperature, pH and metal salts on the flocculating activities.
#### **3.2 MATERIALS AND METHODS**

# **3.2.1** Determination of the growth patterns of bacterial isolates and measurement of flocculating activity

The flocculating activity of the bacterial isolates was evaluated by measurement of the turbidity of a kaolin suspension. In all the experiments, 9 ml of kaolin suspension (5.5 g/l) was mixed with 1 ml of 0.5 M CaCl<sub>2</sub> in 9 mM glycine-NaOH buffer (pH 7.0) in a test tube. The six bacterial cultures used to produce bioflocculants in this study were grown in 250 ml of YMPG medium for 84 hrs, at 28°C with shaking (150 rpm). Culture broth (50  $\mu$ l) was then added to the kaolin suspension every 12 hrs for 84 hrs. The test tube was mixed vigorously for 20 s and left to stand, without shaking, for 5 min. The turbidity of the sample supernatant (A) and a control experiment without the culture broth (B) were measured at 550 nm with spectrophotometer (LKB ultrospec II) (Salehizadeh and Shojaosadati, 2002). The flocculating activity was expressed as the concentration of the flocculant in parts per million (ppm) when the OD<sub>550</sub> was (1/10) x OD<sub>550</sub> of the control (Nakata and Kurane, 1999). The percentage removal of kaolin suspension was calculated by the equations of Kurane and Matsuyama (1994) and Kurane *et al.* (1994b) as follows:

Removal (%) = 
$$\frac{B-A}{B} \times 100$$

In addition, flocculating activity was also determined using various concentrations of purified bioflocculants instead of the culture broth.

#### 3.2.2 Flocculation of microbial cultures

The following microbial cultures, obtained from the stock culture collection of the Discipline of Microbiology (Westville campus) UKZN, South Africa were used: *Pseudomonas aeruginosa, Proteus mirabilis, Serratia marcescens, Alcaligenes faecalis,* 

Citrobacter freundii, Bacillus coagulans, Bacillus cereus, Clostridium hystolyticum, Streptococcus pyogenes, and Saccharomyces cerevisiae. The bacterial isolates used for the production of flocculants were also used to measure the flocculation of these cultures. Microbial cultures were cultivated in 30 ml of YMPG medium in 250 ml Erlenmeyer flasks for 20 hrs at 28°C with shaking (220 rpm). A 10 ml aliquot of the culture was washed with and suspended in an equal volume of deionised water in a test tube. Onehundred microlitres of flocculant solution (1 g/l) and then 100  $\mu$ l of CaCl<sub>2</sub> solution (3 g/l) were added to the test tube. The mixture was vortexed for 5 s and left to stand for 5 min and the OD measured with a spectrophotometer at 550 nm. Flocculating activity was compared to the control without the flocculant or CaCl<sub>2</sub> (Nakata and Kurane, 1999). The flocculating activity was determined as described in Section 3.2.1.

#### **3.2.3 Flocculation inhibition assay**

One-hundred microlitres of different concentrations of potential inhibitors  $(K_2HPO_4, NaNO_3, CH_2COONa, Na_2CO_3, and D-GLU)$ , 100 µl of bioflocculant solution (1 g/l), and 100 µl of CaCl\_2.2H\_2O (30 g/l) were added to 10 ml of kaolin suspension (5 g/l) in a test tube. The mixture was vortexed for 5 s and left to stand for 5 min and the OD measured with a spectrophotometer at 550 nm. Flocculation activity was compared to the control without the salts. The flocculating activity was expressed as described in Section 3.2.1.

### 3.2.4 Flocculating activities of bacterial bioflocculants and alum

In order to compare the flocculating activity of the bioflocculants with alum the former was substituted with 10 ppm (0.01 g) alum. Different concentrations (10–50 ppm) of bacterial bioflocculants were added to 500 ml of raw water in 1-litre Erlenmeyer flasks and left to stand at room temperature for 1 hr. The control was performed without the addition of bacterial bioflocculants and the OD was determined spectrophotometerically at 550 nm for all the samples. The flocculating activity was calculated as described in Section 3.2.1.

# **3.2.5** Determination of the effect of pH, temperature, and cationic/metal salts on the flocculating activity of bioflocculants

Flocculating activity was determined as described in Section 3.2.1. The pH of the kaolin suspension was adjusted using 2 N HCl or NaOH to between 6 and 10 in order to examine the effect of pH on flocculating activity. To determine the effect of temperature on flocculating activity, the flocculation experiment was conducted at 28°C and 37°C. Cationic compounds (MgSO<sub>4</sub>.7H<sub>2</sub>O, MnCl<sub>2</sub>.7H<sub>2</sub>O and CTAB) were added to the mixture instead of CaCl<sub>2</sub>.2H<sub>2</sub>O in order to determine their effect on flocculating activity (Nakata and Kurane, 1999).

#### **3.3 RESULTS**

# **3.3.1** The growth patterns of the bacterial isolates in YMPG media and flocculating activities

Figure 3.1 shows the growth patterns of the bacterial isolates in the YMPG medium. Maximum cell growth was observed for isolate A22 after 24 hrs, after which the growth decreased and then remained constant. The other five isolates displayed similar growth patterns. The flocculating activity of the culture broth increased during the logarithmic phase of growth in YMPG medium and decreased during the late log phase. The best flocculating activity was observed in isolate A17 after 24 hrs (Fig. 3.2).

Generally, the flocculating activity of the bioflocculants increased to a maximum before decreasing to a constant level. However, there was no decrease in activity after 84 hrs for isolate E1. The effect of time on the removal of kaolin suspension by crude bioflocculants is depicted in Fig. 3.3. Isolate A17 removed more kaolin (65%) after 24 hrs compared to the other isolates. The pattern of removal first increased and reached a maximum after which it decreased and remained constant except for isolate E1 where the removal of kaolin did not decrease after 84 hrs.

The flocculating activity of the bacterial bioflocculants is shown in Fig. 3.4. Lower concentrations of bioflocculants were required for flocculation using isolates A22, A17, and A14. The flocculating activity of isolates D1, R2, and E1 required more bioflocculants for flocculation. Therefore, low concentrations of bioflocculants led to better flocculation as compared to higher concentrations.



Fig. 3.1: Growth patterns of the bacterial isolates in YMPG medium.



**Fig. 3.2:** Effect of time on the flocculating activity of crude bioflocculants using a kaolin suspension.



Fig. 3.3: Effect of time on the removal of a kaolin suspension by crude bioflocculants.



Fig. 3.4: Flocculating activity of bioflocculants using a kaolin suspension.

### 3.3.2 Flocculation of microbial cultures

The flocculating activity of the bacteria by their bioflocculants is depicted in Fig. 3.5. The best flocculating activity was shown by isolate R2 while that for isolate E1 was the lowest. Figure 3.6 shows the flocculation of Gram-positive and Gram-negative bacteria by the bioflocculants. All the bacterial bioflocculants were very effective in flocculating *C. hystolyticum, S. cerevisiae,* and *A. faecalis.* Other microbial cultures flocculated but to a lesser extent.



Fig. 3.5: Flocculating activity of bacteria by their bioflocculants.

### **3.3.3 Inhibition of flocculating activity**

The inhibition of flocculating activity was tested by adding different concentrations of salts to the kaolin suspension, which was used as the test material (Table 3.1). High concentrations (10 000 ppm) of  $K_2$ HPO<sub>4</sub>, CH<sub>2</sub>COONa, and Na<sub>2</sub>CO<sub>3</sub> inhibited flocculation. D-GLU and NaNO<sub>3</sub> improved the flocculating activity at both high (10 000 ppm) and low (10 ppm) concentrations. These observations were similar for all the bacterial isolates used in this study.



Fig. 3.6: Flocculation of microbial cultures using bacterial bioflocculants.

# 3.3.4 Comparison of flocculating activities between bacterial bioflocculants and alum

The effect of bioflocculant concentration on the flocculating activity with respect to 10 ppm alum using pond water is depicted in Fig. 3.7. In this case, the flocculating activity of alum was taken as 100% at 10 ppm. The activity of the bacterial bioflocculants was 70-75% at 20-30 ppm when compared to that of alum at 10 ppm. With an increase in bioflocculant concentration up to 50 ppm, the flocculating activity increased significantly. This was achieved by isolates D1, A17, A22, and R2 (Fig. 3.7).

Isolates	Additive	Flocculation of kaolin clay with additive (ppm)							
		10000	7500	5000	2500	1000	500	100	10
E1	K <sub>2</sub> HPO <sub>4</sub>	-	-	-	-	-	+	+	+
	NaNO <sub>3</sub>	+	+	+	+	+	+	+	+
	CH <sub>2</sub> COONa	-	-	-	-	+	+	+	+
	Na <sub>2</sub> CO <sub>3</sub>	-	-	-	-	-	+	+	+
	D-GLU	+	+	+	+	+	+	+	+
A14	K <sub>2</sub> HPO <sub>4</sub>	-	-	-	-	+	+	+	+
	NaNO <sub>3</sub>	+	+	+	+	+	+	+	+
	CH <sub>2</sub> COONa	-	-	-	+	+	+	+	+
	Na <sub>2</sub> CO <sub>3</sub>	-	-	-	-	-	-	+	+
	D-GLU	+	+	+	+	+	+	+	+
A17	K <sub>2</sub> HPO <sub>4</sub>	-	-	-	-	+	+	+	+
	NaNO <sub>3</sub>	+	+	+	+	+	+	+	+
	CH <sub>2</sub> COONa	-	-	-	+	+	+	+	+
	Na <sub>2</sub> CO <sub>3</sub>	-	-	-	-	-	+	+	+
	D-GLU	+	+	+	+	+	+	+	+
R2	K <sub>2</sub> HPO <sub>4</sub>	-	-	-	-	+	+	+	+
	NaNO <sub>3</sub>	+	+	+	+	+	+	+	+
	CH <sub>2</sub> COONa	-	-	+	+	+	+	+	+
	Na <sub>2</sub> CO <sub>3</sub>	-	-	-	-	-	+	+	+
	D-GLU	+	+	+	+	+	+	+	+
D1	K <sub>2</sub> HPO <sub>4</sub>	-	-	-	-	+	+	+	+
	NaNO <sub>3</sub>	+	+	+	+	+	+	+	+
	CH <sub>2</sub> COONa	-	-	-	+	+	+	+	+
	Na <sub>2</sub> CO <sub>3</sub>	-	-	-	-	-	-	+	+
	D-GLU	+	+	+	+	+	+	+	+
A22	K <sub>2</sub> HPO <sub>4</sub>	-	-	-	-	+	+	+	+
	NaNO <sub>3</sub>	+	+	+	+	+	+	+	+
	CH <sub>2</sub> COONa	-	-	-	+	+	+	+	+
	Na <sub>2</sub> CO <sub>3</sub>	-	-	-	-	-	-	+	+
	D-GLU	+	+	+	+	+	+	+	+

+ = flocculated;

- = did not flocculate



**Fig. 3.7:** Effect of flocculant concentration on the flocculating activity with respect to 10 ppm alum using pond water. Symbols: ■, 10 ppm; ■, 20 ppm<sub>4</sub>; ■, 30ppm; ■, 50 ppm.

## **3.3.5 Effect of pH, temperature and cationic compounds on flocculating** activity

The flocculating activities of the bacterial bioflocculants were found to be dependent on the pH and temperature of the kaolin clay (Fig. 3.8 and 3.9). Optimum pH for the flocculating activity was at pH 6 for isolates D1, A17, and A22 (Fig. 3.8). Isolate E1 and R2 showed the best flocculation at pH 8 while for isolate A14 best flocculation was achieved at pH 9. The best flocculating activity for each isolate was observed at 28°C (Fig. 3.9). These observations were based on the amount of bioflocculant required for flocculation. Low concentrations (2 ppm) of bioflocculants were required for flocculation at pH between 6 and 9 and at 28°C. Of the cations tested for their ability to enhance the flocculating activity, MgSO<sub>4</sub> and MnCl<sub>2</sub> improved the flocculating activities of all the bacterial isolates except for that of A22 (Fig. 3.10). CTAB was more effective in increasing the flocculating activity of A22. These observations were also based on the amount of bioflocculant required for flocculating activity of A22.



Fig. 3.8: Effect of pH on the flocculating activity of bacterial biofloccunts.



**Fig. 3.9:** Effect of temperature on the flocculating activity of bacterial bioflocculants. Symbols: ■, 37°C; ■, 28°C.



**Fig. 3.10:** Effect of cationic compounds on the flocculating activity of bacterial bioflocculants. Symbols: ■, CTAB; ■, MgSO<sub>4</sub>; ■, MnCl<sub>2</sub>; ■, CaCl<sub>2</sub>.

### **3.4 DISCUSSION**

The present results indicate that environmental and nutritional parameters play an important role in the production of bioflocculants and in the flocculating activity. The flocculating activities were influenced by temperature, pH, and cationic compounds. The flocculating activity started to decrease rapidly after 36 hrs and this may be due to cell lysis and enzymatic activity. This was also noted by Kurane *et al.* (1994b). Salehizadeh and Shojaosadati (2002) have also reported that the decrease in flocculating activity could be due to over-saturation of the many binding sites of kaolin surface particles, thus the attractive forces of other particles were reduced. During the cultivation of the bacterial strains in YMPG medium, the flocculating activity increased in parallel with its cell growth, indicating that bioflocculants were accumulated extracellularly in the medium during the active phase of growth. This suggests that the bioflocculants were not produced by cell autolysis but by biosynthesis (Nakamura *et al.*, 1976b; Kurane *et al.*,

1986b). The correlation between cell growth and secretion of extracellular biopolymeric flocculants (EBFs) was originally reported by McKinney (1956).

Fujita et al. (2000) noted that the biological flocculation does not occur until the microorganisms have entered into an endogenous phase. In this study bioflocculant production remained constant after 84 hrs. This could be because carbon and nitrogen sources in the medium were used up. In a study done by Norberg and Enfors (1982) on Z. ramigera, the flocculant production ended after 90 hrs in the stationary phase. The production of the flocculant by S. griseus was not growth-related. For S. griseus, the flocculating activity increased rapidly with increasing time of cultivation after the third day and reached a maximum value after 4 days (Shimofuruya et al., 1996). Flavobacterium sp. showed flocculating activity at the end of exponential growth phase and the beginning of the stationary phase (Hantula and Bamford, 1991a; b). In contrast to those observations, the flocculant production in R. erythropolis (Kurane et al., 1991), A. sojae (Nakamura et al., 1976b), Zoogloea MP6 (Unz and Farrah, 1976), and Alcaligenes latus (Kurane and Nohata, 1991) have been found to be parallel to cell growth. This observation is consistent with the findings of the present study where flocculant production, flocculating activity and removal of kaolin clay were parallel to the cell growth.

It is clear that with an increase in flocculant concentration the percentage removal of kaolin clay increases and then a decrease in kaolin removal was observed with a further increase in concentration level. This may be because an optimum amount of flocculants in the suspension causes a larger amount of kaolin particles to aggregate and settle. However, according to Chan and Chiang (1995) the amount exceeding the optimum concentration of flocculants is known to cause the aggregated particle to redisperse and would also disturb particle settling. This behaviour could also be caused by an increase in the repulsive energy between the flocculants and kaolin in solution, which causes hindrance in floc formation (Mishra *et al.*, 2004). The basal surfaces of kaolinite are believed to carry a constant structural charge due to the isomorphous substitution of Si<sup>4+</sup> by Al<sup>3+</sup>, whereas the charge on the edges are due to the

protonation/deprotonation of exposed hydroxyl groups and depend on the pH of the solution. Johnson *et al.* (2000) suggested that the charge on the basal surface is pH dependent. It has been shown that an edge surface which should carry a positive double layer in acid solution, and a negative double layer in alkaline solution, with a point of zero charge (PZC) in the region of pH 7, dependent on the particular kaolinite crystal structure (Hu and Liu, 2003).

In this study, all the bacterial bioflocculants were effective in flocculating *C. hystolyticum, S. cerevisiae,* and *A. faecalis.* Other bacterial cultures flocculated but to a lesser extent. Flocculation in *S. cerevisiae* is due to the presence of dominant flocculation genes *FLO1* and *FLO2* and a recessive gene *flo3* (Lewis *et al.,* 1976 – cited by Jin and Speers, 1998). The European Brewery Convention (EBC) suggested that the aggregation of yeast cells into flocs may be due to either non-separation of cells after budding or coalescence of single cells into clumps (EBC Microbiologica, 1981 – cited by Jin and Speers, 1998). Yeast flocculation has been defined as the phenomenon wherein yeast cells adhere in clumps and sediment rapidly from the medium in which they are suspended (Stewart *et al.,* 1976 – cited by Jin and Speers, 1998). Bacterial bioflocculants flocculated 76 bacterial species in a floc and caused 15 species to float in a floc. The remaining 9 species were flocculated little if at all. Bacteria that precipitated included *P. aeruginosa* IFO 3924, *P. fluorescens* S272 and *E. coli* K12 (Nakata and Kurane, 1999).

The application of bioflocculants for the removal of suspended fine particles and organic matter from raw water was examined in comparison with a conventional coagulant agent, alum. The results indicated that the bioflocculants were efficient for the removal of these particles and organic matter. Furthermore, the bioflocculants produced similar results, as did the use of alum, but at a slightly higher dosage. Fujita *et al.* (2000) indicated that the flocculation of kaolin by the *Citrobacter* sp. TKF04 was comparable to or slightly lower than that of PAA (polyacrylamide) and much higher than that of PAC (polyaluminum chloride).

Of the various cations tested on the flocculating activity of the bioflocculants the most effective was  $Mn^{2+}$  and  $Mg^{2+}$ . The flocculating activity was not enhanced by the addition of  $Ca^{2+}$ . Shimofuruya *et al.* (1996) reported that a high concentration of  $Ca^{2+}$  led to the decrease in flocculating activity. The divalent cations accelerate the initial adsorption of the biopolymer on kaolin particles by decreasing the negative electrical charge of kaolin particles and the biopolymer flocculants (Salehizadeh and Shojaosadati, 2002). Divalent cations have a significant effect on the coagulation of natural colloidal particles. Black et al. (1966) suggested that Mg<sup>2+</sup> affects the stability of anionic polymerclay. Three mechanisms are possible: firstly, divalent cations compress the double layer of colloid; secondly, the repulsive forces between polymers and clay particles are reduced by the cations that enhance adsorption of the polymer on the clay particle, and finally the range of repulsive barrier between adsorbed anionic polymers is probably reduced by Mg<sup>2+</sup>. This is reasonably strong evidence that indicates that divalent ions are necessary for polymers to flocculate negative colloids. In this study, anions such as carbonic and phosphate ions prevented proper flocculation by forming weak or loose structures often decreasing the floc size (Faust and Aly, 1998) (Table 3.1).

The optimum pH for the flocculating activity was observed between pH 6 and 9 (Fig. 3.8). In contrast to the finding of the current study Kurane *et al.* (1994a) reported that flocculation did not decrease with an alkaline pH of up to 10. The possible reason for this observation could be that different genera and species of bacteria was used in this study. Also, these bacteria were isolated from different environments. With respect to temperature the optimum flocculating activity was observed at 28°C (Fig. 3.9). Yokoi *et al.* (1996a) showed that the effective flocculation of kaolin suspension by *Bacillus licheniformis* occurred between the temperatures of 4-90°C. Lian *et al.* (2007) found that the flocculation ratio varies from approximately 85% to 89% in the temperature range of 23 to 70°C, and only begins to decrease noticeably with further temperature increase from 70 to 90 °C. The slight increase in the flocculation ratio from 23 to 40°C may be explained by the higher random motion of the flocculant molecules, and hence, higher collision frequency with kaolin particles. Thus, it appears that temperature has little impact on the physical and chemical properties of the flocculant molecules in the

temperature range of 23–70°C. Fujita *et al.* (2000) indicated that efficient kaolin removal by the bioflocculant produced by *Citrobacter* sp. TKF04, could be performed in a pH range of 2-8 and temperature range of 3-95°C and it could flocculate a variety of organic and inorganic particles.

In conclusion, the bioflocculants produced by these bacterial strains have a satisfactory level of flocculating activity. These results suggest that these bioflocculants can be successfully applied for the clarification of river water or wastewaters under various environmental conditions. Overall, it can be concluded that these bioflocculants exhibit flocculating activity comparable or superior to that of existing inorganic flocculants (alum).

#### **CHAPTER FOUR**

## MICROBIAL DECOLOURIZATION OF EFFLUENTS CONTAINING <u>TEXTILE-DYES</u>

#### **4.1 INTRODUCTION**

The use of synthetic chemical dyes in various industrial processes has increased considerably over the last few years. Some areas where these chemicals are frequently used are paper and pulp manufacturing, plastics, dyeing of cloth, leather treatment and printing (Aksu, 2005). Industrial wastewater containing such dyes is generally discarded as effluents. Since some of these dyes are toxic in nature, their presence in from the industrial effluents is a major environmental problem, because they are recalcitrant to microbial degradation (Pagga and Brown, 1986). The wastewater, which is highly coloured, can block the penetration of sunlight and oxygen, which are essential for the survival of various aquatic forms. Moreover, the dye solution can also undergo anaerobic degradation to form potentially carcinogenic compounds, which can end up in the food chain. Many approaches, including physical and/or chemical processes have been used in the treatment of dye containing industrial wastewater; however, such methods are often very costly (Nigam *et al.*, 1996; Rauf *et al.*, 2006).

In recent times, industries have been faced with more stringent effluent regulations. For instance, the textile, food, and pharmaceutical industry are required to lower the colour content in their wastewater (Pinheiro *et al.*, 2004). Flocculation and precipitation processes have proved to be an effective procedure for the decolourization of such effluents (Mishra and Bajpai, 2005). Physical-chemical flocculation with metal hydroxides assisted by polymer flocculants is the most widely used method of treatment for coloured effluents (Choy *et al.*, 2001). However, other alternatives such as powdered activated carbon and activated bentonites can also be used (Pala and Tokat, 2002; Yavuz and Aydin, 2002). The major disadvantages of this technique are the large amount of

sludge, which has to be buried, and the low efficiency with respect to some dyes (Pearce *et al.*, 2003).

Colour removal is also usually effective and fairly rapid using ozone. However, not all the methods employed give satisfactory results especially for some dispersed dyes. Therefore, new flocculation mechanisms have been attracting attention (Petzold *et al.*, 2003a). Salts alone or in combination with polymers were used for the neutralization of charged particles to obtain coagulation. The flocculation mechanism depends on the properties of polymers, especially the type of charge (negative, positive or uncharged), the charge density, and the molecular weight. Highly charged polyelectrolytes with low molecular weight can cause flocculation by interaction between differently charged regions of the particles (patch flocculation); whereas polymers of very high molecular weight (several millions) can cause bridging. The combined use of cationic flocculant and anionic polyelectrolytes of high molecular weight (step by step) is successful because the two flocculation mechanisms can be combined: at first "patching" is obtained by the highly charged polycation and, in a second step, bridging is caused by the high molecular weight polyanion. This mechanism works very well for small particles, such as clay or cellulose-clay mixtures (Petzold *et al.*, 2003b; Petzold *et al.*, 2004).

Another, more practicable method is the application of pre-mixed polyelectrolyte complexes made by the interaction of aqueous solutions of polycation and polyanion that was first described for clay (Petzold *et al.*, 1998). However, because dye molecules or their aggregates are incomparably smaller than such inorganic particles and, in some cases, they are also uncharged, it is necessary to apply other flocculation principles, for instance the inclusion of dye within complexes. Such complex particles, the so-called particle forming flocculants, are able to bind disperse–dyes effectively over large distances due to their size and structure. Complex particles with hydrophobic parts and positive or negative charge are able to bind the dye via hydrophobic as well as electrostatic interaction forces (Buchhammer *et al.*, 2001).

Textile industries consume substantial volumes of water and chemicals for wet processing of textiles. These chemicals are used for desiring, scouring, bleaching, dyeing, printing, and finishing. They range from inorganic compounds and elements to polymers and organic products. There are more than 8 000 chemical products associated with the dyeing process listed in the Colour Index (Society of Dyers and Colourists, 1976 – cited by Banat *et al.*, 1996). These dyes include several structural varieties of dyes, such as acidic, reactive, basic, disperse, azo, diazo, anthraquinone-based and metal-complex dyes. The only aspect in common is their ability to absorb light in the visible region (Song *et al.*, 2006).

The removal of colour from wastewaters is often more important than the removal of the soluble colourless organic substances, which usually contribute the major fraction of the biochemical oxygen demand (BOD). Methods for the removal of BOD from most effluents are fairly well established; dyes, however, are more difficult to treat because of their synthetic origin and mainly complex aromatic molecular structures. Such structures are often synthesized to resist fading on exposure to sweat, soap, water, light or oxidizing agents (Aksu, 2005; Khan and Husain 2007) and this renders them more stable and less amenable to biodegradation (Fewson, 1988; Seshadri *et al.*, 1994).

Dyes with simple structures and low molecular weights exhibit higher rates of colour removal, whereas colour removal is more difficult with highly substituted, high molecular weight dyes (Sani and Banerjee, 1999). The dye removal rates are influenced by changes in electron density in the region of the azo group. The substitution of electron withdrawing groups (–SO<sub>3</sub>H,–SO<sub>2</sub>NH<sub>2</sub>) in the para position of the phenyl ring, relative to the azo bond, causes an increase in the reduction rate (Yilmaz *et al.*, 2007). Nigam *et al.* (1996) established that azo compounds with a hydroxyl group or with an amino group are more likely to be removed than are those with a methyl, methoxy, sulpho or nitro groups. Colour removal is also related to the number of azo bonds in the dye molecule. The colour of monoazo dyes is removed faster than the colour of diazo or triazo dyes (Nigam *et al.*, 1996).

Government legislation is becoming more stringent in most developed countries regarding the removal of dyes from industrial effluents, which is in turn becoming an increasing problem for the textile industries. Environmental-protection agencies in Europe are promoting prevention of transferral of pollution problems from one part of the environment to another. This means that for most textile industries, developing on-site or in-plant facilities to treat their own effluents before discharge is fast approaching actuality. Recently, state and federal agencies in the USA have been requiring lower effluent colour limits (< 200 units of American Dye Manufacturers Institute, ADMI) (McCurdy *et al.*, 1992).

Interest in the pollution potential of textile dyes has been primarily prompted by concern over their possible toxicity and carcinogenicity. This is mainly because many dyes are made from known carcinogens, such as benzidine and other aromatic compounds, all of which might be reformed because of microbial metabolism (Khan and Husain 2007). It has been shown that azo and nitro compounds are reduced in sediments (Weber and Wolfe, 1987) and in the intestinal environment (Sirianuntapiboon and Srisornsak, 2007), resulting in the regeneration of the parent toxic amines. Anthraquinone-based dyes are most resistant to degradation due to their fused aromatic structures, which remain coloured for long periods. Basic dyes have high brilliance and therefore higher colour intensity, making them more difficult to decolourize, while metal-based complex dyes, such as chromium-based dyes, can lead to the release of chromium, which is carcinogenic in nature, into water supplies. Some disperse dyes have also been shown to have a tendency to bio-accumulate (Baughman and Perenich, 1988) and heavy-metal ions from textile effluents have also been reported at high concentrations in both algae and higher plants exposed to such effluents (Srivastava and Prakash, 1991).

The lack of data on the properties of many dyes has been the main problem in assessing broad classes of dyes to identify common characteristics. Although dyes constitute only a small portion of the total volume of waste discharge in textile processing, these compounds are not readily removed by typical microbial-based waste-treatment processes (Li *et al.*, 2007). Furthermore, dyes can be detrimental to the

microbial population present in such treatment works and may lead to decreased efficiency or treatment failure in such plants (Ogawa *et al.*, 1988). Similar adverse effects have also been detected for aquatic microbial populations and the aquatic environment in general (Pearce *et al.*, 2003) or for laboratory cultures exposed to such dyes (Ogawa *et al.*, 1989).

Azo dyes, which are difficult to degrade biologically and chemically, constitute the largest group of colorants used in industry. They are commonly found in considerable amounts in wastewater released by dye-house effluents. Their presence in dyeing and production of dye wastewater causes high concentration of dissolved organic matter and deep colour. If these wastewaters are not treated properly, they can flow into lakes, rivers, and seas through public sewage and then contaminate the environments where people live. It is reported that azo dyes themselves are not toxic; however, under anaerobic conditions azo dyes are cleaved by microorganisms to form potentially carcinogenic aromatic amines (Li et al., 2007). Since many textile plants have rural locations and municipal treatment costs are increasing, both industries and scientists are becoming compelled to search for innovative novel treatments and technologies directed particularly towards the decolourization of dyes in effluents. Dyes usually have a very low rate of removal ratio for BOD to COD (BOD/COD less than 0.1). Biological methods, being cheap and simple to use, have been the focus of recent studies on dye degradation and decolourization (Sirianuntapiboon and Srisornsak, 2007). Therefore, the objective of this chapter was to evaluate the ability of the bacterial bioflocculants to remove dyes and chemicals from the textile industrial effluents.

#### **4.2 MATERIALS AND METHODS**

#### 4.2.1 Textile dyes used in this study

The three types of dispersible dyes selected for use in this study were whale, medi-blue, fawn and a mixture of dyes (see Section 4.2.2). The chemical properties of these dyes are described in Table 4.1.

Colour	Classification	Dyes	State	Bulk density (kg/m <sup>3</sup> )	Concentration (%)
Whale	Azo	Dianix yellow S-6G	Powder	≈600	0.3700000%
		Dianix rubine S-3B	Powder		0.0850000%
		Dianix navy CC	Powder		1.700000%
Medi-blue	Anthraquinone	Avolan 15 LIQ	Powder	400-600	0.3000000%
		Dianix turquois blue S-BG	Powder		0.350000%
		Dianix blue KFBL	Powder		0.0084000%
Fawn	Azo	Dianix yellow S-6G	Powder	450-520	0.0480000%
		Tiacron/rubine – C-BT 200	Powder		0.0380000%
		Dianix blue K-FBL	Powder		0.0180000%

**Table 4.1:** Chemical properties of the textile dyes used in this study

### **4.2.2 Sample collection**

The three dyes (whale, medi-blue, and fawn) were collected from a textile industry in Hammarsdale (KwaZulu-Natal). These dyes were collected directly from the large silver storage tanks immediately after the dyes were cooled. Mixed dyes were collected from the textile treatment plant also in Hammarsdale. It was composed of the variety of dyes from all the textile industries around Hammarsdale.

#### **4.2.3 Effect of flocculant concentration on dye removal**

Four dyes (whale, medi-blue, fawn and mixed dyes) were used in the decolourization experiment. In a test tube, 9 ml of undiluted dye effluent was mixed with different concentrations of the bacterial bioflocculants (2-10 ppm). After the addition of bioflocculants, the components of the test tube were mixed using a Labcon shaker at 200 rpm for 1 min, and then at 60 rpm for another 5 min. The dyes were left to settle for 60 min and the OD was measured with a spectrophotometer at 550 nm. The flocculating activity was expressed as the concentration of the flocculant in parts per million (ppm) when the OD<sub>550</sub> was (1/10) x OD<sub>550c</sub> of the control (Nakata and Kurane, 1999). The decolourization efficiency or the percentage removal of dyes was calculated using the equation:

Percentage removal/decolourization = 
$$\frac{C_0 - C}{C_0} \times 100$$

Where:  $C_0$  is the absorbance of the untreated dye and C is the absorbance after the treatment (Mishra and Bajpal, 2005; Shubo *et al.*, 2005).

#### 4.2.4 Effect of pH on dye removal

In the experiments on pH effect, the initial pH of dye wastewater in the test tube was adjusted from 6 - 10 using 2 N HCl or NaOH. The decolourization efficiency or the percentage removal of dyes was calculated as described in Section 4.2.3.

#### 4.2.5 Effect of temperature on dye removal

To determine the effect of temperature on the removal of dyes, the test tubes containing dye wastewater were incubated at different temperatures 28°C, 35°C, 40°C, and 45°C. The decolourization efficiency or the percentage removal of dyes was calculated as described in Section 4.2.3.

#### 4.2.6 Effect of cations on dye removal

Different cationic compounds were used to determine the effect of salts. Solutions of CaCl<sub>2</sub>.2H<sub>2</sub>O, MgSO<sub>4</sub>.7H<sub>2</sub>O, MnCl<sub>2</sub>·7H<sub>2</sub>O and CTAB were used as the source of cations. The optimum pH and temperature were used to determine the effect of cations on dye removal. The decolourization efficiency or the percentage removal of dyes was calculated as described in Section 4.2.2.

#### **4.3 RESULTS**

The results shown in this chapter are only for the experiment using 10 ppm (high concentration) of bacterial bioflocculants except for the experiment on the effect of flocculant concentration on dye removal. However, data for the experiment using 2, 4, 6, and 8 ppm are included in Appendix B. Ten ppm was chosen based on the high percentage of dye removal.

## 4.3.1 Effect of flocculant concentration on the flocculating activity and the removal of whale dye

Figure 4.1 shows the effect of flocculant concentration on the removal of whale dye. All the isolates were effective in the removal of whale dye even at low concentrations. Bioflocculants from isolates D1, A22, A17, and A14 removed 60% of whale dye at 2 ppm while isolate D1 removed 99.9% at 10 ppm. Therefore, an increase in flocculant concentration led to an increase in dye removal. The flocculating activity of the bacterial bioflocculants on whale dye is depicted in Fig. 4.2. The best flocculating activity was shown by isolate A14 while E1 showed the least.



Fig. 4.1: Effect of flocculant concentration on the removal of whale dye.



Fig. 4.2: Flocculation of whale dye by the bacterial bioflocculants.

#### 4.3.2 Effect of pH, temperature, and cations on the removal of whale dye

pH is the most important parameter affecting the removal of various dyes from textile industries. The effect of pH on the removal of whale dye at 10 ppm flocculant concentration is shown in Fig. 4.3. The optimum pH for the removal of whale dye was pH 7 for all the isolates. At pH 6, 8, 9, and 10 there was a slight decrease in the removal of whale dye. At pH 10, 70% of whale dye was removed by isolates E1, R2, A17 and A14 while at pH 7, 99% of the dye was removed by all the bacterial isolates.

The optimum temperature for the removal of whale dye was 35°C for all the isolates where 99% of the dye was removed (Fig. 4.4). At 45°C, there was a decrease in the percentage removal of whale dye. This is shown clearly by isolates E1 and A17, where 58% and 62% of the dye was removed, respectively. The effect of cations on the removal of whale dye is depicted in Fig. 4.5. The most effective cation for the removal of whale dye was MnCl<sub>2</sub>, followed by MgSO<sub>4</sub> and CaCl<sub>2</sub>. Ninety-nine percent of whale dye was removed upon the addition of MnCl<sub>2</sub>. CTAB was the least effective of all the cations tested.



Fig. 4.3: Effect of pH on the removal of whale dye at 10 ppm.



**Fig. 4.4:** Effect of temperature on the removal of whale dye at 10 ppm. Symbols: **•**,28°C; **•**, 35°C; **•**, 40°C; **•**, 45°C.



**Fig. 4.5:** Effect of cations on the removal of whale dye at 10 ppm. Symbols: ■, CTAB; ■, CaCl<sub>2</sub>; ■, MnCl<sub>2</sub>; ■, MgSO<sub>4</sub>.

## 4.3.3 Effect of flocculant concentration on the flocculating activity and the removal of medi-blue dye

The effect of flocculant concentration on the removal of medi-blue dye is shown in Fig. 4.6. All the isolates were effective in the removal of medi-blue dye, even at low concentrations. At 10 ppm, 80% of medi-blue dye was removed by isolates E1, R2, A17, and A14. Isolate D1 removed 68% of the dye. Therefore, an increase in flocculant concentration led to an increase in the removal of dye. The flocculating activity of the bacterial bioflocculants are shown in Fig. 4.7. The best flocculating activity was achieved by isolate D1 while A22 removed the least dye.



Fig. 4.6: Effect of flocculant concentration on the removal of medi-blue dye.



Fig. 4.7: Flocculation of medi-blue dye by the bacterial bioflocculants.

# 4.3.4 Effect of pH, temperature, and cations on the removal of the medi-blue dye

The effect of pH on the removal of medi-blue dye at 10 ppm is shown in Fig. 4.8. The optimum pH for the removal of medi-blue dye was 7 for all the isolates. At pH 10, 70% of medi-blue dye was removed by isolates E1, R2, A17, and A14. At pH 6, 8 and 9, the removal of medi-blue dye ranged between 70 and 90% while at pH 7, 99.9% of the dye was removed.

Figure 4.9 shows the effect of temperature on the removal of medi-blue dye. The optimum temperature for the removal of medi-blue dye was  $35^{\circ}$ C for all the isolates, where 70% of the dye was removed by isolates E1, R2, A22, A17, and A14. Isolate D1 removed 75% of the dye. With an increase in temperature from 40°C to 45°C, there was a decrease in the removal of the dye. The effect of cations on the removal of the medi-blue dye is depicted in Fig. 4.10. The most effective cation for the removal of medi-blue dye was MnCl<sub>2</sub> for all the isolates followed by MgSO<sub>4</sub> and CaCl<sub>2</sub>. CTAB was the least

effective of all the cations tested. Only 24% of the dye was removed by isolates R2, and A22 in the presence of CTAB and only 32% was removed by isolates A17 and A14.



Fig. 4.8: Effect of pH on the removal of medi-blue dye at 10 ppm.



**Fig. 4.9:** Effect of temperature on the removal of medi-blue dye at 10 ppm. Symbols: **a**, 28°C; **b**, 35°C; **b**, 40°C; **b**, 45°C.



**Fig. 4.10:** Effect of cations on the removal of medi-blue dye at 10 ppm. Symbols: ■,CTAB; ■, CaCl<sub>2</sub>; ■, MnCl<sub>2</sub>; ■, MgSO<sub>4</sub>.

## 4.3.5 Effect of flocculant concentration on the flocculating activity and the removal of fawn dye

The effect of flocculant concentration on the removal of fawn dye is shown in Fig. 4.11. Isolate D1 showed the best removal at 10 ppm where 99% of fawn dye was removed followed by isolate E1 where 80% of the dye was removed at 10 ppm. At 2 ppm, the removal of the dye by isolates D1 and E1 were 90% and 70%, respectively. Only 50% of fawn dye was removed by isolate R2 at 10 ppm. The removal of fawn dye by the isolates A22, A17, and A14 was less effective even with an increase in the flocculant concentration. The flocculating activity of the bacterial bioflocculants are depicted in Fig. 4.12. Isolate D1 showed the best flocculating activity while isolate A17 showed the least amount of activity. The flocculating activities of isolates E1, R2, A14, and A22 ranged between  $10 - 50 \text{ OD}^{-1}$ .



Fig. 4.11: Effect of flocculant concentration on the removal of fawn dye.



Fig. 4.12: Flocculation of fawn dye by the bacterial bioflocculants.

#### 4.3.6 Effect of pH, temperature, and cations on the removal of fawn dye

The effect of pH on the removal of fawn dye at 10 ppm bioflocculant concentration is depicted in Fig. 4.13. The optimum pH for the removal of fawn dye was 10 for all the isolates. At pH 10, isolates E1 and R2 removed 62% of fawn dye; isolates D1 and A22 removed 58% while A17 and A14 removed only 55%. There was an increase in the removal of fawn dye with an increase in pH. Figure 4.14 shows the effect of temperature on the removal of fawn dye. The optimum temperature for the removal of fawn dye was 40°C for isolates E1 and A22. The optimum temperature for the removal of the fawn dye was 45°C for isolates D1, R2, A17, and A14. The effect of cations on the removal of fawn dye is shown in Fig. 4.15. The most effective cation was CTAB followed by MnCl<sub>2</sub>, and MgSO<sub>4</sub> for isolates E1, D1, R2, and A22 while CaCl<sub>2</sub> was the least effective. For isolates A17 and A14, CaCl<sub>2</sub> was the most effective cation in the removal of fawn dye followed by MnCl<sub>2</sub>, and MgSO<sub>4</sub> while CTAB was the least effective.



Fig. 4.13: Effect of pH on the removal of fawn dye at 10 ppm.



**Fig. 4.14:** Effect of temperature on the removal of fawn dye at 10 ppm. Symbols: ■,28°C; ■, 35°C; ■, 40°C; ■, 45°C.



**Fig. 4.15:** Effect of cations on the removal of fawn dye at 10 ppm. Symbols: ,CTAB;, CaCl<sub>2</sub>; , MnCl<sub>2</sub>; , MgSO<sub>4</sub>.

## 4.3.7 Effect of flocculant concentration on the flocculating activity and the removal of mixed dyes

Figure 4.16 illustrates the effect of flocculant concentration on the removal of mixed dyes. All isolates were effective in the removal of mixed dyes even at low concentrations. Therefore, an increase in flocculant concentration led to an increase in the removal of the dye. At 2 ppm, 62% of mixed dyes were removed by isolates D1, R2 and A14 while at 10 ppm, 75% was removed by isolates D1, E1, R2, A22 and A14. The flocculating activity of the bacterial bioflocculants is depicted in Fig. 4.17. The best flocculating activity was achieved by isolate R2 while isolate E1 removed the least dye.



Fig. 4.16: Effect of flocculant concentration on the removal of mixed dyes.



Fig. 4.17: Flocculation of mixed dyes by the bacterial bioflocculants.
### 4.3.8 Effect of pH, temperature, and cations on the removal of mixed dyes

The effect of pH on the removal of mixed dyes at 10 ppm bioflocculant concentration is shown in Fig. 4.18. The optimum pH for the removal of mixed dyes was 10 for all isolates. At pH 10, 97% of the dyes were removed by isolate R2; while 85% was removed by isolates D1, E1, and A17. The optimum temperature for the removal of mixed dyes was 35°C for isolates E1, D1 and A14 and 40°C for isolates R2, A22 and A17 (Fig. 4.19). At 35°C, 99% of the dyes were removed by isolates E1, D1 and A14 while at 45°C, 99.9% was removed by R2 and A17. The effect of inorganic salts on the removal of dyes is an important parameter since in textile wastewater effluents, dyes are found in solutions of high concentrations of sulphates and phosphates salts. The effect of cations on the removal of mixed dyes is depicted in Fig. 4.20. The most effective cation was MnCl<sub>2</sub> for all the isolates followed by CaCl<sub>2</sub> and MgSO<sub>4</sub>. CTAB was the least effective of all the cations tested.



Fig. 4.18: Effect of pH on the removal of mixed dyes at 10 ppm.



**Fig. 4.19:** Effect of temperature on the removal of mixed dyes at 10 ppm. Symbols: ■, 28°C; ■, 35°C; ■, 40°C; ■, 45°C.



Fig. 4.20: Effect of cations on the removal of mixed dyes at 10 ppm. Symbols: ■,CTAB; ■, CaCl<sub>2</sub>; ■, MnCl<sub>2</sub>; ■, MgSO<sub>4</sub>.

# 4.4 DISCUSSION

In this study, the effect of flocculant concentration on the removal of dyes was investigated. The results have shown that the removal of all the dyes tested were directly proportional to the flocculant concentration (Fig. 4.1; Fig. 4.6; Fig. 4.11; Fig. 4.16). The flocculants cause aggregation of particles and cells by bridging and charge neutralization (Salehizadeh and Sojaosadati, 2001). Bridging occurs if the flocculant extends from the particle's surface into the solution for a distance greater than the distance over which the interparticle repulsion acts. In this case, the biopolymer can adsorb to other particles to form flocs. This mechanism explains flocculation by neutral or like-charged bioflocculants (Hantula and Bamford, 1991b; Levy *et al.*, 1992). Shubo *et al.* (2005) reported that higher decolourization of the dyes can be achieved by increasing the concentration of the bioflocculants.

The flocculating capacity of the bioflocculants increased with an increase in concentration and remained constant except for fawn dye where there was a slight increase in flocculating capacity with an increase in flocculant concentration (Fig. 4.1; Fig. 4.6; Fig. 4.11; Fig. 4.16). This observation may be due to a particle-polymer-particle complex formation in which polymer serves as a bridge. To be effective in destabilization, a polymer molecule must contain chemical groups, which can interact with sites on the surface of the colloidal particle. When a polymer molecule comes into contact with a colloidal particle, some of these groups adsorb at the particle surface, leaving the remainder of the molecule extending out into the solution. If a second particle with some vacant adsorption sites comes into contact with these extended segments, attachment can occur. A particle-polymer-particle complex is thus formed in which polymer serves as a bridge. If a second particle is not available, in time the extended segments may eventually adsorb on other sites on the original particle, so that the polymer is no longer capable of serving as a bridge (Salehizadeh and Sojaosadati, 2001; Salehizadeh and Sojaosadati, 2002). Mishra and Bajpai (2005) indicated that there is direct stoichiometric relationship between optimum polymer dosage and colloid concentration, and restabilization due to overdosing can occur.

In this study, the optimum pH was observed at pH 7 for whale and medi-blue dyes (Fig.4.3, Fig.4.8) while for fawn and mixed dyes it was observed at pH 10 (Fig. 4.13; Fig.4.18). According to Willmott (1997), the optimum pH for colour removal is often at a neutral pH value or a slightly alkaline pH value and the rate of colour removal tends to decrease rapidly at strongly acid or strongly alkaline pH values. As a result, the coloured wastewater is often buffered to enhance the colour removal performance. Colour removal in the alkaline pH range is presumably due to adsorption onto hydroxide flocs. Biological reduction of the azo bond of whale and fawn dye can result in an increase in the pH due to the formation of aromatic amine metabolites, which are more basic than the original azo compound (Willmott, 1997). Altering the pH within a range of 7.0 to 9.5 has very little effect on the dye reduction process. Chang et al. (2001) found that the dye reduction rate increased nearly 2.5-fold as the pH was raised from 5.0 to 7.0, while the rate became insensitive to pH in the range of 7.0-9.5. This is in accordance with the results obtained in this study. On the other hand Mittal and Gupta (1996), studied the effect of pH on the biosorption of three cationic dyes, Orlamar Red BG, Orlamar Blue G and Orlamar Red GTL by the fungus Fomitopsis carnea and their results showed that colour removal decreased with decreasing pH due to repulsive forces between coloured dye cations in solution and biosorbent surface charged positively at pH values lower than 3.0.

In many systems, the rate of colour removal increases with increasing temperature, within a defined range that depends on the system (Chang *et al.*, 2001). The temperature required to produce the maximum rate of colour removal was found to range between 35-45°C for all the textile dyes tested (Fig. 4.4; Fig. 4.9; Fig. 4.14; Fig. 4.19). The results are consistent with a study done by Pearce *et al.* (2003) regarding the removal of colour from textile wastewater using whole bacterial cells. The decline in colour removal activity at higher temperatures can be attributed to the loss of cell viability (Pearce *et al.*, 2003). Aksu and Tezer (2000), also investigated the effect of temperature on the biosorption of Remazol Black B reactive dye by *Rhizopus arrhizus* and their results indicated that optimum adsorption temperature was 35°C and adsorption decreased with further increasing temperature due to the decreased surface activity.

The addition of the divalent cations such as  $Mn^{2+}$ ,  $Mg^{2+}$ , and  $Ca^{2+}$  enhanced both the flocculating activity and the decolourization of the dyes (Fig. 4.5; Fig. 4.10; Fig. 4.15; Fig. 4.20). Cations stimulate flocculating activity by neutralizing and stabilizing the residual negative charge of functional groups and by forming bridges between particles. The role of bivalent and trivalent cations is to increase the initial adsorption of biopolymers on suspended particles by decreasing the negative charge on both the polymer and the particle (Levy et al., 1992). The results are consistent with the findings of Kurane et al. (1994b) who reported that divalent cations namely Mn<sup>2+</sup>, Mg<sup>2+</sup>, and Ca<sup>2+</sup> bind to the bioflocculants and form complexes thus stimulating flocculation. Fujita et al. (2000) and Yim et al. (2007) indicated that the flocculating activity of Citrobacter sp. TKF04 and Gyrodinium impudicum KG03 was not enhanced by the addition of any cations including Ca<sup>2+</sup>. Dyeing processes consume large amounts of salts. Therefore, salt concentration in dye wastewater is one of the important factors that influence the biosorption capacity (Zhou and Banks, 1991; Zhou and Banks, 1993). Textile wastewaters may include metal ions beside dyes and salts due to metal-containing dyes used in textile industry. Metal ions would be a factor influencing biosorption rate and capacity. They might compete with dye molecules for the binding sites or stimulate the biosorption of dye onto biomass (Zhou and Banks, 1993).

Among the four dyes used in this study, whale dye was easily decolourized followed by medi-blue and mixed dyes. Fawn dye was decolourized the least. According to Pearce *et al.* (2003), a possible reason for this observation could be that fawn dye is an acidic dye. Acid dyes are the most problematic and difficult to decolourize due to their inert chemical structure and an attached phenyl group, methyl, methoxy, nitro and a sulphonate groups [PhNH; O=S=O;  $(CH_2)_3-OMe$ ;  $NO_2$ ]. Also Sanghi *et al.* (2006) suggested that removal of colour from dye solutions is complex and may be due to physicochemical mechanisms of coagulation and or chelation–complexation type reactions. The colour removal data suggests that the colour removal mechanism is predominantly physicochemical. The structure of the dyes appears to be conducive to chelation/complex formation reaction with coagulants leading to the formation of insoluble metal dye complexes, which may precipitate, from solution. In this study,

colour removal was accomplished by aggregation or precipitation and adsorption of colouring substances onto the coagulant species. Hitz *et al.* (1978), concluded that acid dyes exhibit low colour removal due to the number of sulphonate groups in the dye, direct dyes exhibit high levels of colour removal that is independent of the number of sulphonate groups in the dye and that reactive dyes exhibit low levels of colour removal. The effect of the sulphonate groups on colour removal is related to the mechanism by which the colour is removed (Pinheiro *et al.*, 2004).

Water is essential in all aspects of the world. If colour could be removed from the dyeing effluent through coagulation/flocculation, wastewater could be reused several times. Decolourization of dye solutions by coagulation with bacterial bioflocculants depended largely on the type of dye, pH, temperature, and flocculants concentration. The bioflocculants were effective to varying degrees in removing the dyes in aqueous solution, in particular whale dye, medi-blue, fawn dye and mixed dyes, with a decolourization efficiency ranging between 20-99.9%. Bacterial bioflocculants may provide a promising alternative to replace or supplement present treatment processes for the removal of very high concentrations of dyes. The use of natural flocculants seems to be an economical and cleaner alternative for textile wastewater treatment, as they are biodegradable and easily available from reproducible resources (Kurane *et al.*, 1986a). Undoubtedly, microbial flocculants offer many promising benefits for commercial purposes in the future and they may be very good alternatives to the chemical coagulants that are used conventionally.

# **CHAPTER FIVE**

# THE TREATMENT OF RIVER WATER BY THE BIOFLOCCULANTS

# **5.1 INTRODUCTION**

Water is the most common and important chemical compound on earth. Only 2.6% of the global water is freshwater and consequently available as potential drinking water. Coagulation-flocculation followed by sedimentation, filtration and disinfection by chlorine, is used worldwide in the water treatment industry before the distribution of treated water to consumers (Ndabigengesere and Narasiah, 1998). The availability of drinking water has been the most critical factor for survival throughout the development of all life. In the history of humankind, cultural centres were always founded in areas with a sufficient supply of freshwater. As the population increased, the natural supply of water became limited, and all of the great cultures developed sophisticated techniques and systems to obtain access to new water reservoirs (e.g. drilling of wells and building of aqueducts) and to distribute water for irrigation and drinking (Hammerton and Sherrat, 1972). Initially, developing communities found that supplying and distributing a sufficient volume of drinking water presented major problems. However, very soon other complications of highly populated areas, such as increasing amounts of waste, wastewater, and other types of contamination, also endangered access to fresh, safe drinking water (Hunter and Quigley, 1998).

Pollutants have been transported by wind and rain to every place on earth. Today, in most industrialized countries, drinking water is ranked as food, and high standards are set for its quality and safety. The strict requirements for microbiological factors specify that bacterial content should be very low and that no pathogenic microorganisms should be detectable. These strict demands for the absence of pathogens, however, are meaningful only for the classical pathogens like *Vibrio cholerae* and *Salmonella typhi* (USEPA, 1991). The discovery of new pathogens and new insights into the microbiology of drinking water required a more detailed investigation toward the occurrence of

potentially pathogenic bacteria, viruses, and parasites. Therefore, guidelines and legislation [e.g. European Union Council Directive 98/83/EC and World Health Organization (WHO) guidelines] state that drinking water should contain pathogenic microorganisms only in such low numbers that the risk for acquiring waterborne infections is below an accepted limit. The fulfilment of these requirements demands resource protection and careful treatment of raw water, as well as accurate quality control of the treatment process. However, evaluation of the behaviour of pathogens in drinking water is also essential as a basis for further improvements of the treatment process and for new regulations (Atherton *et al.*, 1995).

Faecal coliforms and enterococci have been widely used as indicators of faecal pollution (Sinton et al., 1998). Both microbial groups can be determined by their enumeration. Different agents can determine the proportion of faecal coliforms/enterococci, or their inactivation. Both bacterial groups include several species. For example, the genus Enterococcus contains 19 recognized species (Manero and Blanch, 1999). Any determination of their diversity in the environment should consider this aspect. Urban or rural wastewaters normally contain many bacterial species, each with a large number of strains. Biological treatment processes at sewage treatment plants could produce selective elimination and/or changes of proportion, in the bacterial populations (Mezrioui and Baleux, 1994). Moreover, the sewage effluent, as well as urban or industrial waste, could modify some microbial populations in the reception waters, such as rivers, lakes, or lagoons (Sinton and Donnison, 1994). This effect could become more important where policies of water re-utilization are applied in regions with poor water resources. The determination of the origin of faecal pollution in waters is important for the management and quality control of water resources. Sub-typing below the species level of bacteria could provide valuable information about the sources of pollution in surface waters (Kuhn et al., 1997).

In recent years, several so-called "new or emerging pathogens" have arisen as problems in drinking-water production and distribution. These include, on the one hand, newly recognized pathogens from faecal sources like *Campylobacter jejuni*, pathogenic *Escherichia coli, Yersinia enterocolitica*, new enteric viruses like rotavirus, calicivirus, small round-structured virus, astrovirus, and the parasites *Giardia lambia*, *Cryptosporidium parvum*, and microsporidia. On the other hand, some new pathogens comprise species of environmental bacteria that are able to grow in water distribution systems and only recently were recognized as relevant pathogens, such as *Legionella* sp., *Aeromonas* sp., *Mycobacterium* sp., and *Pseudomonas aeruginosa* (Brugha *et al.*, 1999).

River water is a widely used but often unappreciated source of water. In the U.S., river water supplies at least 100 million people with drinking water. In rural and suburban areas, 90-95% of the drinking water comes from river water (Prescott *et al.*, 1996). Several techniques are used in the treatment of river water however; they all have their advantages and drawbacks. The retention of dissolved and dispersed organic and/or inorganic water contaminants with membrane processes for the (direct) treatment of surface waters has recently become more important. The interest in ultra-filtration (UF) and micro-filtration (MF) membranes has increased due to the extremely high water quality with respect to hygiene and microbiological safety, documented by a growing number of UF and MF membrane installations, research projects and pilot plant trials. Low-pressure membranes provide a complete barrier against microorganisms and particles. These are, for instance, the possibility of fully automatic operation, a compact system design in connection with good space utilisation and flexibility in system enlargement, modernisation, and new installations (Lerch *et al.*, 2005).

Photocatalytic oxidation mediated by semi-conductor catalysts is one of the emerging advanced oxidation processes used in the treatment of river water (Meng *et al.*, 2005). By applying ultraviolet (UV) radiation on photocatalysts, powerful active oxidants of hydroxyls can be formed (Ollis *et al.*, 1996); therefore, photocatalytic oxidation technology is commonly considered capable of decomposing almost all types of organic contaminants. However, from a viewpoint of practical application, the feasibility of the photocatalytic process for the treatment of various river waters is of more interest. So far, the reported treatment objectives of applications or application-oriented experiments have encompassed contaminated ground waters, industrial wastewaters, and effluents of

biologically treated wastewaters and polluted river water (Dillert *et al.*, 1999; Meng *et al.*, 2005). Nevertheless, traditional slurry photocatalytic oxidation systems were usually not favoured because catalyst separation and catalyst loss were too severe to warrant a long-term operation. Furthermore, the use of photocatalytic oxidation system is economically unfeasible (Rodriguez *et al.*, 1996; Crittenden *et al.*, 1997). Therefore, there is a great need to develop cheap and effective methods for the treatment of river water.

Aluminum salts are by far the most widely used coagulants in water and wastewater treatment. However, studies have pointed out that there are several serious disadvantages of using aluminum salts including Alzheimer's disease and similar health related problems associated with residual aluminum in treated waters (Yokoi *et al.*, 1995). There is also a problem of reaction of alum with natural alkalinity present in the water leading to a reduction of pH, and a low efficiency in coagulation of cold waters. A significant economic factor is that many developing countries can hardly afford the high costs of imported chemicals for water and wastewater treatment. Therefore, it is desirable that other cost effective and more environmentally acceptable alternative coagulants be developed to supplement if not replace alum, ferric salts, and synthetic polymers (Ndabigengesere and Narasiah, 1998). Hence, the objective of this chapter was to evaluate the efficacy of the bacterial bioflocculants as an alternative to alum in decreasing both the microbial load and turbidity of river water.

# **5.2 MATERIALS AND METHODS**

### **5.2.1** Microbiological analysis of river water

The river water used in the following experiment was collected from Palmiet River close to the University of KwaZulu-Natal (Westville campus). Serial dilutions  $(10^{-1}-10^{-6})$  of river water were carried out to enumerate the different microorganisms present. Aliquots of 0.1 ml from each dilution were plated on nutrient agar (NA); mannitol salt agar (MS); eosin-methylene blue agar (EMB) and Salmonella-Shigella agar (SS). All the

reagents used for the analysis of river water were purchased from Merck. Nutrient agar, (NA) was used to grow all the different bacteria present in river water, MS was used to isolate *Staphylococci*, while EMB and SS agar were used to isolate *E. coli*, *Salmonella* and *Shigella* species respectively. The plates were incubated overnight at 37°C and colonies were then counted (Prescott *et al.*, 1996).

# 5.2.2 Determination of flocculating activity

Different concentrations of bacterial bioflocculants (10-50 ppm) were added to 49 ml of river water spiked with 1 ml of *E. coli* (OD of 1). The tubes were left to stand for 1 hr and the results were recorded at 30 min intervals. For alum, the procedure was carried out as described above but instead of bacterial bioflocculants, different concentrations of alum (10-50 ppm) were added. Two controls were included: for the positive control 49 ml of river water was spiked with 1 ml of *E. coli* but without the bacterial bioflocculants; the negative control had only river water without the bacterial bioflocculants and *E. coli*. The turbidity and the flocculating activity of river water were measured using a HACH 2100P turbidometer in NTU and spectrophotometer (LKB ultrospec II) (OD<sub>550nm</sub>), respectively. The flocculating activity was expressed as the concentration of the flocculant in parts per million (ppm) when the OD<sub>550</sub> was (1/10) x OD<sub>550c</sub> of the control (Nakata and Kurane, 1999). The removal rate were determined according to the method of Kurane *et al.* (1994a, b) as follows:

Removal (%) = 
$$\frac{B-A}{B} \times 100$$

Where: A is the experiment with the bioflocculants and B is the control without the bioflocculants.

# 5.2.3 Reduction of river water turbidity and microbial load

Different concentrations of bacterial bioflocculants (10-50 ppm) were added to 49 ml of river water. The tubes were left to stand for 2 hrs. The turbidity and the flocculating activity of river water was measured using a turbidometer in NTU and spectrophotometer ( $OD_{550nm}$ ), respectively. The flocculating activity and percentage removal was determined as described in Section 5.2.2. The control was conducted without the addition of bacterial bioflocculants. Aliquots of 0.1 ml from each tube was plated out on a NA and incubated at 37°C for 24 hrs. The number of colonies on NA plates were counted and compared to that of the control (refer to Appendix B).

### 5.2.4 Effect of pH on decreasing the microbial load

The pH of the river water was adjusted to 9 and was sterilised by autoclaving and allowed to cool before spiking. Two gram-positive and two gram-negative bacteria were used to spike the river water. The four bacterial cultures used in this experiment were *Streptococcus faecalis, Staphylococcus aureus, Klebsiella oxytoca,* and *E. coli.* Serial dilutions of bacterial cultures were first carried out to enumerate bacterial population. Different concentrations of bacterial bioflocculants (10-50 ppm) were added to 49.5 ml of river water spiked with 0.5 ml of  $10^5$  cfu/ml of bacterial cultures. The effects of alum on decreasing the microbial load was conducted as mentioned above, but instead of bacterial bioflocculants, alum (10-50 ppm) was added. Two controls were also included; for the positive control, 49.5 ml of river water was spiked with 0.5 ml of  $10^5$  cfu/ml of bacterial bioflocculants. The negative control was conducted by the addition of 0.5 ml of distilled water to 49.5 ml of river water, also without the addition of 0.5 ml of distilled water to 49.5 ml of river water, also without the addition of 0.5 ml of distilled water to 49.5 ml of river water, also without the addition of bacterial bioflocculants and the culture. The flocculating activity and percentage removal was determined according to the method of Nakata and Kurane (1999) and Kurane *et al.* (1994a, b) as described in Section 5.2.2.

# **5.3 RESULTS**

The results in this chapter are only for the experiment using 10 ppm (lowest concentration) and 50 ppm, which is the highest concentration of bacterial bioflocculants. However, data for the experiment using 20 and 30 ppm are included in Appendix B. These concentrations of bioflocculants were chosen in order to compare the reduction of turbidity and microbial load of river water at low and high concentrations.

### 5.3.1 Microbiological analysis of river water

The river water used in the current study was found to be contaminated with various Gram-positive and Gram-negative bacteria. The most predominant genera were *Staphylococci, Salmonella, Shigella, Bacillus, E. coli*, and *Proteus* species. The presence of *E. coli* in river water indicated that it was contaminated by faecal matter.

# 5.3.2 The reduction of river water turbidity by the bacterial bioflocculants and the flocculating activities

The effect of bacterial bioflocculants and alum on the turbidity of river water at 10 and 50 ppm is depicted in Fig. 5.1 - 5.2. Sixty eight percent of river water turbidity was removed by isolate A17 at 120 min. With an increase in the bioflocculant concentration (50 ppm), there was a further reduction in turbidity. There was 81% reduction by isolate A22 at 50 ppm. The reduction of river water turbidity upon the addition of alum was similar for isolates D1, E1, and A14 at 10 and 50 ppm. Figure 5.3 illustrates the flocculating activity of the bacterial bioflocculants at the different time intervals. Isolate D1 showed the best flocculating activity at 120 min while E1 showed the least. The flocculating activity of alum was similar to that of isolate A14.

The pH of the river water before and after the addition of bacterial bioflocculants and alum is shown in Fig. 5.4. Before the addition of the bacterial bioflocculants, the pH of the river water was 7.38, which is close to neutral. After the addition of the bacterial bioflocculants, the pH ranged from 6.55-6.92, which is slightly acidic. The pH of river water dropped from 7.38 to 4.14 upon the addition of alum. Therefore, the pH shifted from neutral to acidic.



Fig. 5.1: Effect of bacterial biofflocculants and alum on the turbidity of river water at 10 ppm.



Fig. 5.2: Effect of bacterial biofflocculants and alum on the turbidity of river water at 50 ppm.



Fig. 5.3: Flocculating activity of the bacterial bioflocculants at different time intervals with *E. coli*.



Fig. 5.4: pH of the river water before and after the addition of the bacterial bioflocculants and alum.

### 5.3.3 Effect of bioflocculants on river water turbidity and microbial load

Isolates A22 and D1 were very effective in reducing the river water turbidity at both low and high concentrations; up to 96% of the turbidity was reduced (Fig. 5.5). The reduction of river water turbidity by isolates E1, A17, A14, and alum were similar; up to 90% of the turbidity was reduced at 50 ppm. At 10 ppm the percentage removal was the least for isolate R2, but as the concentration of the bioflocculants increased, there was also an increase in the reduction of river water turbidity.

The flocculating activity of the bacterial bioflocculants at the different time intervals is depicted in Fig. 5.6. The best flocculating activity was achieved for isolate D1 followed by A22, R2, and A17 while alum and isolate E1 had the least activity. Figure 5.7 shows the reduction of the microbial load by the bioflocculants at different concentrations compared to alum. Up to 92% of the microbial load was reduced by the isolates D1, E1, A17, A22, and alum at 50 ppm. Isolates A14, and R2 reduced the microbial load by 87%.



Fig. 5.5: Effect of bioflocculant concentration and alum on the turbidity of river water.



Fig. 5.6: Flocculating activity of bioflocculants compared to alum using river water.



Fig. 5.7: Effect of bioflocculant concentration and alum on the microbial load in river water.

## 5.3.4 Effect of pH on decreasing the microbial load

Figure 5.8 illustrates the effect of pH on the reduction of river water turbidity by the bacterial bioflocculants at different concentrations compared to alum. Ninety-six percent of river water turbidity was reduced by isolate A22 at 50 ppm, while 95% of the river water turbidity was reduced by the isolates D1, E1, A17, A14, and alum at 50 ppm. The reduction of river water turbidity was directly proportional to the bioflocculant concentration. The best flocculating activity was achieved by isolate A14 followed by A22, E1, and alum, while for R2 was only 25 OD<sup>-1</sup>. The flocculating activity of A17 and D1 ranged from 17-20 OD<sup>-1</sup>, respectively (Fig. 5.9). The effect of pH on the reduction of the microbial load by the bioflocculants at different concentrations compared to alum is shown in Fig. 5.10. Ninety-eight percent of the microbial load was reduced by alum at 50 ppm whereas 96% was removed by isolates A14 and R2. There was a 95% reduction of the microbial load by isolate D1 whereas 94% was removed by isolates E1, A17, and A22 at 50 ppm.



**Fig. 5.8:** The effect of pH on the reduction of river water turbidity by the bacterial bioflocculants at different concentrations compared to alum.



**Fig. 5.9:** The effect of pH on the flocculating activity of the bacterial bioflocculants compared to alum.



Fig. 5.10: The effect of pH on the reduction of the microbial load by the bioflocculants at different concentrations compared to alum.

### 5.3.5 Effect of bioflocculants on river water spiked with bacteria

The reduction of river water turbidity spiked with two gram-positive and two gram-negative bacteria by the bacterial bioflocculants compared to alum at different concentrations is depicted in Fig. 5.11 - 5.12. was by all The bacterial bioflocculants decreased the number of *K. oxytoca* at different concentrations followed by *E. coli*. The turbidity was reduced up to 100%. The same pattern was observed for the reduction of *S. faecalis* and *S. aureus* where there was up to 94% reduction of turbidity. The increase in concentration of the bacterial bioflocculants had no significant effect on the reduction of the river water turbidity when compared to alum. Alum, reduced river water turbidity the least at 10 ppm but with an increase in concentration of alum (50 ppm) there was an increase in the removal of river water turbidity. There was 85% reduction of *S. faecalis* followed by *K. oxytoca* and *S. aureus* where 75% and 65% were reduced, respectively on river water spiked with these bacteria. The turbidity of *E. coli* was reduced the least (45%) from spiked river water.

The flocculating activity of bacterial bioflocculants compared to alum is depicted in Fig. 5.13. The best flocculating activity was achieved by all the isolates when the river water was spiked with *S. faecalis*. When the river water was spiked with *E. coli*, the flocculating activity was very weak. The reduction of the microbial load by the bioflocculants at different concentrations compared to alum is shown in Fig. 5.14 - 5.15. The reduction of *S. faecalis* by isolates D1 and A14 was the least at 10 ppm, where there was only 20% reduction by D1 and 24% by isolate A14. With an increase in concentration of these bioflocculants, there was an increase in the removal of the microbial load. One hundred percent of the microbial load was removed by isolates A22, A17, R2, A14, E1, and alum at 50 ppm.



**Fig. 5.11:** The reduction of river water turbidity spiked with two Gram-positive and Gram negative bacteria by the bacterial bioflocculants compared to alum at 10 ppm (*Strep* = *S. faecalis, Staph* = *S. aureus, Kleb* = *K. oxytoca, E. coli* = *E. coli*).



Fig. 5.12: The reduction of river water turbidity spiked with two Gram-positive and Gramnegative bacteria by the bacterial bioflocculants compared to alum at 50 ppm. (*Strep = S. faecalis, Staph = S. aureus, Kleb = K. oxytoca, E. coli = E. coli*).



**Fig. 5.13:** Flocculating activity of bioflocculants compared to alum using river water spiked with two Gram-positive and Gram-negative bacteria. (*Strep = S. faecalis, Staph = S. aureus, Kleb = K. oxytoca, E. coli = E. coli*).



**Fig. 5.14:** The reduction of the microbial load by the bioflocculants at different concentrations compared to alum at 10 ppm. (*Strep = S. faecalis, Staph = S. aureus, Kleb = K. oxytoca, E. coli = E. coli*).



**Fig. 5.15:** The reduction of the microbial load by the bioflocculants at different concentrations compared to alum at 50 ppm. (*Strep = S. faecalis, Staph = S. aureus, Kleb = K. oxytoca, E. coli = E. coli*).

## **5.4 DISCUSSION**

River water turbidity decreased with an increase in flocculant concentration of 50 ppm, and then remained constant with a further increase in flocculant level. This occurs because the optimum amount of flocculants in the suspension causes the microorganisms and the fine particles to aggregate and settle. However, when the optimum concentration of flocculant is exceeded it is known to cause the aggregated particles to redisperse and this disturbs particle-settling (Chan and Chiang, 1995). Mishra *et al.* (2004) explained that this behaviour could be based on an increase in the repulsive energy between the flocculants and the microorganisms, which causes hindrance in floc formation.

The pH of the river water prior to the addition of the bacterial bioflocculants and alum was neutral, with a subsequent decrease in pH upon the addition of bacterial bioflocculants and alum. The addition of alum caused the pH to drop to 4.14, which is more acidic, which means that in practical terms, further chemical addition is necessary in order to correct the pH of the finished water to values between 6.5 and 8.5 (USEPA, 1991). Stumm and Morgan (1981) and Nordstrom and May (1989), reported that the reduction in pH is attributed to alum hydrolysis and production of H<sup>+</sup>; alum dissociates and dissolved alum undergoes a series of hydrolysis reactions that result in the generation of acidity and a decrease in pH. The magnitude of the pH shift is related to the pH of the water and alum dosage. Coagulation/flocculation was improved by using coagulant aids such as alum. Alum helps form large flocs that settle out rapidly. Their concentration is an important parameter since excessive dosage can inhibit flocculation. Coagulation merely transfers pathogenic microorganisms from water to the flocculated material (Stumm and Morgan, 1981; Faust and Aly, 1998).

The pH of the water is probably the most significant factor affecting coagulation/flocculation. In this study the pH of river water was maintained at 9. Other factors include turbidity, temperature, and mixing regime. Coagulation is the most important process used in water treatment plants for clarification of coloured and turbid waters (Bitton, 1994). There was further reduction of river water turbidity as well as the microbial load at pH 9 compared to when the pH was not adjusted (Fig. 5.5 and 5.7). Turbid water contains, in addition to dissolved and settleable solids, colloids, which are electrically charged (Hammerton and Sherratt, 1972). Immediately after the addition of a flocculating agent such as alum to the water, reaction with the water and other ions occurs, resulting in the production of multi-positive hydroxo and polynuclear species of compounds. The coagulant species are rapidly adsorbed onto the surface of the turbidity particles, which ultimately become "coated" with coagulant. The electrostatic attraction between the negatively charged particle and the positively charged hydrolysis products enhances the deposition. The net result is that the electric charges on the particles are reduced. Depending on pH and coagulant dose, the charge on the particle may vary from slightly negative to neutral to slightly positive. The suspension becomes destabilized and the process of flocculation, where the particle can agglomerate to a settleable size, can precede unhindered (Hannah et al., 1967; Ndabigengesere and Narasiah, 1998).

Bacterial bioflocculants were very effective in reducing both the turbidity and the microbial load of river water. Different bacterial isolates used to spike river water were flocculated randomly by the bioflocculants (Fig. 5.11 - 5.15). In this study, there was a maximum removal of microbial load and turbidity of river water by both the bacterial bioflocculants and alum. Bitton (1994) indicated that removal of bacteria, although variable may exceed 90% during the flocculation process, furthermore, coagulation removes 74-99.4% of E. coli and coliforms. Kurane et al. (1986a) reported that the flocculant produced by Rhodococcus erythropolis could efficiently flocculate all suspended solids in aqueous solutions tested and had a wide flocculating activity against both organic and inorganic materials. Among those effectively tested were microrganisms such as E. coli, and alcohol yeast, activated sludge, Microcystis aeruginosa (AOKO), kaolin clay, muddy water, river dredging water, river bottom sediment (HEDORO), ash from a stream-power station and charcoal. Takagi and Kadowaki (1985) reported that the *Paecilomyces* flocculant also had the ability to flocculate all suspended solids from organic materials such as microorganisms to inorganic materials such as aluminium oxide and that Paecilomyces flocculant was a polysaccharide composed of galactosamine.

The application of bioflocculants for the reduction of microbial load and turbidity from river water was examined in comparison with a conventional coagulant agent, alum (Fig. 5.11 - 5.15). The results indicated that the bioflocculants were efficient for the reduction of these bacteria as well as the turbidity. Furthermore, the bioflocculants produced similar results as alum did, but at a slightly lower dosage. The use of alum produced the best results in the removal of the microbial load (Fig. 5.15). Higher concentrations of alum were required to reduce the river water turbidity compared to the use of the bacterial bioflocculants (Fig. 5.11 and 5.13). This can be explained by the production of aluminium hydroxide as a precipitate. In the case of bacterial bioflocculants, only initial suspended particles are agglomerated into larger and settleable flocs, but no additional precipitate is formed. Besides being voluminous, the alum sludges are gelatinous, acidic, and difficult to dewater and dispose in the environment (Degremont, 1989 – cited by Ndabigengesere and Narasiah, 1998). Faust and Aly (1998)

showed that alum was not effective in removing bacteria within the range of 5–10 mg/l. A removal of 99.7% was achieved with 50 mg/l when 14 nephelometric units (NTU) of turbidity was present.

Alum is a widely used coagulant in wastewater treatment. However, medical reports indicated that aluminum might induce Alzheimer's disease, while residual aluminum concentrations in treated water can also impose health problems apart from the production of high amounts of sludge (Letterman and Driscoll, 1988). The maximum contaminant level of aluminum in drinking water was set to 200  $\mu$ g/l (Zouboulisa *et al.*, 2004). Therefore, the use of high concentrations of alum in the treatment of river water must be avoided.

High turbidity and/or colour impart an aesthetically displeasing appearance to water. Apart from a displeasing appearance, turbidity provides adsorption sites for biological organisms and interferes with disinfection. Only a turbidity of 1 NTU is allowed in drinking water (Bitton, 1994). The river water used in this study is not suitable for human consumption because the turbidity was 11.7 NTU. Compared with USEPA Standards (1991), which state that the turbidity of drinking water should be less than 1 ntu, the value of 11.7 NTU is quite excessive. Although turbidity has no serious health effects, it can interfere with disinfection and provide a medium for microbial growth. Turbidity has been shown through scientific studies to be correlated with the contamination of water supplies (typically surface water supplies) with Giardia and Cryptosporidium (USEPA, 1991). Excessive turbidity is often associated with unacceptable tastes, odours, and colour in water and may represent a health concern where heavy metal ions, pesticides or waterborne disease causing organisms may attach to the suspended particles. These organisms include bacteria, viruses, and parasites that can cause symptoms such as nausea, cramps, diarrhoea, and associated headaches (Vigneswaran and Visvanathan, 1995).

It is anticipated that bacterial bioflocculants will be utilized in the areas of wastewater treatment. Due to their relative harmlessness towards humans and the environment, they can also be used in drinking water, downstream processing, in food and fermentation industry. Using natural coagulants in developing countries could effectively alleviate their economic situation and allow further extension of water supply in rural areas. The application of bacterial bioflocculants in the treatment of river water is a promising alternative to using alum. To the best of our knowledge, this is the first study demonstrating the use of bacterial bioflocculants for removal of microorganisms from contaminated water and as such, it was difficult to compare the results with other publications. The removal of organic and inorganic matter from river water using bioflocculants is still in the research stages. However, more studies are required to develop practical applications.

# **CHAPTER SIX**

### CONCLUDING REMARKS

# **6.1 THE RESEARCH IN PERSPECTIVE**

The main objectives of this study were to characterize the properties of the bioflocculants from bacteria, to evaluate the efficacy of the bioflocculant as an alternative to alum in decreasing the microbial load of river water, and to evaluate the ability of the bacterial bioflocculants to remove dyes and chemicals from the textile industries. Six bioflocculant producing bacteria were isolated from Northern Wastewater Treatment Plant. The bacterial isolates were identified and their bioflocculants were purified and analyzed. The bioflocculants were found to be composed of carbohydrates, proteins, uronic acid and amino sugars in varying quantities.

The bioflocculants produced by these bacteria were capable of flocculating kaolin clay, dyes and microbes in river water. The results of the experiments described here demonstrate that these flocculants could efficiently flocculate all suspended solids in aqueous solution and had a wide flocculating activity against both inorganic and organic materials. Flocculant concentration, temperature, pH, time, and cations or salts influenced flocculation by increasing or decreasing the flocculating activity and percentage removal.

The bioflocculants produced by these bacterial strains had a satisfactory level of flocculating activity. These results suggest that these bioflocculants can be successfully applied for the clarification of river water or wastewaters under various environmental conditions. These bioflocculants exhibited flocculating activity comparable or superior to that of existing inorganic flocculants (alum), where up to 99% microbial load and turbidity were reduced.

Coloured-dye-wastewater treatment and decolourization presents an arduous task. Wide ranges of pH, salt concentrations, and chemical structures often add to the complication (Banat *et al.*, 1996; Pinheiro *et al.*, 2004). This study revealed that the bacterial isolates were capable of producing bioflocculants with very good flocculating activity. The bioflocculants were effective to varying degrees in removing the dyes in aqueous solution, in particular whale dye, medi-blue, fawn dye and mixed dyes, with a decolourization efficiency ranging between 20-99.9%. Thus, these bioflocculants may be used in the coagulation process instead of alum. However, more research still needs to be conducted to optimize the conditions for maximum flocculation. Among the most economically viable choices available for effluent treatment/decolourization, and the most practical in terms of labour requirements and running expenses to adopt and develop, appear to be the biological systems. At present, biological systems are known to be capable of dealing with BOD and COD reduction or removal through conventional aerobic biodegradation. They have however, an inherent problem in their inability to remove colour (Banat *et al.*, 1996).

Although decolourization is a challenging process to both the textile industry and the wastewater-treatment facilities that must treat them, the literature suggests a great potential for microbial decolourizing systems for achieving total colour removal and (occasionally) with only a few hours of exposure. Such biological processes could be adopted as a pre-treatment decolourization step, combined with the conventional treatment system (e.g. activated sludge) to reduce the BOD and COD, as an effective alternative for use by the textile-dyeing industries (Pereira et al., 2003). Concerted efforts are still required to establish biological decolourization systems. The techniques by which decolourization occurs vary and among them adsorption seems of great significance for future development in bio-removal or bio-recovery of dye substances. It is important to develop a novel biodegradable and eco-friendly organic coagulant without secondary pollution for wastewater treatment. Unlike some synthetic flocculants, bioflocculants are generally non-toxic and benign to the environment. They have a potential to improve productivities and product quality in bioprocessing, wastewater treatment, and many other industrial operations (Sanghi et al., 2006). Bioflocculants can be produced relatively inexpensively from a variety of microorganisms. Microbial flocculation is a promising alternative to replace or supplement present treatment processes for river water and the removal of very high concentrations of dyes.

### 6.2 POTENTIAL FOR FUTURE DEVELOPMENT OF THIS WORK

Undoubtedly, low-cost bacterial bioflocculants offer many promising benefits for commercial purposes in the future. However, despite a number of papers published on low-cost flocculants, there is little information containing a full study of comparison between flocculants. Although a lot has been accomplished in the area of flocculants, more work is necessary (i) to predict the performance of the adsorption processes for dye removal from industrial effluents under a range of operating conditions, (ii) to better understand the flocculation or adsorption mechanisms and (iii) to demonstrate the use of inexpensive flocculants at an industrial scale (Crini, 2006).

One of the routes still to be explored is the use of thermotolerant or thermophilic microorganisms in decolourization systems. This would be of advantage as many textile and other dye effluents are produced at relatively high temperatures (50-60°C), even after a cooling or heat-exchange step. The availability of thermotolerant organisms may consequently reduce cost significantly, through removing the need for further removal of low-grade heat and through allowing more immediate treatment (Banat *et al.*, 1996).

Techniques used in studies of polysaccharides, including chemical composition, linkage pattern, and higher order structures are in constant development. They provide information necessary for understanding of the polysaccharide properties and functions. Recent advancements in studies of the polysaccharides at the single-molecule level are essential. These techniques can be used to investigate properties of single molecules close to physiological conditions. This field is expected to have increasing impact on the further advancement of the molecular understanding of the role of polysaccharides in various biological processes such as recognition and cell adhesion. Since the primary structure of polysaccharides is not coded directly in the genetic sequence, the advancement in primary structure determination has not evolved as rapidly within the polysaccharide field as it has for proteins (Sletmoen *et al.*, 2003). This, together with the fact that the experimental procedures for determination of the relative contents and arrangement of the monosaccharides are technically more demanding, makes the description of the polysaccharide primary structure not an easy task.

The development of sensitive detection methods will provide very useful information that will aid the structural elucidation of these extracellular polysaccharides. The use of accurate equipment such as Fourier transform infrared, X-ray photoelectron spectroscopy, and High performance liquid chromatography etc. in the future will aid in the analysis of the chemical compositions of the extracellular polysaccharides. The role of molecular biology has yet to feature prominently in this vital area of environmental protection (Shubo *et al.*, 2005). More research on these areas mentioned will offer a better understanding of the function and properties of the bacterial bioflocculants.

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# **APPENDIX A: 16S rDNA sequences**

### 16S rDNA sequence of Bacillus subtilis (E1)

#### 16S rDNA sequence of *Pseudomonas pseudoalcaligenes* (A17)

TATTTAGCGTCTCTGGACGGGTGAGTAATGCCTTAGGAATCTGCCTGGTAGTGGGGGGATAACG TTCCGAAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGCAGGGGACCTTCGGGCCT TGCGCTATCAGATGAGCCTAGGTCGGATTAGCTAGTTGGTGAGGTAATGGCTCACCAAGGCGA CGATCCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACCTGAGACACGGTCCAGACT CCTACGGGAGGCAGCAGTGGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCG CGTGTGTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCATTAACCTA ATACGTTAGTGTTTTGACGTTACCAACAGAATAAGCACCGGCTAACTTCGTGCCAGCAGCCGC GGTAATACGAAGGGTGCAAGCGTTAATCGGAATTACTGGGCGTAAAGCGCGCGTAGGTGGTT CGTTAAGTTGGATGTGAAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAAACTGGCGAGCT AGAGTACGGTAGAGGGTAGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAGG AACACCAGTGGCGAAGGCGACTACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGG AGCAAACAGGATTAAGATACCTGGTAGTCCACGCCGTAAACGTGTCAACTAGCCGTTGGAA TCCTTGAGATTTAGTGGCGCAGCTAACCGCATTTG

#### 16S rDNA sequence of Exiguobacterium acetylicum D1

### 16S rDNA sequence of *Staphylococcus aureus* (A22)

#### 16S rDNA sequence of Klebsiella terrigena (R2)

#### 16S rDNA sequence of *Pseudomonas plecoglossicida* (A14)

CATCAGCGCGTGGACGGGTGAGTAATGCCTAGGAATCTGCCTGGTAGTGGGGGGACAACGTTT CGAAAGGAACGCTAATACCGCATACGTCCTACGGGAGAAAGAGGGGACCTTCGGGCCTTGCG CTATCAGATGAGCCTAGGTCGGATTAGCTAGTGGTGGGGTAATGGCTCACCAAGGCGACGAT CCGTAACTGGTCTGAGAGGATGATCAGTCACACTGGAACTGAGACACGGTCCAGACTCCTAC GGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCAGCCATGCCGCGTGT GTGAAGAAGGTCTTCGGATTGTAAAGCACTTTAAGTTGGGAGGAAGGGCAGTAAGTTAATAC CTTGCTGTTTTGACGTTACCGACAGAATAAGCACCGGCTAACTCTGTGCCAGCAGCGCGCGGTA ATACAGAGGGTGCAAGCGTTAATCGGAATTACTGGGAGCAACTCTGTGCCAGCAGCCGCGGTA ATACAGAGGGTGCAAGCCCCGGGCTCAACCTGGGAACTGCATCCAAACTGGCAAGCTAGAG TACGGTAGAGGGTGGTGGAATTTCCTGTGTAGCGGTGAAATGCGTAGATATAGGAAAGGAAC ACAGTGGCGAAGGCGACCACCTGGACTGATACTGACACTGAGGTGCGAAAGCGTGGGAGCA AACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCAACTAGCCGTGGGAACCT GAGATTAGTG

Isolate code	percentage probability
A22	78% Staphylococcus
A14	83% Pseudomonas
A17	77% Pseudomonas
D1	70% Corynebacterium
E1	93% Bacillus
R2	88% Klebsiella

**Table 6.1:** Identity of bacterial isolates based on the API (percentage probability)

# **APPENDIX B: Data**

Figures in parenthesis appear in the text

<b>Table 7.1:</b> Production of bioflocculants	by different l	bacterial isolates	(Fig. 2.2)
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Isolate	Amount of polysaccharide produced (g\l)
A11	3.000
A12	6.333
A13	3.667
A14*	8.333
A15	2.333
A16	7.333
A17*	15.167
A18	9.333
A21	1.000
A22*	10.833
A23	7.667
A24	8.667
D1*	10.167
D2	5.000
E1*	6.333
E2	0.667
E3	4.333
E4	2.667
E5	6.667
R1	4.667
R2*	27.660
R3	4.333
R4	1.333
R5	5.000
R6	7.667

# \*Bacteria selected for further study

- A1 = activated sludge (aerobic)
- A2 =activated sludge (anaerobic)
- D1 = digested sludge
- E1 = effluent clarifier

# (a) Phenol-sulfuric acid assay for the determination of carbohydrates

Sensitivity: glucose (0.05–2mM)

*Final volume*: 1.4 ml

Reagents:

- (a) phenol dissolved in water (5% w/v).
- (b) Concentrated sulphuric acid.

Method

- Mix samples, standards and control solutions (200 µl containing up to 100 µg carbohydrate) with 200 µl of reagent A.
- (ii) Add 1.0 ml of reagent B rapidly and directly to the solution surface without touching the sides of the tube.
- (iii) Leave the solutions undisturbed for 10 min before shaking vigorously.
- (iv) Determine the absorbance at 490 nm after a further 30 min.

# (b) Folin-Lowry method for the determination of protein

Sensitivity: Bovine serum albumin (0.002–2.000mM)

# Final volume: 6.5 ml

Reagents:

- (a) 2% Na<sub>2</sub>CO<sub>3</sub> in 0.1 N NaOH
- (b) 1% NaK Tartrate in  $H_2O$
- (c) 0.5% CuSO<sub>4</sub>.5 H<sub>2</sub>O in H<sub>2</sub>O
- (d) 48 ml of A, 1 ml of B, 1 ml C
- (e) Phenol Reagent 1 part Folin-Phenol (2 N): 1 part water

# Method

- (i) Add 5 ml of reagent D to 1 ml of the test solution.
- (ii) Mix thoroughly and allow to stand for 10 min or longer.
- (iii) Add 0.5 ml of reagent E rapidly with immediate mixing.
- (iv) After 30 min read the extinction against the appropriate blank at 750 nm

 Estimate the protein concentration of the unknown solution after preparing a standard curve.

# (c) Carbazole assay for the determination of uronic acid

Sensitivity: D-glucurono-6,3-lactone (0.001–0.050mM)

# Final volume: 1.8 ml

# Reagents:

- (a) Dissolve 0.95 g of sodium tetraborate decahydrates in 2.0 ml of hot water and add
   98 ml of ice-cold concentrated sulphuric acid carefully with stirring.
- (b) Dissolve 125 mg of carbazole (recrystallized from ethanol) in 100 ml of absolute ethanol to give a stable reagent.

#### Method

- (i) Cool the samples, standards and controls  $(250 \ \mu l)$  in an ice bath.
- (ii) Add ice-cold reagent A (1.5 ml) with mixing and cooling in the ice bath.
- (iii) Heat the mixtures at  $100^{\circ}$ C for 10 min.
- (iv) Cool rapidly in the ice-bath.
- (v) Add 50  $\mu$ l of reagent B and mix well.
- (vi) Reheat at  $100^{\circ}$ C for 15 min.
- (vii) Cool rapidly at room temperature and determine the absorbance at 525 nm.

# (d) Morgan-Elson assay for the determination of hexosamine

Sensitivity: 2-acetamido-2-deoxy-D-glucose(0.001–0.110 mM)

# Final volume: 1.8 ml

# Reagents:

- (a) Dissolve 6.1 g of di-potassium tetraborate tetrahydrate in 80 ml of water and make up to 100 ml with water.
- (b) Add 1.5 ml of water to 11 ml of concentrated hydrochloric acid. Add a further 87.5 ml of glacial acetic acid and dissolve 10 g of 4-(*N*,*N*-dimethylamino)-

benzaldehyde in this mixture. Dilute 10 ml to 100 ml with glacial acetic acid immediately prior to use.

# Method

- (i) Add samples, standards and controls (250 µl) to 50 µl of reagent A
- (ii) Heat each mixture at  $100^{\circ}$ C for 3 min.
- (iii) After cooling rapidly to room temperature, add 1.5 ml of reagent B, washing down any condensate formed.
- (iv) Incubate the samples at  $37^{\circ}$ C for 20 min.
- (v) After cooling to room temperature, determine the absorbance at 585 nm.

Conc (mM)	OD <sub>490nm</sub>	Average	Standard deviation
0.002	0.054	0.057	0.006
	0.066		
	0.051		
0.004	0.138	0.123	0.012
	0.108		
	0.123		
0.006	0.141	0.132	0.560
	1.320		
	0.123		
0.008	0.270	0.180	0.037
	0.180		
	0.210		
0.01	0.195	0.187	0.006
	0.180		
	0.189		
0.050	0.231	0.219	0.010
	0.219		
	0.207		
0.100	0.399	0.395	0.004
	0.390		
	0.396		
0.300	0.633	0.642	0.006
	0.648		
	0.645		
0.500	0.984	0.985	0.004
	0.981		
	0.990		
1	1.293	1.302	0.007
	1.302		
	1.311		
1.500	2.067	2.064	0.009
	2.073		
	2.052		
2	2.856	2.853	0.002
	2.850		

**Table 7.2:** Determination of the total sugar content using Phenol Sulphuric Acid<br/>assay at  $OD_{490nm}$ 



Fig.7.1: Standard curve for the determination of D-Glucose concentration at OD<sub>490nm</sub>.

Conc (mM)	OD <sub>750nm</sub>	Average	Standard deviation
0.002	0.021	0.021	0.003
	0.015		
	0.027		
0.004	0.03	0.038	0.006
	0.039		
	0.045		
0.006	0.039	0.049	0.007
	0.051		
	0.057		
0.008	0.057	0.055	0.007
	0.063		
	0.045		
0.010	0.099	0.088	0.009
	0.087		
	0.078		
0.050	0.216	0.209	0.006
	0.201		
	0.210		
0.100	0.378	0.370	0.006
	0.369		
	0.363		
0.500	1.410	1.404	0.004
	1.401		
	1.401		
1.500	2.559	2.562	0.009
	2.574		
	2.553		
2	2.610	2.616	0.005
	2.616		
	2.622		

**Table 7.3:** Determination of the total protein content using the Folin-Lowry method at OD<sub>750nm</sub>



- **Fig. 7.2:** Standard curve for the determination of Bovine serum album (BSA) concentration at OD<sub>750nm</sub>.
- Table 7.4: Determination of the uronic acid content using the Carbazole assay at OD<sub>750nm</sub>

Conc (mM)	OD <sub>750nm</sub>	Average	Standard deviation
0.001	0.630	0.540	0.073
	0.540		
	0.450		
0.003	0.57	0.570	0.073
	0.660		
	0.480		
0.005	0.999	1.002	0.003
	1.005		
	1.002		
0.010	2.613	2.628	0.012
	2.628		
	2.643		
0.050	2.790	3	0.218
	2.910		
	3.300		



**Fig. 7.3:** Standard curve for the determination of D- Glucurono-6,3-lactone concentration at OD<sub>750nm</sub>.

Table 7.5:         Determination	of the hexosamine (amino	sugars) content	using the
Morgan-Elson	assay at OD <sub>585nm</sub>		

Conc (mM)	OD7 <sub>585nm</sub>	Average	Standard deviation
0.001	0.003	0.002	0.001
	0		
	0.003		
0.005	0.006	0.014	0.007
	0.021		
	0.015		
0.010	0.030	0.026	0.004
	0.027		
	0.021		
0.030	0.048	0.055	0.006
	0.054		
	0.063		
0.050	0.111	0.123	0.009
	0.126		
	0.132		
0.070	0.198	0.199	0.009
	0.210		
	0.189		
0.090	0.249	0.242	0.008
	0.231		
	0.246		
0.110	0.300	0.298	0.001
	0.297		
	0.297		



**Fig.7.4:** Standard curve for the determination of 2-acetamido-2deoxy-D- Glucuse concentration at OD<sub>585nm</sub>.

<b>X</b> 1	X X 111 1	01.05	01.10	01.15	01.00
Isolates	Undiluted	01:05	01:10	01:15	01:20
R 2	0.624	0.120	0.114	0.039	0.048
	0.630	0.132	0.093	0.051	0.036
	0.612	0.141	0.105	0.045	0.039
Average	0.622	0.134	0.104	0.045	0.041
Standard					
deviation	0.007	0.009	0.009	0.005	0.005
E1	0.309	0.048	0.063	0.033	0.018
	0.291	0.066	0.051	0.039	0.009
	0.297	0.072	0.045	0.030	0.015
Average	0.299	0.062	0.053	0.034	0.014
Standard					
deviation	0.007	0.010	0.007	0.004	0.004
A14	1.092	0.066	0.057	0.030	0.033
	1.107	0.084	0.048	0.042	0.027
	1.077	0.096	0.063	0.033	0.024
Average	1.092	0.082	0.056	0.035	0.028
Standard					
deviation	0.012	0.012	0.006	0.005	0.004
A17	0.225	0.186	0.165	0.105	0.090
	0.231	0.192	0.183	0.090	0.099
	0.219	0.177	0.177	0.114	0.111
Average	0.225	0.185	0.175	0.103	0.100
Standard					
deviation	0.005	0.006	0.007	0.010	0.009
D1	0.174	0.099	0.153	0.075	0.051
	0.183	0.117	0.126	0.084	0.093
	0.195	0.099	0.144	0.066	0.072
Average	0.184	0.105	0.141	0.075	0.072
Standard					
deviation	0.009	0.008	0.011	0.007	0.017
A22	0.789	0.186	0.135	0.069	0.039
	0.777	0.207	0.159	0.093	0.030
	0.771	0.219	0.111	0.060	0.063
Average	0.779	0.204	0.135	0.074	0.044
Standard					
deviation	0.007	0.013	0.020	0.014	0.014

**Table 7.6:** OD<sub>490nm</sub> values of various dilutions of bioflocculants used for the determination of total sugar concentration
Isolates	Undiluted	01:05	01:10	01:15	01:20
R 2	0.117	0.090	0.033	0.039	0.051
	0.126	0.081	0.048	0.045	0.042
	0.138	0.066	0.063	0.048	0.027
Average	0.127	0.079	0.048	0.044	0.04
Standard					
deviation	0.009	0.011	0.012	0.004	0.010
E1	0.300	0.141	0.081	0.063	0.051
	0.297	0.132	0.060	0.057	0.045
	0.291	0.129	0.039	0.045	0.033
Average	0.296	0.134	0.060	0.055	0.043
Standard					
deviation	0.004	0.005	0.018	0.007	0.007
A14	0.162	0.138	0.126	0.081	0.069
	0.189	0.123	0.105	0.066	0.057
	0.201	0.111	0.087	0.051	0.045
Average	0.184	0.124	0.106	0.066	0.057
Standard					
deviation	0.016	0.011	0.016	0.012	0.010
A17	0.231	0.186	0.153	0.144	0.15
	0.249	0.177	0.132	0.135	0.135
	0.216	0.168	0.120	0.120	0.108
Average	0.232	0.177	0.135	0.133	0.131
Standard					
deviation	0.013	0.007	0.013	0.010	0.017
D1	0.129	0.123	0.135	0.057	0.066
	0.156	0.108	0.099	0.075	0.054
	0.183	0.096	0.087	0.084	0.039
Average	0.156	0.109	0.107	0.072	0.053
Standard					
deviation	0.022	0.011	0.020	0.011	0.011
A22	0.135	0.081	0.072	0.093	0.084
	0.123	0.096	0.081	0.048	0.054
	0.147	0.111	0.069	0.057	0.057
Average	0.135	0.096	0.074	0.066	0.065
Standard					
deviation	0.011	0.012	0.005	0.019	0.013

### **Table 7.7:** OD<sub>750nm</sub> values of various dilutions of bioflocculants used for the determination of protein concentration

**Table 7.8:** Final concentrations (mM) of the unknown carbohydrates and proteins in<br/>undiluted bioflocculants as calculated from the standard curves<br/>(Fig. 7.1 and 7.2) and OD values (Table 7.2, 7.3, 7.6 and 7.7) (Fig. 2.3)

Bioflocculants	Carbohydrates (mM)	Proteins (mM)
R2	0.356	0.004
E1	0.107	0.111
A14	0.706	0.040
A17	0.056	0.070
D1	0.020	0.022
A22	0.470	0.009

Isolates	Undiluted	01:05	01:10	01:15	01:20
R 2	0.987	0.597	0.297	0.264	0.207
	0.972	0.591	0.303	0.255	0.183
	0.963	0.585	0.303	0.246	0.189
Average	0.974	0.591	0.301	0.255	0.193
Standard					
deviation	0.010	0.005	0.003	0.007	0.010
E1	0.597	0.297	0.183	0.159	0.075
	0.579	0.282	0.171	0.144	0.066
	0.561	0.273	0.159	0.132	0.054
Average	0.579	0.284	0.171	0.145	0.065
Standard					
deviation	0.015	0.012	0.010	0.011	0.009
A14	0.591	0.351	0.315	0.177	0.129
	0.567	0.363	0.303	0.162	0.141
	0.546	0.339	0.297	0.144	0.111
Average	0.568	0.351	0.305	0.161	0.127
Standard					
deviation	0.018	0.009	0.008	0.013	0.012
A17	0.579	0.366	0.213	0.135	0.204
	0.573	0.381	0.207	0.129	0.195
	0.561	0.351	0.177	0.117	0.183
Average	0.571	0.366	0.199	0.127	0.194
Standard					
deviation	0.007	0.012	0.016	0.007	0.009
D1	0.567	0.360	0.270	0.210	0.069
	0.558	0.354	0.255	0.201	0.054
	0.549	0.345	0.237	0.192	0.042
Average	0.558	0.353	0.254	0.201	0.055
Standard					
deviation	0.007	0.006	0.013	0.007	0.011
A22	0.564	0.327	0.273	0.141	0.045
	0.555	0.312	0.267	0.129	0.033
	0.543	0.294	0.261	0.111	0.039
Average	0.554	0.311	0.267	0.127	0.039
Standard					
deviation	0.009	0.013	0.005	0.012	0.005

### **Table 7.9:** OD<sub>525nm</sub> values of various dilutions of bioflocculants used for the determination of uronic acid concentration

**Table 7.10:** Final concentration of the unknown uronic acid (mM) in undilutedbioflocculants as calculated from the standard curve (Fig.7.3) and OD values(Table 7.4 and 7.9) (Fig. 2.4)

Bioflocculants	Concentration (mM)
R2	45.330
E1	27.318
A14	26.817
A17	26.954
D1	26.361
A22	26.178

Isolates	Undiluted	01:05	01:10	01:15	01:20
A17	0.018	0.012	0.006	0.003	0
	0.021	0.015	0.006	0.006	0.003
	0.027	0.006	0.003	0.003	0.003
Average	0.022	0.011	0.005	0.004	0.002
Standard					
deviation	0.003	0.004	0.001	0.001	0.001
A14	0.003	0	0	0	0
	0.003	0	0	0	0
	0	0	0	0	0
Average	0.002	0	0	0	0
Standard					
deviation	0.001	0	0	0	0
A22	0.003	0.003	0	0	0
	0.006	0.003	0	0	0
	0.003	0	0	0	0
Average	0.004	0.002	0	0	0
Standard					
deviation	0.001	0.001	0	0	0
D1	0	0	0	0	0
	0	0	0	0	0
	0	0	0	0	0
Average	0	0	0	0	0
Standard					
deviation	0	0	0	0	0
E1	0.021	0.003	0	0	0
	0.012	0.006	0	0	0
	0.018	0.003	0	0	0
Average	0.017	0.004	0	0	0
Standard					
deviation	0.00374	0.00141	0	0	0
R 2	0.003	0	0	0	0
	0.003	0.003	0	0	0
	0.003	0	0	0	0
Average	0.003	0.001	0	0	0
Standard			_		
deviation	0	0.00141	0	0	0
A17	0.021	0.012	0.006	0.003	0
	0.018	0.015	0.006	0.006	0.003
	0.027	0.006	0.003	0.003	0.003
Average	0.022	0.011	0.005	0.004	0.002
Standard		0.551			
deviation	0.004	0.004	0.001	0.001	0.001

## **Table 7.11:** OD<sub>585nm</sub> values of various dilutions of bioflocculants used for the determination of hexose amine

**Table 7.12:** Final concentration of the unknown hexosamine (mM) in undiluted<br/>bioflocculants as calculated from the standard curve (Fig.7.4) and OD values<br/>(Table 7.5 and 7.11) (Fig. 2.5)

Bioflocculants	Concentration (mM)
A17	0.054
E1	0.041
A22	0.005
R2	0.002
A14	0.002
D1	0.000

Isolates	0	12	24	36	48	60	72	84
E1	0.147	1.302	1.737	1.773	1.848	1.773	1.752	1.749
	0.141	1.293	1.728	1.755	1.842	1.767	1.734	1.734
	0.156	1.308	1.746	1.788	1.854	1.782	1.767	1.767
Average	0.148	1.301	1.737	1.772	1.848	1.774	1.751	1.75
Standard								
deviation	0.006	0.006	0.007	0.013	0.005	0.006	0.013	0.013
R 2	0.147	1.125	1.419	1.485	1.527	1.572	1.521	1.761
	0.141	1.113	1.401	1.482	1.521	1.566	1.503	1.746
	0.156	1.134	1.437	1.491	1.536	1.578	1.536	1.779
Average	0.148	1.126	1.419	1.486	1.528	1.572	1.52	1.762
Standard								
deviation	0.006	0.009	0.014	0.004	0.006	0.005	0.013	0.013
A17	0.147	0.768	1.35	1.383	1.644	1.632	1.683	1.44
	0.141	0.765	1.2	1.365	1.635	1.614	1.671	1.35
	0.156	0.774	1.5	1.401	1.653	1.65	1.698	1.53
Average	0.148	0.769	1.35	1.383	1.644	1.632	1.684	1.44
Standard								
deviation	0.006	0.004	0.122	0.015	0.007	0.015	0.011	0.073
A14	0.147	1.029	1.617	1.632	1.797	1.803	1.869	1.53
	0.141	1.008	1.602	1.62	1.8	1.785	1.86	1.515
	0.156	1.047	1.632	1.641	1.794	1.821	1.878	1.548
Average	0.148	1.028	1.617	1.631	1.797	1.803	1.869	1.531
Standard								
deviation	0.003	0.016	0.012	0.009	0.00245	0.0147	0.00735	0.01349
A22	0.147	0.498	1.941	1.659	1.608	1.566	1.557	1.554
	0.141	0.492	1.923	1.644	1.602	1.557	1.542	1.557
	0.156	0.504	1.959	1.674	1.617	1.572	1.572	1.554
Average	0.148	0.498	1.941	1.659	1.609	1.565	1.557	1.555
Standard								
deviation	0.006	0.005	0.015	0.012	0.006	0.006	0.012	0.001
D1	0.147	1.368	1.539	1.554	1.569	1.551	1.539	1.539
	0.141	1.356	1.527	1.545	1.566	1.533	1.527	1.527
	0.156	1.377	1.554	1.563	1.575	1.569	1.554	1.554
Average	0.148	1.367	1.54	1.554	1.57	1.551	1.54	1.54
Standard								
deviation	0.006	0.009	0.011	0.007	0.004	0.015	0.011	0.011
Control	0.147	0.147	0.147	0.147	0.147	0.147	0.147	0.147
	0.141	0.141	0.141	0.141	0.141	0.141	0.141	0.141
	0.156	0.156	0.156	0.156	0.156	0.156	0.156	0.156
Average	0.148	0.148	0.148	0.148	0.148	0.148	0.148	0.148
Standard								
deviation	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006

Table 7.13: Growth patterns of bacterial isolates with time at  $OD_{550nm}$  (Fig. 3.1)

Isolates	0	12	24	36	48	60	72	84
E1	0.654	0.378	0.180	0.258	0.249	0.225	0.219	0.219
	0.648	0.375	0.270	0.240	0.237	0.219	0.204	0.204
	0.663	0.384	0.360	0.276	0.258	0.231	0.237	0.237
Average	0.655	0.379	0.270	0.258	0.248	0.225	0.220	0.220
Standard								
deviation	0.006	0.004	0.073	0.015	0.009	0.005	0.013	0.013
R 2	0.654	0.357	0.327	0.258	0.237	0.294	0.330	0.330
	0.648	0.354	0.315	0.255	0.225	0.3	0.315	0.315
	0.663	0.363	0.342	0.264	0.246	0.285	0.348	0.348
Average	0.655	0.358	0.328	0.259	0.236	0.293	0.331	0.331
Standard								
deviation	0.006	0.004	0.011	0.004	0.009	0.006	0.013	0.013
A17	0.654	0.480	0.192	0.273	0.309	0.315	0.324	0.324
	0.648	0.390	0.177	0.252	0.291	0.306	0.318	0.318
	0.663	0.570	0.104	0.291	0.324	0.321	0.333	0.333
Average	0.655	0.48	0.191	0.272	0.308	0.314	0.325	0.325
Standard								
deviation	0.006	0.073	0.038	0.016	0.013	0.006	0.006	0.006
A14	0.654	0.357	0.297	0.279	0.225	0.315	0.354	0.354
	0.648	0.354	0.306	0.258	0.216	0.306	0.339	0.339
	0.663	0.363	0.288	0.297	0.234	0.321	0.372	0.372
Average	0.655	0.538	0.297	0.278	0.225	0.314	0.355	0.355
Standard								
deviation	0.006	0.004	0.007	0.016	0.007	0.006	0.013	0.013
A22	0.654	0.576	0.273	0.219	0.219	0.330	0.333	0.333
	0.648	0.567	0.252	0.204	0.201	0.330	0.321	0.321
	0.663	0.585	0.291	0.237	0.234	0.360	0.348	0.348
Average	0.655	0.576	0.272	0.22	0.218	0.33	0.334	0.334
Standard								
deviation	0.006	0.007	0.015	0.013	0.013	0.014	0.011	0.011
D1	0.654	0.369	0.318	0.282	0.231	0.285	0.342	0.342
	0.648	0.360	0.306	0.297	0.213	0.279	0.336	0.336
	0.663	0.375	0.327	0.273	0.249	0.294	0.348	0.348
Average	0.655	0.368	0.317	0.284	0.231	0.286	0.342	0.342
Standard								
deviation	0.006	0.006	0.009	0.010	0.015	0.006	0.005	0.005
Control	0.654	0.654	0.654	0.654	0.654	0.654	0.654	0.654
	0.648	0.648	0.648	0.648	0.648	0.648	0.648	0.648
	0.663	0.663	0.663	0.663	0.663	0.663	0.663	0.663
Average	0.655	0.655	0.655	0.655	0.655	0.655	0.655	0.655
Standard								
deviation	0.006	0.006	0.006	0.006	0.006	0.006	0.006	0.006

**Table 7.14:** OD<sub>550nm</sub> values at 12 hr time intervals for the determination of flocculating activity

Isolate	0	12hrs	24hrs	36hrs	48hrs	60hrs	72hrs	84hrs
E1	0	1.112	2.177	2.349	2.505	2.917	3.018	3.018
R2	0	1.267	1.522	2.334	2.710	1.886	1.494	1.494
A17	0	0.556	3.709	2.149	1.720	1.658	1.550	1.550
A14	0	0.332	1.840	2.070	2.395	1.658	1.290	1.290
A22	0	0.371	2.149	3.018	3.060	1.503	1.467	1.467
D1	0	1.190	1.628	1.994	2.802	1.970	1.397	1.397
Control	0	0	0	0	0	0	0	0

**Table 7.15:** Flocculating activity of the culture broth with time as derived from Table7.14 using an equation for flocculating activity in Section 3.2.1 (Fig. 3.2)

**Table 7.16:** Percentage removal (B–A/B x 100) of kaolin clay with time by the culture broth as derived from Table 7.14 (Fig. 3.3)

Isolate	0	12	24	36	48	60	72	84
E1	0	42.137	58.779	60.611	62.137	65.649	66.412	66.412
R2	0	45.344	49.924	60.458	63.969	55.267	49.466	49.466
A17	0	26.718	70.840	58.473	52.977	52.061	50.382	50.382
A14	0	17.863	54.656	57.557	61.069	52.061	45.802	45.802
A22	0	12.672	58.473	66.412	66.718	49.618	49.008	49.008
D1	0	43.817	51.603	56.641	64.733	56.336	47.786	47.786
Control	0	0	0	0	0	0	0	0

Isolates	10	8	6	4	2
A17	1.308	0.948	0.750	0.570	0.324
	1.302	0.939	0.600	0.600	0.315
	1.317	0.954	0.900	0.540	0.330
Average	1.309	0.947	0.75	0.570	0.323
Standard					
deviation	0.006	0.006	0.122	0.024	0.006
A14	1.572	1.539	0.876	0.549	0.411
	1.554	1.530	0.861	0.531	0.339
	1.590	1.548	0.894	0.567	0.420
Average	1.572	1.539	0.877	0.549	0.410
Standard					
deviation	0.015	0.007	0.013	0.015	0.036
D1	1.617	0.948	0.747	0.534	0.312
	1.602	0.936	0.741	0.522	0.300
	1.635	0.957	0.753	0.549	0.321
Average	1.618	0.947	0.747	0.535	0.311
Standard					
deviation	0.013	0.009	0.005	0.011	0.009
R 2	1.317	1.185	0.594	0.465	0.300
	1.341	1.197	0.609	0.459	0.297
	1.299	1.206	0.579	0.471	0.300
Average	1.319	1.197	0.594	0.465	0.299
Standard					
deviation	0.017	0.009	0.012	0.005	0.001
E1	1.995	1.563	0.630	0.405	0.210
	2.013	1.545	0.618	0.396	0.207
	1.974	1.581	0.645	0.414	0.216
Average	1.994	1.563	0.631	0.405	0.211
Standard					
deviation	0.015	0.015	0.011	0.007	0.004
A22	1.374	1.218	0.846	0.579	0.378
	1.362	1.209	0.828	0.561	0.360
	1.383	1.224	0.864	0.597	0.396
Average	1.373	1.217	0.846	0.579	0.378
Standard					
deviation	0.009				
Control	2.883				
	2.862				
	2.892				
Average	2.879				
Standard					
deviation	0.013				

**Table 7.17:** OD<sub>550nm</sub> values for the determination of flocculating activity assay of the bacterial bioflocculants

**Table 7.18:** Flocculating activity assay of the bacterial bioflocculants as derived from<br/>Table 7.17 using an equation for flocculating activity in Section 3.2.1<br/>(Fig. 3.4)

Isolate	Flocculating activity	Standard deviation
E1	3.362	0.159
A14	2.072	0.213
A17	1.885	0.407
D1	2.701	0.215
R2	2.746	0.383
A22	1.567	0.411

Table 7.19: OD<sub>550nm</sub> values for the determination of flocculation of bacterial cells

Isolates	OD <sub>550nm</sub>	Average	Standard deviation
Control	0.231	2.332	0
	0.231		
	0.231		
A14	1.929	1.929	0.012
	1.944		
	1.914		
A17	2.004	2.005	0.011
	2.019		
	1.992		
A22	1.917	1.919	0.010
	1.932		
	1.908		
D1	1.416	1.417	0.011
	1.431		
	1.404		
E1	1.200	1.201	0.011
	1.215		
	1.188		
R 2	2.073	2.073	0.007
	2.082		
	2.064		

**Table 7.20:** Flocculation of the bacterial cells as derived from Table 7.19 using anequation for flocculating activity in Section 3.2.1 (Fig. 3.5)

Isolate	Flocculating activity	Standard deviation
A14	2.072	0.145
A17	1.885	0.099
A22	1.567	0.100
D1	2.701	0.152
E1	3.362	0.127
R2	1.103	0.119

(115	. 5.0)						
	A17	A14	D1	E1	R 2	A22	Control
P. aeruginosa	1.674	1.713	1.644	1.707	1.734	1.599	1.74
	1.689	1.725	1.659	1.722	1.731	1.632	1.728
	1.653	1.704	1.626	1.737	1.692	1.653	1.719
Average	1.672	1.714	1.643	1.722	1.719	1.628	1.729
Standard deviation	0.015	0.009	0.013	0.012	0.019	0.022	0.009
P. maribilis	1.395	1.344	1.362	1.299	1.344	1.344	1.398
	1.407	1.362	1.401	1.317	1.374	1.353	1.416
	1.383	1.323	1.383	1.308	1.359	1.347	1.407
Average	1.394	1.343	1.384	1.308	1.360	1.348	1.407
Standard deviation	0.099	0.016	0.016	0.007	0.012	0.004	0.007
S. marcescens	1.794	1.794	1.827	1.809	1.803	1.647	1.839
	1.821	1.821	1.827	1.830	1.827	1.626	1.863
	1.809	1.809	1.833	1.818	1.815	1.635	1.857
Average	1.808	1.808	1.829	1.819	1.815	1.636	1.853
Standard deviation	0.011	0.011	0.003	0.009	0.010	0.009	0.010
A. faecalis	0.573	0.645	0.576	0.621	0.627	0.588	0.708
	0.552	0.657	0.561	0.585	0.618	0.606	0.717
	0.564	0.651	0.567	0.606	0.621	0.6	0.696
Average	0.563	0.651	0.568	0.604	0.622	0.598	0.707
Standard deviation	0.009	0.005	0.006	0.015	0.004	0.007	0.009
C. fruendii	1.386	1.407	1.296	1.359	1.374	1.389	1.401
· · ·	1.365	1.374	1.32	1.335	1.341	1.371	1.389
	1.377	1.392	1.308	1.347	1.359	1.38	1.413
Average	1.376	1.391	1.308	1.347	1.358	1.381	1.4
Standard deviation	0.009	0.013	0.010	0.010	0.013	0.007	0.0010
B. coagulans	1.656	1.653	1.659	1.677	1.683	1.665	1.677
	1.629	1.629	1.650	1.656	1.668	1.638	1.692
	1.644	1.626	1.671	1.668	1.677	1.650	1.665
Average	1.643	1.642	1.660	1.667	1.676	1.651	1.678
Standard deviation	0.011	0.012	0.009	0.009	0.006	0.011	0.011
B. cereus	1.455	1.383	1.443	1.437	1.443	1.401	1.455
	1.443	1.404	1.431	1.404	1.416	1.386	1.44
	1.449	1392	1.437	1.422	1.428	1.392	1.47
Average	1.449	1.393	1.437	1.421	1.429	1.393	1.455
Standard deviation	0.005	0.065	0.005	0.013	0.011	0.006	0.012
C. hvstolvticum	0.033	0.069	0.081	0.072	0.051	0.051	0.105
	0.024	0.036	0.048	0.051	0.036	0.069	0.078
	0.027	0.054	0.066	0.078	0.042	0.060	0.093
Average	0.028	0.053	0.065	0.067	0.043	0.06	0.092
Standard deviation	0.003	0.013	0.013	0.011	0.006	0.007	0.011
S. pyogenes	0.693	0.69	0.759	0.702	0.741	0.681	0.768
	0.690	0.717	0.741	0.687	0.735	0.666	0.759
	0.699	0.702	0.750	0.693	0.738	0.672	0.774
Average	0.694	0.703	0.750	0.694	0.738	0.673	0.767
Standard deviation	0.004	0.011	0.007	0.006	0.002	0.006	0.006
S. cerevisiae	0.087	0.075	0.099	0.093	0.054	0.003	0.111
	0.081	0.063	0.066	0.066	0.051	0	0.093
	0.093	0.069	0.084	0.081	0.06	0.003	0.102
Average	0.087	0.069	0.083	0.08	0.055	0.002	0.102
Standard deviation	0.005	0.005	0.013	0.011	0.004	0.001	0.007
	1	0.000	0.000			1	

**Fig. 7.21:** OD<sub>550nm</sub> values for the determination of flocculation of microbial cultures (Fig. 3.6)

Isolates	10	20	30	50
Control	0.084	0.084	0.084	0.084
	0.075	0.075	0.075	0.075
	0.069	0.069	0.069	0.069
Average	0.076	0.076	0.076	0.076
Standard deviation	0.006	0.006	0.006	0.006
Alum	0.015	0.015	0.015	0.015
	0.006	0.006	0.006	0.006
	0.021	0.021	0.021	0.021
Average	0.014	0.014	0.014	0.014
Standard deviation	0.006	0.006	0.006	0.006
D1	0.027	0.024	0.015	0.006
	0.027	0.030	0.003	0.015
	0.030	0.015	0.021	0.012
Average	0.028	0.023	0.022	0.011
Standard deviation	0.001	0.006	0.007	0.004
A14	0.063	0.054	0.033	0.024
	0.048	0.042	0.018	0.009
	0.057	0.048	0.027	0.015
Average	0.056	0.048	0.0026	0.016
Standard deviation	0.006	0.005	0.006	0.006
A17	0.024	0.015	0.006	0.009
	0.033	0.027	0.015	0.003
	0.027	0.036	0.012	0.006
Average	0.028	0.026	0.011	0.006
Standard deviation	0.004	0.009	0.004	0.002
A22	0.033	0.027	0.009	0.006
	0.027	0.009	0.006	0.003
	0.039	0.018	0.006	0.006
Average	0.033	0.018	0.007	0.005
Standard deviation	0.005	0.007	0.001	0.00
R 2	0.03	0.027	0.024	0.123
	0.015	0.012	0.006	0.111
	0.021	0.018	0.015	0.096
Average	0.022	0.019	0.015	0.011
Standard deviation	0.006	0.006	0.007	0.011

**Table 7.22:** OD<sub>550nm</sub> values for the determination of comparison between flocculating activity of alum and bacterial bioflocculants

**Table 7.23:** Comparison between flocculating activity of alum and bacterialbioflocculants as derived from Table 7.22 using an equation forflocculating activity in Section 3.2.1 (Fig. 3.7)

Conc (ppm)	Control	Alum	D1	A14	A17	A22	R2	E1	Standard deviation
10	0	58.271	22.556	4.699	22.556	17.145	32.297	13.869	1.407
20	0	0	30.32	7.675	25.304	42.398	39.474	15.413	1.853
30	0	0	32.197	36.842	77.751	129.699	53.509	17.145	0.707
50	0	0	77.751	49.342	153.589	186.842	77.751	42.397	1.400

**Table 7.24:** OD<sub>550nm</sub> values for the determination of effect of pH on the flocculating activity

pH6	Isolates	10	8	6	4	2
	A22	0.387	0.375	0.261	0.261	0.198
		0.393	0.387	0.300	0.264	0.213
		0.390	0.381	0.297	0.261	0.207
	Average	0.390	0.381	0.297	0.262	0.206
	Standard deviation	0.002	0.005	0.018	0.001	0.006
	D1	0.306	0.285	0.261	0.243	0.204
		0.318	0.300	0.279	0.246	0.219
		0.312	0.294	0.276	0.243	0.213
	Average	0.312	0.293	0.272	0.244	0.212
	Standard deviation	0.005	0.006	0.008	0.001	0.006
	A17	0.369	0.300	0.273	0.267	0.195
		0.381	0.315	0.297	0.273	0.210
		0.375	0.309	0.291	0.267	0.204
	Average	0.375	0.308	0.287	0.269	0.203
	Standard deviation	0.005	0.006	0.010	0.003	0.006
	A14	0.336	0.240	0.222	0.204	0.147
		0.339	0.258	0.228	0.219	0.159
		0.336	0.255	0.222	0.210	0.153
	Average	0.337	0.251	0.224	0.211	0.153
	Standard deviation	0.001	0.008	0.003	0.006	0.005
	E1	0.324	0.270	0.249	0.243	0.180
		0.333	0.279	0.258	0.252	0.186
		0.327	0.273	0.252	0.246	0.183
	Average	0.328	0.274	0.253	0.247	0.183
	Standard deviation	0.004	0.004	0.004	0.004	0.00245
	R 2	0.387	0.246	0.195	0.192	0.111
		0.393	0.255	0.213	0.201	0.126
		0.387	0.249	0.204	0.195	0.120
	Average	0.389	0.250	0.204	0.196	0.119
	Standard deviation	0.003	0.004	0.007	0.004	0.006
	Control	2.043				
		2.160				
		2.100				
	Standard deviation	0.048				

pH7 Isolates 10 8 6 4	2
A22 0.366 0.297 0.261 0.249	0.201
0.375 0.285 0.267 0.252	0.207
0.357 0.27 0.258 0.246	0.198
Average 0.366 0.284 0.262 0.249	0.202
Standard	
deviation 0.007 0.011 0.004 0.002	0.004
D1 0.330 0.249 0.237 0.225	0.126
0.342 0.252 0.246 0.228	0.123
0.321 0.246 0.228 0.222	0.132
Average         0.331         0.249         0.237         0.225	0.127
Standard	
deviation 0.009 0.002 0.007 0.002	0.004
A17 0.357 0.339 0.261 0.213	0.171
0.354 0.33 0.255 0.195	0.162
0.366 0.333 0.270 0.228	0.177
Average         0.359         0.334         0.262         0.212	0.17
Standard	
deviation 0.005 0.004 0.006 0.013	0.006
A14 0.357 0.333 0.261 0.213	0.171
0.354 0.318 0.255 0.195	0.162
0.366 0.351 0.270 0.228	0.177
Average 0.359 0.334 0.262 0.212	0.170
Standard	0.110
deviation 0.005 0.014 0.006 0.013	0.006
E1 0.327 0.318 0.294 0.228	0.216
0.309 0.306 0.291 0.216	0.201
0.342 0.33 0.297 0.237	0.231
Average 0.326 0.318 0.294 0.227	0.216
Standard	
deviation 0.013 0.010 0.002 0.009	0.012
R 2 0.345 0.339 0.237 0.213	0.192
0.336 0.327 0.225 0.201	0.186
0.357 0.354 0.246 0.225	0.198
Average 0.346 0.34 0.236 0.213	0.192
Standard	
deviation 0.009 0.011 0.009 0.010	0.005
Control 2.256	
2.256	
2.259	
Average 2.257	
Standard	
deviation 0.001	

pH8	Isolates	10	8	6	4	2
	A22	0.615	0.507	0.438	0.216	0.153
		0.621	0.516	0.447	0.228	0.138
		0.612	0.495	0.432	0.207	0.165
	Average	0.616	0.506	0.439	0.217	0.152
	Standard					
	deviation	0.004	0.009	0.006	0.009	0.011
	D1	0.825	0.726	0.591	0.315	0.138
		0.828	0.714	0.588	0.321	0.150
		0.819	0.735	0.597	0.309	0.129
	Average	0.824	0.725	0.592	0.315	0.139
	Standard					
	deviation	0.004	0.009	0.004	0.005	0.009
	A17	0.759	0.561	0.426	0.318	0.156
		0.771	0.555	0.435	0.312	0.156
		0.744	0.567	0.420	0.324	0.159
	Average	0.758	0.561	0.427	0.318	0.157
	Standard	0.011	0.005	0.000	0.005	0.001
	deviation	0.011	0.005	0.006	0.005	0.001
	A14	0.690	0.552	0.339	0.207	0.102
		0.681	0.543	0.333	0.201	0.090
		0.702	0.558	0.342	0.216	0.111
	Average	0.691	0.551	0.338	0.208	0.101
	Standard	0.009	0.006	0.004	0.006	0.000
	E1	0.003	0.000	0.585	0.000	0.003
		0.834	0.720	0.585	0.372	0.102
		0.822	0.717	0.573	0.300	0.192
	A	0.849	0.738	0.594	0.375	0.207
	Average	0.835	0.727	0.584	0.3/1	0.200
	deviation	0.011	0.009	0.009	0.004	0.006
	R 2	0.450	0.546	0.486	0 309	0.138
	112	0.450	0.540	0.474	0.306	0.123
		0.450	0.555	0.495	0.300	0.150
	Average	0.190	0.535	0.195	0.312	0.130
	Standard	0.000	0.047	0.405	0.507	0.137
	deviation	0	0.006	0.0089	0.002	0.011
	Control	1.809				
		1.794				
		1.821				
	Average	1.808			1	1
	Standard deviation	0.011				
	1				1	

pH9	Isolates	10	8	6	4	2
	A22	0.891	0.684	0.513	0.423	0.255
		0.885	0.675	0.504	0.411	0.252
		0.897	0.690	0.519	0.435	0.261
	Average	0.891	0.683	0.512	0.423	0.256
	Standard					
	deviation	0.005	0.006	0.006	0.010	0.004
	D1	0.714	0.627	0.588	0.414	0.222
		0.711	0.621	0.582	0.408	0.219
		0.741	0.633	0.597	0.423	0.228
	Average	0.715	0.627	0.589	0.415	0.223
	Standard					
	deviation	0.01	0.005	0.006	0.006	0.004
	A17	0.873	0.723	0.618	0.405	0.210
		0.855	0.717	0.612	0.399	0.201
		0.888	0.729	0.627	0.408	0.222
	Average	0.872	0.723	0.619	0.404	0.211
	Standard					
	deviation	0.013	0.005	0.006	0.004	0.009
	A14	0.918	0.783	0.630	0.573	0.234
		0.912	0.783	0.624	0.561	0.222
		0.927	0.780	0.639	0.582	0.249
	Average	0.919	0.782	0.631	0.572	0.235
	Standard					
	deviation	0.006	0.001	0.006	0.009	0.011
	E1	0.657	0.567	0.405	0.216	0.138
		0.648	0.564	0.408	0.207	0.129
		0.69	0.576	0.399	0.225	0.147
	Average	0.658	0.569	0.404	0.216	0.138
	Standard					
	deviation	0.018	0.005	0.004	0.007	0.007
	R 2	0.831	0.78	0.528	0.303	0.219
		0.816	0.771	0.519	0.294	0.213
		0.849	0.792	0.537	0.312	0.225
	Average	0.832	0.781	0.528	0.303	0.219
	Standard					
	deviation	0.014	0.009	0.007	0.007	0.005
ļ	Control	2.313				
		2.304				
		2.322				
	Average	2.313				
	Standard					
	deviation	0.007				

·				1		
pH10	Isolates	10	8	6	4	2
	A22	0.825	0.684	0.438	0.216	0.159
		0.813	0.675	0.432	0.204	0.156
		0.834	0.690	0.447	0.225	0.156
	Average	0.824	0.683	0.439	0.215	0.158
	Standard					
	deviation	0.009	0.006	0.006	0.009	0.001
	D1	0.765	0.675	0.531	0.357	0.210
		0.753	0.669	0.525	0.348	0.195
		0.777	0.678	0.540	0.366	0.228
	Average	0.765	0.674	0.532	0.357	0.211
	Standard					
	deviation	0.010	0.004	0.006	0.007	0.013
	A17	0.951	0.732	0.618	0.504	0.231
		0.945	0.720	0.606	0.492	0.222
		0.957	0.741	0.627	0.519	0.243
	Average	0.951	0.731	0.617	0.505	0.232
	Standard					
	deviation	0.005	0.0086	0.008602325	0.01105	0.0086
	A14	0.738	0.663	0.519	0.378	0.201
		0.732	0.651	0.516	0.369	0.192
-		0.744	0.678	0.522	0.384	0.207
-	Average	0.738	0.664	0.519	0.377	0.2
-	Standard					
	deviation	0.005	0.011	0.002	0.006	0.006
	E1	0.618	0.582	0.426	0.222	0.162
		0.612	0.570	0.429	0.222	0.153
		0.627	0.591	0.426	0.225	0.168
	Average	0.619	0.581	0.427	0.223	0.161
	Standard					
	deviation	0.006	0.009	0.001	0.001	0.006
	R 2	0.594	0.402	0.357	0.255	0.138
		0.597	0.393	0.345	0.243	0.132
		0.588	0.414	0.369	0.267	0.147
	Average	0.593	0.403	0.357	0.255	0.139
-	Standard					
	deviation	0.004	0.009	0.010	0.010	0.006
	Control	1.473				
		1.464				İ
		1.479				
	Average	1.472				
	Standard					
	deviation	0.006				

							Standard
pН	A22	D1	A17	A14	E1	R2	deviation
6	2.169	1.519	2.144	4.867	3.278	5.356	0.137
7	3.653	5.669	4.359	4.359	3.034	4.359	0.158
8	2.745	2.316	2.389	3.448	1.601	2.232	0.385
9	1.863	1.591	1.984	1.295	3.664	2.605	0.217
10	2.586	2.992	2.625	2.918	2.175	2.301	0.417

Table 7.25: Effect of pH on the flocculating activity as derived from Tab	le 7.24
using an equation for flocculating activity in Section 3.2.1 (F	ig. 3.8)

## Table 7.26: OD<sub>550nm</sub> values for the determination of effect of temperature on flocculating activity

$28^{\circ}C$	Isolates	10	8	6	4	2
	A22	0.513	0.459	0.435	0.333	0.216
		0.495	0.444	0.459	0.321	0.222
		0.507	0.471	0.447	0.327	0.225
	Average	0.505	0.452	0.447	0.327	0.221
	Standard deviation	0.007	0.011	0.010	0.005	0.004
	D1	0.558	0.471	0.417	0.381	0.294
		0.540	0.453	0.408	0.357	0.276
		0.549	0.462	0.411	0.375	0.285
	Average	0.549	0.462	0.412	0.371	0.285
	Standard deviation	0.007	0.007	0.004	0.010	0.007
	A17	0.501	0.480	0.429	0.405	0.273
		0.471	0.450	0.411	0.384	0.243
		0.492	0.471	0.420	0.393	0.258
	Average	0.488	0.467	0.42	0.394	0.258
	Standard deviation	0.013	0.012	0.007	0.009	0.012
	A14	0.417	0.375	0.363	0.333	0.327
		0.402	0.366	0.354	0.306	0.309
		0.411	0.369	0.357	0.321	0.321
	Average	0.410	0.370	0.358	0.320	0.317
	Standard deviation	0.006	0.004	0.004	0.011	0.007
	E1	0.345	0.339	0.285	0.273	0.255
		0.318	0.318	0.303	0.264	0.246
		0.336	0.330	0.294	0.267	0.249
	Average	0.332	0.329	0.294	0.268	0.250
	Standard deviation	0.011	0.009	0.007	0.004	0.004
	R 2	0.351	0.288	0.273	0.261	0.243
		0.339	0.294	0.261	0.252	0.228
		0.345	0.297	0.267	0.255	0.237
	Average	0.345	0.293	0.267	0.256	0.236
		0.005	0.004	0.005	0.007	0.006
	Control	2.874				
		2.883				
		2.868				
	Average	2.875				
	Standard deviation	0.006				

37 <sup>0</sup> C	Isolates	10	8	6	4	2
	A22	0.657	0.495	0.429	0.354	0.282
		0.636	0.471	0.405	0.348	0.264
		0.648	0.483	0.423	0.351	0.273
	Average	0.647	0.483	0.419	0.351	0.273
	Standard deviation	0.009	0.010	0.010	0.002	0.007
	D1	0.585	0.489	0.447	0.381	0.243
		0.555	0.462	0.432	0.363	0.234
		0.576	0.486	0.438	0.372	0.237
	Average	0.572	0.479	0.439	0.372	0.238
	Standard deviation	0.012	0.012	0.006	0.007	0.004
	A17	0.477	0.423	0.402	0.321	0.294
		0.456	0.408	0.402	0.294	0.279
		0.465	0.417	0.399	0.309	0.285
	Average	0.466	0.416	0.401	0.308	0.286
	Standard deviation	0.009	0.006	0.001	0.011	0.006
	A14	0.366	0.363	0.345	0.267	0.210
		0.381	0.357	0.321	0.249	0.210
		0.381	0.357	0.336	0.258	0.210
	Average	0.376	0.359	0.334	0.258	0.021
	Standard deviation	0.007	0.003	0.010	0.007	0
	E1	0.261	0.243	0.243	0.240	0.168
		0.249	0.249	0.240	0.228	0.144
		0.255	0.252	0.240	0.234	0.156
	Average	0.255	0.248	0.241	0.734	0.156
	Standard deviation	0.005	0.004	0.001	0.004	0.010
	R 2	0.225	0.273	0.261	0.213	0.189
		0.213	0.267	0.240	0.198	0.159
		0.219	0.270	0.249	0.207	0.174
	Average	0.219	0.270	0.250	0.206	0.174
	Standard deviation	0.005	0.002	0.009	0.006	0.012
	Control	2.874				
		2.883				
		2.868				
	Average	2.875				
	Standard deviation	0.006				

# **Table 7.27:** Effect of temperature on the flocculating activity as derived from<br/>Table 7.26 using an equation for flocculating activity in Section<br/>3.2.1 (Fig. 3.9)

	A22	D1	A17	A14	E1	R2
37°C	3.301	2.707	2.430	5.138	9.953	9.478
Standard deviation	0.183	0.178	0.168	0.315	0.163	0.155
28°C	2.796	1.928	2.155	0.625	5.395	6.585
Standard deviation	0.217	0.300	0.041	0.091	0.382	0.110

CTAB	Isolates	2	4	6	8	10
	A22	0.348	0.414	0.528	0.597	0.657
		0.348	0.387	0.498	0.582	0.648
		0.354	0.402	0.519	0.588	0.651
	Average	0.350	0.401	0.515	0.234	0.652
	Standard					
	deviation	0.003	0.011	0.013	0.006	0.004
	D1	0.237	0.423	0.576	0.651	0.702
		0.240	0.402	0.573	0.639	0.699
		0.237	0.414	0.570	0.642	0.699
	Average	0.238	0.413	0.571	0.644	0.7
	Standard					
	deviation	0.001	0.009	0.002	0.005	0.001
	A17	0.276	0.351	0.567	0.651	0.660
		0.264	0.351	0.552	0.636	0.669
		0.267	0.354	0.561	0.645	0.681
	Average	0.269	0.352	0.560	0.644	0.670
	Standard					
	deviation	0.005	0.001	0.006	0.006	0.009
	A14	0.321	0.432	0.597	0.603	0.621
		0.297	0.402	0.594	0.630	0.642
		0.309	0.423	0.594	0.618	0.630
	Average	0.309	0.419	0.595	0.617	0.631
	Standard					
	deviation	0.010	0.013	0.001	0.011	0.009
	E1	0.195	0.327	0.432	0.597	0.666
		0.174	0.321	0.438	0.588	0.645
		0.186	0.324	0.441	0.591	0.657
	Average	0.182	0.324	0.437	0.592	0.656
	Standard					
	deviation	0.009	0.002	0.004	0.004	0.009
	R 2	0.213	0.387	0.477	0.687	0.735
		0.195	0.375	0.462	0.672	0.729
		0.204	0.381	0.468	0.678	0.732
	Average	0.204	0.381	0.469	0.679	0.732
	Standard					
	deviation	0.007	0.005	0.006	0.006	0.002
	Control	2.718				
		2.688				
		2.709				
	Average	2.705				
	Standard					
	deviation	0.013				

**Table 7.28:** OD<sub>550nm</sub> values for the determination of effect of cationic compounds on the flocculating activity

MgSO <sub>4</sub>	Isolates	2	4	6	8	10
	A22	0.246	0.393	0.477	0.564	0.675
		0.216	0.381	0.468	0.546	0.669
		0.231	0.387	0.471	0.555	0.672
	Average	0.231	0.387	0.471	0.555	0.672
	Standard					
	deviation	0.013	0.005	0.004	0.007	0.002
	D1	0.258	0.426	0.519	0.624	0.687
		0.240	0.423	0.495	0.606	0.678
		0.249	0.432	0.507	0.615	0.681
	Average	0.248	0.432	0.507	0.615	0.682
	Standard					
	deviation	0.007	0.004	0.010	0.007	0.004
	A17	0.378	0.465	0.471	0.531	0.624
		0.351	0.435	0.450	0.516	0.615
		0.366	0.456	0.459	0.522	0.618
	Average	0.365	0.452	0.46	0.523	0.619
	Standard					
	deviation	0.011	0.013	0.009	0.006	0.004
	A14	0.252	0.396	0.465	0.537	0.645
		0.264	0.363	0.456	0.519	0.624
		0.258	0.381	0.459	0.528	0.633
	Average	0.258	0.380	0.460	0.528	0.634
	Standard					
	deviation	0.005	0.014	0.004	0.007	0.009
	E1	0.363	0.447	0.591	0.597	0.633
		0.384	0.411	0.585	0.588	0.618
		0.372	0.426	0.588	0.591	0.624
	Average	0.373	0.431	0.588	0.592	0.625
	Standard					
	deviation	0.009	0.015	0.004	0.004	0.006
	R 2	0.315	0.477	0.516	0.693	0.708
		0.291	0.462	0.528	0.675	0.669
		0.303	0.468	0.528	0.684	0.699
	Average	0.303	0.469	0.524	0.684	0.692
	Standard					
	deviation	0.010	0.006	0.006	0.007	0.017
	Control	2.742				
		2.733				
		2.751				
	Average	2.742				
	Standard deviation	0.007				

-			1		1	
MnCl <sub>2</sub>	Isolates	2	4	6	8	10
	A22	0.207	0.423	0.447	0.579	0.609
		0.201	0.405	0.435	0.579	0.594
		0.216	0.441	0.459	0.582	0.621
	Average	0.208	0.423	0.447	0.58	0.608
	Standard					
	deviation	0.006	0.015	0.099	0.001	0.011
	D1	0.306	0.480	0.540	0.576	0.690
		0.297	0.468	0.528	0.561	0.681
		0.318	0.492	0.555	0.588	0.702
	Average	0.307	0.48	0.541	0.575	0.691
	Standard					
	deviation	0.009	0.010	0.011	0.011	0.009
	A17	0.279	0.477	0.501	0.579	0.582
		0.267	0.471	0.495	0.573	0.576
		0.288	0.486	0.507	0.582	0.591
	Average	0.278	0.478	0.501	0.578	0.583
	Standard					
	deviation	0.009	0.006	0.005	0.004	0.006
	A14	0.336	0.462	0.477	0.525	0.657
		0.330	0.465	0.471	0.519	0.642
		0.345	0.462	0.486	0.531	0.669
	Average	0.337	0.463	0.478	0.525	0.656
	Standard					
	deviation	0.006	0.001	0.006	0.005	0.011
	E1	0.372	0.456	0.477	0.576	0.594
		0.363	0.441	0.477	0.567	0.588
		0.378	0.468	0.483	0.582	0.597
	Average	0.371	0.455	0.479	0.575	0.593
	Standard					
	deviation	0.006	0.011	0.003	0.006	0.004
	R 2	0.300	0.417	0.465	0.468	0.486
		0.297	0.402	0.459	0.465	0.48
		0.306	0.432	0.471	0.474	0.495
	Average	0.301	0.417	0.465	0.469	0.487
	Standard					
	deviation	0.004	0.012	0.005	0.004	0.006
	Control	2.853				
		2.838				
		2.868				
	Average	2.853			1	Ì
	Standard					
	deviation	0.012				

CaCl <sub>2</sub>	Isolates	10	8	6	4	2
	A22	1.308	0.948	0.750	0.570	0.324
		1.302	0.939	0.720	0.480	0.315
		1.317	0.954	0.780	0.660	0.330
	Average	1.309	0.947	0.750	0.510	0.323
	Standard					
	deviation	0.006	0.006	0.024	0.073	0.006
	D1	1.572	1.539	0.876	0.549	0.411
		1.569	1.527	0.867	0.543	0.402
		1.575	1.551	0.888	0.555	0.417
	Average	1.572	1.539	0.877	0.549	0.410
	Standard					
	deviation	0.003	0.0010	0.009	0.005	0.006
	A17	1.617	0.948	0.747	0.534	0.312
		1.611	0.939	0.738	0.525	0.303
		1.626	0.954	0.756	0.546	0.318
	Average	1.618	0.947	0.747	0.535	0.311
	Standard					
	deviation	0.006	0.006	0.007	0.009	0.006
	A14	1.317	1.197	0.594	0.465	0.297
		1.311	1.200	0.600	0.456	0.300
		1.329	1.194	0.588	0.474	0.300
	Average	1.319	1.197	0.594	0.465	0.299
	Standard					
	deviation	0.007	0.002	0.005	0.007	0.001
	E1	1.995	1.563	0.630	0.405	0.210
		1.986	1.554	0.621	0.402	0.198
		2.001	1.572	0.642	0.408	0.225
	Average	1.994	1.563	0.631	0.405	0.211
	Standard					
	deviation	0.006	0.007	0.009	0.002	0.011
	R 2	1.374	1.218	0.846	0.579	0.378
		1.365	1.206	0.837	0.561	0.369
		1.380	1.227	0.855	0.597	0.387
	Average	1.373	1.217	0.846	0.579	0.378
	Standard					
	deviation	0.006	0.009	0.007	0.015	0.007
	Control	2.877				
		2.874				
		2.886				
	Average	2.879				
	Standard					
	deviation	0.0051				

Isolate	СТАВ	MgSO <sub>4</sub>	MnCl <sub>2</sub>	CaCl <sub>2</sub>
A22	0.244	2.450	2.821	1.567
Standard				
deviation	0.111	0.003	0.004	0.084
D1	2.027	1.954	0.941	2.701
Standard				
deviation	0.125	0.139	0.013	0.027
A17	2.109	0.836	1.414	1.885
	0.125	0.171	0.398	0.300
A14	0.989	2.087	0.550	2.072
Standard				
deviation	0.133	0.217	0.147	0.168
E1	3.253	0.542	1.104	3.362
Standard				
deviation	0.099	0.155	0.119	0.161
R2	1.713	1.085	0.695	2.746
Standard				
deviation	0.0238	0.178	0.119	0.100

**Table 7.29:** Effect of cationic compounds on the flocculating activity as derived from Table 7.28 using an equation for flocculating activity in Section 3.2.1 (Fig. 3.10)

**Table 7.30:** OD<sub>550nm</sub> values for the determination of flocculation inhibition assay at different concentration of potential inhibitors (Table 3.1)

E1	Conc (ppm)	K <sub>2</sub> HPO <sub>4</sub>	NaNO <sub>3</sub>	CH <sub>2</sub> COONa	Na <sub>2</sub> CO <sub>3</sub>	D-GLU
	10 000	0.747	0.010	0.919	1.025	0.015
	7 500	0.743	0.115	0.859	0.886	0.112
	5 000	0.663	0.221	0.737	0.740	0.135
	2 500	0.612	0.239	0.391	0.518	0.233
	1 000	0.471	0.257	0.242	0.495	0.241
	500	0.285	0.261	0.207	0.301	0.257
	100	0.253	0.283	0.142	0.218	0.262
	10	0.131	0.298	0.113	0.151	0.283
A14	Conc (pp	m) K <sub>2</sub> HPO <sub>4</sub>	NaNO <sub>3</sub>	CH <sub>2</sub> COONa	Na <sub>2</sub> CO <sub>3</sub>	D-GLU
	10 000	0.697	0.125	0.951	0.954	0.124
	7 500	0.449	0.175	0.787	0.842	0.151
	5 000	0.431	0.101	0.635	0 720	0.210

5 000	0.431	0.191	0.635	0.729	0.210
2 500	0.385	0.217	0.299	0.677	0.254
1 000	0.255	0.228	0.282	0.445	0.253
500	0.227	0.256	0.251	0.215	0.291
100	0.213	0.282	0.173	0.201	0.315
10	0.157	0.291	0.139	0.123	0.337

	1	1	1	1	1	1
DI	Conc (ppm)	K <sub>2</sub> HPO <sub>4</sub>	NaNO <sub>3</sub>	CH <sub>2</sub> COONa	Na <sub>2</sub> CO <sub>3</sub>	D-GLU
	10 000	0.953	0.117	0.640	1.570	0.110
	7 500	0.875	0.158	0.511	1.385	0.171
	5 000	0.724	0.172	0.382	0.612	0.218
	2 500	0.453	0.205	0.315	0.367	0.235
	1 000	0.320	0.213	0.297	0.359	0.257
	500	0.268	0.237	0.273	0.392	0.291
	100	0.241	0.281	0.162	0.261	0.297
	10	0.157	0.299	0.138	0.254	0.301
			1	I	1	
A17	Conc	K <sub>2</sub> HPO <sub>4</sub>	NaNO <sub>3</sub>	CH <sub>2</sub> COONa	Na <sub>2</sub> CO <sub>3</sub>	D-GLU
	(ppm)		0.100			
	10 000	0.872	0.139	0.903	0.825	0.105
	7 500	0.777	0.202	0.824	0.633	0.127
	5 000	0.653	0.218	0.688	0.618	0.153
	2 500	0.417	0.257	0.308	0.542	0.192
	1 000	0.251	0.289	0.273	0.486	0.215
	500	0.232	0.260	0.277	0.320	0.238
	100	0.213	0.277	0.285	0.218	0.261
	10	0.135	0.286	0.193	0.207	0.266
DO				CH COON		D CI II
R2	Conc	$K_2HPO_4$	NaNO <sub>3</sub>	CH <sub>2</sub> COONa	$Na_2CO_3$	D-GLU
	10,000	1 411	0.119	0.937	0.993	0.151
	7 500	0.824	0.151	0.612	0.838	0.131
	5 000	0.024	0.131	0.315	0.542	0.172
	2 500	0.740	0.212	0.208	0.342	0.178
	1 000	0.472	0.220	0.258	0.396	0.211
	500	0.237	0.237	0.203	0.390	0.223
	100	0.220	0.289	0.209	0.172	0.201
	100	0.212	0.289	0.132	0.103	0.201
	10	0.181	0.311	0.152	0.195	0.307
A22	Conc	K <sub>2</sub> HPO4	NaNO	CH <sub>2</sub> COONa	Na <sub>2</sub> CO <sub>2</sub>	D-GLU
1122	(ppm)	<b>R</b> 2 <b>H</b> 04	1111103	CH2COON	1142003	D GLC
	10 000	1.534	0.032	0.897	1.868	0.195
	7 500	0.985	0.105	0.738	1.835	0.172
	5 000	0.716	0.138	0.651	0.967	0.132
	2 500	0.567	0.213	0.325	0.857	0.258
	1 000	0.312	0.228	0.255	0.621	0.217
	500	0.267	0.257	0.281	0.426	0.231
	100	0.231	0.275	0.215	0.311	0.209
	10	0.216	0.288	0.173	0.230	0.317

Isolates	10	8	6	4	2
E1	0.165	0.174	0.369	0.501	0.561
	0.156	0.165	0.363	0.492	0.555
	0.174	0.180	0.378	0.510	0.567
Average	0.165	0.173	0.370	0.501	0.561
Standard					
deviation	0.007	0.006	0.006	0.007	0.005
D1	0.009	0.252	0.333	0.543	0.612
	0.003	0.252	0.321	0.528	0.591
	0.015	0.255	0.342	0.558	0.630
Average	0.009	0.253	0.332	0.543	0.611
Standard					
deviation	0.005	0.001	0.009	0.012	0.016
R 2	0.081	0.168	0.186	0.270	0.543
	0.072	0.159	0.177	0.255	0.543
	0.087	0.177	0.192	0.288	0.546
Average	0.080	0.168	0.185	0.271	0.544
Standard					
deviation	0.006	0.007	0.006	0.013	0.00141
A22	0.054	0.237	0.264	0.360	0.507
	0.039	0.234	0.261	0.348	0.495
	0.072	0.246	0.267	0.375	0.519
Average	0.055	0.239	0.264	0.361	0.507
Standard					
deviation	0.013	0.005	0.002	0.011	0.010
A17	0.057	0.096	0.138	0.255	0.456
	0.048	0.096	0.126	0.246	0.494
	0.066	0.099	0.150	0.261	0.465
Average	0.057	0.097	0.138	0.254	0.427
Standard					
deviation	0.007	0.001	0.010	0.006	0.016
A14	0.045	0.063	0.075	0.180	0.414
	0.030	0.051	0.063	0.165	0.423
	0.060	0.072	0.087	0.198	0.417
Average	0.045	0.062	0.075	0.181	0.418
Standard					
deviation	0.012	0.009	0.010	0.013	0.004
Control	1.521				
	1.512				
	1.527				
Average	1.520				
Standard deviation	0.006				
	1	1	1	1	1

**Table 7.31:** OD<sub>550nm</sub> values for the determination of flocculating activity of whale dye using different concentrations of bioflocculants

Conc (ppm)	E1	D1	R2	A22	A17	A14
10	89.145	99.408	94.737	96.382	96.118	97.039
8	88.618	83.355	88.947	84.276	93.618	95.921
6	75.658	78.158	87.829	82.632	90.921	95.066
4	67.039	64.276	82.171	76.250	83.289	88.092
2	63.092	59.803	70.066	66.645	69.934	72.500

**Table 7.32:** Percentage removal  $(C_0-C/C_0)$  of whale dye using different concentrations of flocculants as derived from Table 7.31 (Fig. 4.1)

**Table 7.33:** Flocculating activity of the whale dye as derived from Table 7.31 using anequation for flocculating activity in Section 4.2.3 (Fig. 4.2)

Isolate	Flocculating activity	Standard deviation
E1	9.397	0.132
D1	8.552	0.009
R2	7.688	0.156
A22	8.473	0.136
A17	6.904	0.022
A14	6.075	0.198

pH6	Isolates	10	8	6	4	2
	E1	0.171	0.213	0.324	0.399	0.447
		0.162	0.210	0.324	0.390	0.441
		0.180	0.216	0.327	0.405	0.450
	Average	0.171	0.213	0.325	0.398	0.446
	Standard					
	deviation	0.007	0.002	0.001	0.006	0.004
	D1	0.177	0.195	0.243	0.435	0.474
		0.174	0.186	0.237	0.426	0.465
		0.186	0.201	0.246	0.441	0.480
	Average	0.179	0.194	0.242	0.434	0.473
	Standard					
	deviation	0.005	0.006	0.004	0.006	0.006
	R 2	0.165	0.285	0.330	0.387	0.468
		0.153	0.279	0.327	0.387	0.459
		0.177	0.291	0.333	0.390	0.474
	Average	0.165	0.285	0.330	0.388	0.467
	Standard					
	deviation	0.010	0.005	0.002	0.001	0.006
	A22	0.267	0.306	0.402	0.471	0.492
		0.252	0.297	0.396	0.468	0.489
		0.279	0.312	0.405	0.477	0.495
	Average	0.266	0.305	0.401	0.472	0.492
	Standard					
	deviation	0.011	0.006	0.004	0.004	0.00245
	A17	0.264	0.321	0.381	0.501	0.519
		0.249	0.318	0.381	0.492	0.519
		0.279	0.327	0.384	0.507	0.522
	Average	0.264	0.322	0.382	0.5	0.52
	Standard					
	deviation	0.012	0.004	0.001	0.006	0.001
	A14	0.156	0.198	0.237	0.474	0.489
		0.141	0.189	0.231	0.489	0.504
		0.171	0.207	0.246	0.459	0.498
	Average	0.156	0.195	0.238	0.474	0.497
	Standard					
	deviation	0.012	0.023	0.006	0.012	0.006
	Control	1.551				
	<u> </u>	1.542				
		1.557				
	Average	1.550				
	Standard	0.006				
	deviation					

**Table 7.34:**  $OD_{550nm}$  values for the determination of effect of pH on the removal of whale<br/>dye and the calculations for the percentage removal ( $C_0$ -C/ $C_0$  x 100)<br/>(Fig. 4.3)

pH 6	Conc (ppm)	E1	D1	R	2	A22		A17		A14
	10	88.968	88.452	89.	08	82.83	9	82.96	8	89.935
	8	86.258	87.284	81.1	38	80.32	3	79.22	6	87.226
	6	79.032	84.387	78.	16	74.12	.9	75.35	5	84.645
	4	74.323	72.000	74.3	322	69.54	8	67.742	2	69.419
	2	71.226	69.484	69.0	)93	68.25	8	66.45	2	67.935
	I	1		I	I		1			
pH 7	Isolates	10		8		6		4		2
	E1	0.03	6	0.063	0.	102	0	.129		0.444
		0.03	0	0.054	0.0	099	0	.120		0.441
		0.03	9	0.069	0.	105	0	.135		0.447
	Average	0.03	5	0.062	0.	102	0	.128		0.444
	Standard		-							
	deviation	0.00	4	0.006	0.0	002	0	.006		0.002
	D1	0.02	1	0.042	0.0	078	0	.312		0.345
		0.01	8	0.039	0.0	075	0	.309		0.336
		0.02	4	0.045	0.0	084	0	.315		0.351
	Average	0.02	1	0.042	0.0	079	0	.312		0.344
	Standard					-	0			
	deviation	0.00	2	0.002	0.0	004	0	.002		0.006
	R 2	0.09	3	0.156	0.2	237	0	.504		0.528
		0.08	4	0.153	0.2	234	0	.501		0.525
		0.09	9	0.159	0.2	243	0	.507		0.534
	Average	0.09	2	0.156	0.2	238	0	.504		0.529
	Standard									
	deviation	0.00	6	0.002	0.0	004	0	.002		0.004
	A22	0.06	9	0.276	0.1	315	0	.420		0.528
		0.08	4	0.273	0.1	309	0	.417		0.522
		0.07	2	0.282	0.3	318	0	.426		0.534
	Average	0.07	0	0.277	0.	314	0	.421		0.527
	Standard									
	deviation	0.00	6	0.004	0.0	004	0	.004		0.005
	A17	0.10	5	0.339	0.3	378	0	.390		0.483
		0.09	9	0.339	0.3	372	0	.381		0.480
		0.11	1	0.342	0.3	381	0	.396		0.486
	Average	0.10	5	0.340	0.	377	0	.389		0.483
	Standard									
	deviation	0.00	5	0.001	0.0	004	0	.006		0.002
	A14	0.07	8	0.123	0.3	324	0	.438		0.483
		0.07	5	0.120	0.3	328	0	.432		0.480
	_	0.08	4	0.126	0.	327	0	.441		0.486
	Average	0.07	9	0.123	0.	323	0	.437		0.483
	Standard			0.005	_					0.005
	deviation	0.00	4	0.002	0.0	002	0	.004		0.002
	Control	1.51	2							
		1.50	6							
		1.51	5							
	Average	1.51	1							
	Standard	0.00	4							
	deviation				1					

pH 7	Conc (ppm)	E1	D1	l	R2		A22	A17	A14
	10	97.684	98.6	10	94.06	5	90.012	93.051	94.772
	8	95.897	97.2	20	89.93	5	75.050	77.498	91.794
	6	93.249	94.7	72	84.64	5	74.249	75.314	78.623
	4	91.529	79.3	51	67.48	4	74.076	74.255	71.079
	2	70.612	77.2	34	65.87	1	70.439	68.034	68.034
							,		
pH 8	Isolates	10			8		6	4	2
	E1	0.26	4	0.	.411		0.420	0.564	0.603
		0.25	8	0.	.405		0.423	0.558	0.600
		0.26	7	0.	.417		0.420	0.570	0.606
	Average	0.26	3	0.	411		0.421	0.564	0.603
	Standard						0.001		
	deviation	0.00	4	0.	.005		0.001	0.005	0.002
	DI	0.06	6	0.	078		0.258	0.396	0.441
		0.06	3	0.	078		0.252	0.396	0.438
		0.07	2	0.	081		0.264	0.399	0.447
	Average	0.06	7	0.	.079		0.258	0.397	0.442
	Standard	0.00	4	0	001		0.005	0.001	0.004
	deviation	0.00	4	0.	227		0.005	0.001	0.004
	<u> </u>	0.18	0	0.	237		0.306	0.339	0.576
		0.17	4	0.	242		0.306	0.333	0.573
	A	0.18	0	0.	243		0.309	0.345	0.579
	Stondard	0.10	U	U	230		0.307	0.339	0.570
	deviation	0.00	5	0	006		0.001	0.005	0.002
		0.00	<u>ј</u>	0	/32		0.001	0.003	0.002
	A22	0.17	4 8	0	426		0.441	0.447	0.515
		0.10	7	0	438		0.450	0.453	0.507
	Average	0.17	3	0	432		0.430	0.439	0.512
	Standard	0.17	0	0.	102		0.110	0.112	0.012
	deviation	0.00	4	0.	.005		0.004	0.003	0.004
	A17	0.24	9	0.	297		0.387	0.627	0.636
		0.24	3	0.	306		0.381	0.621	0.630
		0.25	2	0.	288		0.390	0.633	0.642
	Average	0.24	8	0.	297		0.386	0.627	0.636
	Standard								
	deviation	0.00	4	0.	.007		0.004	0.005	0.005
	A14	0.14	7	0.	.342		0.519	0.588	0.591
		0.14	1	0	.339		0.513	0.582	0.585
		0.15	5	0.	.348		0.522	0.594	0.594
	Average	0.14	6	0.	.343		0.518	0.588	0.59
	Standard								
	deviation	0.00	4	0.	.004		0.004	0.005	0.004
	Control	1.56	3						
		1.55	7						
		1.56	6						
	Average	1.56	2						
		0.00	4						

	Care (mmm)	E1	D1	D2		22	A 17	A 1 4
рн 8	Conc (ppm)	EI	DI	K2	A	22	A1/	A14
	10	83.163	95.711	88.47	6 86.	494	84.123	90.653
	8	73.688	94.942	84.89	91 74.	068	80.986	78.041
	6	73.892	83.483	80.34	46 73.	744	75.288	66.837
	4	63.892	74.584	78.29	97 71.	583	59.859	62.356
	2	61.396	71.703	63.12	24 <u>6</u> 9.	746	59.283	62.227
pH 9	E1	0.36	3	0.411	0.417		0.456	0.471
		0.35	7	0.405	0.411		0.447	0.471
		0.360	6	0.417	0.420		0.462	0.474
	Average	0.36	2	0.411	0.416		0.455	0.472
	Standard		-		00110			
	deviation	0.004	4	0.005	0.004		0.006	0.001
	D1	0.19	8	0.306	0.336		0.354	0.423
		0.19	5	0.297	0.330		0.345	0.423
		0.19	1	0.312	0.330		0.36	0.426
	Average	0.20	8	0.312	0.339		0.353	0.420
	Standard	0.130		0.000	0.000		0.000	V•747
	deviation	0.00	2	0.006	0.004		0.006	0.001
		0.002	0	0.000	0.004		0.000	0.555
	<u>K</u> 2	0.110	8	0.141	0.403		0.323	0.555
		0.17	/	0.140	0.399		0.522	0.552
		0.18	9	0.143	0.411		0.531	0.558
	Average	0.18.	3	0.140	0.405		0.526	0.555
	Standard	0.02		0.001	0.005		0.004	0.000
	deviation	0.03	1	0.001	0.005		0.004	0.002
	A22	0.249	9	0.480	0.486		0.525	0.567
		0.249	9	0.474	0.483		0.522	0.543
		0.252	2	0.486	0.489		0.531	0.570
	Average	0.25	0	0.480	0.486		0.276	0.560
	Standard							
	deviation	0.00	1	0.005	0.002		0.004	0.012
	A17	0.252	2	0.411	0.438		0.492	0.507
		0.249	9	0.405	0.435		0.489	0.507
		0.25	8	0.414	0.444		0.495	0.513
	Average	0.252	2	0.410	0.439		0.492	0.509
	Standard							
	deviation	0.004	4	0.004	0.004		0.002	0.003
	A14	0.384	4	0.522	0.531		0.546	0.570
		0.384	4	0.519	0.528		0.543	0.567
		0.38	7	0.528	0.537		0.549	0.573
	Average	0.38	5	0.523	0.532		0.546	0.570
	Standard							
	deviation	0.001	0	0.004	0.004		0.002	0.002
	Control	1.73	1			1		
		1.73	1					
		1.734	4					
	Average	1.73	2					
	Standard							
	deviation	0.00	1					

pH 9	Conc (ppm)	E1	]	D1	R	2	A22	A17	A14
	10	79.099	88	.568	89.4	-34	95.519	85.393	77.771
	8	76.270	82	.390	78.0	02	82.266	76.328	69.804
	6	75.982	80	.658	76.6	17	79.898	74.654	69.284
	4	73.730	79	.619	69.6	30	73.047	71.594	68.822
	2	72.748	75	.520	67.9	56	66.261	70.612	67.090
<u> </u>		•			•		•	·	·
pH 10	Isolates	10			8		6	4	2
	E1	0.564		0.5	576	(	0.591	0.591	0.615
		0.561		0.5	570	(	0.588	0.588	0.612
		0.567		0.5	582	(	0.594	0.597	0.618
	Average	0.564		0.4	576	(	0.591	0.592	0.615
	Standard								
	deviation	0.002		0.0	005	(	0.002	0.004	0.002
	D1	0.459		0.5	537	(	0.543	0.549	0.582
		0.453		0.5	528	(	0.540	0.546	0.582
		0.462		0.5	543	(	0.546	0.555	0.585
	Average	0.458		0.	536	(	0.543	0.55	0.583
	Standard								
	deviation	0.004		0.0	006	(	0.002	0.004	0.001
	R 2	0.522		0.5	537	(	0.537	0.558	0.561
		0.513		0.	531	(	0.534	0.552	0.555
		0.528		0.5	540	(	0.543	0.561	0.567
	Average	0.521		0.4	536	(	0.538	0.557	0.561
	Standard	0.000			201			0.004	0.005
	deviation	0.006		0.0	004	(	0.004	0.004	0.005
	A22	0.255		0.	393	(	0.399	0.42	0.477
		0.249		0.	387	(	0.399	0.414	0.474
	<b>A</b>	0.258		0	399	(	0.402	0.426	0.480
	Average	0.254		U.,	393		0.4	0.42	0.4//
	Standard	0.004			005		0.001	0.005	0.002
		0.004		0.0	510		0.001	0.003	0.558
	A1/	0.495		0.	507		0.513	0.522	0.555
		0.493		0.	516		0.515	0.510	0.555
	Average	0.490		0.	510		0.178	0.520	0.501
<u> </u>	Standard	0.470					U . I / U		0.000
	deviation	0.001		0.0	004	(	0.004	0.005	0.002
	A14	0.501		0.4	519	(	0.564	0.579	0.636
		0.495		0.1	513	(	0.564	0.573	0.636
		0.507		0.1	525	(	0.567	0.585	0.639
	Average	0.501		0.	519		0.565	0.579	0.637
	Standard				-				
	deviation	0.005		0.0	005	(	0.001	0.005	0.001
	Control	1.851							
		1.845							
		1.857							
	Average	1.851							
	Standard								
	deviation	0.005							

pH 10	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	69.530	75.257	71.853	83.190	73.204	72.934
	8	68.882	71.043	71.043	73.991	72.393	71.961
	6	68.071	70.665	70.935	73.527	72.015	69.476
	4	68.017	70.286	69.908	72.204	71.799	68.720
	2	66.775	68.504	69.692	68.432	69.854	65.586

**Table 7.35:**  $OD_{550nm}$  values for the determination of effect of temperature on the removal<br/>of whale dye and the calculations for the percentage removal<br/> $(C_0-C/C_0 \ge 100)$  (Fig. 4.4)

28°C	Isolates	10	8	6	4	2
	E1	0.096	0.153	0.156	0.174	0.210
		0.096	0.147	0.159	0.171	0.210
		0.099	0.159	0.156	0.180	0.213
	Average	0.097	0.153	0.157	0.175	0.211
	Standard deviation	0.001	0.005	0.001	0.004	0.001
	D1	0.102	0.111	0.132	0.141	0.219
		0.105	0.105	0.129	0.138	0.213
		0.108	0.114	0.138	0.144	0.222
	Average	0.105	0.110	0.133	0.141	0.218
	Standard deviation	0.002	0.004	0.004	0.002	0.004
	R 2	0.141	0.156	0.219	0.249	0.300
		0.147	0.156	0.228	0.249	0.315
		0.132	0.159	0.213	0.252	0.285
	Average	0.140	0.157	0.220	0.250	0.300
	Standard deviation	0.006	0.001	0.006	0.001	0.012
	A22	0.051	0.129	0.243	0.282	0.297
		0.054	0.141	0.240	0.285	0.294
		0.045	0.135	0.249	0.288	0.297
	Average	0.050	0.135	0.244	0.285	0.294
	Standard deviation	0.004	0.005	0.004	0.002	0.001
	A17	0.090	0.102	0.225	0.246	0.291
		0.087	0.102	0.225	0.249	0.297
		0.096	0.105	0.222	0.240	0.312
	Average	0.091	0.103	0.224	0.245	0.292
	Standard deviation	0.004	0.001	0.001	0.004	0.009
	A14	0.051	0.063	0.186	0.186	0.294
		0.045	0.057	0.183	0.183	0.294
		0.057	0.066	0.189	0.189	0.297
	Average	0.051	0.062	0.186	0.186	0.295
	Standard deviation	0.005	0.004	0.002	0.002	0.001
	Control	0.48				
		0.477				
		0.486				
	Average	0.481				
	Standard deviation	0.004				

28°C	Conc (ppm)	E1	D1	I	R2	A22	A17	A14
	10	79.834	78.17	0 76	299	88.009	81.081	87.770
	8	68.191	77.13	1 67	360	67.626	78.586	85.132
	6	67.360	72.24	9 54	262	41.487	53.430	67.386
	4	63.617	70.68	70.686 46.362		31.655	49.064	55.396
	2	56.133	54.67	8 37	630	29.496	39.293	29.257
I			L				L	
35°C	Isolates	10		8		6	4	2
	E1	0.00	9	0.033		0.117	0.123	0.174
		0.00	6	0.024		0.111	0.117	0.168
		0.01	5	0.039		0.120	0.129	0.180
	Average	0.01	0	0.032		0.116	0.122	0.174
	Standard							
	deviation	0.00	4	0.006		0.004	0.005	0.005
	D1	0.00	6	0.201		0.207	0.228	0.255
		0.00	3	0.201		0.204	0.228	0.246
		0.00	6	0.204		0.213	0.231	0.261
	Average	0.00	5	0.202		0.208	0.229	0.254
	Standard							
	deviation	0.00	1	0.001		0.004	0.001	0.006
	R 2	0.00	6	0.042		0.057	0.087	0.132
		0.00	6	0.039		0.057	0.087	0.129
		0.00	6	0.048		0.060	0.093	0.135
	Average	0.00	6	0.043		0.058	0.089	0.132
	Standard			0.004		0.001	0.000	0.005
	deviation	0	2	0.004		0.001	0.003	0.005
	A22	0.01	2	0.066		0.108	0.114	0.117
		0.00	6 2	0.075		0.105	0.114	0.108
	A	0.01	5	0.063		0.114	0.117	0.123
	Average	0.01	1	0.068	_	0.109	0.115	0.116
	Standard	0.00	4	0.005		0.004	0.001	0.006
		0.00	4	0.003		0.004	0.001	0.000
	A1/	0.02	5	0.087		0.129	0.102	0.210
		0.01	3 7	0.001	_	0.123	0.155	0.210
	Average	0.02	1	0.090		0.132	0.108	0.219
	Standard	0.02	1	0.000	_	0.120	0.101	0.213
	deviation	0.00	5	0.004		0.004	0.006	0.004
	Δ1Δ	0.00	9	0.007		0.072	0.114	0.117
		0.00	2	0.039		0.069	0.105	0.117
		0.01	6	0.039		0.075	0.12	0.123
	Average	0.00	9	0.043		0.072	0.112	0.123
	Standard	0.00	-	01010		510 / All		VILI/
	deviation	0.00	2	0.004		0.002	0.006	0.004
	Control	0.41	7					
		0.41	4					
		0.40	2					
	Average	0.41	7					
	Standard							
	deviation	0.00	6					

35°C	Conc (ppm)	E1	D1	R2		A22	A17	A14
	10	97.602	98.993	98.50	51	97.713	94.964	98.129
	8	92.326	59.256	89.68	38	85.863	79.376	91.06
	6	72.182	58.149	86.09	91	77.339	69.305	85.031
	4	70.743	53.924	78.6	57	76.091	61.391	76.507
	2	58.273	48.893	68.34	45	75.884	48.441	75.676
				I	I			•
40°C	C Isolates	10		8	6		4	2
	E1	0.02	1	0.114	0.1	71	0.186	0.192
		0.01	5	0.108	0.10	68	0.186	0.183
		0.02	7	0.117	0.1	77	0.189	0.198
	Average	0.02	1	0.113	0.1	72	0.187	0.191
	Standard							
	deviation	0.00	5	0.004	0.00	04	0.001	0.006
	D1	0.11	1	0.150	0.13	59	0.186	0.210
		0.10	5	0.150	0.15	53	0.186	0.210
		0.114	4	0.153	0.10	65	0.189	0.213
	Average	0.11	0	0.151	0.1	59	0.187	0.211
	Standard							
	deviation	0.004	4	0.001	0.00	05	0.001	0.001
	R 2	0.084	4	0.12	0.10	68	0.243	0.297
		0.084	4	0.117	0.13	59	0.237	0.306
		0.08	7	0.126	0.1	74	0.246	0.288
	Average	0.08	5	0.121	0.10	67	0.242	0.297
	Standard							
	deviation	0.00	1	0.004	0.00	06	0.004	0.007
	A22	0.06	3	0.174	0.18	83	0.240	0.279
		0.060	)	0.174	0.1	//	0.240	0.270
		0.060	5	0.177	0.13	89	0.243	0.285
	Average	0.06.	3	0.178	0.13	83	0.241	0.278
	Standard	0.00	- I	0.001	0.00	05	0.001	0.006
		0.00	1	0.001	0.00	00	0.001	0.000
	A1/	0.08	0	0.087	0.10	02	0.129	0.150
		0.07	0 7	0.087	0.05	99	0.120	0.159
	Average	0.08	, <b>,</b>	0.09	0.10	03	0.135	0.139
	Standard	0.002	-	0.000	0.10	00	0.130	0.130
	deviation	0.004	4	0.001	0.00	04	0.004	0.004
	A14	0.00	2	0.195	0.00	49	0.276	0.300
		0.15	6	0.186	0.24	49	0.270	0.297
		0.16	5	0.201	0.2	52	0.279	0.306
	Average	0.16	1	0.194	0.2	5	0.275	0.301
	Standard					-		
	deviation	0.004	4	0.006	0.00	01	0.004	0.004
	Control	0.498	8					-
		0.489	9		1			
		0.495	5		1			
	Average	0.49	7					
	Standard							
	deviation	0.004	4					

40°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	94.866	73.105	82.89	97 87.32	4 79.951	67.606
	8	72.372	63.081	75.65	64.78	9 78.484	60.966
	6	57.946	61.125	66.39	08 63.17	9 74.817	49.698
	4	54.279	54.279	51.30	08 51.50	9 68.215	44.668
	2	53.301	48.411	40.24	44.06	61.858	39.437
<u> </u>					1	I	
45°C	C Isolates	10		8	6	4	2
	E1	0.20	7	0.237	0.273	0.300	0.333
		0.210	)	0.234	0.264	0.297	0.330
		0.210	)	0.240	0.279	0.306	0.336
	Average	0.20	)	0.237	0.272	0.301	0.333
	Standard						
	deviation	0.00	1	0.002	0.006	0.004	0.002
	D1	0.129	)	0.234	0.282	0.303	0.339
		0.129	)	0.231	0.282	0.300	0.336
		0.132	2	0.237	0.285	0.306	0.345
	Average	0.13	)	0.234	0.283	0.303	0.340
	Standard						
	deviation	0.00	1	0.002	0.001	0.002	0.004
	R 2	0.10	5	0.228	0.150	0.231	0.252
		0.102	2	0.102	0.147	0.228	0.246
		0.108	3	0.114	0.156	0.234	0.255
	Average	0.10	5	0.108	0.151	0.231	0.251
	Standard						
	deviation	0.002	2	0.057	0.004	0.002	0.004
	A22	0.075	5	0.120	0.174	0.180	0.198
		0.072	2	0.114	0.168	0.180	0.195
		0.078	3	0.126	0.177	0.183	0.204
	Average	0.075	5	0.120	0.173	0.181	0.199
	Standard	0.00		0.005	0.004	0.001	0.004
	deviation	0.002	2	0.005	0.004	0.001	0.004
	A1/	0.17	-	0.180	0.243	0.276	0.300
		0.16	2	0.1/4	0.237	0.270	0.297
	A 17	0.17	/	0.180	0.246	0.279	0.306
	A1/	0.17	1	0.180	0.243	0.276	0.300
	Standard	0.004		0.005	0.004	0.004	0.004
		0.00	, I	0.003	0.004	0.004	0.004
	A14	0.14		0.249	0.203	0.294	0.300
		0.14	1	0.240	0.283	0.297	0.297
	Average	0.14	т )	0.232	0.200	0.294	0.300
	Standard	0.14		V.477	0.200	0.270	0.301
	deviation	0.00		0.002	0.001	0.001	0.004
	Control	0.00	3	0.002	0.001	0.001	0.001
	Control	0.404	5				
		0.414	1				
	Average	0.40	)				
	Standard						
	deviation	0.004	4				

45°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	57.948	68.825	74.328	81.663	65.594	65.281
	8	52.314	43.884	73.594	70.660	63.783	39.120
	6	45.272	32.134	63.081	57.702	51.308	31.540
	4	39.437	27.338	43.521	55.746	44.668	27.873
	2	32.998	18.465	38.631	51.345	39.437	26.406

**Table 7.36:**  $OD_{550nm}$  values for the determination of effect of cations on the removal of<br/>whale dye and the calculations for the percentage removal ( $C_0$ -C/C $_0$  x 100)<br/>(Fig. 4.5)

CTAB	Isolates	10	8	6	4	2			
	E1	0.729	0.879	0.891	0.894	0.909			
		0.729	0.873	0.888	0.894	0.903			
		0.732	0.885	0.897	0.897	0.918			
	Average	0.730	0.879	0.892	0.895	0.910			
	Standard deviation	0.001	0.005	0.004	0.001	0.006			
	D1	0.441	0.531	0.768	0.879	0.951			
		0.438	0.525	0.762	0.864	0.933			
		0.447	0.540	0.771	0.891	0.942			
	Average	0.442	0.532	0.767	0.878	0.942			
	Standard deviation	0.004	0.006	0.004	0.011	0.007			
	R 2	0.825	0.846	0.873	0.888	0.966			
		0.807	0.831	0.870	0.882	0.957			
		0.840	0.828	0.876	0.891	0.978			
	Average	0.824	0.845	0.873	0.887	0.967			
	Standard deviation	0.013	0.008	0.002	0.004	0.009			
	A22	0.816	0.834	0.861	0.897	0.915			
		0.804	0.825	0.852	0.897	0.928			
		0.825	0.840	0.870	0.900	0.927			
	Average	0.815	0.833	0.861	0.898	0.914			
	Standard deviation	0.009	0.006	0.007	0.001	0.006			
	A17	0.717	0.834	0.864	0.891	0.921			
		0.711	0.825	0.852	0.888	0.918			
		0.723	0.84	0.879	0.894	0.927			
	Average	0.717	0.833	0.865	0.891	0.322			
	Standard deviation	0.005	0.006	0.011	0.002	0.004			
	A14	0.702	0.726	0.813	0.903	0.924			
		0.696	0.711	0.804	0.897	0.915			
		0.711	0.738	0.822	0.912	0.936			
	Average	0.703	0.725	0.813	0.904	0.925			
	Standard deviation	0.006	0.011	0.007	0.006	0.007			
	Control	1.152							
		1.146							
		1.155							
	Average	1.151							
	Standard deviation	0.004							
CTAB	Conc (ppm)	E1	D	1	R2		A22	A17	A14
----------	------------	--------	--------	----------	-------	----	--------	--------	----------
	10	36.577	61.5	599	28.41	10	29.192	37.706	38.923
	8	23.632	53.7	779	26.58	36	27.628	27.628	37.011
	6	22.502	33.3	362	24.15	53	25.195	24.848	29.366
	4	22.242	23.7	719	22.93	37	21.981	22.589	21.460
	2	20.938	18.1	158	15.98	36	20.591	19.896	19.635
I					1		1		
CaCl	2 Isolates	10			8		6	4	2
	E1	0.087	7	0.	.087		0.09	0.09	0.144
		0.075	5	0.	.078		0.087	0.099	0.135
		0.099	)	0.	102		0.096	0.096	0.15
	Average	0.087	1	0.	.089		0.091	0.097	0.143
	Standard								
	deviation	0.008	3	0.	.010		0.004	0.004	0.006
	D1	0.066	5	0.	.084		0.087	0.099	0.102
		0.048	3	0.	.078		0.072	0.09	0.096
		0.081		0.	.090		0.102	0.108	0.108
	Average	0.065	;	0.	.084		0.087	0.099	0.102
	Standard								
	deviation	0.013	;	0.	.005		0.012	0.007	0.005
	R 2	0.072	2	0.	.096		0.111	0.123	0.147
		0.060	)	0.	.084		0.105	0.108	0.138
		0.084	ŀ	0.	108		0.117	0.135	0.156
	Average	0.072	2	0.	.096		0.111	0.122	0.147
	Standard								
	deviation	0.010	)	0.	.010		0.005	0.011	0.007
	A22	0.063	;	0.	.072		0.084	0.084	0.114
		0.057	1	0.	.063		0.078	0.078	0.108
		0.066	5	0.	.078		0.087	0.093	0.123
	Average	0.062	2	0.	.071		0.083	0.085	0.115
	Standard				0.0.4			0.007	0.007
	deviation	0.004	-	0.	.006		0.004	0.006	0.006
	Al7	0.069	)	0.	078		0.084	0.09	0.135
		0.066	)	0.	.069		0.066	0.078	0.132
		0.072	2	0.	.087		0.102	0.102	0.141
	Average	0.069	,	0.	078		0.084	0.09	0.136
	Standard	0.000	,	0	007		0.015	0.010	0.004
		0.002		0.	072		0.013	0.010	0.004
	A14	0.069	, )	0.	066		0.078	0.060	0.090
		0.000	,	0.	000		0.009	0.009	0.075
	Avoraça	0.081		0.	073		0.004	0.103	0.103
	Standard	0.070	,	U.	0/3		0.0//	0.007	0.090
	deviation	0.000	)	0	006		0.006	0.015	0.012
<u> </u>	Control	0.005	, ,	0.	000		0.000	0.015	0.012
	Colluol	0.270	, 1	<u> </u>					<u> </u>
		0.207	)						<u> </u>
	Average	0.282	, ,						<u> </u>
	Standard	0.41	,						<u> </u>
	deviation	0.006	5						

CaCl <sub>2</sub>	Conc (ppm)	E1	D1		R2		A22	A17	A14
	10	68.364	75.30	64	73.81	8	77.455	74.909	74.545
	8	67.636	69.45	55	65.09	1	74.182	71.636	73.455
	6	66.909	68.30	64	60.00	0	69.818	69.455	72.000
	4	64.727	64.00	00	55.63	6	69.091	67.273	68.364
	2	48.000	62.90	09	46.54	6	58.182	50.545	67.273
MnCl <sub>2</sub>	Isolates	10			8		6	4	2
	E1	0.00	3	0	.006	(	0.009	0.012	0.015
		0		0	.009	(	0.012	0.006	0.009
		0		0	.006	(	0.006	0.015	0.018
	Average	0.00	1	0	.007	(	0.009	0.011	0.014
	Standard								
	deviation	0.00	1	0	.001	(	0.002	0.004	0.004
	DI	0.00	3	0	.009	(	0.012	0.018	0.024
		0.00	5	0	.012		0.000	0.009	0.009
	A	0	-	0	000		0.021	0.02/	0.036
	Average	0.00	4	0	.009		0.013	0.018	0.023
	deviation	0.00	1	0	002		0.006	0.007	0.011
		0.00	3	0	002		0.000	0.007	0.011
	K 2	0.00	3	0	006		0.006	0.016	0.021
		0.00	5	0	003		0.021	0.000	0.027
	Average	0.00	2	0	.003		0.014	0.017	0.022
	Standard								
	deviation	0.00	1	0	.001		0.006	0.005	0.004
	A22	0.00	3	0	.009	(	0.015	0.021	0.024
		0		0	.012	(	0.006	0.018	0.018
		0		0	.006	(	0.024	0.024	0.030
	Average	0.00	1	0	.009	(	0.015	0.021	0.024
	Standard								
	deviation	0.00	1	0	.002	(	0.007	0.002	0.005
	A17	0.00	3	0	.003	(	0.006	0.009	0.009
		0		0	.006	(	0.003	0.012	0.012
		0	1	0	.003		0.012	0.006	0.009
	Average	0.00	1	0	.004		0.007	0.009	0.010
	Standard	0.00	5	0	001		0.004	0.002	0.001
		0.00	3	0	000		0.004	0.002	0.001
	A14	0.00	3	0	012		0.012	0.013	0.009
		0.00	3	0	006		0.021	0.012	0.018
	Average	0.00	3	0	.009		0.013	0.016	0.018
	Standard	0.00	-	0					
	deviation	0		0	.002	(	0.006	0.004	0.004
	Control	0.11	1						
		0.10	5						
		0.11	7						
	Average	0.11	1						
	Standard		T						
	deviation	0.00	5						

MnCl <sub>2</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	99.099	98.198	98.198	99.099	99.099	97.209
	8	93.694	91.892	96.396	91.892	96.396	91.892
	6	91.892	88.288	87.387	86.486	93.694	88.288
	4	90.090	83.784	84.685	81.081	91.892	85.586
	2	87.387	79.279	80.180	78.378	90.991	83.784

MgSQ	Isolates	10	8	6	4	2
1115004	E1	0.003	0.003	0.006	0.009	0.012
	LI	0.005	0.003	0.000	0.009	0.012
		0	0.003	0.005	0.005	0.000
	Average	0.001	0.003	0.000	0.000	0.013
	Standard	0.001	0.005	0.005	0.000	0.011
	deviation	0.001	0	0.001	0.001	0.004
	D1	0.001	0.015	0.001	0.001	0.004
		0.002	0.013	0.010	0.046	0.031
		0.005	0.012	0.021	0.050	0.045
	Average	0.013	0.015	0.010	0.037	0.057
	Standard	0.012	0.015	0.017	0.047	0.051
	deviation	0.002	0.002	0.001	0.009	0.005
	R 2	0.002	0.021	0.027	0.039	0.039
	112	0.003	0.018	0.03	0.033	0.03
		0.009	0.021	0.027	0.033	0.051
	Average	0.005	0.020	0.028	0.038	0.04
	Standard	0.000	01020	01020	01020	0001
	deviation	0.002	0.001	0.001	0.004	0.009
	A22	0.027	0.030	0.036	0.039	0.042
		0.021	0.027	0.03	0.036	0.030
		0.033	0.036	0.039	0.042	0.054
	Average	0.027	0.131	0.035	0.039	0.042
	Standard			01000		
	deviation	0.005	0.004	0.004	0.002	0.010
	A17	0.015	0.021	0.027	0.033	0.030
		0.012	0.012	0.027	0.033	0.030
		0.018	0.027	0.033	0.03	0.045
	Average	0.015	0.02	0.029	0.032	0.035
	Standard					
	deviation	0.002	0.006	0.003	0.001	0.007
	A14	0.012	0.012	0.018	0.024	0.027
		0.006	0.006	0.012	0.018	0.021
		0.015	0.021	0.021	0.03	0.033
	Average	0.011	0.013	0.017	0.024	0.027
	Standard					
	deviation	0.004	0.006	0.004	0.005	0.005
	Control	0.234				
		0.234				
		0.237				
	Average	0.235				
	Standard					
	deviation	0.001				

MgSO <sub>4</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	99.574	94.894	97.447	88.511	93.617	95.319
	8	98.723	93.617	91.489	86.809	91.489	94.468
	6	97.872	91.915	88.085	85.106	87.660	92.766
	4	96.596	80.000	83.830	83.404	86.383	89.787
	2	95.319	78.298	82.979	82.128	85.106	88.511

Table 7.37: OD <sub>550nm</sub> values for the determination of flocculating activity of medi-bl	lue
dye using different concentrations of bioflocculants	

Isolates	10	8	6	4	2
E1	0.117	0.114	0.126	0.138	0.141
	0.084	0.117	0.117	0.114	0.126
	0.111	0.123	0.120	0.126	0.132
Average	0.104	0.118	0.121	0.126	0.133
Standard deviation	0.014	0.004	0.004	0.010	0.006
D1	0.111	0.129	0.147	0.156	0.147
	0.123	0.111	0.129	0.135	0.165
	0.117	0.120	0.138	0.147	0.156
Average	0.117	0.12	0.138	0.046	0.156
Standard deviation	0.005	0.007	0.007	0.009	0.007
R 2	0.111	0.114	0.123	0.111	0.135
	0.087	0.093	0.096	0.126	0.12
	0.099	0.102	0.108	0.117	0.129
Average	0.099	0.103	0.109	0.118	0.128
Standard deviation	0.010	0.009	0.011	0.006	0.006
A22	0.114	0.129	0.123	0.138	0.141
	0.102	0.102	0.108	0.12	0.117
	0.108	0.117	0.138	0.129	0.135
Average	0.108	0.116	0.123	0.129	0.131
Standard deviation	0.005	0.011	0.012	0.007	0.010
A17	0.111	0.126	0.114	0.126	0.129
	0.087	0.078	0.105	0.117	0.132
	0.099	0.108	0.108	0.12	0.12
Average	0.099	0.104	0.109	0.121	0.127
Standard deviation	0.010	0.020	0.004	0.004	0.005
A14	0.105	0.111	0.12	0.123	0.126
	0.087	0.087	0.086	0.105	0.114
	0.096	0.105	0.117	0.114	0.112
Average	0.096	0.101	0.107	0.114	0.12
Standard deviation	0.007	0.010	0.015	0.007	0.006
Control	0.513				
	0.477				
	0.495				
Average	0.495				
Standard deviation	0.015				

Conc (ppm)	E1	D1	R2	A22	A17	A14
10	78.990	76.364	80.000	78.182	80.000	80.606
8	76.162	75.758	79.192	76.566	78.990	79.596
6	75.556	72.121	77.980	75.152	77.980	78.384
4	74.545	70.505	76.162	73.939	75.556	76.970
2	73.131	68.485	74.141	73.535	74.343	75.758

**Table 7.38:** Percentage removal ( $C_0$ – $C/C_0 \ge 100$ ) of medi-blue dye using different concentrations of flocculants as derived from Table 7.37 (Fig. 4.6)

**Table 7.39:** Flocculating activity of the medi-blue dye as derived from Table 7.37 using<br/>an equation for flocculating activity in Section 4.2.3 (Fig. 4.7)

Isolate	Flocculating activity	Standard deviation		
E1	26.117	0.177		
D1	21.964	0.102		
R2	22.456	0.063		
A22	29.489	0.154		
A17	22.651	0.218		
A14	24.993	0.127		

$\begin{array}{c c c c c c c c c c c c c c c c c c c $				1	1	1	1
E1         0.228         0.213         0.234         0.243         0.224           0.219         0.237         0.219         0.222         0.228           Average         0.222         0.225         0.227         0.232         0.232           Average         0.223         0.225         0.227         0.232         0.232           deviation         0.004         0.010         0.006         0.009         0.009           D1         0.207         0.243         0.252         0.235         0.243           0.231         0.213         0.228         0.246         0.225           0.237         0.234         0.240         0.249         0.234           deviation         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.240         0.276           0.213         0.237         0.225         0.216         0.255         0.234           0.228         0.228         0.231         0.237         0.240         0.237           0.228         0.221         0.234         0.265         0.240         0.234           0.216         0.222         0.231         0	рН б	Isolates	10	8	6	4	2
0.219         0.237         0.219         0.222         0.228           Average         0.223         0.225         0.228         0.231         0.240           Average         0.223         0.225         0.232         0.232         0.232         0.232           Standard         0.004         0.010         0.006         0.009         0.009           D1         0.207         0.243         0.252         0.235         0.243           0.231         0.213         0.228         0.246         0.225           0.237         0.234         0.240         0.249         0.234           Average         0.225         0.230         0.240         0.249         0.234           deviation         0.013         0.013         0.010         0.004         0.007           R 2         0.240         0.225         0.231         0.237         0.264           Average         0.227         0.228         0.231         0.237         0.264           Average         0.215         0.221         0.231         0.237         0.264           Average         0.216         0.222         0.228         0.231         0.237           Gandard		E1	0.228	0.213	0.234	0.243	0.249
0.222         0.225         0.228         0.231         0.240           Average         0.223         0.225         0.227         0.232         0.239           Standard         0.004         0.010         0.006         0.009         0.009           D1         0.207         0.243         0.252         0.255         0.243           0.231         0.213         0.225         0.234         0.240         0.249         0.234           Average         0.237         0.234         0.240         0.249         0.234           Average         0.237         0.234         0.240         0.249         0.234           Average         0.213         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.265         0.264           0.213         0.237         0.228         0.231         0.237         0.264           Average         0.228         0.231         0.237         0.264           Average         0.216         0.228         0.231         0.234         0.265           Standard         0.011         0.006         0.004         0.014         0.009         0.234			0.219	0.237	0.219	0.222	0.228
Average         0.223         0.225         0.227         0.232         0.239           Standard deviation         0.004         0.010         0.006         0.009         0.009           D1         0.207         0.243         0.252         0.255         0.243           0.231         0.213         0.228         0.246         0.225           0.237         0.234         0.240         0.249         0.234           Average         0.225         0.230         0.240         0.250         0.234           Standard         0.013         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.255           0.228         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.234         0.265           Standard         0.216         0.228         0.244         0.234           deviation         0.011         0.006         0.004         0.014         0.009           Average         0.215         0.223         0.227         0.			0.222	0.225	0.228	0.231	0.240
Standard deviation         0.004         0.010         0.006         0.009         0.009           D1         0.207         0.243         0.252         0.255         0.243           0.231         0.213         0.228         0.246         0.225           0.237         0.234         0.240         0.249         0.234           Average         0.225         0.230         0.240         0.250         0.234           Standard deviation         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.255         0.216         0.255           0.228         0.228         0.231         0.237         0.264         0.265           Marage         0.213         0.227         0.23         0.234         0.265           Standard		Average	0.223	0.225	0.227	0.232	0.239
deviation         0.004         0.010         0.006         0.009         0.009           D1         0.207         0.243         0.252         0.255         0.243           0.231         0.213         0.228         0.246         0.225           Average         0.227         0.234         0.240         0.249         0.234           Average         0.225         0.230         0.240         0.250         0.234           Standard         deviation         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.249         0.276           Average         0.227         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard         0.011         0.006         0.004         0.014         0.009           Average         0.225         0.231         0.225         0.231         0.237           Average         0.216         0.228         0.241         0.234           0.204         0.216         0.228         0.231         0.237           Average         0.216<		Standard					
D1         0.207         0.243         0.252         0.255         0.243           0.231         0.213         0.228         0.246         0.225           Average         0.225         0.230         0.240         0.249         0.234           Average         0.225         0.230         0.240         0.250         0.234           Standard         0.013         0.013         0.010         0.004         0.007           R 2         0.240         0.225         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.255           0.213         0.237         0.225         0.216         0.255           Average         0.228         0.228         0.231         0.237         0.264           Average         0.227         0.228         0.234         0.265         0.240           Standard		deviation	0.004	0.010	0.006	0.009	0.009
Image: Network of the system of the		D1	0.207	0.243	0.252	0.255	0.243
0.237         0.234         0.240         0.249         0.234           Average         0.225         0.230         0.240         0.250         0.234           Standard         0.013         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.255           0.228         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.227         0.232         0.237           Average         0.216         0.228         0.240         0.214         0.204           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard         0         0.216         0.216         0.231         0.237         0.237           Standard         0.215			0.231	0.213	0.228	0.246	0.225
Average         0.225         0.230         0.240         0.250         0.234           Standard deviation         0.013         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.255           0.218         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard         deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.234         0.240           A22         0.225         0.231         0.225         0.240         0.240           0.216         0.222         0.228         0.231         0.237         0.241           0.216         0.223         0.227         0.232         0.231         0.237           Average         0.216         0.213         0.237         0.243         0.246           0.201         0.213         0.237         0.243         0.255           0.216 <td></td> <td></td> <td>0.237</td> <td>0.234</td> <td>0.240</td> <td>0.249</td> <td>0.234</td>			0.237	0.234	0.240	0.249	0.234
$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$		Average	0.225	0.230	0.240	0.250	0.234
deviation         0.013         0.013         0.010         0.004         0.007           R 2         0.240         0.222         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.258           0.228         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard         deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.240         0.216           0.216         0.228         0.224         0.234         0.237           Average         0.216         0.222         0.228         0.231         0.237           Average         0.216         0.223         0.227         0.232         0.237           Standard		Standard					
R 2         0.240         0.222         0.234         0.249         0.276           0.213         0.237         0.225         0.216         0.255           0.228         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard         deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.225         0.240           0.204         0.216         0.228         0.24         0.237           Average         0.216         0.222         0.228         0.231         0.237           Average         0.216         0.222         0.228         0.231         0.237           Standard         0.216         0.221         0.228         0.231         0.237           Standard         0.201         0.213         0.227         0.232         0.237           Standard         0.201         0.213         0.231         0.225           0.213         0.213         0.231         0.237         0.252           0.210         0.214         0.231		deviation	0.013	0.013	0.010	0.004	0.007
0.213         0.237         0.225         0.216         0.255           Average         0.228         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard         deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.232         0.234         0.234           0.204         0.216         0.228         0.24         0.234         0.237           Average         0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard         deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246         0.252           0.213         0.213         0.231         0.237         0.252         0.252           0.214         0.231         0.238         0.251         0.252         0.231         0.237         0.244           0.213 <td></td> <td>R 2</td> <td>0.240</td> <td>0.222</td> <td>0.234</td> <td>0.249</td> <td>0.276</td>		R 2	0.240	0.222	0.234	0.249	0.276
0.228         0.228         0.231         0.237         0.264           Average         0.227         0.229         0.23         0.234         0.265           Standard deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.225         0.240         0.234           0.204         0.216         0.228         0.24         0.234         0.234           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.231         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.252         0.234         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard deviation         0.006         0.004         0.004         0.243 <td></td> <td></td> <td>0.213</td> <td>0.237</td> <td>0.225</td> <td>0.216</td> <td>0.255</td>			0.213	0.237	0.225	0.216	0.255
Average         0.227         0.229         0.23         0.234         0.265           Standard deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.225         0.240           0.204         0.216         0.228         0.24         0.234           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.255           0.201         0.213         0.237         0.232         0.237         0.252           0.213         0.213         0.231         0.237         0.252           0.210         0.214         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.237         0.243           0.213         0.212         0.225         0.231         0.243         0.252           Average         0.216			0.228	0.228	0.231	0.237	0.264
Standard deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.225         0.240           0.204         0.216         0.228         0.24         0.234           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard         deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.252           0.213         0.213         0.231         0.237         0.252           0.214         0.231         0.238         0.251           Standard deviation         0.006         0.004         0.004         0.004           Average         0.219         0.225         0.231         0.243           0.219         0.222         0.231         0.237         0.249		Average	0.227	0.229	0.23	0.234	0.265
deviation         0.011         0.006         0.004         0.014         0.009           A22         0.225         0.231         0.225         0.225         0.240           0.204         0.216         0.228         0.24         0.234           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard		Standard					
A22         0.225         0.231         0.225         0.240           0.204         0.216         0.228         0.24         0.234           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.234         0.246           0.213         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard         0.216         0.219         0.222         0.224         0.252           Quertarian         0.006         0.004         0.004         0.004           Average         0.216         0.219         0.225         0.231         0.237         0.243           Matrix         0.219         0.222         0.231         0.237		deviation	0.011	0.006	0.004	0.014	0.009
0.204         0.216         0.228         0.24         0.234           0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.243         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard deviation         0.006         0.004         0.005         0.004         0.004           Al4         0.222         0.225         0.231         0.243         0.243           0.219         0.222         0.236         0.243         0.243           0.219         0.222         0.236         0.248         0.243           Standard deviation         0.002         0.002         0.004		A22	0.225	0.231	0.225	0.225	0.240
0.216         0.222         0.228         0.231         0.237           Average         0.215         0.223         0.227         0.232         0.237           Standard deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.243           Average         0.210         0.213         0.237         0.243         0.252           Average         0.210         0.214         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard         0.206         0.004         0.005         0.004         0.004           Al4         0.222         0.225         0.231         0.243           0.219         0.222         0.236         0.249           Average         0.219         0.222         0.236         0.248           Maddard         0.002         0.002         0.004         0.004         0.00			0.204	0.216	0.228	0.24	0.234
Average         0.215         0.223         0.227         0.232         0.237           Standard deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.243         0.252           Average         0.210         0.213         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard         0.006         0.004         0.005         0.004         0.004           deviation         0.006         0.004         0.005         0.004         0.252           0.216         0.219         0.225         0.231         0.237         0.243           0.219         0.222         0.231         0.237         0.243           0.219         0.222         0.236         0.248         0.248           Standard <td< td=""><td></td><td></td><td>0.216</td><td>0.222</td><td>0.228</td><td>0.231</td><td>0.237</td></td<>			0.216	0.222	0.228	0.231	0.237
Standard deviation         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.243         0.252           Average         0.210         0.214         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.237         0.252           Standard         deviation         0.006         0.004         0.005         0.004         0.004           Mathematical deviation         0.006         0.004         0.005         0.004         0.004           Mathematical deviation         0.006         0.004         0.005         0.004         0.004           Mathematical deviation         0.006         0.219         0.225         0.231         0.243           Mathematical deviation         0.002         0.002         0.004         0.004         0.004           Mathematical deviation         0.002         0.002         0.004         0.004         0.004           Mathematical deviation		Average	0.215	0.223	0.227	0.232	0.237
Initial         0.009         0.006         0.001         0.006         0.002           A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard         0.006         0.004         0.005         0.004         0.004           deviation         0.006         0.004         0.005         0.004         0.004           A14         0.222         0.225         0.231         0.237         0.243           0.219         0.222         0.231         0.237         0.243           0.219         0.222         0.231         0.237         0.243           Average         0.219         0.222         0.231         0.237         0.243           Average         0.219         0.222         0.236         0.248         0.249           Average         0.219         0.222         0.236         0.248         0.248           Standard         0.002         0.002		Standard					
A17         0.216         0.219         0.225         0.234         0.246           0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.243         0.252           Average         0.210         0.214         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard         0.006         0.004         0.005         0.004         0.004           deviation         0.006         0.004         0.005         0.004         0.252           A14         0.222         0.225         0.221         0.243         0.243           0.216         0.219         0.225         0.231         0.243           0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.236         0.248           Standard         0.002         0.002         0.004         0.004         0.004           Control         0.426		deviation	0.009	0.006	0.001	0.006	0.002
0.201         0.210         0.237         0.243         0.255           0.213         0.213         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.237         0.252           Standard         0.210         0.214         0.231         0.238         0.251           Standard         0.006         0.004         0.005         0.004         0.004           Al4         0.222         0.225         0.231         0.243         0.252           0.216         0.219         0.225         0.231         0.243         0.243           0.219         0.222         0.231         0.237         0.243           0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.236         0.248           Standard         0.002         0.002         0.004         0.004           0.414         0.390         0.414         0.414         0.414           Average         0.410         0.415         0.415         0.415		A17	0.216	0.219	0.225	0.234	0.246
0.213         0.213         0.231         0.237         0.252           Average         0.210         0.214         0.231         0.238         0.251           Standard deviation         0.006         0.004         0.005         0.004         0.004           A14         0.222         0.225         0.222         0.231         0.237         0.252           0.216         0.219         0.225         0.231         0.243         0.243           0.219         0.222         0.231         0.237         0.243           Average         0.219         0.222         0.231         0.237         0.243           Average         0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.236         0.248           Standard         0.002         0.002         0.004         0.004         0.004           O.1414			0.201	0.210	0.237	0.243	0.255
Average         0.210         0.214         0.231         0.238         0.251           Standard deviation         0.006         0.004         0.005         0.004         0.004           A14         0.222         0.225         0.222         0.24         0.252           0.216         0.219         0.225         0.231         0.243           0.219         0.222         0.231         0.237         0.243           Average         0.219         0.222         0.236         0.243           Standard         0.002         0.002         0.004         0.004         0.004           Octrol         0.426         0.004         0.004         0.004         0.004         0.004           0.390         0.414         0.014         0.015         0.015         0.015         0.015			0.213	0.213	0.231	0.237	0.252
Standard deviation         0.006         0.004         0.005         0.004         0.004           A14         0.222         0.225         0.222         0.24         0.252           0.216         0.219         0.225         0.231         0.243           0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.236         0.248           Standard deviation         0.002         0.002         0.004         0.004           Standard deviation         0.002         0.002         0.004         0.004           0.390         0.002         0.004         0.004         0.004           0.414         0.414         0.414         0.414         0.414		Average	0.210	0.214	0.231	0.238	0.251
deviation         0.006         0.004         0.005         0.004         0.004           A14         0.222         0.225         0.222         0.24         0.252           0.216         0.219         0.225         0.231         0.243           0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.236         0.248           Standard         0.002         0.002         0.004         0.004         0.004           Control         0.426		Standard					
A14       0.222       0.225       0.222       0.24       0.252         0.216       0.219       0.225       0.231       0.243         0.219       0.222       0.231       0.237       0.249         Average       0.219       0.222       0.236       0.248         Standard       0.002       0.002       0.004       0.004       0.004         Control       0.426       0.004       0.004       0.004       0.004         Average       0.414       0.414       0.414       0.414       0.414         Average       0.410       0.015       0.015       0.015       0.015		deviation	0.006	0.004	0.005	0.004	0.004
0.216         0.219         0.225         0.231         0.243           0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.236         0.249           Average         0.219         0.222         0.236         0.249           Standard         0.002         0.002         0.004         0.004           Control         0.426         0.004         0.004         0.004           0.390         0.414         0.414         0.414         0.414           Average         0.410         0.015         0.015         0.015		A14	0.222	0.225	0.222	0.24	0.252
0.219         0.222         0.231         0.237         0.249           Average         0.219         0.222         0.226         0.236         0.248           Standard         0.002         0.002         0.004         0.004         0.004           Control         0.426         0.390         0.004         0.004         0.004           Average         0.414         0.414         0.414         0.414         0.414         0.015			0.216	0.219	0.225	0.231	0.243
Average         0.219         0.222         0.226         0.236         0.248           Standard deviation         0.002         0.002         0.004         0.004         0.004           Control         0.426			0.219	0.222	0.231	0.237	0.249
Standard deviation         0.002         0.002         0.004         0.004         0.004           Control         0.426         0.004         0.004         0.004         0.004           0.390         0.414         0.014         0.004         0.004         0.004           Average         0.410         0.015         0.015         0.015         0.015		Average	0.219	0.222	0.226	0.236	0.248
deviation         0.002         0.002         0.004         0.004         0.004           Control         0.426		Standard	00212			0.200	01210
Control         0.426         0.001         0.001         0.001           0.390         0.414         0		deviation	0.002	0.002	0.004	0.004	0.004
0.390         0.414           Average         0.410           Standard         0.015		Control	0.426				
0.414           Average         0.410           Standard			0.390				
Average     0.410       Standard     0.015		+ +	0.414			1	1
Standard		Average	0.410	1		1	1
		Standard	VIIV	+			
deviation UUIS		deviation	0.015				

**Table 7.40:**  $OD_{550nm}$  values for the determination of effect of pH on the removal of<br/>medi-blue dye and the calculations for the percentage removal<br/> $(C_0-C/C_0 \ge 100)$  (Fig. 4.8)

pH 6	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	45.610	45.122	52.43	47.56	1 48.780	46.585
	8	45.122	43.902	51.22	45.61	0 47.805	45.854
	6	44.634	41.463	46.82	44.63	4 43.659	44.878
	4	43.415	39.024	46.09	43.41	5 41.951	42.439
	2	41.707	38.293	40.97	42.19	5 38.780	39.512
				·			·
pH 7	Isolates	10		8	6	4	2
	E1	0.234	L I	0.249	0.249	0.252	0.27
		0.240	)	0.234	0.246	0.249	0.261
		0.231		0.243	0.246	0.249	0.264
	Average	0.232	2	0.247	0.247	0.250	0.265
	Standard			0.007	0.004		
	deviation	0.004		0.006	0.001	0.001	0.004
	D1	0.234		0.234	0.24	0.243	0.258
		0.219	<i>י</i>	0.228	0.231	0.24	0.243
		0.228		0.231	0.234	0.24	0.246
	Average	0.227	/	0.231	0.285	0.241	0.046
	deviation	0.004		0.002	0.004	0.001	0.006
	R 2	0.000	2	0.002	0.004	0.001	0.000
	K 2	0.220	2	0.198	0.210	0.225	0.249
		0.220	, i	0.201	0.210	0.210	0.234
	Average	0.195	5	0.201	0.222	0.222	0.243
	Standard	0.170	, 	0.200	0.210	01221	01212
	deviation	0.001		0.001	0.003	0.004	0.006
	A22	0.219	)	0.231	0.243	0.240	0.267
		0.234	k	0.228	0.228	0.240	0.252
		0.225	5	0.228	0.234	0.240	0.261
	Average	0.226	5	0.229	0.235	0.240	0.260
	Standard						
	deviation	0.006	5	0.001	0.006	0	0.006
	A17	0.219	)	0.246	0.243	0.246	0.276
		0.216	5	0.225	0.234	0.249	0.291
		0.216	5	0.237	0.240	0.246	0.285
	Average	0.217	/	0.236	0.239	0.247	0.284
	Standard	0.001		0.000	0.004	0.001	0.007
	deviation	0.00		0.009	0.004	0.001	0.006
	A14	0.228	)	0.237	0.255	0.291	0.297
		0.222	:	0.225	0.252	0.279	0.297
	Average	0.223	,	0.231	0.232	0.283	0.297
	Standard	0.22	,	0.231	0.233	0.204	0.271
	deviation	0.002		0.005	0.001	0.005	0
	Control	0.450	)	0.005	0.001	0.005	
	Control	0.447	1			1	
		0.456	5				
	Average	0.451					
	Standard						
	deviation	0.004	↓				

pH 7	Conc (ppm)	E1	D1	R2	A2	2 A17	A14
-	10	48.559	49.667	49.66	57 50.5	54 51.885	50.111
	8	46.341	48.780	49.22	24 49.6	67 47.672	48.780
	6	45.233	47.894	49.00	)2 48.7	78 47.007	43.902
	4	44.568	46.563	48.11	48.3	37 45.233	37.029
	2	41.242	45.455	41.24	46.3	41 37.029	34.146
					•	ľ	
pH 8	Isolates	10		8	6	4	2
	E1	0.639	)	0.675	0.702	0.738	0.738
		0.621		0.630	0.684	0.711	0.720
		0.630	)	0.657	0.693	0.720	0.729
	Average	0.210	)	0.218	0.231	0.241	0.243
	Standard						
	deviation	0.007	1	0.018	0.007	0.011	0.007
	D1	0.675	5	0.684	0.711	0.729	0.765
		0.657	1	0.639	0.702	0.702	0.729
		0.657	7	0.72	0.675	0.711	0.747
	Average	0.221		0.227	0.232	0.238	0.249
	Standard						
	deviation	300.0	3	0.033	0.015	0.011	0.015
	R 2	0.666	5	0.738	0.765	0.801	0.774
		0.657	7	0.72	0.765	0.756	0.801
		0.657	7	0.729	0.783	0.774	0.792
	Average	0.220	)	0.243	0.257	0.259	0.263
	Standard						
	deviation	0.004		0.007	0.008	0.018	0.011
	A22	0.666	5	0.666	0.711	0.702	0.801
		0.639	)	0.666	0.684	0.729	0.819
		0.657	1	0.657	0.693	0.72	0.792
	Average	0.218	3	0.221	0.232	0.239	0.266
	Standard	0.011		0.004	0.011	0.011	0.011
	deviation	0.01		0.004	0.011	0.011	0.011
	A17	0.729	)	0.747	0.720	0.783	0.801
		0.693	5	0.711	0.765	0.720	0.747
		0.71		0.729	0.747	0.756	0.774
	Average	0.237	'	0.245	0.248	0.251	0.258
	Standard	0.014	.	0.015	0.010	0.026	0.022
		0.013	2	0.013	0.019	0.020	0.022
	A14	0.228		0.231	0.240	0.249	0.232
		0.220		0.237	0.234	0.24	0.255
	Average	0.225	, 7	0.234	0.240	0.240	0.255
	Standard	0.221		0.407	0.240	0.243	0.433
	deviation	0.001		0.002	0.005	0.004	0.002
	Control	0.001	5	0.002	0.005	0.007	0.002
	Control	0.42	·				
		0.434	5				
	Average	0.425	7				
	Standard						1
	deviation	0.006	5				

pH 8	Conc (ppm)	E1	D1		R2		A22	A	17	A14	
	10	50.820	48.24	4	48.478	3	47.076	44	.496	46.838	3
	8	48 946	46.83	8	43 091		46 370	43	091	45 199	 )
	6	45 902	45.66	7	39.813	2	44 965	41	920	43 794	1
	4	43.560	43.00	2	30 3//	1	/3 70/	41	218	42.623	2
	4	42.001	41.60	2	20.405	7	20.110		.210	40.001	, 1
	2	43.091	41.68	6	38.407	/	39.110	39	.578	40.281	1
pH 9	Isolates	1(	)		8		6	4		2	
	E1	0.1	98	0.	.204	(	0.231	0.22	5	0.228	
		0.1	95	0.	.219	(	0.204	0.21	9	0.228	
		0.1	95	0	0.21	(	0.216	0.21	9	0.225	
	Average	0.1	94	0.	.211	(	0.217	0.22	1	0.227	
	Standard	0.0	21	0	000		0.011	0.00	2	0.001	
		0.0	JI 12	0.	.006	(	0.011	0.00	3	0.001	
	DI	0.2	10	0.	207	(	) 216	0.21	y 5	0.231	
		0.2	07	0.	212	(	) 216	0.22	$\frac{s}{0}$	0.210	
	D1	0.2	13	0.	210	(	) 222	0.21	$\frac{7}{0}$	0.223	
	Standard	0.2	15	0.	.219	(	J.ZZZ	0.21	9	0.231	
	deviation	0.0	13	0	005	(	0.003	0.00	3	0.006	
	R 2	0.0	) <u>4</u>	0	216	(	) 228	0.00	4	0.000	
	1 Z	0.2	10	0	219	(	) 225	0.23	8	0.243	
		0.2	16	0	216	(	).219	0.22	1	0.234	-
	Average	0.2	10	0.	.217	(	0.224	0.23	1	0.235	-
	Standard										
	deviation	0.0	06	0.	.001	(	0.004	0.00	3	0.006	
	A22	0.0	27	0.	.030	(	0.036	0.05	7	0.075	
		0.0	30	0.	.039	(	0.042	0.04	5	0.060	
		0.0	36	0.	.045	(	0.048	0.05	1	0.069	
	Average	0.0	31	0.	.038	(	0.042	0.05	1	0.068	
	Standard										
	deviation	0.0	04	0.	.006	(	0.005	0.00	5	0.006	
	A17	0.20	)4	0.	.219	(	).222	0.22	2	0.237	
		0.2	13	0.	.210	(	0.216	0.21	9	0.231	
	A	0.2	19	0.	216	(	0.219	0.22	2	0.234	
	Average	0.2	12	U.	.215	(	0.219	0.22	1	0.234	
	deviation	0.0	16	0	004	(	0.002	0.00	1	0.002	
		0.0	19	0.	216		) 219	0.00	0	0.002	_
	A14	0.2	1) 1	0	2220		) 222	0.21	0	0.240	
		0.2	16	0	.216	(	).222	0.24	8	0.223	-
	Average	0.2	12	0.	.218		0.222	0.22	9	0.233	
	Standard		-						-+		
	deviation	0.0	08	0.	.003	(	0.001	0.00	9	0.006	
	Control	0.4	38								
		0.4	32								
		0.4	35								
	Average	0.4	35								
	Standard										
	deviation	0.0	02								

pH 9	Conc (ppm)	E1	Ι	D1	R	2	A22	A17	A14
	10	55.402	51	.724	51.7	24	49.885	51.264	51.264
	8	51.494	51	.034	50.1	15	49.195	50.575	49.885
	6	50.115	49	.885	48.5	506	46.667	49.655	48.966
	4	49.195	49	.195	46.8	397	45.057	49.195	47.356
	2	47.816	48	.506	45.9	977	38.851	46.207	46.437
					•		•		•
pH 10	Isolates	10		:	8		6	4	2
	E1	0.123		0.1	138	(	0.165	0.168	0.177
		0.144		0.1	138	(	0.150	0.153	0.171
		0.132		0.1	138	(	0.159	0.162	0.174
	Average	0.133		0.1	139	(	0.158	0.161	0.174
	Standard				_				
	deviation	0.009		(	0	(	0.006	0.006	0.006
	D1	0.117		0.1	111	(	).129	0.141	0.153
		0.105		0.1	114	(	).144	0.138	0.147
		0.111		0.	12	(	0.123	0.144	0.150
	Average	0.111		0.]	115		0.122	0.140	0.150
	Standard	0.005		0.0	004		000	0.002	0.002
		0.003		0.0	)75		) 123	0.002	0.153
	<u> </u>	0.030		0.0	)78		) 108	0.129	0.133
		0.030		0.0	)81		) 117	0.125	0.138
	Average	0.030		0.0	<b>78</b>		0.116	0.120	0.144
	Standard	0.002			//0			0.120	01110
	deviation	0.003		0.0	002	(	0.006	0.004	0.006
	A17	0.039		0.0	)48	(	0.048	0.069	0.069
		0.048		0.0	)57	(	0.060	0.06	0.066
		0.054		0.0	)63	(	0.069	0.063	0.066
	Average	0.047		0.0	)56	(	0.059	0.064	0.067
	Standard								
	deviation	0.006		0.0	)06	(	0.009	0.004	0.001
	A14	0.039		0.0	)66	(	0.057	0.072	0.093
		0.036		0.0	)54	(	0.063	0.078	0.081
		0.036		0.0	)42	(	0.066	0.087	0.087
	Average	0.037		0.0	)54	(	0.062	0.079	0.087
	Standard	0.001			10		2 004	0.007	0.005
	deviation	0.001		0.0	)1U )21		0.004	0.006	0.005
	AZZ	0.225		0.2	201		) 221	0.237	0.249
		0.222		0.2	222 028		) 237	0.234	0.234
	Average	0.222		0.2	220 ))7		0.231	0.220	0.243
	Standard	0.223		0.4				0.400	V.474
	deviation	0.001		0.0	)04	(	0.005	0.004	0.006
	Control	0.468		Cor	ntrol			0.001	0.000
		0.462							
		0.453							
	Average	0.461							
	Standard						İ		
	deviation	0.006							

pH 10	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	71.150	75.922	93.059	93.275	89.805	91.974
	8	69.848	75.054	83.080	91.757	87.852	88.286
	6	65.727	73.536	74.837	90.889	87.202	86.551
	4	65.076	69.631	72.668	88.937	86.117	82.863
	2	62.256	67.462	68.547	85.249	85.466	81.128

**Table 7.41:**  $OD_{550nm}$  values for the determination of effect of temperature on the removal<br/>of medi-blue dye and the calculations for the percentage removal<br/> $(C_0-C/C_0 \times 100)$  (Fig. 4.9)

28°C	Isolates	10	8	6	4	2
	E1	0.114	0.123	0.132	0.147	0.165
		0.126	0.132	0.141	0.147	0.153
		0.120	0.129	0.135	0.153	0.159
	Average	0.120	0.128	0.136	0.149	0.159
	Standard deviation	0.005	0.004	0.004	0.003	0.005
	D1	1.230	0.135	0.138	0.141	0.153
		1.320	0.138	0.141	0.150	0.159
		1.290	0.135	0.147	0.144	0.156
	Average	0.128	0.136	0.142	0.145	0.156
	Standard deviation	0.037	0.001	0.004	0.004	0.002
	R 2	0.114	0.117	0.120	0.126	0.135
		0.120	0.123	0.132	0.141	0.138
		0.117	0.120	0.126	0.135	0.135
	Average	0.117	0.120	0.126	0.134	0.136
	Standard deviation	0.002	0.002	0.005	0.006	0.001
	A22	0.123	0.126	0.135	0.144	0.129
		0.129	0.132	0.123	0.126	0.138
		0.126	0.129	0.135	0.132	0.141
	Average	0.126	0.128	0.131	0.134	0.136
	Standard deviation	0.002	0.002	0.006	0.007	0.005
	A17	0.120	0.120	0.129	0.135	0.150
		0.117	0.123	0.135	0.141	0.156
		0.114	0.117	0.132	0.138	0.153
	Average	0.117	0.12	0.132	0.138	0.153
	Standard deviation	0.002	0.002	0.002	0.002	0.002
	A14	0.108	0.120	0.114	0.120	0.132
		0.117	0.120	0.123	0.129	0.132
		0.114	0.111	0.123	0.129	0.129
	Average	0.113	0.117	0.12	0.126	0.13
	Standard deviation	0.004	0.004	0.004	0.004	0.001
	Control	0.252				
		0.261				
		0.258				
	Average	0.257				
	Standard deviation	0.004				

28°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	53.307	50.195	54.47	75 50.972	2 54.475	56.031
	8	50.195	47.082	2 53.30	07 50.195	5 53.307	54.475
	6	47.082	44.747	50.97	49.027	48.638	53.307
	4	42.023	40.078	47.86	60 47.860	) 46.304	50.973
	2	38.132	39.300	46.69	93 47.082	2 40.467	49.416
·							•
35°C	C Isolates	10		8	6	4	2
	E1	0.15	6	0.159	0.165	0.168	0.150
		0.14	1	0.144	0.144	0.147	0.153
		0.15	0	0.153	0.126	0.159	0.159
	Average	0.14	9	0.152	0.155	0.158	0.16
	Standard						
	deviation	0.00	6	0.006	0.016	0.009	0.004
	D1	0.12	9	0.135	0.147	0.144	0.150
		0.11	1	0.120	0.108	0.141	0.150
		0.12	0	0.126	0.141	0.141	0.147
	Average	0.12	2	0.127	0.132	0.142	0.149
	Standard		_	0.001	0.017	0.001	0.001
	deviation	0.00	7	0.006	0.017	0.001	0.001
	R 2	0.15	6	0.156	0.159	0.165	0.165
		0.12	6	0.138	0.141	0.150	0.159
	A	0.14	/	0.147	0.150	0.156	0.162
	Average	0.14	3	0.147	0.15	0.15/	0.162
	Standard	0.01	2	0.007	0.007	0.006	0.002
		0.01	3	0.007	0.007	0.000	0.002
	ALL	0.14	6	0.133	0.130	0.141	0.177
		0.12	8	0.129	0.133	0.102	0.150
	Average	0.13	7	0.141	0.144	0.150	0.105
	Standard	0.15	/	0.141	0.145	0.101	0.100
	deviation	0.00	9	0.010	0.009	0.009	0.009
	A17	0.15	9	0.144	0.171	0.165	0.183
		0.13	8	0.159	0.141	0.150	0.150
		0.15	0	0.153	0.153	0.159	0.171
	Average	0.14	9	0.152	0.155	0.158	0.171
	Standard						
	deviation	0.00	9	0.006	0.012	0.006	0.014
	A14	0.14	4	0.132	0.141	0.153	0.171
		0.12	9	0.144	0.144	0.150	0.162
		0.13	5	0.138	0.135	0.144	0.165
	Average	0.13	6	0.138	0.14	0.149	0.166
	Standard						
	deviation	0.00	6	0.005	0.004	0.004	0.004
	Control	0.47	1				
		0.45	9				
		0.48	3				
	Average	0.47	1				
	Standard						
	deviation	0.01	0				

35°C	Conc (ppm)	E1	D1		R2		A22	A17	A14
	10	68.365	74.52	22	69.639	)	70.913	68.365	71.125
	8	67.728	73.03	36	68.970	)	70.064	67.091	70.701
	6	67.091	71.9	75	68.153	3	69.214	67.091	70.276
	4	66.454	69.85	51	66.667	7	67.941	66.454	68.365
	2	66.030	68.30	65	65.605	5	64.756	63.694	64.756
<u> </u>				I					
40°C	C Isolates	10		8			6	4	2
	E1	0.16	5	0.1	83	0.	.162	0.195	0.198
		0.16	5	0.1	53	0.	.183	0.18	0.189
		0.17	1	0.1	74	0.	.174	0.189	0.192
	Average	0.16	7	0.1	70	0.	.173	0.188	0.193
	Standard								
	deviation	0.00	3	0.0	13	0.	.009	0.006	0.004
	D1	0.18	0	0.1	83	0.	.195	0.195	0.198
		0.15	6	0.1	62	0.	.177	0.186	0.198
		0.17	4	0.1	74	0.	.186	0.192	0.195
	Average	0.17	0	0.1	73	0.	.186	0.191	0.197
	Standard								
	deviation	0.01	1	0.0	09	0.	.007	0.004	0.001
	R 2	0.16	2	0.1	59	0.	.183	0.186	0.195
		0.13	8	0.1	68	0.	.174	0.183	0.183
		0.15	6	0.1	62	0.	.177	0.183	0.189
	Average	0.15	2	0.1	63	0.	.178	0.184	0.189
	Standard								
	deviation	0.01	0	0.0	04	0.	.004	0.001	0.005
	A22	0.18	6	0.1	95	0.	.198	0.189	0.207
		0.16	5	0.1	83	0.	.189	0.201	0.198
		0.17	7	0.1	89	0.	.192	0.195	0.189
	Average	0.17	6	0.1	89	0.	.193	0.195	0.198
	Standard	0.00		0.0	~ ~	0	0.0.4	0.005	0.005
	deviation	0.00	9	0.0	05	0.	.004	0.005	0.007
	A17	0.16	5	0.10	68	0.	.174	0.192	0.201
		0.15	6	0.1	/1	0.	.180	0.177	0.213
		0.15	9	0.10	68	0.	.177	0.186	0.207
	Average	0.16	U	0.1	69	0.	.177	0.185	0.207
	Standard	0.00	4	0.0	01	0	002	0.007	0.005
	deviation	0.004	1	0.0	20	0.	210	0.000	0.005
	A14	0.17	1	0.1	00	0.	.219	0.210	0.249
		0.18	0	0.1	9J	0.	212	0.223	0.240
	A 1/080 22	0.18	0	0.1	טיש 20	0.	.213	0.219	0.243
	Stondard	0.17	7	0.1	00	0		0.410	V.244
	deviation	0.00	6	0.0	06	0	004	0.006	0.004
	Control	0.00	7	0.0		0.		0.000	0.004
	Control	0.41	0						
		0.42	7						
	Average	0.41	8						
	Standard	0.410							1
	deviation	0.00	$1 \mid $						

$40^{\circ}$ C	Conc (ppm)	F1	1	D1	R	)	Δ22	A17	Δ14
40 C	10	60.048	50	330	63.6	36	57.895	61 722	57 177
	8	59 330	58	.550 .612	61.0	05	54 785	59 569	55.024
	6	58.612	55	502	57.4	.16	53 828	57.656	49 761
	4	55 024	54	306	55.9	81	53 349	55 742	47.847
	2	53.828	52	871	54.7	85	52 632	50.478	41 627
	2	55.020	52		54.7	05	52.052	50.470	41.027
45°C	Isolates	10			8		6	4	2
	F1	0.213		0.2	216	(	0.225	0 231	0.246
		0.198		0.2	201		0.225	0.231	0.240
		0.198		0.2	201		0.210	0.225	0.222
	Average	0.204		0.2	208		0.219	0.225	0.234
	Standard	0.205		0.4	200		0.210	0.220	0.254
	deviation	0.0061		0.0	006	(	0.006	0.004	0.010
	D1	0.210		0.0	210	(	0.219	0.225	0.225
		0.195		0.2	204	(	0 204	0.204	0.213
		0 201		0.2	207	(	0.210	0.216	0.219
	Average	0.202		0.2	207		0.211	0.215	0.219
	Standard	0.202		0.2	-07			0.210	0.217
	deviation	0.006		0.0	002	(	0.006	0.009	0.005
	R 2	0.180		0.2	201	(	0.201	0.213	0.225
		0.171		0.1	183	(	0.189	0.201	0.213
		0.174		0.1	189	(	0.195	0.207	0.219
	Average	0.175		0.1	189		0.195	0.207	0.219
	Standard								
	deviation	0.004		0.0	008	(	0.005	0.005	0.005
	A22	0.189		0.1	189	(	0.189	0.231	0.267
		0.180		0.1	189	(	0.195	0.219	0.261
		0.186		0.1	189	(	0.192	0.225	0.264
	Average	0.185		0.1	189	(	0.192	0.225	0.264
	Standard								
	deviation	0.004		(	0	(	0.005	0.005	0.002
	A17	0.201		0.2	207	(	0.213	0.216	0.225
		0.186		0.1	189	(	0.189	0.198	0.204
		0.195		0.1	198	(	0.201	0.207	0.213
	Average	0.194		0.1	198		0.201	0.207	0.214
	Standard								
	deviation	0.006		0.0	007	(	0.010	0.007	0.009
	A14	0.207		0.2	219	(	0.216	0.231	0.234
		0.186		0.2	204	(	0.210	0.216	0.225
		0.198		0.2	210	(	0.213	0.225	0.231
	Average	0.197		0.2	211	(	0.213	0.224	0.23
	Standard								
	deviation	0.009		0.0	)06	(	0.002	0.006	0.004
	Control	0.348							
		0.339							
		0.342							
	Average	0.343							
	Standard deviation	0.004							

45°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	40.233	41.108	48.980	46.064	43.440	42.566
	8	39.359	39.650	44.898	44.898	42.274	38.484
	6	36.443	38.484	43.149	44.023	41.399	37.901
	4	34.111	37.318	39.650	34.402	39.650	34.694
	2	31.778	36.152	36.152	23.032	37.609	32.945

**Table 7.42:** OD<sub>550nm</sub> values for the determination of effect of cations on the removal of<br/>medi-blue dye and the calculations for the percentage removal<br/> $(C_0-C/C_0 \ge 100)$  (Fig. 4.10)

CTAB	Isolates	10	8	6	4	2
	E1	0.591	0.915	0.975	0.984	1.089
		0.573	0.900	0.957	0.969	1.080
		0.564	0.906	0.966	0.978	1.068
	Average	0.572	0.907	0.966	0.977	1.079
	Standard deviation	0.011	0.006	0.007	0.006	0.009
	D1	0.588	0.873	0.873	0.915	0.948
		0.576	0.864	0.858	0.903	0.933
		0.582	0.867	0.885	0.909	0.942
	Average	0.582	0.868	0.885	0.909	0.941
	Standard deviation	0.005	0.004	0.011	0.005	0.006
	R 2	0.501	0.768	0.813	0.834	1.104
		0.483	0.756	0.798	0.819	1.083
		0.492	0.762	0.807	0.828	1.095
	Average	0.492	0.762	0.806	0.827	1.094
	Standard deviation	0.007	0.005	0.006	0.006	0.009
	A22	0.711	1.026	1.047	1.071	1.125
		0.699	1.011	1.038	1.044	1.107
		0.705	1.017	1.044	1.059	1.116
	Average	0.705	1.018	1.043	0.058	1.116
	Standard deviation	0.005	0.006	0.011	0.011	0.007
	A17	0.351	0.693	0.705	0.831	1.080
		0.330	0.678	0.678	0.816	1.068
		0.342	0.684	0.690	0.822	1.074
	Average	0.341	0.685	0.691	0.823	1.074
	Standard deviation	0.0086	0.006	0.011	0.006	0.005
	A14	0.483	0.777	0.783	0.984	1.002
		0.486	0.765	0.768	0.963	1.023
		0.483	0.771	0.777	0.975	1.014
	Average	0.484	0.771	0.776	0.974	1.013
	Standard deviation	0.001	0.005	0.006	0.009	0.009
	Control	2.115				
		2.100				
		2.109				
	Average	2.108				
	Standard deviation	0.006				

CTAB	Conc (ppm)	E1	D	1	R2	A22	2	A17	A14
	10	72.865	72.3	91	76.660	66.5	56	83.824	77.039
	8	56.973	58.8	324	63.852	51.70	08	67.505	63.425
	6	54.175	58.0	)17	61.765	50.52	22	67.220	63.188
	4	53.653	56.8	379	60.769	49.8	1	61.103	53.795
	2	48.814	55.3	861	48.102	47.0	59	49.051	51.945
						÷		·	
CaCl <sub>2</sub>	Isolates	10			8	6		4	2
	E1	0.38	1	0	.447	0.45		0.462	0.507
		0.35	4	0	.438	0.438		0.450	0.453
		0.36	9	0	.441	0.444		0.456	0.501
	Average	0.36	8	0	.442	0.444		0.456	0.487
	Standard								
	deviation	0.01	1	0	.004	0.005		0.005	0.024
	D1	0.37	8	0	.405	0.411		0.420	0.435
		0.37	2	0	.390	0.390		0.405	0.417
		0.37	5	0	.399	0.402		0.414	0.426
	Average	0.37	5	0	.398	0.401		0.413	0.1426
	Standard				0.0.7			0.005	
	deviation	0.00	2	0	.006	0.009		0.006	0.007
	R 2	0.34	8	0	.381	0.426	_	0.453	0.459
		0.33	3	0	.360	0.414	_	0.438	0.477
		0.34	2	0	.369	0.417		0.447	0.468
	Average	0.34	1	(	).37	0.419	_	0.446	0.468
	Standard	0.00		0	000	0.005		0.000	0.007
	deviation	0.00	0	0	.009	0.005		0.006	0.007
	A22	0.38		0	.432	0.438	_	0.483	0.495
		0.30	2	0	.423	0.423	_	0.471	0.480
	Averege	0.37	2 1	0	.429	0.432		0.477	0.301
	Standard	0.37	1	U	.420	0.431		0.477	0.490
	deviation	0.00	a	0	004	0.006		0.005	0.006
		0.00	2 7	0	435	0.000		0.003	0.000
		0.33	, 8	0	438	0.447		0.468	0.301
		0.34	1	0	438	0.444		0.400	0.405
	Average	0.35	2	0	<b>473</b>	0.444		0.473	0.495
	Standard	0.00.		0		0.111		0.475	0.475
	deviation	0.00	4	0	.001	0.002		0.003	0.005
	A14	0.33	3	0	.417	0.423		0.450	0.489
		0.31	8	0	.396	0.411		0.444	0.477
		0.32	4	0	.405	0.417		0.447	0.483
	Average	0.32	5	0	.406	0.417		0.447	0.483
	Standard								
	deviation	0.00	6	0	.009	0.005		0.002	0.005
	Control	0.74	7						
		0.73	5						
		0.74	1						
	Average	0.74	1						
	Standard								
	deviation	0.00	5						

CaCl <sub>2</sub>	Conc (ppm)	E1	D	1	R2	A22	A17	A14
	10	50.337	49.3	93	53.981	49.933	52,497	56.140
	8	40.351	46.2	89	50.067	42.240	41.026	45.209
	6	40.081	45.8	84	43.455	41.835	40.081	43.725
	4	38.462	44.2	65	39.811	35.628	36.167	39.676
	2	34.278	42.5	10	36.842	33.873	33.198	34.818
<u> </u>	I				1	1		1
MnCl	Isolates	10			8	6	4	2
	E1	0.00	3	0	.015	0.027	0.057	0.069
		0		0	.006	0.012	0.045	0.06
		0		0	.012	0.018	0.051	0.06
	Average	0.00	1	0	.011	0.019	0.051	0.065
	Standard							
	deviation	0.00	1	0	.004	0.006	0.005	0.004
	D1	0.03	0	0	.048	0.054	0.051	0.057
		0.04	5	0	.036	0.045	0.057	0.066
		0.03	9	0	.042	0.051	0.054	0.060
	Average	0.03	8	0	.042	0.05	0.054	0.061
	Standard							
	deviation	0.00	6	0	.005	0.004	0.002	0.004
	R 2	0.00	3	0	.018	0.036	0.039	0.051
		0.02	4	0	.021	0.033	0.045	0.063
		0.01	5	0	.021	0.033	0.039	0.057
	Average		4	0	.020	0.034	0.041	0.057
	Standard							
	deviation	0.00	9	0	.001	0.001	0.003	0.005
	A22	0.02	1	0	.030	0.060	0.06	0.084
		0.03	6	0	.033	0.069	0.075	0.075
		0.03	0	0	.030	0.063	0.069	0.078
	Average	0.02	9	0	.031	0.064	0.068	0.079
	Standard	0.00	<i>(</i>	0	0.01	0.004	0.007	0.004
	deviation	0.00	6	0	.001	0.004	0.006	0.004
	AI7	0.01	8	0	.051	0.069	0.069	0.105
		0.00	6	0	.063	0.054	0.075	0.078
		0.01	2	0	.060	0.06	0.072	0.093
	Average	0.01	2	0	.058	0.061	0.072	0.092
	Standard	0.00	5	_	005	0.007	0.002	0.011
		0.00	з 6	0	042	0.006	0.002	0.011
	A14	0.00	5	0	024	0.045	0.039	0.03/
		0.01	<u> </u>	0	024	0.030	0.039	0.043
	Average	0.00	7	0	033	0.039	0.042	0.031
	Standard	0.01	v	U	.033	0.030	V.V4	0.031
	deviation	0.00	4	Λ	004	0.006	0.001	0.005
	Control	0.00	- 6	0		0.000	0.001	0.005
	Control	0.24	1					
		0.23	7					
	Average	0.23	, 8					
	Standard	0.20	~	<u> </u>				
	deviation	0.00	6					

MnCl <sub>2</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	99.580	84.034	94.118	87.815	94.958	95.798
	8	95.378	82.353	91.597	86.975	75.630	86.134
	6	92.017	78.992	85.714	73.109	74.370	84.034
	4	78.571	77.311	82.778	71.429	69.748	83.193
	2	72.689	74.370	76.050	66.807	61.345	78.571

MgSQ4	Isolates	10	8	6	4	2
	E1	0.060	0.081	0.078	0.075	0.084
		0.060	0.063	0.072	0.084	0.075
		0.060	0.072	0.075	0.081	0.081
	Average	0.060	0.072	0.075	0.08	0.080
	Standard					
	deviation	0	0.0070	0.0020	0.004	0.004
	D1	0.081	0.096	0.096	0.108	0.126
		0.078	0.075	0.090	0.111	0.132
		0.078	0.087	0.090	0.114	0.129
	Average	0.079	0.086	0.092	0.110	0.129
	Standard					
	deviation	0.001	0.009	0.003	0.002	0.002
	R 2	0.045	0.069	0.075	0.081	0.111
		0.030	0.069	0.063	0.084	0.096
		0.039	0.066	0.069	0.090	0.105
	Average	0.038	0.065	0.069	0.085	0.104
	Standard					
	deviation	0.006	0.004	0.005	0.004	0.006
	A22	0.060	0.075	0.069	0.093	0.093
		0.051	0.069	0.090	0.087	0.093
		0.054	0.072	0.081	0.090	0.099
	Average	0.055	0.072	0.079	0.090	0.095
	Standard					
	deviation	0.004	0.002	0.009	0.002	0.003
	A17	0.051	0.078	0.072	0.087	0.096
		0.048	0.057	0.078	0.081	0.099
		0.048	0.069	0.075	0.075	0.096
	Average	0.049	0.068	0.075	0.081	0.097
	Standard					
	deviation	0.001	0.009	0.005	0.0049	0.00141
	A14	0.027	0.036	0.087	0.093	0.105
		0.030	0.045	0.072	0.075	0.108
		0.030	0.042	0.081	0.0843	0.105
	Average	0.029	0.041	0.08	0.084	0.106
	Standard					
	deviation	0.001	0.004	0.006	0.007	0.001
	Control	0.264				
		0.273				
		0.270				
	Average	0.269				
	Standard					
	deviation	0.004				

MgSO <sub>4</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	77.695	70.632	85.874	79.554	81.784	89.219
	8	73.234	68.030	75.836	73.234	74.721	84.758
	6	72.119	65.799	74.349	70.632	72.119	70.260
	4	70.260	59.108	68.401	66.543	69.888	68.773
	2	67.286	52.045	61.338	64.684	63.941	60.595

**Table 7.43:** OD<sub>550nm</sub> values for the determination of flocculating activity of fawn dye using different concentrations of bioflocculants

Isolates	10	8	6	4	2
E1	0.135	0.207	0.228	0.246	0.252
	0.132	0.210	0.222	0.246	0.246
	0.141	0.210	0.234	0.090	0.258
Average	0.136	0.209	0.228	0.247	0.252
Standard deviation	0.004	0.001	0.004	0.074	0.005
D1	0.042	0.045	0.063	0.087	0.105
	0.036	0.036	0.057	0.078	0.099
	0.045	0.051	0.066	0.093	0.108
Average	0.041	0.044	0.062	0.086	0.104
Standard deviation	0.004	0.006	0.004	0.006	0.004
R 2	0.378	0.552	0.636	0.642	0.645
	0.369	0.549	0.633	0.636	0.642
	0.384	0.555	0.642	0.645	0.651
Average	0.377	0.552	0.637	0.641	0.646
Standard deviation	0.006	0.002	0.004	0.004	0.004
A22	0.597	0.603	0.633	0.642	0.654
	0.600	0.597	0.630	0.636	0.651
	0.594	0.606	0.636	0.645	0.657
Average	0.597	0.602	0.633	0.641	0.654
	0.002	0.004	0.002	0.004	0.002
A17	0.630	0.639	0.645	0.651	0.663
	0.624	0.630	0.636	0.648	0.657
	0.636	0.645	0.651	0.654	0.669
Average	0.63	0.638	0.644	0.651	0.663
Standard deviation	0.005	0.006	0.006	0.002	0.005
A14	0.582	0.627	0.633	0.639	0.672
	0.573	0.594	0.63	0.633	0.669
	0.588	0.660	0.636	0.645	0.675
Average	0.581	0.627	0.633	0.369	0.272
Standard deviation	0.006	0.027	0.002	0.005	0.002
Control	0.807				
	0.81				
	0.81				
Average	0.809				
Standard deviation	0.001				

Conc (ppm)	E1	D1	R2	A22	A17	A14
10	83.189	94.932	53.399	26.205	22.126	28.183
8	74.166	94.561	31.768	25.587	21.137	22.467
6	71.817	92.336	21.261	21.755	20.396	21.755
4	69.468	89.369	20.766	20.766	19.530	21.014
2	68.850	87.145	20.148	19.159	18.047	16.934

**Table 7.44:** Percentage removal ( $C_0$ – $C/C_0 \ge 100$ ) of fawn dye using different concentrations of flocculants as derived from Table 7.43 (Fig. 4.11)

**Table 7.45:** Flocculating activity of fawn dye as derived from Table 7.43 using anequation for flocculating activity in Section 4.2.3 (Fig. 4.12)

Isolate	Flocculating activity	Standard deviation		
E1	14.158	0.198		
D1	4.468	0.152		
R2	17.613	0.369		
A22	73.368	0.215		
A17	146.413	0.166		
A14	56.011	0.200		

pH 6	Isolates	10	8	6	4	2
	E1	0.618	0.627	0.630	0.654	0.696
		0.612	0.618	0.624	0.648	0.693
		0.621	0.633	0.636	0.657	0.702
	Average	0.617	0.626	0.630	0.653	0.697
	Standard					
	deviation	0.004	0.006	0.005	0.004	0.004
	D1	0.585	0.591	0.600	0.609	0.609
		0.576	0.588	0.600	0.600	0.609
		0.591	0.594	0.603	0.615	0.612
	Average	0.584	0.591	0.601	0.608	0.61
		0.006	0.002	0.001	0.006	0.001
	R 2	0.558	0.573	0.576	0.579	0.591
		0.555	0.564	0.570	0.576	0.591
		0.561	0.579	0.579	0.585	0.594
	Average	0.558	0.572	0.575	0.58	0.592
	Standard					
	deviation	0.002	0.006	0.004	0.004	0.001
	A22	0.591	0.600	0.603	0.603	0.609
		0.588	0.600	0.597	0.600	0.603
		0.597	0.600	0.606	0.609	0.612
	Average	0.592	0.600	0.602	0.604	0.608
	Standard					
	deviation	0.004	0	0.004	0.004	0.004
	A17	0.576	0.582	0.588	0.597	0.597
		0.576	0.582	0.594	0.600	0.603
		0.579	0.585	0.582	0.591	0.597
	Average	0.577	0.583	0.588	0.596	0.599
	Standard					
	deviation	0.001	0.001	0.005	0.005	0.003
	A14	0.567	0.579	0.585	0.591	0.666
		0.570	0.570	0.582	0.588	0.657
		0.570	0.585	0.588	0.594	0.672
	Average	0.569	0.578	0.585	0.591	0.665
	Standard					
	deviation	0.001	0.006	0.002	0.002	0.006
	Control	0.714				
		0.711				
		0.720				
	Average	0.715				
	Standard deviation	0.004				

**Table 7.46:**  $OD_{550nm}$  values for the determination of effect of pH on the removal of fawn<br/>dye and the calculations for the percentage removal ( $C_0$ – $C/C_0 \ge 100$ )<br/>(Fig. 4.13)

pH 6	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	22.970	18.322	21.958	17.203	19.301	20.420
	8	21.848	17.343	20.000	16.084	18.462	19.161
	6	21.348	15.944	19.580	15.804	17.762	18.182
	4	18.477	14.965	18.881	15.524	16.643	17.343
	2	14.921	14.685	17.203	14.965	16.224	6.993

pH 7	Isolates	10	8	6	4	2
	E1	0.579	0.591	0.600	0.609	0.618
		0.573	0.588	0.597	0.609	0.612
		0.582	0.597	0.606	0.612	0.624
	Average	0.578	0.592	0.601	0.610	0.618
	Standard					
	deviation	0.004	0.004	0.004	0.001	0.005
	D1	0.621	0.63	0.636	0.642	0.648
		0.615	0.624	0.63	0.636	0.639
		0.624	0.636	0.639	0.645	0.654
	Average	0.620	0.630	0.635	0.641	0.647
	Standard					
	deviation	0.004	0.005	0.004	0.004	0.006
	R 2	0.624	0.636	0.642	0.642	0.645
		0.621	0.636	0.636	0.639	0.642
		0.627	0.639	0.645	0.648	0.648
	Average	0.624	0.637	0.641	0.643	0.645
	Standard					
	deviation	0.002	0.001	0.004	0.004	0.002
	A22	0.576	0.636	0.642	0.645	0.648
		0.567	0.636	0.636	0.645	0.645
		0.582	0.639	0.348	0.648	0.654
	Average	0.575	0.637	0.642	0.646	0.649
	Standard					
	deviation	0.006	0.001	0.137	0.001	0.004
	A17	0.639	0.642	0.648	0.651	0.687
		0.636	0.639	0.639	0.645	0.684
		0.642	0.648	0.654	0.654	0.69
	Average	0.639	0.643	0.647	0.650	0.687
	Standard					
	deviation	0.002	0.004	0.006	0.004	0.002
	A14	0.633	0.648	0.651	0.666	0.681
		0.630	0.645	0.648	0.666	0.681
		0.639	0.651	0.657	0.669	0.684
	Average	0.234	0.648	0.652	0.667	0.682
	Standard					
	deviation	0.004	0.002	0.004	0.001	0.001
	Control	0.822				
		0.816				
		0.825				
	Average	0.821				
	Standard					
	deviation	0.004				

pH 7	Conc (ppm)	E1	D1		R2	A22	2	A17	A14
	10	29.598	22.597	22	2.097	28.2	15	20.225	20.849
	8	27.893	21.348	20	).474	20.47	74	19.725	19.101
	6	26.797	20.724	19	0.975	19.85	50	19.226	18.602
	4	25.700	19.975	19	0.725	19.35	51	18.851	16.729
	2	24.726	19.226	19	0.476	18.97	76	14.232	14.856
					-				
pH 8	Isolates	10	8		6			4	2
	E1	0.489	0.57		0.5	82	(	0.597	0.645
		0.483	0.56	7	0.5	82	(	0.600	0.642
		0.492	0.57	6	0.5	85	(	0.600	0.651
	Average	0.488	0.57	1	0.5	83	(	0.597	0.646
	Standard	0.004	0.00	4	0.0	01		0.001	0.004
	deviation	0.004	0.004	4	0.0	01	(	0.001	0.004
	DI	0.588	0.59	4 0	0.5	94	(	0.597	0.397
		0.585	0.58	8 7	0.5	94	(	0.600	0.600
	Auorogo	0.394	0.39	/	0.5	97		0.000	0.000
	Standard	0.569	0.59	3	0.5	95		0.397	0.599
	deviation	0.004	0.00	4	0.0	01	(	0.001	0.001
	R 2	0.591	0.59	<u> </u>	0.0	00		0.001	0.615
	1 C 2	0.591	0.5%	4	0.0	97	(	0.002	0.609
		0.594	0.59	7	0.6	06	(	0.612	0.621
	Average	0.590	0.59	5	0.6	01		0.609	0.615
	Standard	0.00220		-					01010
	deviation	0.004	0.00	1	0.0	04	(	0.002	0.005
	A22	0.585	0.59	1	0.5	97	(	0.600	0.603
		0.579	0.59	1	0.6	00	(	0.540	0.600
		0.591	0.594	4	0.6	00	(	0.660	0.609
	Average	0.585	0.592	2	0.5	97	(	0.600	0.604
	Standard								
	deviation	0.005	0.00	1	0.0	01	(	0.049	0.002
	A17	0.594	0.60	9	0.6	12	(	0.618	0.630
		0.591	0.60	9	0.6	06	(	0.618	0.624
		0.597	0.612	2	0.6	18	(	0.621	0.816
	Average	0.594	0.61	0	0.6	12	(	0.619	0.630
	Standard	0.000	0.00	1		05	,	0.001	0.000
	deviation	0.002	0.00	1	0.0	12	(	0.001	0.089
	A14	0.585	0.00	2	0.0	03		0.012	0.021
		0.382	0.60	5 6	0.0	19		0.012	0.618
	Average	0.391	0.00	4	0.0	10		0.013	0.027
	Standard	0.500	0.00	т	0.0	11		0.015	0.022
	deviation	0.004	0.00	1	0.0	06	(	0.001	0.004
	Control	0.801	0.00		0.0				0.001
	Control	0.807							
		0.795							
	Average	0.801			İ				
	Standard deviation	0.005							

pH 8	Conc (ppm)	E1	Ι	D1	F	R2	A22		A17	A14
	10	31.748	28.	.258	28.	136	28.74	-5	27.649	28.624
	8	20.140	27.	.771	27.	771	27.89	3	25.700	26.431
	6	18.462	27.	.527	27.	797	27.28	3	25.457	25.579
	4	16.503	27.	.284	25.	822	26.91	8	24.604	25.335
	2	9.650	27.	.040	25.	.091	26.43	1	23.264	24.239
				•			•			•
pH 9	Isolates	10		8			6		4	2
	E1	0.345		0.34	8	0.	354		0.366	0.387
		0.342		0.34	2	0.	354		0.366	0.378
		0.351		0.35	4	0.	357		0.372	0.393
	Average	0.346		0.34	8	0.	355		0.368	0.386
	Standard									
	deviation	0.004		0.00	5	0.	001		0.003	0.006
	D1	0.348		0.35	4	0.	357		0.360	0.366
		0.342		0.35	1	0.	351		0.357	0.363
		0.354		0.35	/	0	.36		0.366	0.372
	Average	0.348		0.35	4	0.	556		0.361	0.367
	Standard	0.005		0.00	2		004		0.004	0.004
		0.003		0.00	2	0.	452		0.004	0.004
	K 2	0.433		0.43	4	0.4	435		0.453	0.402
		0.432		0.44	+ 3	0.	444 450		0.455	0.450
	Average	0.441		0.43	<u>0</u>	0.	452		0.450	0.405
	Standard	0.150		0.11	/	0.			0.121	0.401
	deviation	0.004		0.00	4	0.	006		0.001	0.004
	A22	0.447		0.45	6	0.4	465		0.471	0.501
		0.444		0.45	3	0.4	459		0.465	0.498
		0.450		0.45	9	0.	471		0.474	0.507
	Average	0.447		0.45	6	0.	465		0.470	0.502
	Standard									
	deviation	0.002		0.00	2	0.	005		0.004	0.004
	A14	0.348		0.35	1	0.	456		0.468	0.510
		0.348		0.34	8	0.	450		0.468	0.504
		0.351		0.35	4	0.	462		0.471	0.516
	Average	0.349		0.35	1	0.	456		0.469	0.51
	Standard	0.001		0.00	2		005		0.001	0.005
	deviation	0.001		0.00	2	0.	005		0.001	0.005
	A1/	0.351		0.36	2	0.	312 266		0.399	0.405
		0.348		0.36	2 2	0.	275		0.390	0.405
	Average	0.337		0.37	ے 7	0.	373 371		0.402	0.408
	Standard	0.352		0.30	1	U.	5/1		0.377	0.400
	deviation	0.004		0.00	4	0	004		0.002	0.001
	Control	0.825		0.00		0.	501		0.002	0.001
		0.822								
		0.828								
	Average	0.825								
	Standard					İ				
	deviation	0.002								

pH 9	Conc (ppm)	E1	D1	I	R2	A22	A	17	A14
	10	58.061	57.818	47	.152	45.81	8 57	.333	57.697
	8	57.818	57.091	45	.576	44.72	7 55	.515	57.455
	6	56.970	56.848	45	.212	44.84	8 55	.030	44.727
	4	55.394	56.242	44	.970	43.03	0 51	.636	43.152
	2	53.212	55.515	44	.121	39.15	2 50	.788	38.182
pH 10	Isolates	10		8		6	4		2
	E1	0.312	0.	321	0.	342	0.348	3	0.366
		0.309	0.	312	0.	339	0.348	3	0.357
		0.315	0.	327	0.	345	0.351		0.372
	Average	0.312	0.	.320	0.	342	0.349	)	0.365
	Standard								
	deviation	0.002	0.	.006	0.0	002	0.001		0.006
	D1	0.339	0	348	0.	354	0.372		0.387
		0.330	0	348	0.	348	0.366	)	0.384
		0.345	0	351	0.	357	0.375	)	0.390
	Average	0.338	0.	.549	0.	353	0.371		0.387
	Standard	0.006	0	001		004	0.004		0.002
		0.000	0	242	0.0	249	0.004	+	0.002
	<u> </u>	0.316	0	220	0.	240	0.331		0.337
		0.313	0	3.15	0.	342	0.340	7	0.351
	Average	0.321	0	343	0.	331 3/7	0.357	,	0.30
	Standard	0.510		574	0.	547	0.002	, 	0.550
	deviation	0.002	0	002	0	004	0.004	L	0.004
	A22	0.339	0	363	0.	366	0.366	)	0.372
		0.333	0	354	0.	357	0.363	;	0.366
		0.345	0	369	0.	372	0.372	2	0.375
	Average	0.339	0.	362	0.	365	0.367	/	0.371
	Standard								
	deviation	0.005	0	.006	0.0	006	0.004	ŀ	0.004
	A17	0.354	0.	360	0.	363	0.369	)	0.384
		0.354	0.	351	0.	354	0.363	;	0.381
		0.357	0.	366	0.	369	0.372	2	0.390
	Average	0.355	0	359	0.	362	0.368	;	0.385
	Standard								
	deviation	0.001	0.	.006	0.0	006	0.004		0.004
	A14	0.354	0.	357	0.	360	0.366	)	0.369
		0.348	0	351	0.	357	0.363	5	0.363
		0.357	0	363	0.1	363	0.369		0.375
	Average	0.353	0.	357	U.	.30	0.366	•	0.369
	Standard	0.004	0	005		002	0.007	,	0.005
	Control	0.004	0.	005	0.0	002	0.002		0.003
	Control	0.825							
		0.823							
	Average	0.037							
	Standard	0.031			1				
	deviation	0.005							

pH 10	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	62.455	59.326	61.733	59.206	57.280	57.521
	8	61.492	58.002	58.845	56.438	56.799	57.040
	6	58.845	56.799	58.243	56.077	56.438	56.979
	4	58.002	55.355	57.641	55.836	55.716	55.957
	2	56.077	53.430	57.160	55.355	53.670	55.596

**Table 7.47:**  $OD_{550nm}$  values for the determination of effect of temperature on the removal<br/>fawn dye and the calculations for the percentage removal ( $C_0$ -C/C $_0$  x 100)<br/>(Fig. 4.14)

28°C	Isolates	10	8	6	4	2
	E1	0.639	0.645	0.648	0.651	0.657
		0.633	0.642	0.642	0.645	0.654
		0.645	0.648	0.651	0.657	0.663
	Average	0.639	0.645	0.647	0.651	0.658
	Standard deviation	0.005	0.002	0.004	0.005	0.004
	D1	0.642	0.651	0.654	0.657	0.663
		0.642	0.648	0.654	0.687	0.657
		0.645	0.657	0.657	0.633	0.669
	Average	0.643	0.652	0.655	0.659	0.663
	Standard deviation	0.001	0.004	0.001	0.020	0.0045
	R 2	0.645	0.648	0.657	0.660	0.663
		0.639	0.648	0.654	0.657	0.654
		0.648	0.651	0.660	0.663	0.669
	Average	0.644	0.649	0.657	0.66	0.662
	Standard deviation	0.004	0.001	0.002	0.002	0.006
	A22	0.642	0.648	0.651	0.660	0.669
		0.636	0.642	0.648	0.657	0.672
		0.645	0.651	0.654	0.663	0.669
	Average	0.641	0.647	0.651	0.660	0.670
	Standard deviation	0.004	0.004	0.002	0.002	0.001
	A17	0.657	0.66	0.663	0.666	0.702
		0.651	0.657	0.657	0.660	0.699
		0.660	0.663	0.669	0.669	0.705
	Average	0.656	0.660	0.663	0.665	0.702
	Standard deviation	0.004	0.002	0.005	0.004	0.002
	A14	0.546	0.612	0.627	0.657	0.666
		0.543	0.606	0.627	0.654	0.660
		0.552	0.615	0.63	0.660	0.669
	Average	0.547	0.611	0.629	0.628	0.665
	Standard deviation	0.004	0.004	0.001	0.003	0.004
	Control	0.858				
		0.846				
		0.867				
	Average	0.857				
	Standard deviation	0.009				

28°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	25.438	24.971	24.854	25.204	23.454	36.173
	8	24.737	23.921	24.271	24.504	22.987	28.705
	6	24.504	23.571	23.337	24.037	22.637	26.721
	4	24.037	23.104	22.987	22.987	22.404	23.337
	2	23.221	22.637	22.754	21.820	18.086	22.404

35°C	Isolates	10	8	6	4	2
	E1	0.444	0.486	0.492	0.498	0.504
		0.438	0.480	0.486	0.489	0.498
		0.447	0.492	0.495	0.480	0.507
	Average	0.443	0.486	0.491	0.497	0.503
	Standard					
	deviation	0.004	0.005	0.004	0.007	0.004
	D1	0.465	0.471	0.483	0.486	0.507
		0.465	0.462	0.477	0.483	0.510
		0.468	0.477	0.486	0.492	0.510
	Average	0.466	0.470	0.482	0.487	0.509
	Standard					
	deviation	0.001	0.006	0.004	0.004	0.001
	R 2	0.477	0.495	0.498	0.504	0.564
		0.471	0.489	0.495	0.498	0.564
		0.480	0.501	0.501	0.510	0.567
	Average	0.476	0.495	0.498	0.504	0.565
	Standard					
	deviation	0.004	0.005	0.002	0.005	0.001
	A22	0.441	0.468	0.471	0.477	0.486
		0.441	0.462	0.465	0.477	0.483
		0.444	0.474	0.474	0.480	0.492
	Average	0.442	0.468	0.47	0.478	0.487
	Standard					
	deviation	0.001	0.005	0.004	0.001	0.004
	A17	0.477	0.495	0.495	0.501	0.507
		0.471	0.489	0.489	0.492	0.504
		0.480	0.498	0.498	0.507	0.504
	Average	0.476	0.494	0.494	0.500	0.505
	Standard					
	deviation	0.004	0.004	0.004	0.006	0.001
	A14	0.471	0.477	0.483	0.495	0.501
		0.465	0.474	0.477	0.492	0.501
		0.474	0.480	0.489	0.501	0.504
	Average	0.470	0.477	0.483	0.496	0.502
	Standard					
	deviation	0.004	0.002	0.005	0.004	0.001
	Control	0.837				
		0.831				
		0.843				
	Average	0.837				
	Standard					
	deviation	0.005				

35°C	Conc (ppm)	E1	D1		R2	A22	2	A17	A14
	10	47.073	44.325	43	3.130	47.19	2	43.130	43.847
	8	41.935	43.847	40	).860	44.08	36	40.980	43.010
	6	41.338	42.413	40	0.502	43.84	7	40.502	42.294
	4	40.621	41.816	39	9.785	42.89	)1	40.263	40.741
	2	39.904	39.188	32	2.497	41.81	.6	39.665	40.024
· · · · ·		•					•		
40°C	C Isolates	10	8		6		4	ł	2
	E1	0.315	0.32	4	0.42	29	0.4	-29	0.444
		0.321	0.32	4	0.4	35	0.4	.44	0.447
		0.318	0.32	4	0.4	32	0.4	38	0.444
	Average	0.318	0.32	6	0.4	32	0.4	37	0.445
	Standard								
	deviation	0.002	0		0.0	02	0.0	06	0.001
	D1	0.420	0.43	2	0.4	35	0.4	·62	0.492
		0.435	0.41	0	0.4	47	0.4	50	0.498
		0.426	0.43	8	0.4	41	0.4	53	0.492
	Average	0.427	0.43	7	0.4	41	0.4	54	0.494
	Standard	0.006	0.012	0	0.0	05	0.0	05	0.002
		0.000	0.012	<u>0</u>	0.0	50	0.0	50	0.003
	<u> </u>	0.433	0.43	0 0	0.4	50	0.4	65	0.492
		0.441	0.45	4	0.4	53	0.4	59	0.498
	Average	0.440	0.44	<u> </u>	0.4	54	0.4	59 58	0.495
	Standard	0.110	0.11	•	0.4		0.1	50	0.475
	deviation	0.004	0.00	5	0.0	04	0.0	06	0.002
	A22	0.306	0.31	5	0.3	21	0.4	44	0.444
		0.312	0.32	7	0.3	36	0.4	38	0.447
		0.309	0.32	1	0.3	30	0.4	41	0.444
	Average	0.309	0.32	1	0.3	29	0.4	41	0.445
	Standard								
	deviation	0.002	0.00	5	0.0	06	0.0	02	0.001
	A17	0.432	0.43	2	0.54	40	0.5	55	0.573
		0.438	0.44	7	0.54	49	0.5	61	0.582
		0.435	0.44	1	0.54	46	0.5	58	0.576
	Average	0.435	0.44	0	0.54	45	0.5	58	0.577
	Standard	0.000	0.00	~			0.0		0.001
	deviation	0.002	0.00	0	0.0	41	0.0	17	0.004
	A14	0.420	0.44	1	0.44	+1	0.4	+/	0.483
		0.429	0.44	+ 1	0.4	17	0.4	15	0.477
	Average	0.423	0.44	2	0.4	46	0.2	15 15	0.477
	Standard	0.727	0.44		0.4	10	V	т	U.T//
	deviation	0.004	0.00	1	0.0	04	0.0	08	0.005
	Control	0.825	0.00		0.0		0.0	- ~	
		0.828			İ				
		0.825							
	Average	0.826							
	Standard								
	deviation	0.001							

40°C	Conc (ppm)	E1	D1		R2	A22	2	A17	A14
	10	61.501	48.305	46	5.731	62.59	)1	47.337	48.668
	8	50.000	47.094	46	5.247	61.13	8	46.731	46.489
	6	47.700	46.610	45	5.036	60.16	59	34.019	46.005
	4	47.094	45.036	44	4.552	46.61	0	32.446	45.521
	2	46.126	40.193	40	).073	46.12	26	30.145	42.252
II	ľ						I		
45°C	C Isolates	10	8		6		4	ŀ	2
	E1	0.405	0.41	7	0.4	38	0.4	44	0.462
		0.399	0.420	0	0.4	35	0.4	38	0.462
		0.411	0.420	0	0.4	44	0.4	47	0.465
	Average	0.405	0.419	9	0.4	39	0.4	43	0.463
	Standard								
	deviation	0.005	0.00	1	0.0	04	0.0	04	0.001
	D1	0.405	0.420	6	0.4	29	0.4	35	0.444
		0.405	0.420	0	0.4	26	0.4	32	0.438
		0.408	0.432	2	0.4	35	0.4	41	0.447
	Average	0.406	0.420	6	0.4	30	0.4	36	0.443
	Standard			_					
	deviation	0.001	0.005	5	0.0	04	0.0	04	0.004
	R 2	0.324	0.32	7	0.3	51	0.3	51	0.393
		0.324	0.324	4	0.3	36	0.3	45	0.387
		0.327	0.33	3	0.3	54	0.3	57	0.396
	Average	0.325	0.328	8	0.3	47	0.3	51	0.392
	Standard	0.001	0.00	4	0.0	0.0	0.0	0.5	0.004
	deviation	0.001	0.004	4	0.0	28	0.0	20	0.004
	AZZ	0.432	0.43	2	0.4	38 41	0.4	38 50	0.447
		0.420	0.42	9	0.4	20	0.4	30	0.444
	A	0.433	0.44	1 5	0.4	20	0.4	44	0.430
	Average	0.431	0.433	3	0.4	39	0.4	44	0.447
	deviation	0.004	0.004	5	0.0	01	0.0	04	0.002
		0.004	0.00	5 7	0.0	20	0.0	<u>14</u>	0.002
		0.408	0.42	<u>,</u>	0.4	23	0.4	38	0.433
		0.400	0.420	0	0.4	32	0.4	<u>47</u>	0.456
	Average	0.412	0.42	9 9	0.4	28	0.4	43	0.452
	Standard	0.412	0.41.	/	0.7		V. <b>T</b>	15	0.704
	deviation	0.004	0.00	1	0.0	04	0.0	04	0.004
	A14	0.411	0.42	-	0.4	23	0.4	26	0.471
		0.408	0.414	4	0.4	12	0.4	29	0.468
		0.417	0.420	6	0.4	26	0.4	20	0.474
	Average	0.412	0.42	1	0.4	23	0.4	25	0.471
	Standard								
	deviation	0.004	0.005	5	0.0	02	0.0	04	0.002
	Control	0.831							
		0.831							
		0.834							
	Average	0.832							
	Standard							T	
	deviation	0.001							

45°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	51.322	51.202	60.938	48.197	50.481	50.481
	8	49.639	48.798	60.577	47.716	49.639	49.519
	6	47.236	48.317	58.293	47.236	48.558	49.159
	4	46.755	47.596	57.813	46.635	46.755	48.918
	2	44.351	46.755	52.885	46.274	45.673	43.389

**Table 7.48:**  $OD_{550nm}$  values for the determination of effect of cations on the removal of<br/>fawn dye and the calculations for the percentage removal ( $C_0$ -C/ $C_0$  x 100)<br/>(Fig. 4.15)

CTAB	Isolates	10	8	6	4	2
	E1	0.012	0.015	0.015	0.072	0.108
		0.012	0.012	0.009	0.066	0.108
		0.015	0.021	0.018	0.078	0.111
	Average	0.013	0.016	0.014	0.072	0.109
	Standard deviation	0.001	0.004	0.004	0.004	0.001
	D1	0.006	0.027	0.039	0.048	0.12
		0.003	0.021	0.036	0.042	0.117
		0.012	0.033	0.042	0.051	0.126
	Average	0.007	0.027	0.039	0.047	0.121
	Standard deviation	0.004	0.005	0.002	0.004	0.004
	R 2	0.135	0.153	0.171	0.225	0.252
		0.108	0.144	0.171	0.216	0.234
		0.153	0.171	0.180	0.234	0.261
	Average	0.044	0.052	0.059	0.075	0.083
	Standard deviation	0.018	0.011	0.004	0.007	0.011
	A22	0.048	0.057	0.060	0.102	0.126
		0.042	0.057	0.057	0.096	0.123
		0.051	0.060	0.066	0.105	0.132
	Average	0.047	0.058	0.061	0.101	0.127
	Standard deviation	0.004	0.001	0.009	0.004	0.004
	A17	0.102	0.132	0.147	0.153	0.192
		0.099	0.132	0.141	0.153	0.186
		0.108	0.135	0.126	0.156	0.198
	Average	0.103	0.133	0.148	0.154	0.192
	Standard deviation	0.004	0.001	0.009	0.001	0.005
	A14	0.219	0.291	0.3	0.354	0.372
		0.213	0.285	0.294	0.354	0.366
		0.222	0.297	0.309	0.357	0.375
	Average	0.218	0.291	0.301	0.355	0.371
	Standard deviation	0.004	0.005	0.006	0.001	0.004
	Control	0.411				
		0.405				
		0.414				
	Average	0.410				
	Standard deviation	0.004				

CTAB	Conc (ppm)	E1	D	1	R2	2	A22		A17	A14
	10	96.829	98.2	293	89.2	68	88.537	7	74.878	46.829
	8	96.098	93.4	415	87.3	17	85.854	1	67.561	29.024
	6	90.244	90.4	188	85.6	10	85.122	2	63.902	26.585
	4	82.195	88.5	537	81.7	07	75.366	5	92.439	13.415
	2	73.415	70.4	188	79.7	56	69.024	1	53.171	9.512
LI		•		ı						-1
CaCl <sub>2</sub>	Isolates	10		8	3		6		4	2
	E1	0.327	'	0.3	351	(	).39		0.399	0.417
		0.327	'	0.3	351	0	.384		0.393	0.417
		0.333		0.3	354	0	.396		0.402	0.423
	Average	0.329	)	0.3	352	0	.390		0.398	0.419
	Standard									
	deviation	0.003		0.0	001	0	.005		0.004	0.003
	D1	0.351		0.3	357	0	.393		0.399	0.411
		0.351		0.3	848	0	.393		0.396	0.405
		0.354		0.3	363	0	.396		0.405	0.417
	Average	0.352		0.3	856	0	.394		0.4	0.411
	Standard									
	deviation	0.001		0.0	006	0	.001		0.004	0.005
	R 2	0.303		0.3	333	0	.348		0.357	0.375
		0.300	)	0.3	330	0	.348		0.357	0.369
		0.309		0.3	339	0	.351		0.360	0.381
	Average	0.304		0.3	334	0	.349		0.358	0.375
	Standard					_				
	deviation	0.004		0.0	004	0	.001		0.001	0.005
	A22	0.330	)	0.3	333	0	.339		0.345	0.369
		0.324		0.3	330	0	.339		0.336	0.366
		0.336	)	0.3	339	0	.342		0.351	0.372
	Average	0.33		0.3	534	0	.340		0.344	0.369
	Standard	0.005		0.0	004	0	001		0.006	0.002
		0.003		0.0	04	0	.001		0.000	0.002
	AI/	0.000	)	0.0	)27	0	.039		0.100	0.174
		0.003	,	0.0	)27	0	.030		0.139	0.171
	Average	0.012	,	0.0	28	0	030		0.1/4	0.17/
	Standard	0.007		0.0	<i>1</i> <u>4</u> 0	0	.037		0.10/	V•1/4
	deviation	0.004		0.0	001	0	002		0.006	0.002
	A14	0.003		0.0	009	0	.015		0.036	0.342
		0.003		0.0	006	0	.009		0.03	0.339
		0.006	;	0.0	)15	0	.018		0.039	0.348
	Average	0.004		0.0	010	0	.014		0.035	0.343
	Standard									
	deviation	0.001		0.0	004	0	.004		0.004	0.004
	Control	0.708								-
		0.702								
		0.711								
	Average	0.707	'							
	Standard									
	deviation	0.004	.							

CaCl <sub>2</sub>	Conc (ppm)	E1	Γ	D1	R2	2	A22		A17	A14
2	10	53.465	50.	212	57.0	01	53.324	4	99.010	99.434
	8	50.212	49.	646	52.6	46	52.75	8	96.040	98.586
	6	44.837	44.	272	50.6	36	51.90	9	94.484	98.020
	4	43.706	43.	423	49.3	64	51.34	4	76.379	95.050
	2	40.736	41.	867	46.9	59	47.80	8	75.389	93.918
LI					•					•
MnCl <sub>2</sub>	Isolates	10			8		6		4	2
	E1	0.120	)	0.	141	0	.159		0.156	0.195
		0.114	ŀ	0.	135	0	.153		0.147	0.189
		0.126	<b>)</b>	0.	144	0	.162		0.162	0.198
	Average	0.120	)	0.	140	0	.158		0.155	0.194
	Standard									
	deviation	0.005	5	0.0	004	0	.004		0.006	0.004
	D1	0.105	5	0.	120	0	.144		0.150	0.189
		0.102	2	0.	117	0	.138		0.141	0.189
		0.108	8	0.	126	0	.147		0.156	0.192
	Average	0.105	5	0.	121	0	.143		0.149	0.190
	Standard	0.000			0.0.4		004		0.007	0.001
	deviation	0.003	5	0.0	004	0	.004		0.006	0.001
	R 2	0.129	)	0.	141	0	.153		0.621	0.168
		0.120	)	0.	141	0	.153		0.612	0.162
	A	0.133	)	0.144		0	.130		0.027	0.1/1
	Average	0.120	)	U	142	U	.154		0.02	0.107
	deviation	0.006	ξ.	0	001	0	001		0.006	0.004
		0.000	2	0.	153	0	162		0.000	0.004
		0.138	2	0.	150	0	156		0.165	0.258
		0.130	,	0	150	0	165		0.103	0.250
	Average	0.139	)	0.	154	0	.161		0.169	0.261
	Standard						101		00107	01201
	deviation	0.001		0.0	004	0	.004		0.006	0.002
	A17	0.123	3	0.	156	0	.177		0.198	0.207
		0.120	)	0.	153	0	.174		0.198	0.204
		0.129	)	0.	162	(	).18		0.201	0.210
	Average	0.124		0.	157	0	.177		0.199	0.207
	Standard									
	deviation	0.004	ŀ	0.0	004	0	.002		0.001	0.002
	A14	0.087	7	0.	126	0	.141		0.144	0.159
		0.090	)	0.	120	0	.141		0.144	0.153
		0.090	)	0.	129	0	.147		0.147	0.165
	Average	0.089	)	0.	125	0	.141		0.145	0.159
	Standard	0.001			0.0.4				0.001	0.005
	deviation	0.001	-	0.0	004	0	.003		0.001	0.005
	Control	0.531								
		0.540	)							
	A	0.522								
	Average	0.531	L							
	deviation	0.007	7							
	deviation	0.007	1							

MnCl <sub>2</sub>	Conc (ppm)	E1	D1	R2	2	A22	A17	A14
	10	77.401	80.226	76.0	38	73.823	76.648	83.239
	8	73.635	77.213	73.2	58	70.998	70.433	76.460
	6	71.186	73.070	70.9	98	69.680	66.667	73.446
	4	70.810	70.056	69.4	92	68.173	62.524	72.693
	2	63.465	64.218	68.5	50	50.847	61.017	70.056
<u> </u> I		11		1	I		1	
MgSO <sub>4</sub>	Isolates	10		8	6	5	4	2
	E1	0.156	(	0.18	0.1	86	0.192	0.198
		0.153	0	.177	0.1	80	0.189	0.189
		0.162	0	.183	0.1	92	0.195	0.204
	Average	0.157	(	0.18	0.1	86	0.192	0.197
	Standard							
	deviation	0.004	0	.002	0.0	05	0.002	0.006
	D1	0.144	0	.162	0.1	65	0.171	0.177
		0.138	0	.156	0.1	59	0.168	0.174
		0.147	0	.165	0.1	68	0.177	0.180
	Average	0.143	0	.161	0.1	64	0.172	0.177
	Standard							
	deviation	0.004	0	.004	0.0	04	0.003	0.002
	R 2	0.141	0	.147	0.1	71	0.192	0.201
		0.135	0	.144	0.1	.68	0.189	0.198
		0.144	0	0.153	0.1	77	0.195	0.204
	Average	0.140	0	.148	0.1	72	0.192	0.201
	Standard							
	deviation	0.004	0	0.004	0.0	004	0.002	0.002
	A22	0.141	0	0.429	0.1	.68	0.186	0.210
		0.135	0	0.153	0.1	.62	0.180	0.210
		0.144	0	0.165	0.1	71	0.192	0.213
	Average	0.140	0	.159	0.1	.67	0.186	0.211
	Standard	0.004		107			0.005	0.001
	deviation	0.004	0	0.127	0.0	04	0.005	0.001
	Al7	0.162	0	0.171	0.1	77	0.183	0.234
		0.156	(	0.165	0.1	/4	0.183	0.231
		0.165	0		0.1	.83	0.186	0.24
	Average	0.161	0	.1/1	0.1	/ð	0.184	0.235
	Standard	0.004		005	0.0	04	0.001	0.004
		0.004		183	0.0	02	0.001	0.004
	A14	0.174		183	0.1	86	0.192	0.193
		0.103		186	0.1	95	0.109	0.193
	Average	0.130		184	0.1	91	0.190	0.190
	Standard	0.175		TUT	0.1		0.175	0,170
	deviation	0.006	6	001	0.0	04	0.004	0.001
	Control	0.543		1	0.0		0.001	0.001
	Control	0.545						
		0.546						
	Average	0.542						
	Standard	010 12						
	deviation	0.0037	4					

MgSO <sub>4</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	71.033	73.616	74.170	74.170	70.295	68.081
	8	67.159	70.295	72.694	70.664	68.450	66.052
	6	65.683	69.742	68.266	69.188	67.159	64.760
	4	64.576	68.266	64.576	65.683	66.052	64.391
	2	63.653	67.343	62.915	61.070	56.642	63.838

**Table 7.49:** OD<sub>550nm</sub> values for the determination of flocculating activity of mixed dyes using different concentrations of bioflocculants (Fig. 4.16)

Isolates	10	8	6	4	2
E1	0.057	0.057	0.051	0.048	0.072
	0.045	0.048	0.06	0.066	0.057
	0.051	0.051	0.054	0.063	0.063
Average	0.050	0.050	0.055	0.059	0.064
Standard					
deviation	0.005	0.004	0.004	0.008	0.006
D1	0.054	0.054	0.060	0.072	0.069
	0.048	0.060	0.063	0.066	0.078
	0.051	0.057	0.060	0.069	0.075
Average	0.051	0.057	0.061	0.069	0.074
Standard					
deviation	0.002	0.002	0.001	0.002	0.004
R 2	0.045	0.048	0.051	0.069	0.069
	0.048	0.051	0.057	0.072	0.078
	0.051	0.057	0.054	0.069	0.075
Average	0.048	0.057	0.054	0.070	0.074
Standard					
deviation	0.002	0.004	0.002	0.001	0.004
A22	0.045	0.048	0.054	0.057	0.066
	0.045	0.051	0.066	0.069	0.069
	0.051	0.051	0.060	0.063	0.066
Average	0.047	0.050	0.060	0.063	0.067
Standard					
deviation	0.003	0.001	0.005	0.005	0.001
A17	0.033	0.042	0.045	0.054	0.063
	0.042	0.051	0.057	0.063	0.066
	0.039	0.048	0.051	0.060	0.063
Average	0.038	0.047	0.051	0.059	0.064
Standard					
deviation	0.004	0.004	0.005	0.004	0.001
A14	0.045	0.048	0.063	0.072	0.072
	0.048	0.063	0.066	0.063	0.078
	0.045	0.057	0.063	0.063	0.075
Average	0.046	0.056	0.064	0.067	0.075
Standard					
deviation	0.001	0.006	0.001	0.004	0.002
Control	0.201				
	0.213				
	0.207				
Average	0.207				
Standard					
deviation	0.005				

Conc (ppm)	E1	D1	R2	A22	A17	A14
10	75.845	75.362	76.812	77.295	81.643	77.778
8	74.879	72.464	75.362	75.845	77.295	72.947
6	73.430	70.531	73.913	71.014	75.362	69.082
4	71.498	66.667	66.184	69.565	71.498	67.633
2	69.082	64.251	63.768	67.633	69.082	63.768

**Table 7.50:** Percentage removal ( $C_0$ – $C/C_0 \ge 100$ ) of mixed dyes using different concentrations of flocculants as derived from Table 7.49 (Fig. 4.16)

**Table 7.51:** Flocculating activity of mixed dyes as derived from Table 7.49 using anequation for flocculating activity in Section 4.2.3 (Fig. 4.17)

Isolate	Flocculating activity	Standard deviation		
E1	25.611	0.315		
D1	20.261	0.279		
R2	15.898	0.127		
A22	19.268	0.199		
A17	15.597	0.249		
A14	17.538	0.328		

pH 6	Isolates	10	8	6	4	2
	E1	0.183	0.192	0.195	0.204	0.213
		0.189	0.195	0.207	0.210	0.216
		0.186	0.192	0.201	0.207	0.213
	Average	0.186	0.193	0.201	0.209	0.214
	Standard					
	deviation	0.002	0.001	0.005	0.002	0.001
	D1	0.186	0.183	0.189	0.192	0.207
		0.183	0.195	0.192	0.198	0.213
		0.186	0.189	0.189	0.195	0.210
	Average	0.185	0.189	0.19	0.195	0.210
	Standard					
	deviation	0.001	0.005	0.001	0.002	0.002
	R 2	0.159	0.18	0.183	0.195	0.201
		0.165	0.195	0.198	0.195	0.210
		0.162	0.189	0.189	0.195	0.207
	Average	0.162	0.188	0.190	0.195	0.206
	Standard					
	deviation	0.002	0.006	0.006	0	0.004
	A22	0.144	0.195	0.216	0.204	0.207
		0.150	0.201	0.189	0.207	0.210
		0.147	0.198	0.195	0.204	0.207
	Average	0.147	0.198	0.200	0.205	0.208
	Standard					
	deviation	0.002	0.002	0.012	0.001	0.001
	A17	0.162	0.171	0.177	0.180	0.183
		0.174	0.168	0.180	0.186	0.192
		0.168	0.171	0.177	0.183	0.189
	Average	0.168	0.170	0.176	0.183	0.183
	Standard					
	deviation	0.005	0.001	0.001	0.002	0.004
	A14	0.177	0.174	0.177	0.186	0.189
		0.165	0.18	0.183	0.195	0.198
		0.168	0.177	0.186	0.192	0.185
	Average	0.170	0.177	0.182	0.191	0.194
	Standard					
	deviation	0.0051	0.002	0.004	0.004	0.005
	Control	0.300				
		0.300				
		0.297				
	Average	0.299				
	Standard					
	deviation	0.001				

**Table 7.52:**  $OD_{550nm}$  values for the determination of effect of pH on the removal of<br/>mixed dyes and the calculations for the percentage removal ( $C_0$ -C/C $_0$  x 100)<br/>(Fig. 4.18)
pH 6	Conc (ppm)	E1	Ľ	D1	R2	2	A22	A17	A1	.4
	10	37.793	38.	127	45.8	20	50.836	43.81	3 43.1	44
	8	35.452	36.	789	37.1	23	33.779	43.14	4 40.8	303
	6	32.776	36.	455	36.4	55	33.110	41.13	7 39.1	30
	4	31.104	34.	782	34.7	83	31.438	38.79	6 36.1	20
	2	28.428	29.	766	31.1	04	30.435	37.12	4 35.1	17
11.7	, T. 1.	10		0			6	4		
рн /	Isolates	10		<u> </u>	_	0	0	4	2	
	EI	0.141		0.18	5	0.	162	0.171	0.17	4
		0.147		0.16	2	0.	105	0.180	0.18	3
	A	0.144		0.159	9	0.	162	0.17/	0.18	0
	Average	0.144		0.155	9	0.	163	0.176	0.17	9
	Standard	0.002		0.010		0	001	0.004	0.00	14
		0.002		0.010	5	0.	156	0.004	0.004	4
	DI	0.144		0.150	) )	0.	150	0.150	0.16	5
		0.130		0.150	3	0.	156	0.103	0.10	<u>5</u>
	Average	0.147		0.15	2	0.	150 157	0.102	0.10	2
	Standard	0.147		0.13.	5	0.	157	0.101	0.10	7
	deviation	0.002		0.00	,	0	001	0.004	0.00	18
	R 2	0.002		0.002	1	0.	147	0.004	0.15	6
	1	0.099		0.14	7	0.	156	0.159	0.15	9
		0.096		0.144	4	0.	153	0.03	0.15	6
	Average	0.097		0.14	4	0.	152	0.154	0.15	7
	Standard				-			01101		-
	deviation	0.001		0.002	2	0.	004	0.059	0.00	1
	A22	0.138		0.147	7	0.	159	0.159	0.17	4
		0.144		0.150	)	0.	153	0.159	0.17	7
		0.141		0.147	7	0.	156	0.162	0.17	4
	Average	0.141		0.149	9	0.	156	0.160	0.17	5
	Standard						1			
	deviation	0.002		0.00	1	0.	002	0.001	0.00	1
	A17	0.144		0.153	3	0.	156	0.162	0.17	1
		0.153		0.150	5	0.	168	0.168	0.174	4
		0.147		0.153	3	0.	162	0.165	0.17	1
	Average	0.148		0.154	4	0.	162	0.165	0.17	2

Standard					
deviation	0.004	0.001	0.005	0.002	0.001
A14	0.147	0.165	0.159	0.174	0.189
	0.162	0.159	0.174	0.171	0.195
	0.156	0.171	0.168	0.174	0.204
Average	0.155	0.165	0.167	0.173	0.196
Standard					
deviation	0.006	0.005	0.006	0.001	0.006
Control	0.276				
	0.297				
	0.288				
Average	0.287				
Standard					
deviation	0.009				

pH 7	Conc (ppm)	E1		D1	R	2	A22		A17	A14
	10	49.826	4	8.780	66.	202	50.871		48.432	45.993
	8	44.599	4	6.690	49.	826	48.08	4	46.341	42.509
	6	43.206	4	5.296	47.	038	45.64	5	43.554	41.812
	4	38.676	4	3.902	46.	341	44.25	1	42.509	39.721
	2	37.631	4	1.115	45.	296	39.02	4	40.070	31.707
LI								I		
pH 8	Isolates	10		8			6		4	2
	E1	0.162		0.1	59	0	.171		0.174	0.183
		0.165		0.1	71	0	.180		0.183	0.183
		0.162		0.1	65	0	.177		0.180	0.183
	Average	0.163		0.1	65	0	.176		0.179	0.182
	Standard									
	deviation	0.001		0.0	05	0	.004		0.004	0
	D1	0.153		0.1	59	0	.168		0.183	0.189
		0.159		0.1	68	0	.174		0.192	0.195
		0.156		0.1	62	0	.171		0.186	0.192
	Average	0.156		0.1	63	0	.171		0.187	0.192
	Standard									
	deviation	0.002		0.0	04	0	.002		0.004	0.002
	R 2	0.144		0.1	5	(	).15		0.159	0.192
		0.15		0.1	56	0	.159		0.171	0.207
		0.159		0.1	53	0	.156		0.165	0.198
	Average	0.151		0.1	53	0	.155		0.165	0.199
	Standard									
	deviation	0.006		0.0	02	0	.004		0.005	0.006
	A22	0.153		0.1	50	0	.153		0.162	0.162
		0.159		0.1	65	0	.168		0.168	0.162
		0.156		0.1	59	0	.162		0.165	0.162
		0.156		0.1	58	0	.161		0.165	0.169
		0.002		0.0	06	0	.006		0.002	0
	A17	0.153		0.1	59	0	.165		0.171	0.186
		0.159		0.1	62	0	.177		0.168	0.192
		0.156		0.1	59	0	.171		0.180	0.189
ļ	Average	0.156		0.1	.6	0	.171		0.176	0.189
	Standard				0.4		0.05		0.005	0.005
	deviation	0.002		0.0	01	0	.005		0.005	0.002
	A14	0.138		0.1	38	0	.147		0.162	0.177
		0.138		0.1	41	(	0.15		0.171	0.183
		0.138		0.14	41	0	.147		0.165	0.180
	Average	0.138		0.14	42	0	.148		U.166	0.180
	Standard				0.4		001		0.004	0.000
	deviation	0 001		0.0	04	0	.001		0.004	0.002
	Control	0.204								
		0.213								
	A	0.210								
	Average	0.209								
	Standard	0.004								
	deviation	0.004								

pH 8	Conc (ppm)	E1		D1	R	2	A22		A17	A14
P-1 0	10	22.010	2	5.359	27	751	25.35	9	25.359	33.971
	8	21.053	2	2.010	26'	794	23.33	)2	23 445	32,057
	6	15 789	1	8 182	25.	37	22.10	7	18 182	29.187
	4	14 354	10	0.526	21.0	153	21.05	3	15 789	20.574
		12 010	- 1	2 13/	4.7	85	10.13	0	0 560	13.876
	2	12.717	0	.1.54	т./	0.5	17.15		7.507	15.070
nH 9	Isolates	10		8			6		4	2
	E1	0.18		0.10	58	0	165		0.174	0.177
		0.159		0.1	50 77	0.	183		0.180	0.186
		0.159		0.1	71	0.	174		0.177	0.183
	Average	0.160		0.1	72	0.	<b>174</b>		0.177	0.185
	Standard	0.107		0.1		0.	1/7		0.177	0.102
	deviation	0.009		0.00	04	0	007		0.002	0.004
	D1	0.147		0.00	55	0	168		0.002	0.183
		0.150		0.1	74	0	174		0.186	0.186
		0.147		0.1	58	0.	171		0.18	0.183
	Average	0.147		0.10	<u>60</u>	0.	171		0.18	0.184
	Standard	0.140		0.10	••	U	11		0.10	VILUT
	deviation	0.001		0.0	)4	0	.002		0.005	0.001
	R 2	0.129		0.0	38	0	144		0.153	0.156
		0.132		0.14	41	0	147		0.162	0.162
		0.129		0.1	38	0	144		0.156	0.159
	Average	0.13		0.1	<u>39</u>	0.	145		0.157	0.159
	Standard								01107	01107
	deviation	0.001		0.0	01	0.	.001		0.004	0.002
	A22	0.135		0.1.	53	0.	.174		0.183	0.195
		0.153		0.10	58	0.	.177		0.195	0.195
		0.144		0.10	52	0.	174		0.189	0.201
	Average	0.144		0.10	61	0.	175		0.188	0.197
	Standard				-					
	deviation	0.007		0.00	06	0.	.001		0.005	0.003
	A17	0.135		0.13	38	0.	.144		0.147	0.168
		0.135		0.14	14	0	.15		0.156	0.165
		0.135		0.14	41	0.	.147		0.153	0.168
	Average	0.136		0.14	41	0.	.147		0.152	0.167
	Standard									
	deviation	0		0.00	02	0.	.002		0.004	0.001
	A14	0.147		0.14	47	0.	.156		0.162	0.174
		0.147		0.1	56	0.	.162		0.168	0.186
		0.153		0.1	53	0.	.159		0.165	0.180
	Average	0.149		0.1	52	0.	.159		0.165	0.180
	Standard									
	deviation	0.003		0.00	)4	0.	.002		0.002	0.005
	Control	0.273								
		0.276								
		0.273								
	Average	0.274								
	Standard									
	deviation	0.001								

pH 9	Conc (ppm)	E1		D1	R	2	A22		A17	A14
-	10	38.321	4	5.985	52.	555	47.44	5	50.365	45.620
	8	37.226	3	8.321	49.	270	41.24	1	48.540	44.526
	6	36.496	3	7.591	47.	080	36.49	6	46.351	41.971
	4	35.401	3	4.307	42.	701	31.38	7	44.526	39.781
	2	33.577	3	2.847	41.	971	28.10	2	39.051	34.307
pH 10	Isolates	10		8			6		4	2
	E1	0.027		0.0	3	0.	.045		0.039	0.042
		0.021		0.02	27	0.	.039		0.042	0.051
		0.024		0.0	30	0.	.030		0.039	0.042
	Average	0.024		0.02	29	0.	.038		0.040	0.046
	Standard						0.0.5		0.001	
	deviation	0.002		0.00	<u>) </u>	0.	.006		0.001	0.004
	DI	0.027		0.03	54	0.	.054		0.063	0.075
		0.036		0.00	53	0.	.072		0.072	0.081
	A	0.030		0.00	50	0.	.069		0.069	0.087
	Average	0.031		0.03	59	0.	.065		0.068	0.081
	deviation	0.004		0.00	74	0	008		0.004	0.005
	R 2	0.004		0.0	) <del>4</del> )1	0.	024		0.004	0.005
	<u> </u>	0.005		0.02	21	0.	027		0.051	0.051
		0.003		0.0	15	0.	021		0.031	0.060
	Average	0.002		0.0	19	0.	.024		0.049	0.059
	Standard				.,				01012	0.0003
	deviation	0.001		0.00	03	0.	.002		0.001	0.006
	A22	0.012		0.0	12	0.	.024		0.048	0.054
		0.018		0.02	27	0.	.027		0.051	0.063
		0.015		0.0	18	0.	.021		0.048	0.060
	Average	0.015		0.0	19	0.	.024		0.049	0.059
	Standard									
	deviation	0.002		0.00	)6	0.	.002		0.001	0.004
	A17	0.012		0.02	24	0.	.036		0.051	0.075
		0.015		0.02	24	0.	.048		0.063	0.081
		0.012		0.02	21	0.	.042		0.066	0.078
	Average	0.013		0.02	23	0.	.042		0.06	0.078
	Standard	0.001			31		005		0.006	0.000
		0.001		0.00	)] )]	0.	020		0.000	0.002
	A14	0.006		0.0	21 27	0.	032		0.030	0.043
		0.000		0.0	∠ / DA	0.	030		0.039	0.054
	Average	0.009		0.02	24	0.	031		0.039	0.031
	Standard	0.007		0.02	- 1				01007	V+VT2
	deviation	0.001		0.0	02	0.	.001		0.002	0.004
	Control	0.246					-			
		0.257								
		0.258								
	Average	0.258								
	Standard									
	deviation	0.005								

pH 10	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	90.698	87.984	99.225	94.186	94.961	97.287
	8	88.760	77.132	96.124	92.636	91.085	90.698
	6	85.271	74.806	95.349	90.698	83.721	87.984
	4	84.496	73.643	92.636	81.008	76.744	84.884
	2	82.171	68.605	89.922	77.132	69.767	82.558

**Table 7.53:**  $OD_{550nm}$  values for the determination of effect of temperature on the removal<br/>mixed dyes and the calculations for the percentage removal ( $C_0$ -C/C $_0$  x 100)<br/>(Fig. 4.19)

28°C	Isolates	10	8	6	4	2
20 0	E1	0.009	0.036	0.036	0.048	0.054
		0.015	0.039	0.048	0.054	0.063
		0.012	0.036	0.042	0.051	0.069
	Average	0.012	0.037	0.042	0.051	0.062
	Standard deviation	0.002	0.001	0.005	0.002	0.006
	D1	0.054	0.066	0.072	0.084	0.960
	21	0.063	0.069	0.075	0.093	0.102
		0.060	0.066	0.072	0.087	0.096
	Average	0.059	0.067	0.073	0.088	0.098
	Standard deviation	0.004	0.001	0.001	0.004	0.406
	R 2	0.018	0.024	0.024	0.051	0.057
		0.012	0.018	0.027	0.045	0.048
		0.021	0.021	0.03	0.051	0.051
	Average	0.017	0.021	0.027	0.049	0.052
	Standard deviation	0.004	0.002	0.002	0.003	0.004
	A22	0.027	0.057	0.066	0.063	0.075
		0.036	0.045	0.057	0.066	0.078
		0.03	0.051	0.063	0.063	0.075
	Average	0.031	0.051	0.062	0.064	0.076
	Standard deviation	0.004	0.005	0.004	0.001	0.001
	A17	0.012	0.018	0.024	0.042	0.048
		0.018	0.024	0.027	0.045	0.048
		0.015	0.021	0.03	0.042	0.051
	Average	0.015	0.021	0.027	0.043	0.049
	Standard deviation	0.002	0.0024	0.002	0.001	0.001
	A14	0.024	0.027	0.024	0.042	0.039
		0.015	0.021	0.03	0.036	0.051
		0.018	0.027	0.033	0.039	0.045
	Average	0.015	0.021	0.027	0.043	0.049
	Standard deviation	0.004	0.003	0.004	0.002	0.005
	Control	0.255				
		0.249				
		0.243				
	Average	0.249				
	Standard deviation	0.005				

28°C	Conc (ppm)	E1	D1	R2	A22	A22 A17	
	10	95.181	76.305	95.283	87.550	93.976	92.369
	8	85.141	73.092	88.208	79.518	91.566	89.960
	6	83.133	70.683	63.208	75.100	89.157	88.353
	4	79.518	64.659	57.075	74.297	82.731	84.337
	2	75.100	60.643	55.189	69.478	80.321	81.928
35°C	Isolates	10	8		6	4	2
	E1	0.003	0.03	9 0	.045	0.051	0.066
		0.003	0.043	3 0.	.048	0.063	0.075
		0.003	0.042	2 0	.048	0.060	0.072
	Average	0.003	0.04.	3 0	.047	0.058	0.071
	Standard						
	deviation	0	0.004	4 0	.001	0.005	0.004
	D1	0	0.03	3 0	.036	0.039	0.066
		0.003	0.03	5 0	.039	0.051	0.057
		0.006	0.03	3 0	.045	0.045	0.06
	Average	0.003	0.034	4 0.	.040	0.045	0.061
		0.002	0.00	1 0	.004	0.005	0.004
	R 2	0.009	0.024	4 0	.075	0.096	0.090
		0.012	0.02	7 0	.081	0.087	0.099
		0.009	0.024	4 0	.078	0.090	0.096
	Average	0.010	0.02	5 0	.078	0.091	0.095
	4.22	0.001	0.00		.002	0.004	0.004
	A22	0.021	0.05		.054	0.078	0.087
		0.030	0.06	<u> </u>	.066	0.075	0.075
	A	0.027	0.05		.000	0.072	0.081
	Average	0.026	0.05		005	0.002	0.005
	A 17	0.004	0.004	+ 0	.003	0.002	0.003
	A17	0.009	0.00	$\frac{0}{0}$	000	0.013	0.018
		0.000	0.00	5 0	015	0.021	0.024
	Average	0.009	0.01	<u> </u>	015	0.018	0.027
	Standard	0.008	0.01		.013	0.010	0.023
	deviation	0.001	0.00	1 0	005	0.002	0.004
	A 14	0.001	0.00	$\frac{1}{2}$	006	0.021	0.030
	111-7	0.003	0.00	$\frac{2}{2}$	021	0.015	0.045
		0.003	0.01	5 0	015	0.006	0.039
	Average	0.003	0.01	$\frac{1}{2}$	.013	0.017	0.038
	Standard	0.000	0.01				
	deviation	0	0.00	2 0	.006	0.006	0.006
	Control	0.195					
		0.207					
		0.201					
	Average	0.201					
	Standard						
	deviation	0.005					

35°C	Conc (ppm)	E1		D1	R	2	A22		A17	A14
	10	98.507	9	8.507	84.0	080	87.73	6	96.020	98.507
	8	78.607	8	3.085	80.	597	73.58	5	95.025	94.030
	6	76.617	8	0.100	74.0	527	71.69	8	92.537	93.035
	4	71.144	7	7.612	69.0	552	64.62	3	91.045	91.542
	2	64.677	6	9.652	63.	184	61.79	2	88.557	81.095
		•					•			
40°C	Isolates	10		8			6		4	2
	E1	0.003		0.0	12	0.	.015		0.018	0.036
		0.006	)	0.0	06	0.	.027		0.027	0.048
		0.003		0.0	09	0.	.018		0.024	0.042
	Average	0.004		0.0	09	0	.02		0.023	0.041
	Standard									
	deviation	0.001		0.0	02	0.	.005		0.004	0.005
	D1	0.006	)	0.0	09	0.	.009		0.018	0.030
		0.009	)	0.0	15	0.	.021		0.036	0.033
		0.006	)	0.0	12	0.	.015		0.027	0.030
	Average	0.007	,	0.0	12	0.	.015		0.027	0.031
	Standard	0.001			0.0		005		0.007	0.001
	deviation	0.001		0.0	02	0.	.005		0.007	0.001
	<u>K 2</u>	0		0.0	12	0.	.000		0.027	0.030
		0.003		0.0	12	0.	015		0.018	0.043
	Average	0.003	1	0.0	00	0.	015		0.024	0.030
	Standard	0.001		0.0	07	0.	.007		0.023	0.037
	deviation	0.001		0.0	04	0	004		0.004	0.006
	A22	0.015		0.0	27	0	0.03		0.024	0.036
		0.024		0.0	18	0.	.021		0.039	0.039
		0.018		0.0	21	0.	.024		0.033	0.042
	Average	0.019	)	0.0	22	0.	.025		0.032	0.039
	Standard									
	deviation	0.004		0.0	04	0.	.004		0.006	0.002
	A17	0		0.0	06	0.	.006		0.006	0.015
		0		0.0	03	0.	.009		0.012	0.015
		0.003		0.0	06	0.	.006		0.009	0.021
	Average	0.001		0.0	05	0.	.007		0.009	0.017
	Standard			_						0.5
	deviation	0.001		0.0	01	0.	.001		0.002	0.003
	A14	0.003		0.0	03	0.	.006		0.009	0.009
		0.003		0.0	00	0.	.009		0.012	0.015
	A	0.006	)	0.0	09	0.	.009		0.009	0.021
	Average	0.004	•	0.0	00	U.	600		0.01	0.015
	deviation	0.001		0.0	02	0	001		0.001	0.005
	Control	0.001		0.0	02	0.	.001		0.001	0.005
	Control	0.204	,							
		0.207								
	Average	0.204								
	Standard	0.200								
	deviation	0.001								

$40^{\circ}\mathrm{C}$	Conc (ppm)	E1		D1	R	2	A22		A17	A14
	10	98.049	9	6.585	99.	512	90.73	2	99.512	98.049
	8	93.780	9.	4.146	96.	585	89.26	8	97.561	97.073
	6	90.244	9	2.683	95.0	510	87.80	5	96.585	96.098
	4	88.780	8	6.829	88.	780	84.39	0	95.610	95.123
	2	80.000	8	4.878	81.0	951	80.97	6	91.707	92.683
		00.000	0		010		00177	0	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	/2:000
45°C	Isolates	10		8			6		4	2
	E1	0.006		0.0	18	0.	.009		0.030	0.033
		0.012		0.0	09	0.	.018		0.021	0.024
		0.009		0.0	12	0.	.027		0.024	0.027
	Average	0.090	)	0.0	13	0.	.018		0.025	0.028
	Standard									
	deviation	0.002		0.0	04	0.	.007		0.004	0.004
	D1	0.012		0.0	09	0.	.018		0.045	0.048
		0.009		0.0	15	0.	.024		0.033	0.063
		0.015		0.0	21	0.	.027		0.039	0.057
	Average	0.012		0.0	15	0.	.023		0.039	0.056
	Standard									
	deviation	0.002		0.0	05	0.	.004		0.005	0.006
	R 2	0.027		0.0	33	0.	.045		0.057	0.066
		0.036		0.04	45	0.	.057		0.066	0.081
		0.033		0.0	39	0.	.051		0.06	0.075
	Average	0.032	r	0.0	39	0.	.051		0.061	0.074
	Standard									
	deviation	0.004		0.0	05	0.	.005		0.004	0.006
	A22	0.051		0.04	48	0.	.051		0.054	0.075
		0.054		0.0	54	0.	.063		0.069	0.078
		0.051		0.0	60	0.	.057		0.063	0.075
	Average	0.052		0.0	54	0.	.056		0.062	0.076
	Standard									
	deviation	0.001		0.0	05	0.	.005		0.006	0.001
	A17	0.048		0.0	72	0.	.078		0.081	0.084
		0.072		0.0	87	0.	.090		0.096	0.099
		0.066		0.0	81	0.	.084		0.090	0.093
	Average	0.062		0.0	80	0.	.084		0.089	0.092
	Standard									
	deviation	0.010	)	0.0	06	0.	.005		0.006	0.006
	A14	0.018		0.0	33	0.	.042		0.042	0.039
		0.021		0.04	45	0.	.051		0.054	0.057
		0.018		0.0	39	0.	.045		0.048	0.054
	Average	0.019	)	0.0	39	0.	.046		0.048	0.05
	Standard									
	deviation	0.001		0.0	05	0.	.004		0.005	0.008
	Control	0.201								
		0.219								
		0.216								
	Average	0.212	r							
	Standard									
	deviation	0.008								

45°C	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	95.755	94.340	93.173	74.129	70.755	91.038
	8	93.868	92.925	91.566	73.134	62.264	81.604
	6	91.509	89.151	89.157	72.139	60.377	78.302
	4	88.208	81.604	80.321	69.154	58.019	77.358
	2	86.792	73.585	79.116	62.189	56.604	76.415

**Table 7.54:**  $OD_{550nm}$  values for the determination of effect of cations on the removal of<br/>mixed dyes and the calculations for the percentage removal (C<sub>0</sub>-C/C<sub>0</sub> x 100)<br/>(Fig. 4.20)

CTAB	Isolates	10	8	6	4	2
	E1	0.156	0.210	0.213	0.219	0.258
		0.165	0.216	0.225	0.228	0.273
		0.150	0.219	0.219	0.222	0.267
	Average	0.157	0.213	0.219	0.223	0.266
	Standard deviation	0.006	0.004	0.005	0.004	0.006
	D1	0.228	0.231	0.249	0.273	0.246
		0.234	0.237	0.228	0.279	0.255
		0.231	0.234	0.240	0.276	0.252
	Average	0.231	0.234	0.239	0.276	0.251
	Standard deviation	0.002	0.002	0.009	0.002	0.004
	R 2	0.237	0.237	0.285	0.309	0.354
		0.228	0.246	0.285	0.315	0.351
		0.234	0.240	0.291	0.312	0.354
	Average	0.233	0.241	0.287	0.312	0.353
	Standard deviation	0.004	0.004	0.003	0.002	0.001
	A22	0.213	0.24	0.267	0.228	0.285
		0.228	0.231	0.276	0.282	0.297
		0.222	0.234	0.270	0.276	0.291
	Average	0.221	0.235	0.271	0.275	0.291
	Standard deviation	0.006	0.004	0.004	0.024	0.005
	A17	0.306	0.303	0.321	0.333	0.372
		0.312	0.318	0.327	0.342	0.387
		0.309	0.312	0.324	0.336	0.381
	Average	0.309	0.311	0.324	0.337	0.38
	Standard deviation	0.002	0.006	0.002	0.004	0.006
	A14	0.246	0.324	0.336	0.369	0.366
		0.258	0.333	0.345	0.375	0.384
		0.252	0.327	0.339	0.372	0.381
	Average	0.252	0.328	0.34	0.372	0.377
	Standard deviation	0.005	0.004	0.004	0.002	0.008
	Control	0.393				
		0.390				
		0.390				
	Average	0.391				
	Standard deviation	0.001				

CTAB	Conc (ppm)	E1		D1	R	2	A22		A17	A14
	10	59.847	4	0.921	40.4	409	43.47	8	20.972	35.294
	8	45.424	4	0.153	38.0	636	39.89	8	20.460	16.113
	6	43.990	3	8.875	26.	598	30.69	1	17.136	13.043
	4	42.967	2	9.412	20.2	205	29.66	8	13.811	4.859
	2	31.969	1	0.230	9.7	719	25.57	5	2.831	3.581
	11						I			
CaCl <sub>2</sub>	Isolates	10		8			6		4	2
	E1	0.039		0.04	42	0.	.045		0.051	0.063
		0.051		0.0	57	0	0.06		0.069	0.066
		0.045		0.04	48	0.	.054		0.060	0.063
	Average	0.045		0.4	90	0.	.053		0.060	0.064
	Standard									
	deviation	0.005		0.0	)6	0.	.006		0.007	0.001
	D1	0.072		0.0	78	0.	.087		0.090	0.093
		0.075		0.0	78	0.	.093		0.096	0.105
		0.072		0.0	34	0.	.090		0.093	0.099
	Average	0.073		0.0	8	0	.09		0.093	0.099
	Standard									
	deviation	0.001		0.0	)3	0.	.002		0.002	0.005
	R 2	0.048		0.0	51	0.	.045		0.069	0.060
		0.054		0.0	50	0.	.075		0.06	0.075
		0.051		0.0	57	0.	.066		0.063	0.066
	Average	0.051		0.0	56	0.	.062		0.064	0.067
	Standard					_				
	deviation	0.002		0.00	)4	0.	.013		0.004	0.006
	A22	0.075		0.0	75	0.	.075		0.081	0.102
		0.078		0.00	59 70	0.	.087		0.087	0.099
		0.075		0.0	/8	0.	.081		0.084	0.096
	Average	0.075		0.0	/9	0.	.081		0.084	0.097
	Standard	0.001		0.0	74	0	005		0.002	0.002
		0.001		0.0	)4 54	0.	072		0.002	0.002
	AI/	0.042		0.0.	56	0.	072		0.009	0.073
		0.048		0.0	50		066		0.073	0.081
	Average	0.045		0.0	6	0	066		0.072	0.078
	Standard	0.045		0.0	U	U			0.074	0.070
	deviation	0.002		0.00	)5	0	006		0.002	0.002
	A14	0.027		0.0	39	0	.042		0.054	0.066
	T	0.027		0.04	45	0	.051		0.057	0.075
		0.033		0.04	42	0	.045		0.054	0.072
	Average	0.033		0.04	42	0.	.046		0.055	0.071
	Standard				_					~~~ * *
	deviation	0.005		0.0	02	0.	.004		0.001	0.004
	Control	0.198								
		0.219								
		0.210								
	Average	0.209								
	Standard									
	deviation	0.009								

CaCl <sub>2</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	78.469	65.072	75.598	64.115	78.469	84.211
	8	76.555	61.722	73.206	62.201	71.292	79.904
	6	74.641	56.938	70.335	61.244	68.421	77.990
	4	71.292	55.938	69.378	59.809	65.550	73.684
	2	69.378	52.632	67.943	53.589	62.679	66.029

MnCl <sub>2</sub>	Isolates	10	8	6	4	2
	E1	0.027	0.045	0.063	0.069	0.084
		0.039	0.051	0.051	0.075	0.093
		0.033	0.054	0.057	0.072	0.084
	Average	0.033	0.050	0.057	0.072	0.087
	Standard					
	deviation	0.005	0.004	0.005	0.002	0.004
	D1	0.039	0.06	0.048	0.045	0.069
		0.051	0.039	0.063	0.075	0.078
		0.045	0.048	0.057	0.066	0.075
	Average	0.045	0.049	0.056	0.062	0.074
	Standard					
	deviation	0.005	0.009	0.006	0.013	0.004
	R 2	0.003	0.012	0.024	0.048	0.072
-		0.003	0.024	0.039	0.051	0.087
		0.003	0.018	0.033	0.048	0.081
	Average	0.003	0.019	0.032	0.049	0.080
	Standard					
	deviation	0	0.005	0.006	0.001	0.006
	A22	0.015	0.024	0.021	0.042	0.036
		0.006	0.027	0.039	0.033	0.051
-		0.009	0.024	0.036	0.036	0.045
	Average	0.010	0.025	0.032	0.037	0.044
	Standard	01010	00020	00002	00001	
	deviation	0.004	0.001	0.008	0.004	0.00616
	A17	0.003	0.006	0.006	0.018	0.018
		0	0.006	0.015	0.018	0.027
-		0.003	0.012	0.012	0.018	0.021
-	Average	0.002	0.008	0.011	0.017	0.022
-	Standard					
	deviation	0.001	0.003	0.00374	0	0.004
	A14	0.003	0.009	0.009	0.012	0.018
		0	0.006	0.009	0.009	0.021
		0.003	0.009	0.009	0.012	0.018
	Average	0.002	0.008	0.009	0.011	0.019
	Standard				00011	
	deviation	0.001	0.001	0	0.001	0.001
	Control	0.192				
		0.210				1
		0.207				
	Average	0.203				
	Standard	01200				
	deviation	0.008				
			1	1	1	1

MnCl <sub>2</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14	Control
	10	0.033	0.045	0.003	0.010	0.002	0.002	0.203
	8	0.050	0.049	0.019	0.025	0.008	0.008	
	6	0.057	0.056	0.032	0.032	0.011	0.009	
	4	0.072	0.062	0.049	0.037	0.017	0.011	
	2	0.087	0.074	0.080	0.044	0.022	0.019	

	1 1		-	~		-
MgSO <sub>4</sub>	Isolates	10	8	6	4	2
	E1	0.078	0.075	0.084	0.096	0.198
		0.084	0.099	0.099	0.117	0.201
		0.081	0.093	0.096	0.108	0.198
	Average	0.081	0.089	0.095	0.107	0.199
	Standard					
	deviation	0.002	0.010	0.006	0.009	0.001
	D1	0.090	0.090	0.105	0.108	0.131
		0.099	0.102	0.111	0.117	0.123
		0.093	0.096	0.108	0.114	0.117
	Average	0.094	0.096	0.018	0.113	0.117
	Standard					
	deviation	0.004	0.005	0.002	0.004	0.006
	R 2	0.060	0.075	0.087	0.09	0.105
		0.075	0.081	0.102	0.108	0.105
		0.069	0.078	0.096	0.099	0.102
	Average	0.068	0.078	0.095	0.099	0.103
	Standard					
	deviation	0.006	0.002	0.006	0.007	0.001
	A22	0.075	0.084	0.090	0.093	0.105
		0.090	0.090	0.093	0.102	0.111
		0.084	0.087	0.090	0.099	0.108
	Average	0.083	0.087	0.091	0.098	0.108
	Standard					
	deviation	0.006	0.002	0.001	0.004	0.002
	A17	0.084	0.078	0.087	0.093	0.111
		0.090	0.099	0.096	0.108	0.111
		0.087	0.090	0.093	0.102	0.108
	Average	0.087	0.089	0.092	0.101	0.107
	Standard					
	deviation	0.002	0.009	0.004	0.006	0.001
	A14	0.099	0.102	0.105	0.105	0.114
		0.105	0.108	0.114	0.117	0.108
		0.102	0.111	0.108	0.111	0.117
	Average	0.102	0.107	0.109	0.111	0.113
	Standard	01102				
	deviation	0.002	0.004	0.004	0.005	0.004
	Control	0.204				
		0.225				
		0.216				
	Average	0.215				
	Standard	UMIC				
	deviation	0.009				
	acriation	0.007		1	1	1

MgSO <sub>4</sub>	Conc (ppm)	E1	D1	R2	A22	A17	A14
	10	62.326	56.279	68.372	61.395	59.535	52.558
	8	58.605	55.349	63.721	59.535	58.605	50.233
	6	58.537	49.767	55.814	57.674	57.209	49.302
	4	50.233	47.442	53.953	54.419	53.023	48.372
	2	44.651	45.581	52.093	49.767	50.233	47.442

Table 7.55: Turbidity	(ntu) of river water	with bioflocculants	and <i>Escherichia coli</i> at
30 min			

30 min	Isolates	10	20	30	50
		17.400	16.290	15.210	13.410
		16.800	16.290	15.180	13.410
		18	16.290	15.210	13.410
	Average	17.400	16.300	15.20	13.40
	Standard deviation	0.489	0	0.014	0
	E1	17.190	14.490	13.110	12.510
		17.160	14.490	13.080	12.510
		17.220	14.490	13.110	12.510
	Average	17.20	14.490	13.100	12.500
	Standard deviation	0.024	0	0.014	0
	A17	14.910	13.500	12.210	11.700
		14.910	12.900	12.210	11.400
		14.910	14.100	12.210	12
	Average	14.900	13.500	12.200	11.700
	Standard deviation	0	0.490	0	0.245
	A14	17.790	16.290	15.810	14.490
		17.790	16.290	15.780	14.490
		17.820	16.290	15.810	14.490
	Average	17.800	16.300	15.800	14.500
	Standard deviation	0.014	0	0.014	0
	R 2	15.990	15.900	14.790	14.400
		15.990	15.600	14.790	13.800
		16.020	16.200	14.790	15
	Average	16	15.900	14.800	14.400
	Standard deviation	0.014	0.245	0	0.490
	A22	17.790	16.200	14.490	10.890
		17.790	15.900	14.490	10.890
		17.820	16.500	14.490	10.890
	Average	17.800	16.200	14.500	10.900
	Standard deviation	0.014	0.245	0	0
	Alum	21	17.910	16.290	14.490
		18	17.910	15.960	14.490
		15	17.910	16.320	14.490
	Average	18	17.900	16.300	14.500
	Standard deviation	2.449	0	0.1631	0

60 min	Isolates	10	20	30	50
	D1	17.100	16.200	14.910	12.210
		16.800	15.600	14.910	12.210
		17.400	16.800	14.910	12.210
	Average	17.100	16.200	14.900	12.200
	Standard				
	deviation	0.245	0.490	0	0
	E1	17.100	14.010	12.900	12.210
		16.800	13.980	12.600	12.210
		17.400	14.010	13.200	12.210
	Average	17.100	14	12.900	12.200
	Standard				
	deviation	0.245	0.014	0.245	0
	A17	14.490	13.110	11.700	10.200
		14.490	13.080	11.400	9.600
		14.490	13.110	12	10.800
	Average	14.500	13.100	11.700	10.200
	Standard				
	deviation	0	0.014	0.245	0.490
	A14	17.310	15.810	12.210	13.200
		17.310	15.780	12.180	12.600
		17.310	15.810	12.210	13.800
	Average	17.300	15.800	15.200	13.200
	Standard				
	deviation	0	0.750	0.014	0.490
	R 2	15.510	15.210	14.100	13.890
		15.510	16.800	13.500	13.890
		15.510	15.210	14.700	13.920
	Average	15.500	15.200	14.100	13.900
	Standard				0.044
	deviation	0	0.750	0.4899	0.014
	A22	17.490	15.990	13.890	9.510
		17.490	15.990	13.890	9.510
		17.520	15.990	13.920	9.510
	Average	17.500	16	13.900	9.500
	Standard	0.014	0	0.014	
	deviation	0.014	0	0.014	0
	Alum	17.700	16.290	15.390	13.800
		17.400	16.290	15.390	13.500
	A	18	16.290	15.420	14.100
	Average	17.700	16.300	15.400	13.800
	Standard	0.245		0.014	0.250
	deviation	0.245	0	0.014	0.250

**Table 7.56:** Turbidity (ntu) of river water with bioflocculants and *Escherichia coli* at<br/>60 min

120 min	Isolates	10	20	30	50
	D1	16.710	15.510	14.190	11.010
		16.710	15.510	14.190	10.980
		16.710	15.510	14.190	11.010
	Average	16.700	15.500	14.200	11
	Standard				
	deviation	0	0	0	0.014
	E1	16.290	13.800	12.210	11.490
		16.290	13.500	12.180	11.490
		16.320	14.100	12.210	11.490
	Average	16.300	13.800	12.200	11.500
	Standard				
	deviation	0.014	0.245	0.014	0
	A17	13.710	12.300	11.100	9.600
		13.710	11.700	10.800	8.700
		13.710	12.900	11.400	10.500
	Average	13.700	12.300	11.100	9.600
	Standard				
	deviation	0	0.490	0.245	0.735
	A14	16.500	14.190	13.710	12.390
		15.900	14.190	13.680	12.390
		17.100	14.190	13.710	12.390
	Average	16.500	14.200	13.700	12.400
	Standard				
	deviation	0.490	0	0.014	0
	R 2	14.700	13.200	12.510	11.190
		14.400	12.600	12.480	11.190
		15	13.800	12.510	11.190
	Average	14.700	13.200	12.500	11.200
	Standard				
	deviation	0.245	0.490	0.014	0
	A22	16.200	13.500	11.400	8.700
		15.600	13.200	10.800	8.400
		16.800	13.800	12	9
	Average	16.200	13.500	11.400	8.700
	Standard				
	deviation	0.490	0.245	0.490	0.245
	Alum	16.410	15.210	13.200	11.100
		16.410	15.180	12.600	10.800
		16.410	15.210	13.800	11.400
	Average	16.400	15.200	13.200	11.100
	Standard		0.014	0.400	0.045
	deviation	0	0.014	0.490	0.245

**Table 7.57:** Turbidity (ntu) of river water with bioflocculants and *Escherichia coli* at120 min

**Table 7.58:** Percentage reduction (B–A/B x 100) of river water turbidity at different time intervals compared to alum at 10 ppm as derived from Table 7.55–7.57 (Fig. 5.1)

Bacterial bioflocculants			
& Alum	30 min	60 min	120 min
D1	60.364	61.047	61.959
E1	60.820	61.047	62.870
A17	66.059	66.973	68.793
A14	59.453	60.592	62.415
R2	63.554	64.692	66.515
A22	59.453	60.137	63.098
Alum	58.998	59.680	62.642

**Table 7.59:** Percentage reduction (B–A/B x 100) of river water turbidity at different time intervals compared to alum at 20 ppm as derived from Table 7.55–7.57

Bacterial bioflocculants			
& Alum	30 min	60 min	120 min
D1	62.870	63.098	64.692
E1	66.970	68.109	68.565
A17	69.248	70.159	71.982
A14	62.870	64.009	67.654
R2	63.781	65.376	69.932
A22	63.979	63.554	69.248
Alum	59.226	62.870	65.376

**Table 7.60:** Percentage reduction (B–A/B x 100) of river water turbidity at different time intervals compared to alum at 30 ppm as derived from Table 7.55–7.57

Bacterial bioflocculants			
& Alum	30 min	60 min	120 min
D1	65.376	66.059	67.654
E1	70.159	70.615	72.209
A17	72.209	73.349	74.715
A14	64.009	65.376	68.793
R2	66.287	67.882	71.526
A22	66.970	68.337	74.032
Alum	62.870	64.920	69.932

(Fig. 5.2)			
Bacterial bioflocculants			
& Alum	30 min	60 min	120 min
D1	69.476	72.209	74.943
E1	71.526	72.209	73.804
A17	73.349	76.765	78.132
A14	66.970	69.205	71.754
R2	67.198	68.337	74.487
A22	75.171	78.359	80.182
Alum	66.970	68.565	74.715

**Table 7.61:** Percentage reduction (B–A/B x 100) of river water turbidity at different timeintervals compared to alum at 50 ppm as derived from Table 7.55–7.57

**Table 7.62:** OD<sub>550nm</sub> values for the determination of flocculating activity of both alum and bioflocculants in 30 min

Inclator	10	20	20	50
Isolates	10	20	30	30
DI	0.099	0.081	0.051	0.036
	0.093	0.078	0.051	0.027
	0.105	0.870	0.054	0.042
Average	0.099	0.082	0.052	0.035
Standard deviation	0.005	0.373	0.001	0.006
E1	0.090	0.087	0.081	0.081
	0.087	0.084	0.078	0.075
	0.093	0.093	0.084	0.084
Average	0.09	0.088	0.081	0.080
Standard deviation	0.002	0.004	0.002	0.004
A17	0.087	0.072	0.069	0.054
	0.090	0.072	0.069	0.054
	0.090	0.075	0.072	0.057
Average	0.089	0.073	0.070	0.055
Standard deviation	0.001	0.001	0.001	0.001
A14	0.105	0.099	0.093	0.087
	0.111	0.096	0.090	0.090
	0.318	0.105	0.099	0.090
Average	0.035	0.100	0.094	0.089
Standard deviation	0.099	0.004	0.004	0.001
R 2	0.099	0.093	0.087	0.084
	0.108	0.084	0.084	0.081
	0.312	0.099	0.093	0.087
Average	0.032	0.092	0.088	0.084
Standard deviation	0	0.004	0.006	0.005
A22	0.012	0.081	0.078	0.033
	0.012	0.078	0.069	0.027
	0.012	0.087	0.084	0.039
Average	0.036	0.082	0.077	0.033
Standard deviation	0	0.004	0.006	0.005
Alum	0.105	0.090	0.084	0.078
	0.114	0.087	0.081	0.075
	0.108	0.093	0.087	0.081
Average	0.109	0.090	0.084	0.078
Ŭ	0.004	0.002	0.002	0.002

Isolates	10	20	30	50
D1	0.096	0.081	0.051	0.033
	0.090	0.075	0.045	0.027
	0.102	0.084	0.057	0.039
Average	0.096	0.08	0.051	0.033
Standard deviation	0.005	0.004	0.005	0.005
E1	0.087	0.084	0.078	0.072
	0.084	0.084	0.069	0.066
	0.093	0.087	0.084	0.078
Average	0.088	0.085	0.077	0.072
Standard deviation	0.004	0.001	0.006	0.005
A17	0.078	0.069	0.066	0.051
	0.081	0.069	0.063	0.054
	0.087	0.072	0.072	0.051
Average	0.082	0.070	0.067	0.052
Standard deviation	0.004	0.001	0.004	0.001
A14	0.102	0.099	0.090	0.084
	0.099	0.093	0.090	0.084
	0.108	0.102	0.093	0.087
Average	0.103	0.098	0.091	0.085
Standard deviation	0.004	0.004	0.001	0.001
R 2	0.102	0.090	0.084	0.078
	0.096	0.060	0.078	0.075
	0.105	0.120	0.087	0.084
Average	0.101	0.09	0.083	0.079
Standard deviation	0.004	0.024	0.004	0.004
A22	0.093	0.081	0.072	0.030
	0.084	0.075	0.072	0.027
	0.099	0.084	0.075	0.036
Average	0.092	0.08	0.073	0.031
Standard deviation	0.006	0.004	0.001	0.004
Alum	0.105	0.087	0.081	0.075
	0.099	0.084	0.078	0.069
	0.108	0.090	0.084	0.081
Average	0.104	0.087	0.081	0.075
Standard deviation	0.004	0.002	0.002	0.005

## **Table 7.63:** OD<sub>550nm</sub> values for the determination of flocculating activity of both alum and bioflocculants in 60 min

Isolates	10	20	30	50
D1	0.093	0.078	0.048	0.027
	0.084	0.069	0.048	0.021
	0.099	0.084	0.051	0.033
Average	0.092	0.077	0.049	0.027
Standard deviation	0.006	0.006	0.001	0.005
E1	0.084	0.081	0.072	0.069
	0.078	0.078	0.069	0.063
	0.087	0.084	0.078	0.075
Average	0.083	0.081	0.073	0.069
Standard deviation	0.004	0.002	0.004	0.005
A17	0.081	0.069	0.063	0.048
	0.075	0.063	0.057	0.048
	0.084	0.072	0.069	0.051
Average	0.08	0.068	0.063	0.049
Standard deviation	0.004	0.004	0.005	0.001
A14	0.099	0.084	0.081	0.078
	0.093	0.084	0.078	0.072
	0.105	0.087	0.084	0.084
Average	0.099	0.085	0.081	0.078
Standard deviation	0.005	0.001	0.002	0.005
R 2	0.096	0.087	0.081	0.066
	0.093	0.078	0.084	0.063
	0.102	0.093	0.078	0.072
Average	0.097	0.086	0.081	0.067
Standard deviation	0.004	0.006	0.002	0.004
A22	0.087	0.078	0.072	0.024
	0.084	0.084	0.066	0.024
	0.09	0.069	0.078	0.027
Average	0.087	0.077	0.072	0.025
Standard deviation	0.002	0.006	0.005	0.001
Alum	0.099	0.084	0.075	0.069
	0.093	0.084	0.069	0.069
	0.105	0.087	0.081	0.072
Average	0.099	0.085	0.075	0.070
Standard deviation	0.005	0.001	0.005	0.001

## **Table 7.64:** OD<sub>550nm</sub> values for the determination of flocculating activity of both alum and bioflocculants in 120 min

#### **Table 7.65:** Turbidity (ntu) and the OD<sub>550nm</sub> for the determination of flocculating activity of the controls

	Turbidity	OD <sub>550nm</sub>
River water + Escherichia coli	43.890	0.150
	43.890	0.180
	43.920	0.120
Average	43.9	0.150
River water + distilled water	0.014	0.024
	11.700	0.102
	11.700	0.108
	11.730	0.096
	11.710	0.102
Average	0.014	0.005

# **Table 7.66:** Flocculating activity of the bacterial bioflocculants at different time intervals compared to alum as derived from Table 7.62–7.65 using an equation for flocculating activity in Section 5.2.2 (Fig. 5.3)

Bacterial bioflocculants & Alum		Standard deviation		Standard deviation		Standard deviation
	30 min		60 min		120 min	
D1	57.268	0.154	56.802	0.163	54.284	0.185
E1	244.444	0.095	180.077	0.090	175.994	0.100
A17	99.397	0.351	94.936	0.327	93.293	0.300
A14	165.005	0.214	147.721	0.239	119.707	0.137
R2	213.229	0.416	196.183	0.216	140.287	0.057
A22	62.532	0.218	61.538	0.233	57.461	0.019
Alum	116.659	0.300	110.752	0.276	113.432	0.277

Bioflocculants/alum	Before	After
A22	7.380	6.800
	7.380	6.800
	7.380	6.800
Average	7.380	6.800
	0	0
A17	7.380	6.600
	7.380	6.60
	7.380	6.600
Average	7.380	6.600
	0	0
A14	7.380	6.830
	7.380	6.830
	7.380	6.830
Average	7.38	6.830
	0	0
R 2	7.380	6.550
	7.380	6.550
	7.380	6.550
Average	7.38	6.550
	0	0
E1	7.380	6.650
	7.380	6.650
	7.380	6.650
Average	7.380	6.650
	0	0
D1	7.380	6.920
	7.380	6.920
	7.380	6.920
Average	7.380	6.920
	0	0
Alum	7.380	4.140
	7.380	4.140
	7.380	4.140
Average	7.380	4.140
	0	0

**Table 7.67:** The pH of river water before and after the addition of bioflocculants and alum (Fig. 5.4)

Isolates	10	20	30	50
D1	0.870	0.810	0.570	0.510
	0.840	0.750	0.570	0.510
	0.900	0.870	0.600	0.570
Average	0.870	0.810	0.580	0.540
Standard deviation	0.024	0.049	0.014	0.028
E1	1.290	3.210	4.500	5.250
	1.290	3.210	3.900	5.250
	1.290	3.240	5.100	5.250
Average	1.280	3.220	4.500	5.260
Standard deviation	0	0.014	0.490	0
A17	1.230	3.180	4.530	4.980
	1.230	3.180	4.530	4.950
	1.260	3.180	4.530	4.980
Average	1.240	3.170	4.520	4.970
Standard deviation	0.014	0	0	0.014
A14	2.010	2.370	3.570	4.320
	2.010	2.370	3.510	4.320
	2.010	2.370	3.600	4.320
Average	2	2.380	3.560	4.320
Standard deviation	0	0	0.037	0
A22	0.870	0.930	0.960	0.990
	0.870	0.930	0.990	1.020
	0.870	0.930	0.960	0.960
Average	0.880	0.920	0.970	0.990
Standard deviation	0	0	0.014	0.024
R 2	2.160	4.530	7.170	10.890
	2.130	4.470	7.140	10.920
	2.160	4.560	7.170	10.890
Average	2.150	4.520	7.160	10.900
Standard deviation	0.014	0.037	0.014	0.014
Alum	1.260	2.520	4.620	4.860
	1.170	2.550	4.560	4.860
	1.320	2.520	4.680	4.890
Average	1.250	2.530	4.620	4.870
Standard deviation	0.061	0.014	0.049	0.014
Control	13.500			
	13.500			
	13.500			
Average	13.500			
Standard deviation	0			

**Table 7.68:** The turbidity (ntu) of river water with different concentrations of bioflocculants and alum

**Table 7.69:** Percentage reduction (B–A/B x 100) of river water turbidity by the bacterial bioflocculants at different concentrations compared to alum as derived from Table 7.68 (Fig. 5.5)

Bacterial				
bioflocculants &				
Alum	10 ppm	20 ppm	30 ppm	50 ppm
D1	93.556	94.000	95.704	96.000
E1	61.037	66.667	76.148	90.519
A17	63.185	66.519	76.519	90.815
A14	68.000	73.629	82.370	85.185
A22	92.667	92.815	93.185	93.481
R 2	19.259	46.963	66.519	84.074
Alum	63.926	65.778	81.259	90.741

Isolates	10	20	30	50
D1	0.072	0.051	0.027	0.015
Standard deviation	0.063	0.045	0.027	0.012
	0.078	0.054	0.030	0.018
Average	0.071	0.05	0.028	0.015
Standard deviation	0.006	0.004	0.001	0.002
E1	0.090	0.072	0.057	0.039
	0.090	0.069	0.057	0.039
	0.093	0.078	0.063	0.042
Average	0.091	0.073	0.059	0.040
Standard deviation	0.001	0.004	0.003	0.001
A17	0.078	0.051	0.045	0.039
	0.075	0.048	0.042	0.033
	0.081	0.057	0.051	0.045
Average	0.078	0.052	0.046	0.039
Standard deviation	0.002	0.004	0.004	0.005
A14	0.087	0.066	0.057	0.069
	0.090	0.057	0.054	0.066
	0.090	0.072	0.063	0.072
Average	0.089	0.065	0.058	0.069
Standard deviation	0.001	0.006	0.004	0.002
A22	0.075	0.057	0.030	0.018
	0.069	0.060	0.027	0.015
	0.081	0.060	0.036	0.021
Average	0.075	0.059	0.031	0.018
Standard deviation	0.005	0.001	0.004	0.002
R 2	0.099	0.072	0.051	0.063
	0.093	0.069	0.045	0.054
	0.105	0.078	0.054	0.069
Average	0.099	0.078	0.005	0.062
Standard deviation	0.005	0.004	0.004	0.006
Alum	0.084	0.075	0.051	0.045
	0.078	0.066	0.051	0.036
	0.087	0.081	0.054	0.051
Average	0.083	0.074	0.052	0.044
	0.004	0.006	0.001	0.006
Control	0.177			
	0.183			
	0.174			
Average	0.178			
	0.004			

# **Table 7.70:** OD<sub>550nm</sub> values for the determination of flocculating activity of both the bioflocculants and alum

**Table 7.71:** Flocculating activity of the bacterial bioflocculants compared to alumas derived from Table 7.70 using an equation for flocculating activityin Section 5.2.2 (Fig. 5.6)

Isolate	Flocculating activity	Standard deviation
D1	45.524	0.517
E1	68.076	0.273
A17	62.564	0.500
A14	64.459	0.215
A22	47.639	0.107
R2	60.685	0.418

·			1	
Isolates	10	20	30	50
D1	300	255	188	156
	303	252	188	150
	300	261	188	162
Average	301	256	188	156
Standard deviation	1.414	3.741	0	4.899
E1	393	354	237	195
	387	354	249	192
	396	357	243	198
Average	392	355	243	195
Standard deviation	3.742	1.414	4.899	2.449
A17	387	324	107	186
	384	318	107	180
	390	327	107	189
Average	387	323	107	185
Standard deviation	2.449	3.742	0	3.742
A14	390	360	321	243
	408	372	321	240
	405	372	321	249
Average	401	368	321	244
Standard deviation	7.874	5.657	0	3.741
A22	300	276	192	168
	318	267	201	168
	318	282	198	171
Average	312	275	197	169
Standard deviation	8.485	6.164	3.741	1.414
R 2	438	399	342	273
	433	393	330	264
	440	402	324	279
Average	437	398	342	272
Standard deviation	2.944	3.742	7.483	6.164
Alum	357	321	243	180
	360	315	234	177
	367	327	249	186
Average	358	321	242	181
Standard deviation	4.189	4.899	6.164	3.742
Control	1980			
	1974			
	1986			
Average	1980			
Standard deviation	4.898			

Table 7.72: Total plate count per 0.1 ml

Bacterial				
bioflocculants &				
Alum	10 ppm	20 ppm	30 ppm	50 ppm
D1	84.798	87.071	90.505	92.121
E1	80.202	82.071	87.727	90.152
A17	80.455	83.687	89.343	90.657
A14	79.748	81.414	83.733	87.677
A22	84.242	86.111	90.051	91.465
R2	77.929	79.899	82.727	86.263
Alum	81,919	83.788	87.778	90.859

**Table 7.73:** Percentage reduction (B–A/B x 100) of bacterial load by bioflocculants at different concentrations compared to alum as derived from Table 7.72 (Fig. 5.7)

Isolates	10	20	30	50
D1	0.840	0.690	0.510	0.480
	0.840	0.690	0.450	0.450
	0.840	0.690	0.570	0.510
Average	0.830	0.700	0.510	0.480
Standard deviation	0	0	0.049	0.024
E1	0.720	0.690	0.690	0.660
	0.690	0.630	0.690	0.600
	0.720	0.750	0.690	0.720
Average	0.710	0.690	0.680	0.660
Standard deviation	0.014	0.049	0	0.049
A17	0.600	0.570	0.540	0.540
	0.600	0.570	0.540	0.480
	0.630	0.570	0.570	0.600
Average	0.610	0.580	0.550	0.540
Standard deviation	0.014	0	0.014	0.049
A14	0.690	0.660	0.660	0.560
	0.690	0.660	0.630	0.540
	0.690	0.690	0.660	0.570
Average	0.700	0.670	0.650	0.550
Standard deviation	0	0.014	0.014	0.012
A22	0.660	0.630	0.510	0.390
	0.630	0.570	0.510	0.390
	0.660	0.690	0.540	0.420
Average	0.650	0.630	0.520	0.40
Standard deviation	0.014	0.049	0.014	0.014
R 2	0.750	0.720	0.600	0.42
	0.750	0.690	0.570	0.42
	0.750	0.720	0.600	0.42
Average	0.740	0.71	0.590	0.43
Standard deviation	0	0.014	0.014	0
Alum	0.750	0.630	0.570	0.450
	0.750	0.570	0.510	0.450
	0.750	0.690	0.630	0.420
Average	0.740	0.630	0.570	0.440
Standard deviation	0	0.04899	0.049	0.014
Control	10.500			
	10.500			
	10.500			
Average	10.500			
Standard deviation	0			

Table 7.74: Turbidity (ntu) of river water with bioflocculants and alum at pH 9

**Table 7.75:** Percentage reduction (B–A/B x 100) of river water turbidity by the bacterial bioflocculants at different concentration compared to alum at pH 9 as derived from Table 7.74 (Fig. 5.8)

Bacterial				
bioflocculants &				
Alum	10 ppm	20 ppm	30 ppm	50 ppm
D1	92.095	93.333	95.143	95.429
E1	93.238	93.429	93.524	93.714
A17	94.190	94.476	94.762	94.857
A14	93.333	93.619	93.809	94.762
A22	93.809	94.000	95.048	96.190
R2	92.952	93.238	94.381	95.905
Alum	92.952	94.000	94.571	95.809

Isolates	10	20	30	50
D1	0.021	0.006	0.003	0.001
	0.015	0.003	0.003	0.001
	0.024	0.006	0.003	0.001
Average	0.020	0.005	0.003	0.001
Standard deviation	0.004	0.001	0	0
E1	0.012	0.009	0.006	0.003
	0.009	0.006	0.003	0.003
	0.015	0.012	0.012	0.006
Average	0.012	0.009	0.007	0.004
Standard deviation	0.002	0.002	0.004	0.001
A17	0.015	0.009	0.006	0.003
	0.012	0.003	0.006	0.003
	0.021	0.015	0.006	0
Average	0.016	0.009	0.005	0.002
Standard deviation	0.004	0.005	0	0.001
A14	0.009	0.009	0.006	0.003
	0.006	0.003	0	0.003
	0.015	0.012	0.009	0.003
Average	0.010	0.008	0.005	0.003
Standard deviation	0.004	0.004	0.004	0
A22	0.009	0.006	0.003	0
	0.003	0.006	0.003	0.003
	0.015	0.009	0.006	0
Average	0.009	0.007	0.004	0.001
Standard deviation	0.005	0.001	0.001	0.001
R 2	0.018	0.012	0.006	0.003
	0.015	0.009	0.003	0.003
	0.024	0.015	0.012	0.006
Average	0.019	0.012	0.007	0.004
Standard deviation	0.004	0.002	0.003	0.001
Alum	0.009	0.006	0.003	0.003
	0.003	0.003	0.003	0
	0.012	0.009	0.003	0
Average	0.008	0.006	0.003	0.001
Standard deviation	0.003	0.002	0	0.001
Control	0.174			
	0.174			
	0.177			
	0.175			
	0.001			

**Table 7.76:** OD<sub>550nm</sub> values for the determination of flocculating activity of both alum and bioflocculants at pH 9

**Table 7.77:** Flocculating activity of both alum and bioflocculants at pH 9 as derived from Table 7.76 using an equation for flocculating activity in Section 5.2.2 (Fig. 5.9)

Isolate	Flocculating activity	Standard deviation
D1	20.739	0.111
E1	10.000	0.641
A17	18.272	0.216
A14	0.776	0.105
A22	2.687	0.129
R2	25.058	0.166
Alum	9.913	0.317

-		1		
Isolates	10	20	30	50
D1	222	171	120	99
	240	162	117	93
	237	177	126	102
Average	233	170	121	98
Standard deviation	7.874	6.164	3.742	3.742
E1	276	270	171	123
	267	261	162	120
	282	276	177	129
Average	275	269	170	124
Standard deviation	6.164	6.164	6.164	3.741
A17	201	132	123	114
	198	129	117	114
	204	138	129	117
Average	201	133	123	115
Standard deviation	2.449	3.742	4.899	1.414
A14	201	168	135	96
	198	162	132	90
	204	171	138	102
Average	199	167	135	96
Standard deviation	2.449	3.742	2.449	4.898
A22	180	177	141	117
	174	171	132	108
	192	183	147	123
Average	182	177	140	116
Standard deviation	7.483	4.898	6.164	6.164
R 2	84	153	150	120
	78	147	144	114
	90	159	153	123
Average	84	153	149	119
Standard deviation	4.899	4.898	3.742	3.742
Alum	87	72	48	36
	72	69	45	33
	105	78	51	42
Average	88	73	48	37
Standard deviation	13.491	3.742	2.450	3.742
Control	1965			
	1982			
	1972			
Average	1978			
Standard deviation	6.976			

Table 7.78: Total plate count per 0.1 ml

**Table 7.79:** Percentage reduction (B–A/B x 100) of bacterial load by at different concentrations of bioflocculants compared to alum at pH 9 as derived from Table 7.78 (Fig. 5.10)

Bacterial				
bioflocculants &				
Alum	10 ppm	20 ppm	30 ppm	50 ppm
D1	88.179	91.750	93.861	95.028
E1	86.048	86.352	91.375	93.709
A17	89.802	93.252	93.759	94.165
A14	89.904	91.527	93.151	95.129
A22	90.766	91.019	92.897	94.115
R 2	92.237	92.440	93.962	95.738
Alum	95.535	96.296	97.565	98.123

**Table 7.80:** Data used for the calculation of flocculating activity (Section 5.2.2) (Table 7.81) percentage reduction in turbidity (Table 7.82) and total plate count (B–A/B x 100) (Table 7.83). Figure 5.11 and 5.12 show the reduction of river water turbidity spiked with two Gram-positive and Gram-negative bacteria by the bacterial bioflocculants compared to alum at 10 and 50 ppm respectively

	OD <sub>550nm</sub>						
S. feacalis	Isolates	10	20	30	50		
	A22	0.051	0.048	0.048	0.039		
		0.060	0.066	0.054	0.042		
		0.042	0.033	0.039	0.033		
	Average	0.051	0.049	0.047	0.038		
	Standard						
	deviation	0.007	0.013	0.006	0.004		
	A17	0.048	0.039	0.030	0.030		
		0.045	0.042	0.030	0.033		
		0.03	0.033	0.036	0.024		
	Average	0.047	0.038	0.031	0.029		
	Standard						
	deviation	0.008	0.004	0.003	0.004		
	D1	0.027	0.027	0.006	0.003		
		0.027	0.03	0.006	0		
		0.003	0.021	0.009	0.003		
	Average	0.028	0.026	0.007	0.002		
	Standard						
	deviation	0.011	0.004	0.001	0.001		
	R 2	0.033	0.027	0.012	0.006		
		0.042	0.03	0.015	0.003		
		0.024	0.03	0.006	0.009		
	Average	0.033	0.029	0.011	0.006		
	Standard						
	deviation	0.007	0.001	0.004	0.002		
	A14	0.054	0.051	0.048	0.021		
		0.060	0.054	0.051	0.027		
		0.051	0.045	0.042	0.018		
	Average	0.055	0.050	0.047	0.022		
	Standard						
	deviation	0.004	0.004	0.004	0.004		
	E1	0.033	0.018	0.069	0.051		
		0.039	0.015	0.075	0.057		
		0.027	0.021	0.066	0.042		
	Average	0.033	0.018	0.07	0.050		
	Standard						
	deviation	0.005	0.002	0.003	0.006		
	Control	1.110					
		1.230					
		0.990					
	Average	1.110					
	Standard						
	deviation	0.098					

	Turbidity (NTU)					
S. feacalis	Isolates	10	20	30	50	
	A22	3.030	2.970	2.880	2.610	
		3.090	2.970	2.910	2.640	
		3	2.970	2.850	2.550	
	Average	3.040	2.970	2.880	2.600	
	Standard					
	deviation	0.037	0	0.024	0.037	
	A17	2.730	2.610	2.520	2.220	
		2.790	2.670	2.55	2.250	
		2.640	2.550	2.460	2.220	
	Average	2.720	2.610	2.510	2.230	
	Standard					
	deviation	0.061	0.049	0.037	0.014	
	D1	3.120	2.580	2.520	2.100	
		3.150	2.640	2.490	2.100	
		3.090	2.550	2.460	2.130	
	Average	3.120	2.590	2.490	2.110	
	Standard					
	deviation	0.024	0.037	0.024	0.014	
	R 2	2.820	2.370	2.250	2.160	
		2.820	2.310	2.280	2.190	
		2.760	2.250	2.190	2.160	
	Average	2.810	2.310	2.240	2.170	
	Standard					
	deviation	0.028	0.048	0.037	0.014	
	A14	2.940	2.940	2.610	2.220	
		2.970	2.880	2.640	2.250	
		2.910	2.970	2.610	2.190	
	Average	2.940	2.930	2.620	2.220	
	Standard					
	deviation	0.024	0.037	0.014	0.024	
	E1	2.400	2.310	2.310	2.130	
		2.430	2.370	2.340	2.190	
		2.370	2.280	2.250	2.100	
	Average	2.400	2.320	2.300	2.140	
	Standard					
	deviation	0.024	0.037	0.037	0.037	
	Control	32.490				
		32.550				
		32.460				
	Average	32.500				
	Standard					
	deviation	0.037				

		Plate coun	t per 0.1 ml			
S. feacalis	Isolates	10	20	30	50	
	A22	6	3	1	0	
		3	2	1	0	
		0	1	1	0	
	Average	3	2	1	0	
	Standard					
	deviation	2.449	0.816	0	0	
	A17	6	9	9	5	
		9	6	3	3	
		6	3	3	3	
	Average	7	6	5	4	
	Standard					
	deviation	1.414	2.449	2.828	0.942	
	D1	138	114	105	81	
		135	117	99	87	
		138	114	95	78	
	Average	137	115	98	82	
	Standard	-				
	deviation	1.414	1.414	4.109	3.742	
	R 2	69	55	9	3	
		70	50	3	3	
		71	51	9	0	
	Average	70	52	7	2	
	Standard					
	deviation	0.816	2.160	2.828	1.414	
	A14	126	1	1	0	
		130	1	1	0	
		122	1	1	0	
	Average	126	1	1	0	
	Standard					
	deviation	3.265	0	0	0	
	E1	18	3	3	1	
		19	3	3	1	
		20	3	0	1	
	Average	19	3	2	1	
	Standard					
	deviation	0.816	0	1.414	0	
	Control	180	-			
		183				
		183				
	Average	182				
	Standard	1.414				
	deviation					
OD <sub>550nm</sub>						
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S. aureas	Isolates	10	20	30	50	
	A22	0.045	0.042	0.039	0.027	
		0.048	0.045	0.045	0.030	
		0.039	0.036	0.030	0.036	
	Average	0.044	0.041	0.038	0.031	
	Standard					
	deviation	0.004	0.004	0.006	0.004	
	A17	0.045	0.039	0.027	0.012	
		0.054	0.045	0.021	0.018	
		0.039	0.033	0.015	0.021	
	Average	0.047	0.038	0.021	0.017	
	Standard					
	deviation	0.006	0.005	0.005	0.004	
	D1	0.060	0.024	0.009	0.003	
		0.030	0.021	0.015	0.003	
		0	0.021	0.006	0.006	
	Average	0.03	0.022	0.01	0.004	
	Standard					
	deviation	0.024	0.001	0.004	0.001	
	R 2	0.033	0.027	0.015	0.009	
		0.036	0.027	0.015	0.012	
		0.033	0.030	0.015	0.006	
	Average	0.034	0.028	0.015	0.009	
	Standard					
	deviation	0.001	0.001	0	0.002	
	A14	0.036	0.033	0.027	0.018	
		0.042	0.036	0.024	0.021	
		0.036	0.027	0.030	0.018	
	Average	0.041	0.032	0.027	0.019	
	Standard					
	deviation	0.003	0.004	0.002	0.001	
	E1	0.039	0.027	0.012	0.006	
		0.042	0.021	0.015	0.003	
		0.036	0.030	0.012	0.003	
	Average	0.039	0.026	0.013	0.004	
	Standard					
	deviation	0.002	0.004	0.001	0.001	
	Control	1.44				
		1.44				
		1.44				
	Average	1.427				
	Standard					
	deviation	0				

	Turbidity (NTU)						
S. aureas	Isolates	10	20	30	50		
	A22	2.550	2.340	2.340	2.310		
		2.520	2.370	2.370	2.340		
		2.490	2.340	2.100	2.250		
	Average	2.540	2.350	2.330	0.300		
	Standard						
	deviation	0.024	0.014	0.1201	0.037		
	A17	2.610	2.340	2.280	2.010		
		2.640	2.370	2.310	2.040		
		2.610	2.310	2.250	2.010		
	Average	2.620	2.340	2.280	2.020		
	Standard						
	deviation	0.014	0.024	0.024	0.014		
	D1	2.640	2.460	2.400	2.310		
		2.610	2.490	2.430	2.310		
		2.580	2.430	2.340	2.310		
	Average	2.630	2.460	2.390	2.310		
	Standard						
	deviation	0.024	0.024	0.037	0		
	R 2	2.520	2.490	2.070	2.040		
		2.550	2.490	2.100	2.070		
		2.490	2.490	2.130	2.010		
	Average	2.520	2.490	2.080	2.040		
	Standard						
	deviation	0.024	0	0.024	0.024		
	A14	3.210	2.400	2.280	2.250		
		3.240	2.400	2.310	2.310		
		3.240	2.400	2.280	2.190		
	Average	3.230	2.390	2.290	2.250		
	Standard						
	deviation	0.014	0	0.014	0.049		
	E1	2.760	2.670	2.370	2.310		
		2.520	2.670	2.400	2.310		
		2.700	2.670	2.310	2.310		
	Average	2.760	2.680	2.360	2.320		
	Standard						
	deviation	0.102	0	0.037	0		
	Control	37.800					
		37.890					
		37.710					
	Average	37.800					
	Standard	0.073					
	deviation						

	Plate count per 0.1 ml						
S.aureas	Isolates	10	20	30	50		
	A22	6	3	3	0		
		3	3	3	0		
		3	3	0	0		
	Average	4	3	2	0		
	Standard						
	deviation	1.414	0	1.414	0		
	A17	6	6	3	0		
		3	3	3	0		
		3	3	3	0		
	Average	4	4	3	0		
	Standard						
	deviation	1.414	1.414	0	0		
	D1	6	9	6	3		
		9	6	3	3		
		3	3	3	3		
	Average	6	6	4	3		
	Standard						
	deviation	2.449	2.449	1.414	0		
	R 2	0	0	0	0		
		0	0	0	0		
		0	0	0	0		
	Average	0	0	0	0		
	Standard						
	deviation	0	0	0	0		
	A14	6	3	3	0		
		3	3	3	0		
		6	3	3	0		
	Average	5	3	3	0		
	Standard						
	deviation	1.414	0	0	0		
	E1	0	0	0	0		
		0	0	0	0		
		0	0	0	0		
	Average	0	0	0	0		
	Standard	_			_		
	deviation	0	0	0	0		
	Control	258					
		260					
		253					
	Average	257					
	Standard						
	deviation	2.944					

$OD_{550nm}$						
K. oxytoca	Isolates	10	20	30	50	
	A22	0.030	0.027	0.015	0.009	
		0.036	0.027	0.018	0.009	
		0.027	0.027	0.012	0.006	
	Average	0.013	0.027	0.015	0.008	
	Standard					
	deviation	0.004	0	0.002	0.001	
	A17	0.033	0.027	0.021	0.018	
		0.033	0.030	0.021	0.015	
		0.036	0.030	0.021	0.018	
	Average	0.034	0.029	0.021	0.017	
	Standard					
	deviation	0.001	0.001	0	0.001	
	D1	0.018	0.012	0.009	0.003	
		0.021	0.009	0.009	0.003	
		0.018	0.018	0.009	0	
	Average	0.019	0.013	0.009	0.002	
	Standard					
	deviation	0.001	0.004	0	0.001	
	R 2	0.009	0.006	0.006	0.003	
		0.012	0.012	0.003	0	
		0.009	0.006	0.003	0	
	Average	0.010	0.009	0.004	0.001	
	Standard					
	deviation	0.001	0.003	0.001	0.001	
	A14	0.018	0.012	0.009	0.003	
		0.018	0.009	0.003	0	
		0.018	0.012	0.003	0	
	Average	0.018	0.011	0.005	0.001	
	Standard					
	deviation	0	0.00141	0.00283	0.0015	
	E1	0.024	0.018	0.009	0.006	
		0.027	0.018	0.006	0.003	
		0.018	0.018	0.006	0.003	
	Average	0.023	0.018	0.007	0.004	
	Standard					
	deviation	0.003	0	0.001	0.001	
	Control	1.272				
		1.272				
		1.272				
	Average	1.271				
	Standard					
	deviation	0				

	Turbidity (NTU)						
K. oxytoca	Isolates	10	20	30	50		
· ·	A22	0.720	0.690	0.540	0.510		
		0.720	0.720	0.570	0.480		
		0.720	0.630	0.510	0.570		
	Average	0.720	0.680	0.540	0.520		
	Standard						
	deviation	0	0.037	0.024	0.037		
	A17	1.620	1.020	0.600	0.510		
		1.620	1.050	0.660	0.540		
		1.620	0.990	0.510	0.600		
	Average	1.610	1.140	0.590	0.550		
	Standard						
	deviation	0	0.024	0.061	0.037		
	D1	2.370	1.140	0.450	0.420		
		2.400	1.170	0.450	0.450		
		2.370	1.110	0.450	0.360		
	Average	2.380	1.140	0.450	0.410		
	Standard						
	deviation	0.014	0.025	0	0.037		
	R 2	0.540	0.510	0.420	0.390		
		0.570	0.510	0.450	0.390		
		0.510	0.510	0.420	0.390		
	Average	0.540	0.510	0.430	0.380		
	Standard						
	deviation	0.024	0	0.014	0		
	A14	0.810	0.480	0.450	0.390		
		0.870	0.510	0.450	0.420		
		0.780	0.480	0.450	0.330		
	Average	0.820	0.490	0.450	0.380		
	Standard						
	deviation	0.037	0.014	0	0.037		
	E1	0.600	0.570	0.420	0.420		
		0.660	0.570	0.450	0.450		
		0.570	0.600	0.420	0.360		
	Average	0.61	0.580	0.430	0.410		
	Standard						
	deviation	0.037	0.014	0.014	0.037		
	Control	34.320					
		34.320					
		34.320					
	Average	34.310					
	Standard	_					
	deviation	0					

Plate count per 0.1 ml						
K. oxytoca	Isolates	10	20	30	50	
	A22	12	9	3	3	
		6	7	2	0	
		6	5	1	0	
	Average	8	5	2	1	
	Standard					
	deviation	2.828	1.633	0.817	1.414	
	A17	0	0	0	0	
		0	0	0	0	
		0	0	0	0	
	Average	0	0	0	0	
	Standard					
	deviation	0	0	0	0	
	D1	15	12	12	6	
		20	13	15	9	
		13	14	9	6	
	Average	15	13	12	7	
	Standard					
	deviation	2.944	0.817	2.449	1.414	
	R 2	12	9	6	3	
		12	6	5	3	
		14	6	4	0	
	Average	13	7	5	2	
	Standard					
	deviation	0.942	1.414	0.817	1.414	
	A14	6	3	1	0	
		3	3	1	0	
		3	3	1	0	
	Average	4	3	1	0	
	Standard					
	deviation	1.414	0	0	0	
	E1	0	0	0	0	
		0	0	0	0	
		0	0	0	0	
	Average	0	0	0	0	
	Standard					
	deviation	0	0	0	0	
	Control	210				
		215				
		208				
	Average	211				
	Standard					
	deviation	2.944				

	OD <sub>550nm</sub>					
E. coli	Isolates	10	20	30	50	
	A22	0.045	0.030	0.027	0.021	
		0.510	0.030	0.024	0.018	
		0.360	0.030	0.027	0.018	
	Average	0.044	0.031	0.026	0.019	
	Standard					
	deviation	0.194	0	0.001	0.001	
	A17	0.039	0.033	0.021	0.012	
		0.042	0.039	0.021	0.015	
		0.036	0.030	0.024	0.006	
	Average	0.039	0.034	0.022	0.011	
	Standard					
	deviation	0.002	0.004	0.001	0.004	
	D1	0.039	0.048	0.048	0.036	
		0.039	0.051	0.048	0.039	
		0.039	0.048	0.048	0.036	
	Average	0.053	0.049	0.048	0.037	
	Standard					
	deviation	0	0.001	0	0.001	
	R 2	0.027	0.021	0.009	0.009	
		0.033	0.021	0.0165	0.012	
		0.027	0.021	0.006	0.003	
	Average	0.029	0.021	0.01	0.008	
	Standard					
	deviation	0.003	0	0.004	0.004	
	A14	0.039	0.039	0.033	0.027	
		0.045	0.042	0.036	0.027	
		0.036	0.033	0.030	0.027	
	Average	0.040	0.038	0.033	0.027	
	Standard					
	deviation	0.004	0.004	0.002	0	
	E1	0.003	0.018	0.009	0.003	
		0.003	0.021	0.009	0.003	
		0	0.018	0.009	0.003	
	Average	0.002	0.019	0.009	0.003	
	Standard					
	deviation	0.001	0.001	0	0	
	Control	2.874		~	~	
		2.880				
		2.865				
	Average	2.873				
	Standard	2070				
	deviation	0.006				

	Turbidity (NTU)					
E.coli	Isolates	10	20	30	50	
	A22	3.060	2.910	2.670	2.430	
		3.060	2.910	2.700	2.490	
		3.060	2.940	2.670	2.370	
	Average	3.060	2.920	2.680	2.430	
	Standard					
	deviation	0	0.014	0.014	0.049	
	A17	0.840	2.640	2.580	2.400	
		0.890	2.640	2.580	2.700	
		0.780	2.640	2.580	2.100	
	Average	0.840	2.650	2.580	2.400	
	Standard					
	deviation	0.045	0	0	0.245	
	D1	2.880	2.760	2.730	2.460	
		2.880	2.790	2.760	2.460	
		2.880	2.730	2.670	2.460	
	Average	2.890	2.760	2.720	2.470	
	Standard					
	deviation	0	0.0245	0.037	0	
	R 2	2.520	2.370	1.020	0.480	
		2.550	2.400	1.050	0.510	
		2.520	2.370	1.020	0.450	
	Average	2.530	2.380	1.030	0.480	
	Standard					
	deviation	0.014	0.014	0.014	0.025	
	A14	2.940	2.820	2.700	2.460	
		2.970	2.850	2.730	2.490	
		2.910	2.790	2.700	2.400	
	Average	2.940	2.820	2.710	2.450	
	Standard					
	deviation	0.024	0.025	0.014	0.037	
	E1	0.840	0.720	0.540	0.450	
		0.870	0.750	0.570	0.450	
		0.840	0.720	0.510	0.480	
	Average	0.850	0.730	0.540	0.460	
	Standard					
	deviation	0.014	0.014	0.024	0.014	
	Control	41.100				
		41.400				
		40.800				
	Average	41.100				
	Standard					
	deviation	0.245				

Plate count per 0.1 ml						
E. coli	Isolates	10	20	30	50	
	A22	10	3	0	0	
		11	3	0	0	
		9	0	0	0	
	Average	10	2	0	0	
	Standard					
	deviation	0.816	1.414	0	0	
	A17	3	3	1	1	
		3	3	1	1	
		3	0	1	1	
	Average	3	2	1	1	
	Standard					
	deviation	0	1.414	0	0	
	D1	6	11	12	18	
		9	6	16	21	
		6	13	11	18	
	Average	7	10	13	19	
	Standard					
	deviation	1.414	2.944	2.160	1.414	
	R 2	6	12	18	24	
		3	21	24	30	
		3	6	15	21	
	Average	4	13	19	25	
	Standard					
	deviation	0	1.414	0	1.414	
	A14	1	3	3	6	
		1	3	3	3	
		1	0	3	3	
	Average	1	2	3	4	
	Standard					
	deviation	0.024	0.024	0.014	0.037	
	E1	0	0	0	0	
		0	0	0	0	
		0	0	0	0	
	Average	0	0	0	0	
	Standard					
	deviation	0	0	0	0	
	Control	1257				
		1259				
		1255				
	Average	1257				
	Standard					
	deviation	0.245				

		OD <sub>550nm</sub>		
Alum	Isolates	10	20	30
	S. feacalis	0.255	0.210	0.147
		0.258	0.210	0.150
		0.252	0.210	0.147
	Average	0.255	0.211	0.148
	Standard deviation	0.002	0	0.001
	S. aureas	0.240	0.231	0.129
		0.249	0.237	0.132
		0.228	0.228	0.126
	Average	0.239	0.232	0.129
	Standard deviation	0.009	0.004	0.002
	K. oxytoca	0.219	0.207	0.153
		0.222	0.210	0.159
		0.216	0.207	0.147
	Average	0.219	0.208	0.153
	Standard deviation	0.002	0.001	0.005
	E. coli	0.333	0.222	0.213
		0.342	0.225	0.219
		0.327	0.219	2.040
	Average	0.334	0.222	0.212
	Standard deviation	0.006	0.002	0.860

		Turbidity (NTU)		
Alum	Isolates	10	20	30
	S. feacalis	20.010	12.600	6.810
		20.040	12.900	6.900
		19.950	12.300	6.690
	Average	20	12.600	6.800
	Standard deviation	0.037	0.245	0.086
	S.aureas	27.690	15	10.410
		27.720	15	10.410
		27.690	15	10.410
	Average	27.700	15	10.400
	Standard deviation	0.014	0	0
	K.oxytoca	21.990	19.710	19.200
		22.020	19.770	19.200
		21.990	19.620	19.200
	Average	22	19.700	19.200
	Standard deviation	0.014	0.061	0
	E.coli	31.110	26.790	19.110
		31.110	26.850	19.050
		31.110	26.760	19.140
	Average	31.100	26.800	19.100
	Standard deviation	0	0.037	0.037

		Plate count per 0.1 n	nl	
Alum	Isolates	10	20	30
	S. feacalis	21	9	4
		20	9	3
		25	6	2
	Average	22	8	3
	STDEVPA	2.160	1.414	0.817
	S. aureas	3	0	0
		3	0	0
		0	0	0
	Average	2	0	0
	STDEVPA	1.414	0	0
	K. oxytoca	9	3	0
		6	0	0
		3	0	0
	Average	5	1	0
	STDEVPA	2.449	1.414	0
	E. coli	0	0	0
		0	0	0
		0	0	0
	Average	0	0	0
	STDEVPA	0	0	0

**Table 7.81:** Flocculating activity of the bacterial bioflocculants compared to alum, as<br/>calculated from Table 7.80 for the removal of test organisms using an<br/>equation for flocculating activity in Section 5.2.2 (Fig. 5.13)

Bacterial	Streptococcus	Staphylococcus	Klebsiella oxytoca	Escherichia coli			
bioflocculants &	faecalis	aureus					
Alum	-						
A22	161.015	291.824	138.887	365.371			
A17	114.481	97.815	190.031	322.624			
D1	86.363	149.053	248.623	557.856			
R2	82.074	144.990	443.446	401.249			
A14	47.904	177.561	232.905	710.876			
E1	56.923	104.109	175.245	106.109			
Alum	34.813	36.603	30.961	16.185			
Standard deviation							
A22	1.235	0.521	0.355	0.127			
A17	0.188	0.374	0.222	0.174			
D1	0.098	0.177	0.208	0.311			
R 2	0.900	0.537	0.418	0.159			
A14	0.139	0.217	0.400	0.960			
E1	0.023	0.369	0.493	0.300			
Alum	0.090	0	0	0.179			

**Table 7.82:** Percentage reduction of river water turbidity (B–A/B x 100) at different concentrations of bacterial bioflocculants compared to alum at pH 9 as calculated from Table 7.80 (Fig. 5.14)

Conc (ppm)		Bacterial Streptococcus		IS	Staphylococcus	Klebsiella	Escherichia	
		bioflocculants	&	faecalis		aureus	oxytoca	coli
		Alum						
10 ppm A22			90.646		93.280	97.901	 92.555	
A17			91.631		93.069	95.307	 97.956	
D1			90.400		93.042	93.063	 92.968	
		R2		91.354		93.333	98.426	93.844
		A14		90.954		91.455	97.610	92.487
		E1		92.615		92.698	98.222	97.932
		Alum		38.462		26.719	35.879	 4.331
<u></u>							•	 1
Conc (ppm)		Bacterial	S	treptococcus	St	aphylococcus	Klebsiella	Escherichia
	bic	oflocculants &		faecalis		aureus	oxytoca	coli
		Alum		•				
20 ppm		A22		90.862		93.783	98.018	92.895
		A17		91.969		93.890	97.027	93.552
		D1		92.030		93.492	96.677	93.285
		R2		92.892		93.413	98.514	94.209
		A14		90.985		93.677	98.572	93.139
		E1		92.862		92.910	98.309	98.224
Alum			61.231		60.317	24.220	34.893	
						I		
Conc (ppm)		Bacterial	S	treptococcus	St	aphylococcus	Klebsiella	Escherichia
	bic	oflocculants &		faecalis		aureus	oxytoca	coli
		Alum		•				
30 ppm		A22		91.138		93.836	93.426	93.479
		A17		92.277		93.968	98.280	93.723
		D1		92.338		93.677	98.688	93.382
		R2		93.108		94.497	98.747	97.494
		A14		91.938		93.942	98.688	93.406
		E1		92.923		93.757	98.747	98.686
		Alum		79.077		72.487	44.040	53.528
<u></u>								
Conc (ppm)		Bacterial	S	treptococcus	St	aphylococcus	Klebsiella	Escherichia
41 /	bic	oflocculants &		faecalis		aureus	oxytoca	coli
		Alum		5			2	
50 ppm		A22		92.000		93.915	98.484	94.088
		A17		93.138		94.656	98.397	94.161
		D1		93.508		93.889	98.805	93.990
		R2		93.323		94.603	98.892	98.832
		A14		93.169		94.048	98.892	94.039
		E1		93.415		93.864	98.805	98.881
		Alum		90.185		75.952	79.102	57.178

**Table 7.83:** Percentage reduction in total bacterial counts (B–A/B x 100) at different concentrations of bacterial bioflocculants compared to alum at pH 9 as calculated from Table 7.80. Figure 5.14 and 5.15 shows the reduction of the microbial load by the bioflocculants at different concentrations compared to alum at 10 ppm and 50 ppm respectively

Conc	Bacterial	Streptococcus	Staphylococcus	Klebsiella	Escherichia
(ppm)	bioflocculants &	faecalis	aureus	oxytoca	coli
	Alum				
10 ppm	A22	98.352	98.444	96.209	99.204
	A17	96.153	98.444	100.000	99.761
	D1	24.725	97.665	92.891	99.443
	R2	61.538	100.000	93.839	99.682
	A14	30.769	98.054	98.104	99.920
	E1	89.560	100.000	100.000	100.000
	Alum	87.912	99.222	97.630	100.000

Conc (ppm)	Bacterial bioflocculants &	Streptococcus faecalis	Staphylococcus aureus	Klebsiella oxytoca	Escherichia coli
	Alum				
20 ppm	A22	98.901	98.833	97.630	99.814
	A17	96.703	98.444	100.000	99.814
	D1	36.813	97.665	93.839	99.204
	R2	71.428	100.000	96.682	98.966
	A14	99.451	98.833	98.578	99.814
	E1	98.351	100.000	100.000	100.000
	Alum	95.604	100.000	99.526	100.000

Conc (ppm)	Bacterial bioflocculants &	Streptococcus faecalis	Staphylococcus aureus	Klebsiella	Escherichia coli
(ppm)	Alum	Juceuns		onyroeu	0011
30 ppm	A22	99.451	99.222	99.052	100.000
	A17	97.530	98.833	100.000	99.920
	D1	46.154	98.444	94.313	98.966
	R2	96.154	100.000	97.630	97.098
	A14	99.451	98.833	99.526	99.761
	E1	98.901	100.000	100.000	100.000
	Alum	98.352	100.000	100.000	100.000

Conc	Bacterial	Streptococcus	Staphylococcus	Klebsiella	Escherichia
(ppm)	bioflocculants &	faecalis	aureus	oxytoca	coli
	Alum				
50 ppm	A22	100.000	100.000	99.526	100
	A17	97.802	100.000	100.000	99.920
	D1	54.945	98.833	96.682	98.488
	R2	98.901	100.000	99.052	97.098
	A14	100.000	100.000	100.000	99.682
	E1	99.451	100.000	100.000	100.000
	Alum	100.000	100.000	100.000	100.000