In Rajasthan state particularly, textile mills represent an important economic sector. Sanganer near Jaipur is famous for dyeing and printing of colorful dresses, bed sheets, curtains, dress material and variety of other textiles. Bulk of the textile products of these industries is exported. There are estimated to be around 500 block and screen printing units in Sanganer.

Effluents of these industries are directly discharged into the drain or directly into the Amanishah Nalla without any pre treatments. Effluents of these industries are continuously deteriorating the water quality of that area. The Amanishah drain originating from the Aravalli hills N.E. of the Jaipur city, receives sewage of the city and industrial wastewaters.

Apart from the Amanishah drain, the untreated dye wastewater is also discharged on the land, forming shallow pools (depth = 60-75 cm) adjoining the dyeing units. Pollution Control Board has listed the dye and dye intermediates industry as one of the heavily polluting industries (CPCB, 1990). They are thus, a potent hazard to the natural sources like soil, water, flora, fauna, livestock and human population.

In the present study the effects of the wastewaters on the moist bank vegetation were monitored at near Gullar ka Bandha sites which are near the Amanishah drain, for which a survey was conducted of the Sanganer area where most of the textile printing and dyeing
factories were concentrated, particularly from where the contaminated factory effluents passed and collected, regarding the available wild flora round the year. Sampling was also done of contaminated water and soil samples from that area where the sample plants were growing. This was done to understand which plant species are hardy enough to sustain the toxicity of the dyes and other factory effluent; and also to study the exact condition of the soil and water where they were growing.

From the survey results it was observed that 15 families dominated the area with 24 plant species, maximum belonging to Asteraceae family. These plants were of all the categories i.e. herb, shrub and tree. From among these plants three plant species were selected for further studies viz. a herb *Parthenium hysterophorus* L. (*Asteraceae*), shrubs *Verbesina encelioides* Cav. (*Asteraceae*) and *Chenopodium album* L. (*Chenopodiaceae*).

The plants are not only the source of providing vital ingredients for human needs. They are also used to remove environmental contaminants such as halocarbons, poly-chlorinated biphenyls, synthetic polymers, alkyl benzyl sulphonate, oil mixture and others. This removing process of pollutants by plants is called “Phytoremediation”. Phytoremediation is the process of cleaning toxic pollutants from soil and ground water, as well as, heavy metal contamination by the use of plants (Robbins, 1965).
Environment pollution is “the contamination of the physical and biological components of the earth/atmosphere system to such an extent that normal environmental processes are adversely affected”. India has been ranked as seventh most environmentally hazardous country in the World by a new ranking released recently. The study is based on evaluation of “absolute” environment impact of 179 countries (Harvard, Princeton, Adelaide University and University of Singapore, 2011).

The organic pollutants, such as pesticides, explosives, solvents, industrial chemicals including dyes are manmade non-natural compounds are the xenobiotic substances (Schlegel, 1995). These complex and recalcitrant compounds cannot be broken down to basic molecules by plant molecules, and hence by phytotransformation there is possibility of treating such contaminants i.e. to a change in chemical structure without complete breakdown of the compound, these are converted into simpler toxic compounds. Thousands of hazardous waste sites have been generated worldwide resulting from the accumulations of xenobiotics in soil and water over the years (Jain, 2005). Xenobiotic compounds are human made chemicals that are present in the environment at unnaturally high concentrations. There are two types of xenobiotic compounds. They may be biodegradable or non degradable /recalcitrant. Biodegradable xenobiotic compounds
are those that get degraded by the action of microbes or other reactions while recalcitrant compounds are resistant to degradation by any reactions. The recalcitrant xenobiotic compounds can be grouped into various groups like halocarbons, polychlorinated biphenyl, oil mixtures, synthetic polymers, alkyl benzyl sulphonates, etc. The potential health hazards of a xenobiotic compound is a function of its persistence in the environment, as well as, the toxicity of the chemical class. They tend to accumulate in the environment and lead to bioaccumulation and biomagnifications (Aelion et al., 1987).

Dye waste water from textile or dye stuff industry is one of the most difficult to treat because dyes have various synthetic origin and they contain complex aromatic molecular structures, which make them more stable and more difficult to be biodegraded (Kim et al., 2004 and Abou-Okeil, 2005).

Man and microorganisms have strong relationship for their livelihood and maintenance. The microorganisms including fungi and bacteria may be friendly or toxic (non-friendly) to human being. A large group of microorganisms harbor the human body as well as living plants apart from free-living in the environment. They may be friendly or may not be. However, human being or the plants without these microorganisms can not live. To facilitate the human life these microorganisms play multi partite role in and out side the body, so it
does with the plants. They provide desired mineral nutrition to the plants in various ways, either by degrading the complex molecules in the soil or converting them into simple components and by absorbing the desired elements in the plants for its benefits.

In recent years, a number of studies have focused on some microorganisms which are able to biodegrade and biosorb the xenobiotic compounds, such as dyes in waste waters. A wide variety of microorganisms capable of decolorizing a wide range of dyes include some bacteria, fungi and algae (Fu and Tiraraghavan, 2002 and 2004; Pazarlioglu et al., 2005). The use of microorganisms for the removal of synthetic dyes from industrial effluents offers considerable advantages. The process is relatively inexpensive, it is simple method and the running costs are low the end products of complete mineralization are not toxic (Zheng et al., 1999; Forgacs et al., 2004 and Park et al., 2006).

Certain microorganisms which throughout or part of its life cycle invade the tissues of living plants termed as “Endophytes” for those microorganisms living inside the plant tissue (De Barry, 1986). He first introduced the term "epiphytes" for fungi that live on the surface of their host and "endophytes" for those living inside the plant tissue.
In its most conservative definition the term endophyte now includes all organisms that at some time of their life cycle lives within plant tissue without producing any symptom. Usually several to hundred of endophyte species can be isolated from a single plant (Tan and Zou, 2001).

Endophytic organisms have received considerable attention after they were found to protect their host against insect, pest, pathogens and even domestic herbivorous (Webber, 1981). Almost all the plant species (~400,000) harbor one or more endophytic organisms (Tan and Zou, 2001). To date, only a few plants are investigated for their endophyte biodiversity and their potential to produce bioactive secondary metabolites. Studies have been conducted at different parts of the world about the endophytic biodiversity, taxonomy, reproduction, host ecology, and their effect on the host (Bandaru, *et al.*, 2006; Dayle, *et al.*, 2001; Selosse and Scardl, 2007; Carroll and Carroll, 1978). Dreyfuss and Chapela (1994) estimated that there may be at least one million species of endophytic fungi alone. Different groups of organisms such as fungi, bacteria, actinomycetes and mycoplasma are reported as endophyte of plants (Bandara, *et al* 2006; Castillo, *et al*, 2006; Azevedo, *et al*, 2000; Petrini, 1985). Endophytic communities are formed mainly by fungi and bacteria.

Many environmental factors influence the plant growth and survival. Endophyte infected plants have been reported to have
increased tolerance to drought, heat, metal toxicity, low pH, and high salinity (Waller, et al., 2005; Rodriguez, et al., 2004; Lewis, 2004). Similarly, salt tolerance is observed in plants infected with endophytes (Waller et al., 2005). The endophytic fungus *Piriformospora indica* was reported to protect barley from salt stress. Endophytes also increase heat tolerance in their host (Redman, et al., 2002). The symbiotic relationship for thermotolerance was observed in endophyte *Curvularia* sp.-infected plant, *Dichanhelium lanuginosum*, exposed to high temperature 65°C for 10 days. All nonsymbiotic plants died during the 65°C heat treatment, whereas symbiotic plants survived (Redman, et al., 2002).

Actinomycetes have also been shown to catalyse hydroxylation, oxidation, and dealkylation reactions against various xenobiotic compounds (Goszczynski et al. 1994). In 1989, Ball et al. screened 20 strains of actinomycetes, representing a wide range of genera, for their ability to decolourise the polymeric dye Poly R (Ball et al. 1989).

Understanding the above facts present study was undertaken to isolate the endophytes from different plant parts of the selected plant species that grew well in the textile dye contaminated soil and water, viz. a herb *Parthenium hysterophorus* L. (Asteraceae), shrubs *Verbesina encelioides* Cav. (Asteraceae) and *Chenopodium album* L. (Chenopodiaceae). The endophytic microorganisms (Bacteria and
Fungi) were isolated from root, stem and leaf part of the selected plants. Among the three plant parts taken for isolation of the endophytes, root harbored maximum number of endophytic microorganisms in all the three plants taken for study followed by leaf. This is because roots are in the soil and hence have an easy approach for the microorganism. Besides, the growth and colonization of the bacteria on plant roots can be influenced by several soil chemical, physical and biological factors (Harries, 1998).

Leaves of the plants photosynthesize and it is transported to roots. The roots in turn, by this energy absorbs minerals and other nutrients from the soil. But if there is no easy accessible minerals and nutrients plants may not survive which can be the case if they are growing in such a polluted area, so is the condition of microorganisms, hence in such a stress conditions a harmony is developed among the living organisms to benefit each other and this leads to symbiotic relationship. According to Kobayashi and Palumbo (2000) endophytes are sheltered from environmental stresses and microbial competition by the host plant and they seem to be ubiquitous in plant tissues, having been isolated from flowers, fruits, leaves, stems, roots and seeds of various plant species. In turn endophytes provide protection to their host from insect, pest and herbivore, and help their host to adapt in different stress conditions.
(Knop, *et al.*, 2007; Clay, 2005; Clay and Schardl, 2002; Malinowski and Beiesky, 2006; Bonnet and Veisseire, 2000). There is sufficient evidence that endophytic fungi play important role in host plant physiology. They received nutrition protection and propagation opportunities from their hosts (Clay and Schardt, 2002; Thrower and Lewis, 1973) and host plant also benefited from this symbiosis. It is believed that the environment has an important role on endophyte biodiversity and species diversity is dependent upon the nature of the host plant and their ecological location. Therefore though growing in the same ecological conditions, the three selected plants harbored not only quantitatively different amount of endophytes e.g. from *Parthenium hysterophorus* maximum number (total 11 isolates) of endophytic microorganisms (9 bacterial and 2 fungal) were isolated from its different plant parts, compared to *Verbesina encelioides* (total 7; 6 bacterial and 1 fungal) and *Chenopodium album* (total 9; 8 bacterial and 1 fungal). It was observed that bacterial colonies outnumbered to a great extent over fungal colonies in all the plant samples studied. This may be due to greater number and smaller size of the bacteria. As the penetration into the host plant may occur via stomata, wounds, or areas of lateral root development, or may even be facilitated by the production of hydrolytic enzymes capable of degrading the cell wall (Souza *et al.*, 2004). Once inside, the
endophytic microorganism may lodge in specific tissues, or even systemically colonize the plant, thereby establishing symbiotic, mutualistic, commensal and tropobiotic relationships (Ulrich et al., 2008). This might result into differential selection of the plant tissues/organs for their localization as has been observed in the present study viz. Maximum number of endophytes (six) have been obtained from roots of *Parthenium hysterophorus*, from stem of *Chenopodium album* (four) and from leaves of *Parthenium hysterophorus* and *Verbesina enceloides* (three each).

Colors gives delightful pleasure to eyesight but at the same time they may act as serious pollutants when their origin is dyes and dyestuffs. Until the latter half of the 19th century, with the exception of a few mineral colors like nila thotha (CuSo4) and tin chloride (SnCl2), all dyes used were vegetable or animals in origin. Now, these natural dyes are almost completely replaced by synthetic dyes. About 3500 dyes are in practical use. Azo dyes contribute 84%, of which sulphonated azo dyes predominate.

The disposal of these dye wastes into receiving waters causes damage to the environment. As a result, the dye wastewaters are extremely toxic to both flora and fauna, including crop plants and human beings (Sharma et.al., 1999). Our present concern is the dye waste water from Textile printing and dyeing factories in Sanganer.
which has been reported to contain heavy metals like Zn, Ni, Cr, Cd and Pb to more than permissible limits (Khan et al. 1995). Thus, dye effluents are found toxic to the crop plants, especially the concentrated ones. Dyes and phenol are such xenobiotic compounds which accumulate in environment after being produced from various industrial operations. Textile dyes are one of the most prevalent type chemicals used today.

The organic pollutants, such as pesticides, explosives, solvents, industrial chemicals including dyes are manmade non-natural compounds are the xenobiotic substances (Schlegel, 1995). These complex and recalcitrant compounds cannot be broken down to basic molecules, and hence by phytotransformation there is possibility of treating such contaminants i.e. to change in chemical structure without complete breakdown of the compound. These are converted into simpler toxic compounds.

Bioremediation is a pollution control technology that uses biological systems to catalyze the degradation or transformation of various toxic chemicals to less harmful forms. This natural process, bioremediation, includes bioengineering the capabilities of intrinsic microorganisms, to clean up the environment, is an effective alternative to conventional remediation methods (Vidali, 2001).

The different mechanism supposed to be involved in the bioremediation of Textile dyes and related xenobiotic chemicals are;
Biodegradation by direct and indirect extracellular enzymes (Kulla et al., 1983; Fewson, 1988), Bioaccumulation: in intracellular milieu and then their further assimilation in living beings specifically microbes (Kuhn & Pfister, 1990), Biotransformation, which involves the detoxification of a chemical or metal by transforming its physical state (by enzymatically or by any chemical reaction) (Ishibashi et al., 1990), Bioadsorption, through ion exchange by living and dead microbial biomass (Zhau & Zimmerman, 1993). Sometimes, a single biological mechanism of an organism may work out for the remediation of any chemical or at times, a combination of any of the aforementioned mechanisms in different organisms can go along together in a series.

Biodegradation is considered as a phenomenon of biological transformation of organic compounds by living organisms particularly microbes. Biodegradation can be divided into three categories i.e. Mineralization, Biotransformation and Co-metabolism. Mineralization is a process where the organic chemical is broken down into inorganic compounds. It is also known as “ultimate biodegradation.

Bioremediation can be defined as the action of microbes or other biological systems to degrade environmental pollutants. Microorganism has the capability of degrading all naturally occurring compounds; this is known as the principle of microbial inflability proposed by Alexander in 1965. Mix cultures of microbes can together
be used to degrade xenobiotic compounds completely because they produce different enzymes that act on recalcitrant compounds and degrade them to simpler form. Smaller compounds are again taken up by other series of microbes and degraded wholly. Since xenobiotics consist of a wide variety of compounds, their degradation occurs via a large number of metabolic pathways. Degradation of alkanes and aromatic hydrocarbons generally occurs as follows: an oxygenase first introduces a hydroxyl group to make the compound reactive, the hydroxyl group is then oxidized to a carboxyl group, the ring structures is opened up (in case of cyclic compounds), the linear molecule is degraded by $\beta$-oxidation to yield acetyl CoA, which is metabolised in the usual manner.

Biodegradation processes may be anaerobic, aerobic or involve a combination of the two ( Forgacs et al., 2004). However, it has been observed in a number of cases that the efficiency of aerobic treatment was inferior to that of anaerobic decolonization process (Sapari, 1996, Young and Yu, 1997, Ramakrishna and Viraraghavan, 2000; Forgacs et al., 2004; Sarioglu and Bisgin, 2007).

Although anaerobic reduction of azo dyes is generally more satisfactory than aerobic degradation, the intermediate products (carcinogenic aromatic amines) have to be degraded by an aerobic process (Forgacs et al., 2004 and Melgoza et al., 2004).
In recent years, a number of studies have focused on some microorganisms which are able to biodegrade and biosorb dyes in waste waters. A wide variety of microorganisms capable of decolorizing a wide range of dyes include some bacteria, fungi and algae (Fu and Tiraraghavan, 2001, Pazarlioglu et al., 2005, Deng et al., 2008). The use of microorganisms for the removal of synthetic dyes from industrial effluents offers considerable advantages. The process is relatively inexpensive, it is simple method, the running costs are low and the end products of complete mineralization are not toxic (Zheng et al., 1999, Forgacs et al., 2004 and Park et al., 2007).

Over the past decade, many fungal strains have been studied for their abilities to degrade a wide variety of structurally diverse pollutants. Recently, many studies have also demonstrated that fungi are able to degrade dyes (Park et al., 2006). White-rot fungi produce a wide variety of extracellular enzymes (laccase, lignin peroxidase, phenol oxidase, Mn dependent peroxidase, and Mn-independent peroxidase) that decompose the highly stable natural compounds (lignin, hemi cellulose, cellulose, etc.) (Moreira et al., 2000; Wesenberg et al., 2003 and Forgacs et al., 2004). Besides, there are various fungi other than white-rot fungi, such as Aspergillus niger, which can also decolorize and / or biosorb diverse dyes (Fu and Tiraraghavan, 2002 and 2004).
Adsorption rather than degradation plays a major role during the decolorization process by fungi and algae, as a result, the dyes remain in the environment. It is well known that bacteria can degrade and even completely mineralize many reactive dyes under certain conditions (Asad et al., 2007; Chen et al., 2003; Moosvi et al., 2005). Some new bacterial strains capable of decolorizing a broad-spectrum of dyes have also been isolated and characterized (Deng et al., 2008). Bacterial degradation of reactive dyes is often initiated under anaerobic conditions by an enzymatic biotransformation step (Carvalho et al., 2008; Park et al., 2007). The resulting products such as aromatic amines are further degraded by multiple-step bioconversion occurring aerobically or anaerobically (Barragan et al., 2007; Xu et al., 2006).

Our present studies were concentrated on four fungal and twenty three bacterial isolates obtained as endophytes from the three experimental plant species Parthenium hysterophorus, Verbesina encelodies and Chenopodium album, which were growing near the contaminated effluents release site of textile dye industry. For the study material as dye contamination five commercial synthetic dyes- Azo dyes (Reactive VS dyes) i.e. Red-5B, Orange-3R, Yellow-GR, Black-B and Turquoise Blue-G, manufactured by Metrochem Industries Ltd., Ahemdabad, were selected for the decolorization
experiments in the present study, as these dyes were being used for printing/dyeing of fabrics in the industries near the selected study sites. All these dyes were used without any purification. In an experiment decolorization of textile dye was studied under different (static and agitated conditions) incubation conditions. It was observed that only 5 bacterial isolates; four from *Parthenium hysterophorus* and one from *Verbesina encelioides* among 23 isolates could grow under static, as well as, agitated conditions of incubation, showing complete decolorizing capabilities of all the five dyes (Orange-3R, Turquoise Blue-G, Red-5B, Black-B and Yellow-GR), while out of total 4 fungal isolates 3 (75%) could grow and decolorized the dyes in both stationary and agitated conditions. Thus it can be inferred that all the fungal isolates from *Parthenium hysterophorus* and *Chenopodium album*, which could be grown on the dye decolorization medium had the capacity to decolorize the dyes. Therefore it can be inferred that fungal isolates are better dye decolorizers than bacterial, though the number of bacterial endophytic isolates were more (23) compared to fungal (4) isolates. Probably the bacterial endophytes had other role to play in the plants and fungi were dye decolorents; or bacteria might be playing a part role in dye decoloration as reported by Pandey *et al.* (2007) even the products of intermediate metabolism during the decolorization process, such as aromatic amines, can be degraded by the hydroxylase and oxygenase produced by bacteria.
Percent decolorization potential of selected microorganism were also studied. In which the dye decolorizing isolates both bacterial and fungal were subjected to increasing concentrations (20, 40, 60, 80 and 100 mg/l) of dyes Orange-3R, Turquoise Blue-G, Red-5B, Black-B and Yellow-GR. From the results it was clearly observed that all the decolorizing fungal isolates gave better response over bacterial decolorizers, as all the three fungal isolates had the potential to decolorize all the five dyes taken for study, to more than 80% decolorization at 20 mg/l concentration, and above 60% at 100 mg/l concentrations; whereas, among the five bacterial decolorizers, only the isolates obtained from Parthenium hysterophorus showed better response i.e. above 70% at 20 mg/l & 55% at 100 mg/l, in all the dyes studied. The reason for better results with fungus might be due to the reason that for living fungal cells, the major mechanism is biodegradation, because they can produce the lignin modifying enzymes, laccase, manganese peroxidase (MnP) and lignin peroxidase (LiP) to mineralize synthetic lignin or dyes (Fu and Tiraraghavan 20001 and Stolz, 2001).

In the present study 23 bacterial and 4 fungal isolates were obtained, among which 5 bacterial and 4 fungal isolates could decolorize the dyes. The microbial cultures which dechlorised the test dyes were identified up to the genus level.
Dyes contain *chromophores*, that delcolized via electron system with conjusted double bonds, and *auxochromes*, electron-withdrawing or electron-donating substituents that cause or intensify the color of the chromophore by altering the overall energy of the electron system. Usual chromophores are –\(\text{C}≡\text{C}\)-, –\(\text{C}≡\text{N}\)-, –\(\text{C}≡\text{O}\)-, –\(\text{N}≡\text{N}\)-, –\(\text{NO}_2\) and quinoid rings and auxochromes are –\(\text{NH}_3\), –\(\text{COOH}\), –\(\text{SO}_3\text{H}\) and –\(\text{OH}\). (Van der Zee, 2002).

Associative nitrogen fixation is also well established as an important nitrogen input for many plant ecosystems. Associative nitrogen fixation is the phenomenon whereby nitrogen-fixing bacteria are not encased within a nodule of the host root tissue but instead are found in the rhizosphere or mycorrhizosphere (van Berkum and Bohlool, 1980). Li and Hung (1987) also reported nitrogen-fixing *Clostridium* spp. and *Azospirillum* spp. isolated from surface-sterilized ectomycorrhizal root tips, which suggests that associative nitrogen-fixing bacteria may reside within the ectomycorrhizae but, again, not within a nodulated structure. In these types of relationships, bacterial species other than those of the genera *Rhizobium*, *Bradyrhizobium* and *Frankia* have been shown to fix nitrogen which is then taken up by the mycorrhizal fungus and, ultimately, by the host plant. Li and Hung (1987) proposed that phosphorus uptake by the ectomycorrhizal fungus increased and enhanced the nitrogen-fixing capabilities of the associative nitrogen-fixing bacteria.
Recently, the culturable nitrogen-fixing bacteria *Paenibacillus pabuli*, *Paenibacillus amylolyticus* and *Methylobacterium mesophilicum* were shown to reside within TEM formed by *Suillus tomentosus* on *Pinus contorta* var. *latifolia* roots (Paul, 2002). These bacteria were isolated from inner tissue and were not found on the surface of the tubercles (Paul, 2002). The presence of nitrogen-fixing bacteria exclusively within a nodular structure – the TEM – suggests an evolutionary parallel to the other types of nodulated loci of significant levels of nitrogen fixation.

Bacteria, commonly known as rhizobia, inhabit nitrogen-fixing nodules on the roots of many legumes. Legume-nodulating bacteria belong to several branches of the a- and b-subgroups of the proteobacteria (van Berkum and Eardly 1998; Moulin *et al.* 2001). Carbon fixed photosynthetically in leaf chloroplasts is translocated to the roots. There the bacteria use it as a source of energy and electrons for the reduction of atmospheric dinitrogen to ammonia, which serves as a nitrogen source for the plants (Van Rhijn and Vanderleyden 1995).

Phosphorus is important for plant growth because it stimulates growth of young plants, promotes a vigorous start and hastens maturity. Consequently, plant growth is diminished, maturity is delayed and yield reduced when an inadequate supply of P is present (Sawyer and Creswell, 2000).
Phosphorus exists in soil in organic and inorganic forms. Each form is a continuum of many P compounds, existing in different phases and in equilibrium with each other. Availability of P ranges from soluble P (plant available) to very stable (plant unavailable) compounds. There is a dynamic and complex relationship among the different forms of P involving soil, plants and microorganisms. Organic P compounds are found in humus and other organic materials including decayed plant, animal and microbial tissues. Organic P is also the principal form of P in manure.

The process of mineralization or immobilization is carried out by microorganisms and is highly influenced by soil moisture and temperature. Mineralization and immobilization are most rapid in warm, well-drained soils (Busman et al., 2002).

For over one hundred years, workers have recognized the ability of soil microorganisms to solubilize Pi from insoluble (i.e. nutritionally unavailable) organic and mineral phosphates (Whitelaw, 2000). Wide ranges of microbial biosolubilization mechanisms exist, so that much of the global cycling of insoluble organic and inorganic soil phosphates is attributed to bacteria and fungi. These associations are assumed to play an important role in phosphorus nutrition in many natural and agro-ecosystems.
Many soil bacteria and fungi have the ability to solubilize P and make it available to growing plants (Antoun et al., 1998). Microorganisms are central to the soil P cycle and play a significant role in mediating the transfer of P between different inorganic and organic soil P fractions, subsequently releasing available P for plant acquisition (McLaughlin, 1988; Oberson, 2001). There are two aspects in microbial P solubilization: 1) P released by solubilization processes (Rodriguez and Fraga, 1999), and 2) P released from accumulated P in biomass of microorganisms (Oehl, 2001).

Phosphate solubilizing microorganisms include different groups of microorganisms, which not only assimilate phosphorus from insoluble forms of phosphates, but they also cause a large portion of soluble phosphates to be released in quantities in excess of their requirements.

Inorganic phosphate solubilizing microorganisms (PSM) constitute various portions of the soil microbial population and vary from soil to soil (Banki and Dey, 1982; Kucey et al., 1989). The populations of PSM are reportedly varied and ranged from very low (less than 102 cfu g-1 of soil) in a soil in Northern Spain to very high (3 x 106 cfu g-1 of soil) in Quebec, Canada (Chabot et al., 1993; Peix et al., 2001). Phosphate solubilizing microorganisms were isolated from rhizosphere soils of different crops (Ponmurugan and Gopi,
2006). The numbers of PSM are more important in rhizosphere than non-rhizosphere soil (Kucey et al., 1989). The PSM represented 0.1 to 0.5% of total bacterial and fungal populations in 29 Alberta soils (Kucey, 1983). PSM occur in both fertile and P-deficient soils and the fastest initial rates of P incorporation were observed in P-deficient soils (Oehl, 2001). Species of Aspergillus and Penicillium are among fungal isolates identified to have phosphate solubilizing capabilities.

Aspergillus niger and some Penicillium species have been tested in fermentation system or inoculated directly into soil in order to solubilized rock phosphate (Kucey, 1987 and Vassilev et al., 1995). Reddy et al., (2002) found that all the isolates of Aspergillus tubingensis and A. niger isolated from rhizospheric soils were found to be capable of solubilizing all the natural forms of rock phosphates.

Among the bacterial genera with this capability are Pseudomonas, Azospirillum, Bacillus, Rhizobium, Burkholderia, Arthrobacter, Alcaligenes, Serratia, Enterobacter, Acinetobacter, Flavobacterium and Erwinia (Rodriguez et al., 1996). Seed or soil inoculation with PSMs is known to improve solubilization of fixed soil phosphorus and applied phosphates resulting in higher crop yields (Jones et al., 1994).

Phosphorus in fertilizers is converted to water-soluble Pi as orthophosphate ions $\text{H}_2\text{PO}_4^-$ and $\text{HPO}_4^{2-}$ in soil within a few hours
after application (Schulte and Kelling, 1996). As the fertilizer enters the soil, moisture from the soil begins to dissolve the fertilizer particles. The concentration of Pi in solution increases around the dissolved fertilizer particles and diffuses a short distance from the fertilizer particles (Busman et al., 2002). These negatively charged P ions attach strongly to the surfaces of minerals containing positively charged ions such as iron (Fe$^{3+}$) and aluminum (Al$^{3+}$) in acidic soils via sorption/desorption processes. Fe$^{3+}$ and Al$^{3+}$ act as the sorption sites for the negatively charged P (Sato and Comerford, 2005).

Phosphate solubilizing fungi are superior to their bacterial counterpart for P solubilization both on precipitated agar and in liquid (Kucey, 1983). Fungal hyphae in liquid culture were attached to P mineral particles shown by scanning electron microscopy, whereas bacteria were not (Chabot et al., 1993).