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EFFECT OF TEXTILE INDUSTRY WASTE WATER ON SOIL MICROBIAL POPULATION

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Abstract

The textile industry is one of the world's most responsible industries for pollution generation and hence, management of its toxic effluent has become a global issue. In the textile effluent some essential minerals are present so these can be used as a source of nutrients but the presence of several toxic elements can deteriorate soil health. Therefore, experiments were conducted to identify the potential of textile effluent amendment of soil to increase the microbial population for agricultural sustainability. In this study, soil was fertilized with different concentrations of textile effluents (*i.e.* 0, 10, 20, 50 and 100%) to accurately. The results indicated that lower concentrations of textile effluent were a good source of microbial population whereas higher concentrations of it were deteriorating soil health. Total number of bacteria, free-living diazotrophs, actinomycetes and fungi increased with increase in the concentration of waste water upto 20% level. After 60 days of incubation, microbial population increased significantly upto 20% concentration of textile waste water amendments and then declined on further incubation showing that textile waste water is being utilized as nutritive source upto 20% at initial stages of incubation, however microbial population was decreased on further increasing the waste water concentrations (20 to 100%) indicating damaging effects of waste water on soil health.

Keywords: Industry, Microbial population, Soil health and Waste water.

Introduction

Textile and clothing is one of the oldest and largest industries present all around the world. However, from the environmental point of view, these industries account for greatest risk by releasing a variety of toxic chemicals. Besides using harmful chemicals, these textile industries also utilize a lot of water for all steps during manufacture. Among all industries, cotton textile and synthetic industries contribute for 82% and 18% respectively, representing a large network of textile industries in India (Sheth and Patel, 2004). Big cities like Bangalore, Kanpur, Mumbai, Ahmadabad, Chennai and Coimbatore, are considered as initial centers for these industries. Many textile processing units are well developed and distributed everywhere in the country. Now adays, textile industries are exploring more rapidly due to its demand by human population (Hassan *et al*., 2013). Disposal of waste water, released from these types of industries, is mainly through dumping into soil or river. The structural organization of soil particle provides a spatially heterogeneous habitat for microorganisms characterized by different nutrients, substrates, oxygen concentrations and water contents as well as pH value. Therefore, due to mixed bag of components ultimately leads to significant change in structural and functional composition of microbes and hence influence the viability of soil for agriculture sustainability.

Microbes are considered as natural recyclers and scavengers of toxic organic compounds by converting into non-toxic simpler products, often carbon dioxide and water. The presence of numerous diverse bacteria, fungi and other microbes in nature play an important role in expanding the variety of chemical pollutants that can be degraded, by this means clean the sites polluted. Various microorganisms have been reported in industrial effluent or nearby places by many researchers. For instance, Sarnaik and Kanekar (1995) isolated four species, characterized as *Pseudomonas*, namely *P. stutzeri*, *P. putida* biovar B, *P. mendocina* and *P. alcaligenes* from the soil samples of the factory manufacturing methyl violet, nearby Pune. There was a reduction and also change in number of *Pseudomonas* species from soil samples collected from the location of a dye factory. Kousar *et al.* (2000) isolated 8 different bacterial and 23 different fungi species from textile polluted habitats and reported *Aspergillus* among the fungi, tobe the most dominant genus. Oved *et al*. (2001) investigated the impact of effluent irrigation on community composition and function of Ammonia-Oxidizing Bacteria (AOB) in soil, using molecular biology and analytical soil chemistry. Result showed a constant and significant shift in the population composition of AOB in soil irrigated with effluent. Keeping in view the probability of finding different microorganisms in industrial effluents, present research work was conducted to study different microbial population and effects of industrial effluent on microbial population with varying concentrations of effluents.

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Methods

Effect of textile industry waste water on soil microbial population under laboratory conditions

To study the effect of textile industrial waste water on soil microbial population, a laboratory experiment was conducted with following treatments -

T1: Soil + 0% waste water (soil + water)

T2: Soil + 10% waste water (waste water: water :: 1:9)

T3: Soil + 20% waste water (waste water: water :: 2:8)

T4: Soil + 50% waste water (waste water: water :: 5:5)

T5: Soil + 100% waste water (undiluted)

For each treatment, 500 g of soil was taken in plastic boxes and amended with different concentrations of waste water to maintain 60% of full water holding capacity. Soil samples from each treatment were withdrawn at 0, 30, 60 and 90 days of incubation for enumeration of microbial population.

Enumeration of microorganisms

Soil samples were analyzed to enumerate total bacterial count, fungi, actinomycetes and free living diazotrophs by using serial dilution and spread plate method. Ten grams of each soil sample was suspended in 90 ml of sterile distilled water and kept on a rotary shaker for about 30 minutes so that microorganism adhered with soil particles get suspended uniformly into the water. Serial dilutions were made in 9 ml water blanks and 0.1 ml of appropriate dilution was spread on specific media (*i.e.* Kenknight Munaier's medium, Martin's Rose Bengal agar medium, nutrient agar medium and Jensen's nitrogen free agar medium to count actinomycetes, fungi, bacterial colony and free living diazotrophs, respectively) in triplicate. The plates were incubated at 28 ± 2°C till visible colonies appeared and number per gram of dry soil was calculated. The colonies of microorganisms appeared on the plates were counted- following standard method (Pramer and Schmidt, 1964).

Effect of textile industry waste water on soil microbial population

Effect of different concentrations of textile waste water was studied on total bacterial, fungal, actinomycetes and diazotrophs populations under laboratory conditions. Soil amended with different concentrations of textile waste water was incubated at 30ºC for 90 days by maintaining moisture level to 60% of water holding capacity in a BOD incubator. Sub samples of soil were withdrawn at 0 day and after 30, 60 and 90 days for determining total bacterial, fungal, actinomycetes and diazotrophs counts on their respective media.

Results and Discussion

It was found that with increase in waste water concentration and incubation time the viable count of bacteria, actinomycetes, diazotrophs and fungal counts were affected.

Effect of textile industry waste water on total bacterial population

Table 1 shows the effect of amendment of different concentrations of textile waste water on bacterial population which varied from 55 to 220×10^6cfu g^{-1} dry soil. Initially, the bacterial count was 56×10^6cfu g^{-1} dry soil, which increased with textile waste water amendment upto 60 days and declined further. Also, with increasing the concentration of textile waste water upto 20%, an increase in bacterial count was observed which decreased with increasing the concentration of the waste water. There was a significant difference in bacterial population with the amendment of different concentrations of textile waste water and at different incubation time. A significant increase in bacterial population was observed up to 20% of textile waste water amendment and at 60 days of incubation.

Effect of textile industry waste water on total actinomycetes population

Table 2 represents actinomycetes count which varied from 35 to 75×10^2cfu g^{-1} dry soil at different waste water concentrations and incubation time. A numerical change in actinomycetes count was observed at different incubation time and different concentration of waste water. However, a significant decrease in actinomycetes count was observed with increasing waste water concentration from 20 to 100% at 30 and 90 days of incubation.

Effect of textile industry waste water on total fungal population

As shown in Table 3, the fungal population varied from 40×10^4 to 79×10^4cfu g^{-1} dry soil with different waste water concentrations and incubation time. Initially, cfu of fungi were 48×10^4 g^{-1} dry soil, which increased with the amendment of different concentration of textile waste water. The difference in fungal population with the amendment of 10 and 20% textile waste water at 30 and 60 days was non-significant. However, a significant increase in fungal population was observed upto 20% of textile waste water amendment at 30, 60 and 90 days, as compared to control, which declined with increasing textile waste water upto 100% level.

Effect of textile industry waste water on total free living diazotrophs population

Table 4 shows the effect of different concentrations of waste water on free living diazotrophs in soils amended with different textile waste water concentration at 30, 60 and 90 days of incubation. The cfu of diazotrophs varied from 18 to 49×10^1cfu g^{-1} dry soil at different concentration of textile waste water and incubation time. The higher level of textile waste water had inhibitory effect on diazotrophs count, which declined significantly at higher concentration of textile waste water.

Conclusion

During the present investigation, effect of different concentrations of textile industry waste water on microbial population was determined by standard plate count technique. After 60 days of incubation, total bacterial, actinomycetes, diazotrophs and fungal population increased significantly upto 20% concentration of textile waste water amendments and then declined on further incubation showing that at initial stages of incubation, textile waste water was being utilized as nutritive source upto 20% but on further increasing the waste water concentration from 20 to 100%, it imposes its toxic effect on total microbial population of soil. It is concluded that concentrations of salts increase with repeated irrigation of soils with textile waste water and will ultimately affect the microbial population. So direct application of textile waste water may be avoided or may be amended after its treatment.

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Table 1: Effect of different concentrations of textile industry waste water on total bacterial population

Textile waste water Concentration (%)	Bacterial count ($\times 10^6$ cfu g^{-1} dry soil)		
	Days		
	30	60	90
0	62	65	55
10	113	190	135
20	125	220	160
50	74	130	85
100	55	65	60
CD at 5% level	8	6	12

Initial bacterial count = 56×10^6 cfu g^{-1} dry soil

Table No 2: Effect of different concentrations of textile industry waste water on total actinomy cetes population

Textile waste water Concentration (%)	Actinomycetes count ($x10^2$ cfu g^{-1} dry soil)		
	Days		
	30	60	90
0	48	54	50
10	52	68	58
20	58	75	65
50	42	52	48
100	35	40	38
CD at 5% level	6	8	7

Initial actinomycetes count = 46 $x10^2$ cfu g^{-1} dry soil

Table 3: Effect of different concentrations of textile industry waste water on total fungal population

Textile waste water Concentration (%)	Fungal count ($x10^4$ cfu g^{-1} dry soil)		
	Days		
	30	60	90
0	48	56	51
10	65	69	62
20	68	79	66
50	42	52	46
100	40	45	38
CD at 5% level	9	8	7

Initial fungal population= 48×10^4 cfu g^{-1} dry soil

Table 4: Effect of different concentrations of textile industry waste water on total free living diazotrophs population

Textile waste water Concentration (%)	Diazotrophs count ($x10^1$ cfu g^{-1} dry soil)		
	Days		
	30	60	90
0	19	24	18
10	34	36	26
20	38	49	31
50	32	36	24
100	18	20	17
CD at 5% level	5	7	6

Initial diazotrophs count = 22×10^1 cfu g^{-1} dry soil