

## ABSTRACT

Bioremediation is an environmentally benign, economical and easiest technique to get rid of the increasing pollution now-a-days. Bioremediation deals with the application of indigenous microflora to reduce the threats to ecosystem. Present study was designed to achieve a better confirmation about bioremediation through decolorization and degradation of textile industry effluents. Wastewater samples were taken from the wastewater discharge points of Nishat Textile Mill and were evaluated for their physicochemical properties to measure the potential of pollution parameters. Water samples were then subjected to bacterial isolation. Two categories of bacteria i.e. halophilic and halotolerant bacteria were isolated through TSB medium having some specified amounts of salts and cultures of isolated bacterial species were maintained on agar plates. Isolated bacteria were further tested for their dye decolorizing potential against Reactive Black-5, Reactive Red-120, Reactive Orange-16 and Reactive Green-19. Reactive azo dyes were selected for their notorious chemically stable nature and harmful effects on aquatic ecosystem. Dyes were tested at different concentrations i.e. 100 ppm, 200 ppm, 500 ppm and 1000 ppm. Halophilic bacterial isolates gave excellent results at 100 and 200 ppm for all the dyes under study but halotolerant bacteria were less capable in that regard. 10 halophilic and 10 halotolerant bacteria were isolated. Out of 20 isolates 9 halophilic isolates and 4 halotolerant isolates that proved themselves very best for decolorization, were selected for consortium development. Three consortia were made and decolorization was investigated. For decolorization optimum conditions were also investigated i.e. 7.2 pH, 34°C temperature and 100 ppm concentration in aerobic condition under shaking incubation (48 h) was the best one. Decolorization was further confirmed by TLC analysis and biodegradation was confirmed through GC-MS analysis. TLC analysis revealed presence of some aromatic amines of unknown identity. GC-MS characterization exhibited numerous peaks for decolorized and degraded sample pointing towards successful break down of reactive azo dyes into smaller fragments of non-toxic and harmless nature. 16S rRNA analysis disclosed that isolate 1 and 4 showed 98% homology with *Bacillus cereus* and isolate 2, 5 and 6 showed 99% homology with *Bacillus subtilis*.