

ABSTRACT

The Bioremediation potential of bacterial isolates retrieved from local industrial effluent samples was assessed to determine the potential of isolates and consortia to biodegrade the fiber reactive azo dyes. The Effluent samples were collected from discharge site of Al-Qaim dyeing industries, Al-Hammad Textile Mills and Ali Raza textile Mills situated on Lahore-Sheikhupura road. Samples were collected from Source point, mid point and discharge point of industries and were named after their collection site. The physico-chemical parameters like temperature, pH, EC, BOD, COD, appearance, texture, odour, TDS, TSS, DO, Turbidity, Salinity and bacterial count of effluents were determined in order to assess the amount of contaminants present in them.

Bacterial isolates from effluent samples were retrieved by serial dilution method. Lysogeny Broth (LB) medium was employed to isolate and screen bacteria on regular basis by streaking and spread plate method. By this procedure, 20 bacterial isolates were retrieved and were used to test the degradation of four fiber reactive azo dyes namely Reactive Red 120, Reactive Green 19, reactive Orange 16 and Reactive Black 5. Biochemical characterization of bacterial isolates was carried out to check the presence of different enzymes like catalase, oxidase, protease and nitrate reduction enzymes. The dyes were tested at different concentrations i.e. 100ppm, 200ppm, 500ppm, 1000ppm and 1500ppm and were selected because of their destructive and hazardous effects on aquatic fauna and flora. The growth parameters i.e. pH, temperature and dye concentration was optimized to determine the optimum conditions for decolorization. All the 20 isolates proved good for decolorizing the media containing the reactive dyes and showed >80% decolorization. These isolates were used to develop consortia and check their decolorization potential for the dyes.

The degradation of dyes was confirmed by using various chromatographic techniques including TLC and GC-MS. Phytotoxicity test was carried out for *Triticum aestivum*, *Vigna radiata* and *Brassica juncea* in order to assure that degraded products were non-toxic in nature. The 20 retrieved isolates were identified using 16S rRNA sequencing technique which clearly showed that the isolates belonged to bacterial genus *Bacillus*, *Pseudomonas*, *Streptococcus*, *Staphylococcus* and *Salmonella*. Of all the 20 isolates, Isolate 8, 11 and 19 showed 99% homology with *Bacillus subtilis*, Isolate 2 and 6

showed 99% homology with *Bacillus cereus*. Isolate 3 and 4 showed 99% homology with *Bacillus pumilus*, Isolate 17 and 20 showed 99% homology with *Pseudomonas aeruginosa*, Isolate 15 and 16 showed 99% homology with *Pseudomonas fluorescens*, Isolate 14 and 18 showed homology to Genus *Staphylococcus* while Isolate 12 and 13 showed homology to Genus *Streptococcus*. Isolate 1, 5 and 9 showed homology to Genus *Bacillus* while isolate 7 and 10 showed homology to Genus *Salmonella* and *Pseudomonas* respectively.