

ABSTRACT

There is an utter necessity to endorse a sustainable progress for humanity with an ecofriendly influence. The present study was an endeavor to deal with the applications of indigenous bacterial flora in the form of isolated strains and consortia to lessen the intimidations of pollution to ecosystem. The study was intended to achieve a healthier endorsement about the process of bioremediation dealt with textile industry effluents. Wastewater samples were collected from the discharge points of a textile industry near Hudiara Drain, 22-Km off from Ferozpur Road Lahore. Five samples were selected namely PD, 1m, 5m, 10m and 100m based on the discharge points of desizing, bleaching, mercerizing, dyeing and finishing sectors of textile industries respectively. The effluent samples were assessed for their physicochemical parameters to estimate the amount of contamination present in the wastewater before and after the experiment. Through serial dilution method, water samples were exposed to bacterial isolation. Indigenous bacteria were screened and isolated through LB medium and the culture was maintained on regular basis. Isolated bacteria were tested against five textile azo dyes namely Direct blue 1 (DB-1), Direct green 6 (DG-6), Mordant yellow 1 (MY-1), Mordant black 11 (MB-11) and Mordant black 17 (MB-17). These textile azo dyes were selected for their consistent nature and destructive effects on the water environment. Dyes were taken at different concentrations i.e. 100ppm, 200ppm, 500ppm, 1000ppm and 1500ppm. All selected bacterial isolates provided exceptional results at 100ppm, 200ppm and 500ppm concentrations for all dyes under study. Thirteen bacterial isolates were isolated and all proved that they are good for decolorizing ability (>75%). All five consortia yielded 85%+ result against all five dyes at given concentrations. Degradation of dyes was additionally confirmed by TLC and GC-MS analysis. Through 16S rRNA sequencing technique, it was clearly showed that out of 13 isolates selected, seven belonged to bacterial genus *Bacillus* and *Pseudomonas*. Isolate 2 and 6 showed 99% homology with *Bacillus thurengensis*. Isolate 3, 5 and 11 exhibited 99% homology with *Bacillus subtilis*. Isolate 4 and 8 presented 99% homology with *Pseudomonas putida*.