

Isolation, Selection and Identification of Bacteria for Bioaugmentation of Paper Mills White Water

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Abstract : Objectives: White water circuits of woodfree paper mills contain suspended, dissolved, and colloidal particles, such as cellulose, starch, paper sizings, and dyes. By closing the white water circuits, these particles start to accumulate and affect the production. Due to high amount of organic matter that scavenge radicals and adsorbs onto catalyst surfaces, treatment of white water with photocatalysis is inappropriate. The most suitable approach should be bioaugmentation-assisted bioremediation. Accordingly, objectives were: - to isolate bacteria capable of degrading organic compounds used for the papermaking process - to select the most active bacteria for bioaugmentation. Status: The state-of-the-art of bioaugmentation of pulp and paper mill effluents is mostly based on biodegradation of lignin. Whereas in white water circuits of woodfree paper mills only papermaking compounds are present. As far as one can tell from the literature, the study on degradation activities of bacteria for all possible compounds of the papermaking process is a novelty. Methodology: The main parameters of the selected white water were systematically analyzed during a period of two months. Bacteria were isolated on selective media with particular carbon source. Organic substances used as carbon source either enter white water circuits as base paper or as recycled broke. The screening of bacterial activities for starch, cellulose, latex, polyvinyl alcohol, alkyl ketene dimers, and resin acids was followed by addition of lugol. Degraders of polycyclic aromatic dyes were selected by cometabolism tests; cometabolism is simultaneous biodegradation of two compounds, in which the degradation of the second compound depends on the presence of the first. The obtained strains were identified by 16S rRNA sequencing. Findings: 335 autochthonous strains were isolated on plates with selected carbon source. The isolated strains were selected according to degradation of the particular carbon source. The ultimate degraders of cationic starch, cellulose, and sizings are *Pseudomonas* sp. NV-CE12-CF and *Aeromonas* sp. NV-RES19-BTP. The most active strains capable of degrading azo dyes are *Aeromonas* sp. NV-RES19-BTP and *Sphingomonas* sp. NV-B14-CF. *Klebsiella* sp. NV-Y14A-BTP degrade polycyclic aromatic direct blue 15 and also yellow dye, *Agromyces* sp. NV-RED15A-BF and *Cellulosimicrobium* sp. NV-A4-BF are specialists for whitener and *Aeromonas* sp. NV-RES19-BTP is general degrader of all compounds. To the white water adapted bacteria were isolated and selected according to their degradation activities for particular organic substances. Mostly isolated bacteria are specialized to lower the competition in the microbial community. Degraders of readily-biodegradable compounds do not degrade recalcitrant polycyclic aromatic dyes and vice versa. General degraders are rare.

Keywords : bioaugmentation, biodegradation of azo dyes, cometabolism, smart wastewater treatment technologies

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