## Algal/Bacterial Membrane Bioreactor for Bioremediation of Chemical Industrial Wastewater Containing 1,4 Dioxane

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Abstract : Oxidation of 1,4 dioxane produces metabolites by-products involving glycolaldehyde and acids that have geno- and cytotoxicity impact on microbial degradation. Thereby, the incorporation of algae with bacteria in the treatment system would eliminate and overcome the accumulation of metabolites that are utilized as a carbon source for the build-up of biomass. Therefore, the aim of the present study is to assess the potential of algae/bacteria-based membrane bioreactor (AB-MBR) for biodegradation of 1,4 dioxane-rich wastewater at a high imposed loading rate. Three identical reactors, i.e., AB-MBR1, AB-MBR2, and AB-MBR3, were operated in parallel at 1,4 dioxane loading rates of 641.7, 320.9, and 160.4 mg/L. d., and HRTs of 6.0, 12 and 24 h. respectively. The AB-MBR1 achieved 1,4 dioxane removal rate of 263.7 mg/L.d., where the residual value in the treated effluent amounted to 94.4±22.9 mg/L. Reducing the 1,4 dioxane loading rate (LR) to 320.9 mg/L.d in the AB-MBR2 maximized the removal rate efficiency of 265.9 mg/L.d., with a removal efficiency of 82.8±3.2%. The minimum value of 1,4 dioxane of 17.3±1.8 mg/L in the treated effluent of AB-MBR3 was obtained at an HRT of 24.0 h and loading rate of 160.4 mg/L.d. The mechanism of 1,4 dioxane degradation in AB-MBR was a combination of volatilization (8.03±0.6%), UV oxidation  $(14.1\pm0.9\%)$ , microbial biodegradation (49.1±3.9%) and absorption/uptake and assimilation by algae (28.8±2.%). Further, the Thioclava, Afipia, and Mycobacterium genera oxidized and produced the required enzymes for hydrolysis and cleavage of the dioxane ring into 2-hydroxy-1,4 dioxane. Moreover, the fungi, i.e., Basidiomycota and Cryptomycota, played a big role in the degradation of the 1,4 dioxane into 2-hydroxy-1,4 dioxane. Xanthobacter and Mesorhizobium were involved in the metabolism process by secreting alcohol dehydrogenase (ADH), aldehyde dehydrogenase (ALDH), and glycolate oxidase. Bacteria and fungi produced dehydrogenase (DH) for the transformation of 2-hydroxy-1,4 dioxane into 2-hydroxy-ethoxyacetaldehyde. The latter is converted into Ethylene glycol by Aldehyde hydrogenase (ALDH). Ethylene glycol is oxidized into acids using Alcohol hydrogenase (ADH). The Diatomea, Chlorophyta, and Streptophyta utilize the metabolites for biomass assimilation and produce the required oxygen for further oxidation of the dioxane and its metabolites by-products of bacteria and fungi. The major portion of metabolites (ethylene glycol, glycolic acid, and oxalic acid were removed due to uptake and absorption by algae  $(43\pm4.3\%)$ , followed by adsorption (18.4 $\pm0.9\%$ ). The volatilization and UV oxidation contribution for the degradation of metabolites were 8.7±0.7% and 12.3±0.8%, respectively. The capabilities of genera Defluviimonas, Thioclava, Luteolibacter, and Afipia. The genera of Defluviimonas, Thioclava, Luteolibacter, and Mycobacterium were grown under a high 1,4 dioxane LR of 641.7 mg/L.d. The Chlorophyta (4.1-43.6%), Streptophyta (2.5-21.7%), and Diatomea (0.8-1.4%) phyla were dominant for degradation of 1,4 dioxane. The results of this study strongly demonstrated that the bioremediation and bioaugmentation process can safely remove 1,4 dioxane from industrial wastewater while minimizing environmental concerns and reducing economic costs.

1

Keywords : wastewater, membrane bioreactor, bacterial community, algal community

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