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Bisphenol A And Bisphenol S Biodegradation In The River Water-Sediment Microcosms And Their Impact On The Biodiversity Of Autochthonous Microbial Community

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Extended Abstract

The concept of the study resulted from numerous concerns around bisphenol A (BPA) and bisphenol S (BPS) in aquatic environments. Previous works demonstrated that bioaugmentation with a pollutant-degrading consortium consisting of two or more microbial species was more effective in removing pollutants than with only a single strain. This effect relies on the fact that intermediates of one strain's catabolic pathway may be further utilized by other strains possessing the desired enzymes. Therefore, in this work, we used a BPA and BPS degrading bacterial consortium formed by *Pseudomonas* sp. BG12 and *Acinetobacter* sp. K1MN to amend river water-sediment microcosms polluted with these BPs. We aimed to (1) assess BPA and BPS biodegradation rates in created microcosms bioaugmented with the consortium during 70-day lasting experiment; (2) monitor the bacteria survival during the incubation period; (3) identify responses of the dominant bacterial community to bioaugmentation and BPs' presence; (4) determine the core-indigenous microorganisms from water and sediment and their enzymes involved in BPS degradation. The effect of bioaugmentation of water-sediment microcosms with the consortium on BPA and BPS removal was assessed. Statistical analysis of obtained data showed significant differences ($p<0.05$) both between the time of sampling points and microcosms. BPA was removed from created microcosms within 40 days. The amount of BPS continuously decreased in all microcosms over the experimental time, but it was still detected in all microcosms at the 70th day of the experiment. Since the introduced consortium did not survive in tested treatments, BPs biodegradation was due to the activity of indigenous microflora. However, introduced bacterial strains can act as biofertilizers and stimulate changes in the composition and structure of an indigenous bacterial community. These changes were observed in our experiment. On day 35, the predominance of *Thiobacillus, Dyella,* and *Hyphomicrobium* were detected in created microcosms. The abundance of reads belonging to the *Pseudomonas* and *Acinetobacter* genera detected on day 35 was very low. Compared to day 35, different composition of bacterial communities in analyzed microcosms was observed on day 70. The predominance of the genus *Thiobacillus, Rhodanobacter, Dyella, Hyphomicrobium,* and *Parvibaculum* were observed. For *Mesorhizobium*, *Achromobacter,* and *Mycobacterium*, PICRUSt2 assigned metabolic pathways based on the calculated OTUs. The presence of protocatechuate and catechol degradation pathways were assigned for *Achromobacter* and *Mycobacterium*, while for *Mesorhizobium* only the catechol degradation pathway was identified. The relative number of OTUs assigned to these pathways was higher on day 35 than on day 70. In contrast, the relative number of OTUs assigned to the protocatechuate degradation pathway identified for *Mycobacterium* was higher at day 70 than 35. This study provides new insights into the effects of bioaugmentation with a bacterial consortium on bacterial diversity and BPs degradation in aquatic environments.