
Aerobic biodegradation of bisphenol A with microbial consortium from e-waste contaminated river sediment

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Abstract

Bisphenol A (BPA) is a synthetic chemical primarily used to produce polycarbonate plastics and epoxy resins, which are used as food-contact surface coatings for consumer goods, including reusable bottles, sports equipment and protective coatings. Mass consumption of BPA-containing products has contributed to the widespread contamination of BPA in various environments. Due to BPA's estrogenic and genotoxic effects on both human beings and other organisms, it has become one of the major environmental concerns. In the natural environment, biodegradation plays a major role in elimination of BPA, but the information on the structure of BPA-degrading microbial community is still lacking. In this work, microcosms with different treatments were constructed to investigate the biodegradation of BPA, and the response microbial community structure in e-waste contaminated river sediment and its change character was also investigated during BPA biodegradation. The results found BPA could be quickly depleted by the bioaugmentation with *Bacillus* sp. GZB in the e-waste contaminated river sediment under aerobic condition. Furthermore, BPA biodegradation was enhanced by adding co-substrates, such as glucose, yeast extract, humic acid and sodium chloride, especially by glucose and yeast extract. Metagenomic analysis of total 16S rRNA genes from BPA-degrading microcosms with bioaugmentation showed that *Bacillus* (13.43-33.39%), *Flaviumibacter* (0.46-3.83%), *Ochrobactrum* (0.31-6.74%) and *Dyella* (3.10-10.69%) were dominant genera, and a consortium of microorganisms from different microbial genera might be involved in BPA biodegradation in e-waste contaminated river sediment. This study provides some new insights towards BPA biodegradation and microbial ecology in BPA-degrading environment.

Keywords: Bisphenol A, Biodegradation, Bmicrobial community, Metagenomic analysis, Sediment

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