Microbial Degradation of Polybrominated Diphenyl Ethers: Current and Future

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Polybrominated Diphenyl Ethers (PBDEs) are flame retardants that have been detected and used in a wide variety of products for their fire retardant properties. They are detectable in the environment because of their global distribution and persistence. Their metabolites accumulate in tissues due to their environmental half-lives, and have been found in humans, animals, and the environment. PBDEs have been identified in wastes, both industrial and municipal, in environmental media, and in human breast milk.

PBDEs are degraded primarily by aerobic and anaerobic bacteria [9-12]. In a word, less-brominated congeners are the main products of PBDEs biodegradation in oxygen-free environment, i.e. reductive debromination is the mechanism of PBDEs anaerobic microbial degradation [8], which is similar to photodegradation and nanoscale zero-valent iron degradation of PBDEs [13,14]. However, in contrast to other degradation methods, selectivity of PBDE anaerobic degradation was observed in many studies. For example, Dehalococcoides-containing cultures can transform an octa-BDE mixture to a variety of hepta- through di-BDEs, but none of these cultures could debrominate deca-BDE [15]. In addition, Qiu et al. [16] studied the effects of electron donors on anaerobic microbial debromination of PBDEs, and found that the percentage of BDE-209 was decreased by 12% (methanol), 11% (ethanol), 8% (acetate), 9% (lactate), 5% (pyruvate), and 11% (no electron donors), meanwhile the microbial community structure was highly correlated with the concentration of BDE-209. Yen et al. [11] reported the change of bacterial communities caused by the variety of PBDE congeners in degradation system. These results indicated that anaerobic degradation of PBDEs in the environment was controlled by the comprehensive effect of microbial community structure, concentration and homologue composition of PBDEs, and electron donors. However, the mechanism of this comprehensive effect is not clear at present.

Meanwhile, PBDEs can also be degraded by aerobic microbes. Currently, only Sphingomonas sp. (SS3, SS33, PH-07) [7-19], white-fruit fungi (Trametes versicolor SBUG 1050, DSM 11269 and DSM 11309, and GIM 3.383) [20,21], Rhodococcus (ostrii RHA1 and sp. RRI), Burkholderia xenovorans LB400, Pseudonocardia dioxanivorans CB1190 [22], Lysinibacillus fusiformis DB-1 [23], Sphomonas (sp., stutzeri BFR01) and Bacillus sp. [24,25], and other unnamed soil microbes [26], were reported having ability to degrade PBDEs. The metabolic products were hydroxylated brominated diphenyl ethers, brominated phenols, brominated catechols and bromide ion, which were different from PBDEs metabolites from anaerobic biodegradation. Moreover, for PBDEs with three or more bromines, the pathway of aerobic biodegradation has not yet been clearly delineated in the literature. Furthermore, the function gene and enzyme involved in the degradation should be investigated in detail.

Thus, further study should be focused on: (1) detecting aerobic biodegradation products of PBDEs, and proposing their pathway; (2) detecting enzymes involving in the anaerobic and aerobic degradation of PBDEs, and finding the genes controlling the process of biodegradation; (3) computing the properties of PBDEs, and establishing the relationship between these properties and the biodegradation pathway of PBDEs; (4) screening some species of exclusive bacteria for anaerobic and aerobic degradation of PBDEs, forming some rules of thumb, and applying them into natural environment, and establishing in situ bioremediation of environments contaminated by PBDEs.

References

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