

sustainable strategies to address the plastic disposal issue and the recovery of harmed natural environments in order to preserve both human and wild lives.

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### 356A - Genome sequence analysis of dibenzofuran degrading bacteria

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Agent Orange containing dioxin compounds, which were sprayed during the Vietnam war, has gravely damaged the environment and caused a wide range of serious health problems. Microorganisms play important roles in the degradation of these hazardous compounds in natural environments. It is therefore important to screen indigenous microorganisms capable of dioxin degradation for using them in bioremediation of these contaminated sites. The soil samples collected from A Luoi district in the central of Vietnam, of which the levels of 2,3,7,8-tetrachlorodibenzo-*p*-dioxin were 20-21 pg/g-dry matter (10-fold of average value monitored in Japan), were used for the isolation of dioxin degraders via enrichment culture with dibenzofuran. We isolated two dominant *Paenibacillus* sp. strains (4B1 and 1-10), a moderate thermophile and a mesophile, respectively, which showed faster growth than another dibenzofuran-degrading bacterium *Paenibacillus* sp. strain YK5. To understand characteristics of their dibenzofuran degradation pathways, their draft genome sequences were determined by MiSeq (Illumina). Isolated *Paenibacillus* genomes contain at least 11 putative genes involved in dibenzofuran degradation. Their putative degradative pathways were initiated with hydroxylation at the angular position of dibenzofuran, then *meta*-cleaved 2,2',3-trihydroxybiphenyl to generate salicylate and 2-hydroxypenta-2,4-dienoate. Subsequently, salicylate could be metabolized by following gentisate metabolic pathway. Furthermore, reverse transcription-PCR analysis of *dbf* genes revealed that these dibenzofuran degradative genes were partially induced by dibenzofuran. Our findings provide valuable insights into the mechanism of these two DF degraders, which might facilitate the application of them in bioremediation of contaminated sites.

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### 357A - Fungal biosorption of uranium using newly isolated *Cladosporium* sp. strain F1

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Biosorption of uranium from various environments has been focused because of its high toxicity and radioactivity. The use of fungal biomass such as *Aspergillus niger*, *Penicillium* spp., *Saccharomyces cerevisiae*, or *Talaromyces emersonii* has been studied for the biosorption of uranium. For the first time, we report a biosorption capability of uranium by using genus *Cladosporium*, the common fungus in indoor and outdoor air. *Cladosporium* sp. strain F1, revealed by internal transcribed spacer (ITS) sequence analysis, was newly isolated in our laboratory. The adsorption of uranyl ions (UO<sub>2</sub>)<sup>2+</sup> and uranium-phosphate nanoplates on the cell surfaces of *Cladosporium* sp. strain F1 was observed and optimized regarding the parameters such as pH, temperature and the presence of heavy metals in aqueous solution. The