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主　論　文　の　要　旨

論文題目 Molecular and physiological characterization of dehalorespiring microbial communities
（脱ハロゲン呼吸微生物群集の分子生物学的および生理学的特性）

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論　文　内　容　の　要　旨

Tetrachloroethene (PCE) and 1,1,2-trichloroethane (112-TCA) are suspected carcinogens and widespread groundwater contaminants that are reductively dechlorinated to either toxic or benign end products by organohalides respiring bacteria (OHRB). This study successfully established both PCE and 112-TCA dechlorinating consortia. The first consortium (named YN3 culture) dechlorinated PCE into non-toxic ethene (ETH) by reductive dechlorination, while the other (named KJ-TCA culture) dechlorinated 112-TCA by dichloroelimination to vinyl chloride (VC), the proven carcinogen. Illumina amplicon analysis indicated the presence of *Dehalococcoides* and *Dehalobacter* as the potential dechlorinators in YN3 and KJ-TCA cultures, respectively. YN3 culture dechlorinated up to 800 μM PCE to ETH within only 14 days. This activity indicated a potential application of YN3 culture to the

bioremediation of the groundwater contaminated with PCE and other chloroethenes (CEs). YN3 metagenome analysis showed the presence of 18 *rdhA* genes (designated *YN3rdhA1–18*) encoding the catalytic subunit of reductive dehalogenase (RdhA), the key enzyme in the reductive dechlorination. Of these 18 *YN3rdhA* genes, four genes were suggested to be involved in the dechlorination of PCE to ETH, based on the significant increases in their transcription levels in response to the addition of CEs. In these four *rdhA* genes, two *rdhAs*, *YN3rdhA6* and *YN3rdhA12*, were never proved before as *rdhA* to be involved in the dechlorination CEs. The *YN3rdhA6* and *YN3rdhA12* genes showed particularly high transcription level upon the addition of VC, suggesting their involvements in the VC dechlorination as novel *rdhA* genes. The metagenome data also indicated the existence of three bacteria taxa belonging to phyla *Bacteroidetes*, *Actinobacteria* and *Firmicutes*. Moreover, analysis of YN3 metagenome indicated that the metagenome of *Bacteroidetes* was the largest and represented by a novel species of the genus *Bacteroides*. *Thereafter, the novel species of the genus Bacteroides, designated strain YN3PY1, was isolated from YN3 culture.* The strain enhanced the dechlorination of *cis*-dichloroethene to ETH by C4C4 culture, which is a *Dehalococcoides* enriched culture obtained from YN3 culture, especially at the early stages of cultivation. However, even the enhanced dechlorination activity is still small if compared with the parent culture YN3 culture. This indicated different mechanisms or microbes enhanced the

dechlorination. This study would contribute to the development of bioremediation technology using *Dehalococcoides* as dehalogenator with the enhancement by coexisting bacteria such as *Bacteroides*. This study provides potential candidates for *in situ* bioaugmentation for remediation of sites contaminated with PCE (using YN3 culture) and 112-TCA using (using YN3 and KJ-TCA cultures).