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PII: S0959-6526(18)31711-6

DOI: [10.1016/j.jclepro.2018.06.061](https://doi.org/10.1016/j.jclepro.2018.06.061)

Reference: JCLP 13207

To appear in: *Journal of Cleaner Production*

Received Date: 28 December 2017

Revised Date: 5 June 2018

Accepted Date: 7 June 2018

Please cite this article as: Song J, Chen L, Chen H, Sheng F, Xing D, Li L, Zhang Y, Rittmann B, Characterization and high-throughput sequencing of a trichlorophenol-dechlorinating microbial community acclimated from sewage sludge, *Journal of Cleaner Production* (2018), doi: 10.1016/j.jclepro.2018.06.061.

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# Characterization and high-throughput sequencing of a trichlorophenol-dechlorinating microbial community acclimated from sewage sludge

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## Abstract

This study reports the dechlorination characteristics of acclimated biomass, high-throughput sequencing of the 16S ribosomal RNA (rRNA) gene harbored by the microorganisms, and analysis of the relation between the dechlorination function and community structure. Anaerobic 2,4,6-trichlorophenol (TCP)-dechlorinating biomass was acclimated from active sludge, and it showed a high TCP-dechlorination rate. It dechlorinated TCP only at the *ortho*-position, with 4-chlorophenol as the terminal product. Illumina HiSeq sequencing analyses of a 16S rRNA gene amplicon indicated that the abundance of the phyla Bacteroidetes and Firmicutes doubled in the acclimation process. Compared with that in raw sludge, Betaproteobacteria disappeared from acclimated biomass, and Deltaproteobacteria was replaced by sulfate-reducing bacteria (SRB) including *Desulfobulbus*, *Desulfovibrio*, *Desulfomicrobium*, and *Syntrophus*. *Syntrophomonas* of the phylum Firmicutes predominated (abundance 6.7%), and it was responsible for the high efficacy of dechlorination. Dechlorinators included *Dechloromonas*, *Clostridium*, SRB and *Geobacter*. The emergence of SRB provided microbiological evidence of the sulfate-reducing ability of the dechlorinating biomass. *Propionicimonas* was discovered during this study, and it is known to produce vitamin B<sub>12</sub>, which is an essential factor for reductive dehalogenase enzymes.

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