P-045

Complete genome analysis of a nonylphenol-degrading bacterium *Sphingobium cloacae* JCM10874^T

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Alkylphenols such as nonylphenol (NP) and octylphenol (OP) are known to be endocrine disrupting agents and found as degradation products of industrial detergents, NP- and OPpolyethoxylates, in the natural environment. In an early work by Fuji et al., a bacterium (JCM10874^T) able to degrade NP was isolated from wastewater of a sewage treatment plant in Tokyo and identified as a novel species, Sphingomonas cloacae, later reclassified as Sphingobium cloacae, in the class Alphaproteobacteria. In this study, we analyzed the complete genome sequence of strain JCM10874^T to characterize the NP degradation genes. Genomic DNA of the strain JCM10874^T was sequenced by the PacBio RS II system and annotated using the MiGap, RAST and BLASTP programs. Strain JCM10874^T consists of 3,767,292-bp one circular chromosome, SCLO1 (coverage of 322-folds) with 64.6% G+C content and contains 3,302 coding sequences (CDSs), 6 rRNA operons and 50 tRNA genes, and five circular plasmids, pSCLO2 (375,493bp, 64.9% G+C, 334 CDSs, coverage of 301-folds), pSCLO3 (151,712bp, 62.8% G+C, 137 CDSs, coverage of 340-folds), pSCLO4 (108,910bp, 63.7% G+C, 92 CDSs, coverage of 225-folds), pSCLO5 (57,701bp, 63.5% G+C, 53 CDSs, coverage of 85-folds), pSCLO7 (33,768bp, 62.9% G+C, 33 CDSs, coverage of 32-folds), and a linear plasmid, pSCLO6 (52,690bp, 62.4% G+C, 51 CDSs, coverage of 99-folds). From the genomic analysis, the strain was found to possess the genes encoding octylphenol 4-monooxygenase (opdA), nonylphenol monooxygenase (*nmoA*) and hydroquinone degradation gene cluster. From these genetic analyses, it can be concluded that both OP and NP are transformed to hydroquinone (HQ) and 1,2,4-benzenetriol by opdA and nmoA, thereafter HQ and 1,2,4-benzenetriol are degraded by hydroquinone degradation enzymes. Further analyses are now in progress to compare the degradation genes of another related OP- and NP-degrading bacterium Sphingobium amiense strain YT^T.