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Functional genomics analysis of *Comamonas testosteroni* strain P19 degrading aromatic compounds

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Aromatic hydrocarbons have attracted concern as a kind of environmental pollutants along with possible health threats. *Comamonas testosteroni* strain P19 was originally isolated as a biphenyl degrader and capable of degrading several aromatic compounds as a sole source of carbon and energy. Here, we describe the metabolic insight by genetic and physiological analysis indicating how aromatic compounds are metabolized in *C. testosteroni* strain P19. The strain has a circular chromosome of 5,633,218 bp with a G+C content of 67.65% and one plasmid. The annotation identified gene clusters encoding essential proteins for metabolizing several aromatic hydrocarbons including anthranilate, benzoate, biphenyl, m-hydroxybenzoate, p-hydroxybenzoate, p-methoxybenzoate, phenol, phthalate, protocatechuate, terephthalate etc. Random plasposon mutagenesis confirmed that the predicted gene clusters were essential in the metabolic pathways of the compounds. In addition, we identified novel metabolite on degradation of ferulate which had very similar structure to vanillate. Based on structural assignment, the unknown product was revealed as a dimer of vanillate that was a novel intermediate in ferulate degradation pathway. Subsequently, genomic approach suggested the metabolic network of aromatic compounds in *C. testosteroni* strain P19.

Biography

Jong-Chan Chae has completed his PhD from Chungbuk National University and Postdoctoral studies from Rutgers University. He is Vice Dean of College of Environmental & Bioresource Sciences, Chonbuk National University. He has been serving as an Editorial Board Member of "Journal of Microbiology and Biotechnology".

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