A genomic analysis of the catabolism of aromatic compounds in *Azospirillum brasilense* SR80

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Key message. We performed a genomic analysis of the presence and organization of oxygenases involved in the hydroxylation of various substrates, including the aromatic ring, and dioxygenases catalyzing a ring-cleavage of the formed hydroxylated intermediates in *A. brasilense* SR80.

Keywords: *Azospirillum brasilense* SR80, genomic sequence analysis, hydroxylated dioxygenases, extradiol dioxygenases, metabolic pathways of aromatic compounds

A. brasilense SR80 showed degradation ability toward petroleum (Muratova et al., 2005), however the molecular mechanisms of aromatic degradation in SR80 are unclear. On the other hand, we are understanding, that many evolution processes have occurred allowing bacteria to adapt and survive in rhizosphere riching of complex aromatic molecules.

In this study, a detailed genomic analysis was performed to identify of the presence, organization and genomic surround among oxygenase-encoding genes involved in aromatic catabolism in the *A. brasilense* SR80.

The draft genome sequence has been assembled, annotated and deposited to GenBank (accession number QXHE000000000.1). Well-characterized key oxygenase sequences from Protein Data Bank (<https://www.rcsb.org/>) were used to search for orthologous sequences. Genomic search of catabolic dioxygenase-encoding genes of four main pathways (catechol, protocatechuate, gentisate and homogentisate) and their peripheral reactions was carried out. Benzoate 1,2-dioxygenase (BenDO), 3-hydroxybenzoate-6-hydroxylase (Mhb6H), nitronate monooxygenase (YrpB), cytochrome P450 (CYP), phthalate 4,5-dioxygenase (PhtDO), aminomethyltransferase (VanOD), *p*-cresol methylhydroxylase (PchH), four markers of the 2OG-Fe oxygenase superfamily (II) and other are represented in genome as nonspecific hydroxylating oxygenases.

The strain SR80 harbored of ring-cleaving extradiol dioxygenases – 4,5-DOPA dioxygenase (LigB), protocatechuate 4,5-dioxygenase subunits alpha and beta (LigAB), type I extradiol dioxygenases, 2,5-dihydroxypyridine 5,6-dioxygenase (NicX), and various transcriptional regulators and transporters in the degradation pathways.

Bioinformatic analysis showed that, in most cases, plant aromatic components were substrates of SR80 catabolic oxygenases. This research significantly improves our understanding of the biodegradative potential of *A. brasilense* SR80 and demonstrates the importance of aromatic catabolism in plant-bacterial interactions.

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