Expression of Novel Salicylate Oxygenase Genes from a *Sphingomonas* strain in *E.coli*

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Bacterial aromatic-ring dioxygenase is a normally three-component enzyme system, which consists of a flavoprotein reductase, a ferredoxin and an iron sulfur protein (terminal oxygenase). *Sphingomonas yanoikuyae* B1 is unique in that it possesses least six different sets of an iron sulfur protein component, which are apparently associated with a single ferredoxin (BphA3) and a reductase (BphA4) components. Previous studies suggested that the gene for one of the multiple oxygenases (*bphA1cA2c*) is responsible for metabolizing salicylate and 1-hydroxy-2-naphthoate during the degradation of naphthalene and phenanthrene (Kim et al., Abstr. Am. Soc. Microbiol., Q299, p. 470. 1998). To investigate the function of the *bphA1cA2c* gene in more detail, the genes for *bphA1cA2c* and *bphA3* were amplified by PCR, and cloned together into an expression vector. The *Escherichia coli* strain harboring the recombinant plasmid converted salicylate, 3-methylsalicylate, 4-methylsalicylate, or 5-methylsalicylate to catechol, 3-methylcatechol, 4-methylcatechol, or 4-methylcatechol, respectively as confirmed by UV-visible spectral, HPLC, and GC/mass-spectrometric analyses. Furthermore, this expression system was also able to oxidize benzoate, *m*-toluate, or 1-hydroxy-2-naphthoate although the metabolite structures have not been identified yet.