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PCBs Degradation of the Enzyme and its Dynamics

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Polychlorinated biphenyls (PCB) are one of the most polluted compounds. Microorganisms are considered to be the most effective tools to repair the PCB contamination in the environment. In most PCB-degrading bacteria, biphenyl rely on a series of enzymes: such as biphenyl dioxygenase (BphA), dihydro-dihydroxybiphenyl dehydrogenase (BphB), 2,3-dihydroxy-biphenyl-dioxygenase (BphC) and biphenyl hydrolase (BphD), transformed into benzoic acid and 2-hydroxy-pentyl 2,4-dienoic acid. 2,3-the biphenyl dioxygenase catalyzed biphenyl ring adjacent to ortho and meta-positioned carbon atoms to produce 2,3-dihydro-2,3-dihydroxy biphenyl (dDBP). Dihydrodihydroxy intermediate via a dependent NAD+ dehydrogenase transformed to generate 2,3-dihydroxybiphenyl (DHBP), then ring splitting enzyme-catalyzed ring-opening formation of benzoic acid and amyl final BphD spray fracture , 4 - dienoic acid.

Rhodococcus R04 gene (bphBCA1A2A3A4D) respectively encoding 2,3-biphenyl dioxygenase (bphA1A2A3A4), trans-2,3-dihydro-2,3-dihydroxybiphenyl dehydrogenase (bphB), 2,3-dihydroxy-1, 2-biphenyl the dioxygenase (bphC) and 2-hydroxy-6-oxo-6 phenyl-2,4 hexadienoic acid hydrolase (bphD) together to form a gene cluster, which play a large role in the biphenyls' metabolism. The *Rhodococcus* R04 bph gene by bphB pilot, then bphC, bphA1A2A3A4 and bphD. Encoding biphenyl dioxygenase α-subunit and bphC an unknown function of orf2 separate. In addition, the nucleic acid fragment of a 330 and 450 are located between the bphA2, and bphA3, bphA3 and bphA4. These details are unlike other biphenyl degrading bacterium *Rhodococcus* R04 bph gene organization. We purified and described the biphenyl metabolic pathways BphC and BphD and proved that they are the high thermal stability of the enzyme. We, BphD pre-steady state kinetic analysis, and experimental data fitting. The results showed that in the 2-hydroxy-6-oxo-6-phenyl-2,4 adipic acid cracking process, Ser-110 being in the leading position; keto group of His-265 is responsible for the substrate and Ser-110, Trp- The 266 join CC fracture. In the BphD catalytic 2 - hydroxy-6 - oxo-6-phenyl-2 ,4 adipic acid cracking process, in addition to the catalytic triad (Ser-110, Asp-237, His-265) in vitro, Trp-266 also plays an important role.

Our goal is to provide readers with some 2-hydroxy-6-oxo-6-phenyl-2,4 adipic acid cracking process 2,3-dihydroxy-1,2-biphenyl dioxygenase and biphenyl hydrolase horizons, including: i) some dihydroxy -1,2 - biphenyl dioxygenase metabolic regulation of PCBs; ii) biphenyl hydrolase directed evolution; iii) biphenyl hydrolase mutant former state kinetics. We hope to do our utmost concern of data for experts in related fields, but also want to cause more happen to readers some of the concerns.

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