

Identification and characterization of the new enoyl-CoA hydratase in *Pseudomonas putida* KT2442

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Polyhydroxyalkanoates (PHAs) are biodegradable and biocompatible polyesters, which are accumulated in many bacteria when the bacteria face the unfavorable growth conditions. Metabolic pathways involved in PHA biosynthesis have been characterized in many natural PHA producing bacteria¹⁾. Many enzymes have been suggested to be responsible for supplying (*R*)-hydroxyacyl-CoAs, substrates for PHA synthases. Enoyl-CoA hydratase and ketoacyl-CoA reductase are the enzymes most extensively studied for their roles in PHA biosynthesis²⁾. This study reports new enoyl-CoA hydratase in *Pseudomonas putida* KT2442. Through protein database search, another enoyl-CoA hydratase homologous to MaoC was found to exist in *P. putida* KT2442. Enoyl-CoA hydratase MaoC involved in the PHA biosynthesis in *P. putida* KT2442, *Ralstonia eutropha* H16, and *Sinorhizobium meliloti* was identified. Co-expression of the *maoC* gene with medium-chain-length(MCL) PHA synthase gene in *E. coli* W3110 resulted in the production of MCL PHA from fatty acid. This work was kindly supported by a Korean Systems Biology Research Grant (M10309020000-03B5002-00000) of the Ministry of Science and Technology, Center for Ultramicrochemical Process Systems and the BK21 project.

References

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