

Development of short-chain alkane production metabolic pathway in *Escherichia Coli*

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Here we report the development of the platform *Escherichia coli* strain by which short chain alkanes (gasoline), free fatty acids (FFAs), fatty esters, and fatty alcohols are able to be produced through the fatty acyl-ACP to fatty acid to fatty acyl-CoA pathway. The *fadE* gene was deleted to block *beta*-oxidation to secure fatty acyl-CoAs. Promoted *fabH* gene, and deletion of *fadR* gene enhanced short-chain fatty acid biosynthesis. Starting from short-chain FFAs generated by a mutated thioesterase, the sequential reactions of *E. coli* fatty acyl-CoA synthetase, *C. acetobutylicum* fatty acyl-CoA reductase, and *A. thaliana* fatty aldehyde decarbonylase generated 580.8 mg/L of short chain alkanes conclusively. [This work was supported by the Advanced Biomass Research and Development Center of Korea (NRF-2010-0029799) through the Global Frontier Research Program of the Ministry of Science, ICT and Future Planning (MSIP) through the National Research Foundation (NRF). Systems metabolic engineering work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries (NRF-2012M1A2A2026556) by MSIP through NRF].