

A metabolically engineered *E. coli* platform for production of short-chain alkanes

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Although enormous efforts on microbial biofuels productions have been made so far, microbial production of highly demanded transport fuel, such as gasoline, has not yet been demonstrated. In this study a platform *Escherichia coli* strain for the production of short-chain alkanes (gasoline), free fatty acids (FFAs), fatty esters, and fatty alcohols using the fatty acid biosynthesis pathway was developed.  $\beta$ -oxidation was blocked through deletion of *fadE*, preventing degradation of fatty acyl-CoAs. The activity of *fabH*, 3-oxoacyl-ACP synthase, was promoted *fadR* gene deletion, which reduced formation of unsaturated fatty acyl-ACPs. Furthermore, a leaderless *tesA* mutant with improved activity towards short-chain fatty acyl-ACPs was used to produce corresponding short-chain FFAs. Next, The sequential reactions of *E. coli* fatty acyl-CoA synthetase, *Clostridium acetobutylicum* fatty acyl-CoA reductase, and *Arabidopsis thaliana* fatty aldehyde decarbonylase converted these FFAs into the corresponding alkanes, resulting in production of up to 580.8 mg/L of short chain alkanes. [This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries from the Ministry of Science, ICT and Future Planning (MSIP) through the National Research Foundation (NRF) of Korea (NRF-2012M1A2A2026556 and NRF-2012M1A2A2026557)]