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Ketoacyl synthase domains of a PUFA synthase in *Thraustochytrium* can function as standalone enzymes in *Escherichia coli*

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Thraustochytrium spp. 26185 accumulates a high level of docosahexaenoic acid (DHA), a nutritionally important ω-3 very long chain unsaturated fatty acid (VLCPUFAs) synthesized primarily by a polyunsaturated fatty acid (PUFA) synthase. However, the molecular mechanism of the PUFA synthase for positioning multiple *cis*-double bonds in the acyl chain remains elusive. The PUFA synthase in this species comprises three large subunits each with multiple catalytic domains. It was hypothesized that among these domains, ketoacyl synthase (KS) domains might be critical for retaining double bonds in the extended acyl chain. To investigate the function of these putative KS domains, two KS domains from SubunitA (KS-A) and from SubunitB (KS-B) of the PUFA synthase were dissected and then expressed as standalone enzymes in *Escherichia coli*. The results showed that both KS-A and KS-B domains, but not the mutagenized ones could complement defective phenotypes of both *E. coli fabB* and *fabF* mutants. Overexpression of these domains in a wildtype *E. coli* showed increases in the total fatty acid production. Successful complementation and functional expression of the embedded KS domains from the PUHA synthase in *E. coli* is the first step forward to study the molecular mechanism of the PUFA synthase for the biosynthesis of VLC-PUFAs.

Biography

Xi Xie has completed her MSc in Food Science from South China Agricultural University, China. She did her PhD in the Department of Food and Byproduct Sciences, University of Saskatchewan. Her research aims at studying the molecular mechanism of DHA biosynthesis through PUFA synthase in *Thraustochytrium*.

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