Phosphopantetheinylation in the green microalgae Chlamydomonas reinhardtii

Microalgal biofuel is a promising solution to the decline of fossil fuels. However, algal fatty acid metabolism, the machinery producing the raw material for biofuels, remains poorly understood. The central unit of the fatty acid synthase (FAS) is the acyl carrier protein (ACP), which is responsible for holding the product. Fatty acid biosynthesis is initiated through posttranslational modification of the ACP by the phosphopantetheinyl transferase (PPTase). We identified two PPTases, PptC1 and PptC2, in the model alga Chlamydomonas reinhardtii by genome analysis and phylogenetic and structural comparison. Both PPTases are of Sfp-type, the archetypical PPTase type for non-ribosomal peptide and polyketide biosynthetic pathways in bacteria and cyanobacteria. In vitro analysis revealed that PptC2 has a broader substrate range than PptC1. Both PPTases were able to activate the cognate ACP of the type II FAS, while PptC2 also recognized ACP of Escherichia coli type II FAS and actinorhodin type II polyketide synthase. Besides FAS as PPTase target, the C. reinhardtii genome encodes a single type I PKS, and we hypothesize that PptC2 is responsible for its activation. Screening of the currently available microalgal genome data revealed that most green microalgae appear to carry two PPTases forming clusters with each C. reinhardtii PPTase, while microalgae of other divisions carry one or two PPTases and do not cluster in the pattern of the green algal data. This new understanding on the PPTases in microalgae shows that microalgae are already primed for biotechnological applications in contrast to other organisms. Thus, microalgae have great potential for metabolic engineering efforts in the realm of biofuel and high-value products including direct engineering of the fatty acid or secondary metabolism using the natural genomic reservoir and as biotechnological platform for heterologous expression.

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