

Long-chain polyunsaturated fatty acid biosynthesis in a land-crab with advanced terrestrial adaptations: Molecular cloning and functional characterization of two fatty acyl elongases

ABSTRACT

Depending on the presence and activities of the front-end fatty acyl desaturases and elongation of very long-chain fatty acid (Elovl) enzymes, animals have different capacities for long-chain ($\geq C_{20}$) polyunsaturated fatty acids (LC-PUFA) biosynthesis. Successful land colonisation in brachyuran crabs requires a shift towards terrestrial food chain with limited LC-PUFA availability. We cloned and functionally characterised two elovl genes from the purple land crab *Gecarcoidea lalandii*. The two Elovl contained all the necessary motifs of a typical polyunsaturated fatty acids (PUFA) Elovl and phylogenetically clustered in the Elovl1 and Elovl6 clades, respectively. The *G. lalandii* Elovl1 elongated saturated fatty acids, with low activities towards C20 and C22 PUFA substrates. Moreover, the *G. lalandii* Elovl6 was particularly active in the elongation of C18 PUFA, although it also recognised monounsaturated fatty acids as substrates for elongation. Collectively, the herein characterised *G. lalandii* elovl paralogues fulfil all the elongation steps involved in the LC-PUFA biosynthetic pathways. Tissue distribution of the *G. lalandii* elovl genes, along with the FA composition analyses, suggest the hepatopancreas and gill as key metabolic sites for fatty acid elongation. However, current data suggest that *G. lalandii* is unable to rely solely on biosynthesis to fulfil LC-PUFA requirements, since front-end desaturase appears to be absent in this species and other decapods.