FUNCTIONAL DIVERSITY OF THE UNSATURATED FATTY ACIDS BIOSYNTHESIS PATHWAY IN BONY FISHES AND CARTILAGINOUS FISHES

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Résumé

The unsaturated fatty acids such as docosahexaenoic acid (DHA) and eicosapentaenoic acid (EPA) are important nutrients, and they are given to fish as feed in aquaculture. To elucidate the functional diversity of the unsaturated fatty acids biosynthesis pathway, we performed the phylogenetic analyses of Elovl2, Elovl5, and Fads2 that are involved in the DHA and EPA biosynthesis pathway in fishes. We found that most of marine fishes lack the *elovl2* gene from their genomes while freshwater fishes have all three genes. A trend was seen in that fishes in the same order belong to the same cluster in the phylogenetic trees of each gene. Based on the multiple alignments of Elovl5 and Fads2, we found that some amino acids were conserved in fishes that have the *elovl2* gene or not respectively (Figure 1). These results shows that marine fishes cannot synthesize the unsaturated fatty acids and need to take them as food from environments. They also suppose that nonsynonymous mutations have occurred when marine fishes eliminated the *elovl2* gene and conserved amino acids are important for the unsaturated fatty acids biosynthesis of freshwater fishes and seawater fishes respectively. We expect that these findings are useful for an appropriate feeding toward a sustainable aquaculture.

Mots-Clés: unsaturated fatty acids biosynthesis, functional diversity, phylogenetic analyses

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