

ω-6和ω-3脂肪酸脱氢酶家族系统进化与功能分化

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摘要 文章利用生物信息学方法对ω-6和ω-3脂肪酸脱氢酶基因家族的氨基酸序列特征、系统进化及功能分化进行分析。结果表明, ω-6和ω-3脂肪酸脱氢酶氨基酸序列均含有3个保守的组氨酸基序(Hisbox)。质体类ω-6和ω-3脂肪酸脱氢酶氨基酸N-端序列均有数目不等的信号肽区域, 并且在信号肽区中部发现1个由10个氨基酸残基组成的相对保守的疏水区, 推测为该类酶信号肽的功能区域。多数植物微体ω-6和ω-3脂肪酸脱氢酶氨基酸C-端均有KKXX-like motif内质网滞留信号, 而红花*CtFAD2-3*、*CtFAD2-4*、*CtFAD2-5*、*CtFAD2-6*和*CtFAD2-7*中没有检测到该滞留信号, 但C-端序列富含芳香族氨基酸, 同样具有内质网滞留信号的作用。系统进化分析可将所有序列分为4大类, 结果显示ω-3脂肪酸脱氢酶在原核生物中由ω-6脂肪酸脱氢酶基因进化而来; 并且植物质体和微体类ω-3脂肪酸脱氢酶均可再划分为单子叶和双子叶植物2个亚类, 表明植物质体和微体类ω-3脂肪酸脱氢酶功能的分化早在单子叶和双子叶植物分化之前就已经形成; 而植物微体类ω-6脂肪酸脱氢酶可细分为种子特异表达型和组成性表达型两类, 是在双子叶植物形成之后才开始分化的。各亚群间的功能分化位点分析表明, 除植物 *FAD3*/植物 *FAD2*外, 在所有存在功能分化的亚群间, 均存在后验概率值超过0.80的氨基酸位点, 而这些位点主要分布在Hisbox I的前后两端以及Hisbox II的前端, 表明这些位点变化对蛋白质功能域的大小或构象有着重要影响, 对于亚群间功能分化起着非常重要的作用。

关键词: 系统进化 组氨酸保守区 信号肽 内质网滞留信号 功能分化

Abstract: The deduced amino acid sequences characteristics, phylogeny, and functional diverge of ω-6 and ω-3 fatty acid desaturase families were analyzed by using Bioinformatics methods. The results showed that all the deduced amino acid sequences shared three highly conserved histidine rich motifs (Hisbox). All the plastidial ω-6 and ω-3 fatty acid desaturases possessed putative N-terminal signal peptide with different amino acids. A relatively conserved hydrophobic region composed of 10 amino-acid residues was found in the middle of signal peptides, which is presumed to be the functional region of the signal peptide of these enzymes. Most of the plant microsomal ω-6 and ω-3 fatty acid desaturases (FAD2 and FAD3) contained a KKXX-like motif of endoplasmic reticulum (ER) retention signal at the C-terminus. However, no such motif was detected in safflower *CtFAD2-3*, *CtFAD2-4*, *CtFAD2-5*, *CtFAD2-6*, and *CtFAD2-7*, while an aromatic aa enriched signal (YKKN) was found at their C-terminus which has been reported to be both necessary and sufficient for maintaining localization of the enzymes in the ER. All the amino acid sequences were divided into four categories through phylogenetic analysis. It was suggested that ω-3 fatty acid desaturase originates in a prokaryotic lineage from ω-6 fatty acid desaturase. Both plastidial and microsomal ω-3 fatty acid desaturases could be divided into dicotyledonous and monocotyledonous subgroups, which inferred that functional differentiation of plastidial and microsomal ω-3 fatty acid desaturases had been formed before the divergence of dicotyledonous and monocotyledonous plants. Seed type and housekeeping type FAD2 diverged after the formation of dicotyledonous plants. Except for plant FAD3/plant FAD2, posterior probability values over 0.80 amino acid sites were identified among the functional differentiation subsets, which were mainly distributed at the front and back end of Hisbox I, and the front end of Hisbox II. This indicated that the variations of these amino acid sites played an important role in the size and conformation of protein functional domains and subfamily functional divergence.

Keywords: phylogenetic analysis, conserved histidine rich motifs, signal peptide, ER-retention signal, functional divergence

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