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个人简历

科研领域描述

本实验室主要兴趣在于:

植物超长链脂肪酸合成途径的研究。

超长链脂肪酸调控植物细胞伸长的分子机制研究。

脂肪酸是指一端含有一个羧基的长的脂肪族碳氢链, 在生物体内大部分脂肪酸都以脂质形式存在。超长链脂肪酸是指碳骨架长度超过20个碳原子的脂肪酸, 在植物体内这类脂肪酸主要集中于细胞膜鞘脂及植物表面蜡质中, 其生物学作用不很清楚。

实验室近几年来以陆地棉和无长绒无短绒突变体为实验材料, 通过构建大规模棉花转录组基因芯片, 分离、鉴定和研究棉花纤维伸长相关基因。其中, 超长链脂肪酸(VLCFA)合成途径是被鉴定为一条重要的在纤维发育期显著上调的代谢途径, 我们克隆并鉴定编码3-酮脂酰-CoA合酶、3-酮脂酰-CoA还原酶及烯酰-CoA还原酶的棉花cDNA。为验证其生物学功能, 将它们互补相对应的酵母突变体中, 并使用气相色谱质谱联用仪对互补棉花基因的酵母突变体中的脂肪酸进行定性和定量分析。我们最新的研究发现VLCFA通过激活乙烯合成途径不仅能够促进棉纤维伸长发育, 而且还能促进拟南芥茎细胞伸长。这是关于VLCFA可能作为植物信号分子的首次报道, 对于VLCFA如何调控植物发育的进一步研究具有重要意义。

Research Description:

We have two major lines for our research: understanding the reaction mechanism of biosynthesis of very-long-chain fatty acids (VLCFA) and VLCFAs modulating cotton fiber cell elongation.

Very-long-chain fatty acids (VLCFAs, >C20) are widely distributed in nature, and they are found mainly in membrane sphingolipids, epi-cuticular waxes, seed storage triacylglycerols of most plant species. VLCFAs are synthesized by the microsomal fatty acid elongation system, which consists of four sequential reactions. Through microarray transcriptome profiling of cotton fiber UniESTs, we identified cDNAs encoding enzymes involved in VLCFA biosynthesis that were preferentially expressed during the fast fiber elongating period. The cotton cDNAs encoding 3-ketoacyl-CoA synthase (KCS), 3-ketoacyl-CoA reductase and trans-2-enoyl-CoA reductase, were cloned, and functionally characterized by heterologous expressing in yeast mutants. With regarding to the function of VLCFAs in cotton cells, we reported that many VLCFA biosynthetic genes are up-regulated during early cotton fiber development. Further, we recently found that saturated VLCFAs promote cotton fiber and Arabidopsis cell elongation by activating ethylene biosynthesis gene ACOs, providing an important link between the VLCFA biosynthesis and cotton fiber elongation

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