

油茶种仁含油量及脂肪酸代谢关键基因的挖掘与分析

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摘要:【目的】为挖掘油茶含油量及脂肪酸代谢的关键基因。【方法】对‘长林 40 号’三个关键发育时期(7 月 7 日, 8 月 14 日和 10 月 3 日)的油茶种仁进行转录组分析, 并对富集的脂肪酸代谢关键基因表达量、含油量和各脂肪酸组分比例进行相关性分析。【结果】转录组测序并分析表明, 共获得 17772 个差异表达基因(Differentially expressed genes, DEGs), 其中上调表达的基因有 11006 个(61.93%), 下调表达的基因有 6766 个(38.07%), 且每个时期上调表达的 DEGs 数量高于下调表达的 DEGs 数量, 在 Em0707vsEm1003 中 DEGs 数量最多。去除重复后共获得 9625 个 DEGs, 其中三个比较组共有的 DEGs 有 1302 个, 在 Em0707vsEm0814、Em0707vsEm1003 和 Em0814vsEm1003 中每个比较组特有的 DEGs 分别为 452 个、1652 个和 676 个。GO (Gene Ontology)分析表明, 三个比较组共有 1302 个 DEGs 富集到 195 个 GO terms, 对每个比较组特有的 DEGs 进行 GO 富集分析显示, Em0707vsEm0814 中 452 个特有的 DEGs 共富集 14 个 GO terms, 包括 10 个生物过程和 4 个分子功能; Em0707vsEm1003 中 1652 个特有的 DEGs 富集 1 个分子功能方面的 GO terms, 为 3-氧代酰基-酰基载体蛋白还原酶(nicotinamide adenine dinucleotide phosphate oxidase, NADPH)活性; Em0814vsEm1003 中 676 个特有的 DEGs 共富集了 17 个 GO terms, 包括 10 个生物过程和 7 个分子功能。进一步地 KEGG 分析显示, 三个比较组共有 DEGs 富集在类黄酮生物合成、苯丙烷生物合成、二芳基庚烷和姜酚生物合成、黄酮和黄酮醇生物合成以及谷胱甘肽代谢 5 条通路中。对三个比较组共有和每个比较组特有的 DEGs 分析发现, 三个比较组共同有的 DEGs 有 5 条 KEGG 通路显著富集, 主要为类黄酮生物合成、苯丙烷生物合成、二芳基庚烷和姜酚的生物合成、黄酮和黄酮醇的生物合成和谷胱甘肽代谢。对每个比较组特有的 DEGs 进行 KEGG 分析发现, 在 Em0707vsEm0814 和 Em0814vsEm1003 比较组中未获得 KEGG 显著性富集通路, 而在 Em0707vsEm1003 比较组中, 有 4 条 KEGG 通路显著富集, 主要包含脂肪酸生物合成、脂肪酸代谢、生物素代谢和丙酮酸代谢。其中, 脂肪酸生物合成和脂肪酸代谢通路共有 12 个 DEGs, 进一步测定不同时期种仁含油量和脂肪酸组分, 并进行相关性分析表明, ACC、KASIII、PATE、KAT2 和 SAD 基因的表达量与种仁含油量和 C18:1n-9c 呈显著正相关, KASIII、ACC、PATE 和 KAT2 基因与 C16:0 呈显著负相关性。【结论】ACC、KASIII、PATE、KAT2 和 SAD 基因可能是调控油茶含油量及脂肪酸代谢相关的关键基因, 上述研究为油茶遗传改良提供了科学依据。

Exploration and Analysis of Key Genes Involved in Oil Content and Fatty Acid Metabolism in *Camellia oleifera* Seeds Kernel

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Abstract: 【Objective】 In order to explore the key genes involved in oil content and fatty acid metabolism in *Camellia oleifera*. **【Method】** transcriptome analysis was performed on the kernels of *Camellia oleifera* seeds at three key developmental stages (July 7, August 14, and October 3), and correlation analysis was conducted on the expression levels of enriched key genes involved in fatty acid metabolism, oil content, and the proportions of various fatty acid components. **【Results】** Transcriptome sequencing and analysis showed that a total of 17772 differentially expressed genes (DEGs) were obtained, of which 11006 (61.93%) were up-regulated and 6766 (38.07%) were down regulated. Moreover, the number of upregulated DEGs was higher than the number of downregulated DEGs at each stage, with the highest number of DEGs observed in Em0707vsEm1003. After removing duplicates, a total of 9625 DEGs were obtained, of which 1302 DEGs were shared among the three comparison groups. The DEGs unique to each comparison group in Em0707vsEm0814, Em0707vsEm1003, and Em0814vsEm1003 were 452, 1652, and 676, respectively. GO (Gene Ontology) analysis showed that a total of 1302 DEGs were enriched to 195 GO terms in the three comparison groups. GO enrichment analysis of each comparison group's unique DEGs showed that 452 unique DEGs were enriched to 14 GO terms in Em0707vsEm0814, including 10 biological processes and 4 molecular functions; In Em0707vsEm1003, 1652 unique DEGs were enriched with one molecular functional GO term, which represents the activity of nicotinamide adenine dinucleotide phosphate oxidase (NADPH), a 3-oxoacyl acyl carrier protein reductase; The 676 unique DEGs in Em0814vsEm1003 collectively enrich 17 GO terms, including 10 biological processes and 7 molecular functions. Further KEGG analysis showed that the three comparison groups shared DEGs enriched in five pathways: flavonoid biosynthesis, phenylpropane biosynthesis, diarylheptane and gingerol biosynthesis, flavonoid and flavonol biosynthesis, and glutathione metabolism. Analysis of DEGs shared and unique to each of the three comparison groups revealed significant enrichment in five KEGG pathways, mainly including flavonoid biosynthesis, phenylpropane biosynthesis, diarylheptane and gingerol biosynthesis, flavonoid and flavonol biosynthesis, and glutathione metabolism. KEGG analysis of DEGs unique to each comparison group revealed that no significant KEGG enrichment pathways were found in the Em0707vsEm0814 and Em0814vsEm1003 comparison groups, while in the Em0707vsEm1003 comparison group, four KEGG pathways were significantly enriched, mainly including fatty acid biosynthesis, fatty acid metabolism, biotin metabolism, and pyruvate metabolism. Among them, there are a total of 12 DEGs involved in fatty acid biosynthesis and fatty acid metabolism pathways. Further determination of oil content and fatty acid composition in seeds at different stages, and correlation analysis showed that the expression levels of *ACC*, *KASIII*, *PATE*, *KAT2*, and *SAD* genes were significantly positively correlated with seed oil content and C18:1n-9c, while *KASIII*, *ACC*, *PATE*, and *KAT2* genes were significantly negatively correlated with C16:0. **【Conclusion】** *ACC*, *KASIII*, *PATE*, *KAT2*, and *SAD* genes may be key genes regulating oil content and fatty acid metabolism in *Camellia oleifera*, providing scientific basis for genetic improvement of *Camellia oleifera*.