

桂花色泽关键基因 *OfCCD4* 互作转录因子的鉴定分析

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摘要: 【目的】明确调控桂花类胡萝卜素代谢关键基因 *OfCCD4* 的转录因子, 探究转录因子与 *OfCCD4* 结合并调控其表达的分子机制, 为解析桂花类胡萝卜素代谢的分子机制及桂花花色的基因工程育种提供理论依据。【方法】选取杭州临安太湖源区桂花花瓣为研究材料, 对前期筛选的类胡萝卜素代谢关键基因 *OfCCD4* 进行转录因子预测, 并利用实时荧光定量 PCR (RT-qPCR)、酵母单杂交等分子生物学试验初步鉴定 *OfCCD4* 的转录因子。【结果】转录组分析发现, 有 10 个转录因子与 *OfCCD4* 表达水平呈现高相关性; Y1H 酵母转录激活活性结果显示, 其中有 8 个转录因子具有一定的转录自激活能力; 酵母单杂交结果表明, 3 个转录因子与 *OfCCD4* 启动子有强相互作用, 3 个转录因子与 *OfCCD4* 启动子存在弱相互作用。【结论】筛选到 3 个具有自激活活性, 且与 *OfCCD4* 存在强互作关系的转录因子, 推测其可能通过调控桂花 *OfCCD4* 基因表达影响花色差异。

关键词: 桂花; 类胡萝卜素; *OfCCD4* 基因; 转录因子; 酵母单杂交

中图分类号: S685.13

文献标志码: A

Identification of transcriptome-based *Osmanthus fragrans* *OfCCD4* interaction transcription factors

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Abstract: 【Objective】Defining the transcription factors of *OfCCD4*, a key gene that regulates carotenoid metabolism in *Osmanthus fragrans*, as well as exploring the molecular mechanism of transcription factors binding to *OfCCD4* and regulating *OfCCD4* expression, which provide a theoretical basis for revealing the molecular mechanism of carotenoids metabolism as well as for *O. fragrans* color genetic engineering breeding. 【Method】The petals of *Osmanthus* flower were obtained in Tai Hu Yuan, which located in Lin'an, Hangzhou City. The transcription factors of *OfCCD4* were predicted through the online websites and further identified by RT-qPCR and yeast-one-hybrid assays. 【Result】Transcriptome analysis showed that 10 transcription factors showed highly correlated with the expression level of *OfCCD4*. Transactivation activity in Y1H yeast showed that 8 transcription factors of them had transactivation activity. Finally, 3 transcription factors displayed strong interaction and 3 exhibited weak interaction with *OfCCD4*.

收稿日期: 2024-01-26

基金项目: 河南省重大公益专项项目 (201300110900); 河南省植物学会人才托举项目 (2022HYTP029); 河南省青年科学基金项目 (222300420183); 河南农业大学科技创新基金项目 (KJCX2021A17); 河南省留学人员科研择优资助项目 (30602425)

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