

油茶 *bHLH* 基因家族鉴定与响应干旱胁迫的基因表达分析3

谢荟清^{1,2}, 刘娟^{1,2*}

(1. 亚热带森林资源培育江西省重点实验室; 2. 江西农业大学林学院, 江西 南昌 330045)

摘要: 【目的】*bHLH* 转录因子在植物生长发育、响应非生物胁迫等过程中起重要调控作用。油茶是我国南方山地丘陵重要的木本油料树种, 其主产区夏秋持续性的伏旱天气, 对油茶生长和集约栽培管理构成了严峻的挑战。探究油茶 *bHLH* 基因家族成员及其应对干旱胁迫的表达调控模式具有重要意义。【方法】基于油茶全基因组数据, 本研究鉴定 *CobHLHs* 成员, 分析其系统发育进化关系, 研究其在油茶染色体上的分布、顺式作用元件预测、家族成员间共线性分析, 探究 *CobHLHs* 的组织表达特异性及其在干旱胁迫、ABA 处理下的表达模式。【结果】本研究共鉴定出 127 个 *CobHLHs*, 根据其系统发育关系, 将其分为 17 个亚族。共线性分析结果显示, 全基因组范围内共发生了 22 次片段复制事件。干旱胁迫下叶组织比较转录组分析结果显示, 共有 106 个 *CobHLHs* 参与油茶干旱胁迫响应过程。组织特异表达分析发现, 参与干旱胁迫的 *CobHLHs* 主要在叶中高表达, 在根中表达相对较低。PEG 模拟干旱胁迫和同源基因功能预测证实, 9 个 *CobHLHs* 的表达均在不同程度上受干旱胁迫诱导, 不同基因表达调控模式存在差异, *CobHLH071* 在干旱胁迫下为低表达, 表现为 12、48h 分别为对照的 0.07 和 0.24 倍; *CobHLH006*、*082* 在干旱胁迫下高表达, *CobHLH006* 在 12、48h 为对照的 8.2、54.1 倍, 而 *CobHLH082* 在 48h 才出现显著高表达。进一步进行 ABA 处理研究其可能的表达调控模式发现, *CobHLH071* 可能通过 ABA 依赖负调控干旱胁迫应答。*CobHLH006*、*082* 可能通过影响 ABA 信号通路相关基因的表达, 正调控油茶干旱胁迫应答, 但两者的响应时间存在差异, 前者可能同时存在非 ABA 依赖调控模式。【结论】本研究为油茶 *bHLH* 基因功能研究奠定了理论基础, 同时也为进一步开展油茶耐旱分子机制研究提供依据。

Identification of *bHLH* gene family in *Camellia oleifera* and analysis of its expression under drought stress

XIE Huiqing LIU Juan*

(a. Jiangxi Key Laboratory of Subtropical Forest Resources Cultivation; b. College of Forestry, Jiangxi Agricultural University, Nanchang 330045, Jiangxi, China)

Abstract: 【Objective】*bHLH* transcription factors play important regulatory roles in plant growth and development, as well as in response to abiotic stress. *Camellia oleifera* is an important woody oilseed tree species in the mountainous and hilly areas of southern China. The continuous summer and autumn drought in its main production area poses a serious challenge to the growth and intensive cultivation management of *C. oleifera*. Exploring the members of the *bHLH* gene family in *C. oleifera* and their expression regulation patterns in response

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第一作者: 谢荟清 (xiehuiqing1999@163.com), 硕士生。通信作者: 刘娟 (liu_juan1122@163.com), 副教授, 博士, 硕士研究生导师。

to drought stress is of great significance. **【Method】** Based on the whole genome data of *C. oleifera*, this study identified members of *CobHLHs*, analyzed their phylogenetic relationships, studied their distribution on *C. oleifera* chromosomes, predicted cis acting elements, and analyzed collinearity among family members, to clarify the tissue expression specificity of *CobHLHs* and their expression patterns under drought stress and ABA treatment. **【Results】** A total of 127 *CobHLHs* were identified in this study. Based on their phylogenetic relationships, they were divided into 17 subfamilies. The results of collinearity analysis showed that a total of 22 fragment duplication events occurred across the entire genome. The comparative transcriptome analysis of leaf tissue under drought stress showed that a total of 106 *CobHLHs* were involved in the response process of *C. oleifera* to drought stress. Organizational specific expression analysis revealed that *CobHLHs* involved in drought stress are mainly highly expressed in leaves and relatively low in roots. PEG simulation of drought stress and homologous gene function prediction confirmed that the expression of 9 *CobHLHs* was induced to varying degrees by drought stress, and there were differences in the regulation modes of different gene expression. *CobHLH071* was low expression under drought stress, with 0.07 and 0.24 time higher expression than the control at 12 and 48 hours, respectively; *CobHLH006* and *082* are highly expressed under drought stress. *CobHLH006* was 8.2 and 54.1 times higher than the control at 12 and 48 hours after drought stress, while *CobHLH082* was significantly higher at 48 hours after drought stress. Further study on the possible expression regulation mode of *CobHLH071* by ABA treatment showed that *CobHLH071* may negatively regulate drought stress response through ABA dependence. *CobHLH006* and *082* may positively regulate the response of *C. oleifera* to drought stress by affecting the expression of genes related to ABA signaling pathway, but the response time of the two may be different. The former may also have an ABA independent regulation mode. **【Conclusion】** This study laid a theoretical foundation for the functional study of *bHLH* gene in *C. oleifera*, and also provided a basis for further study on the molecular mechanism of drought tolerance in *C. oleifera*.