

闽楠 DOF 基因家族的鉴定和表征及其在非生物胁迫 ——干旱、高温和光胁迫中的作用*

郑珂晖¹ 吕萌萌² 钱佳颖³ 连怡然⁴ 刘小敏^{5,*} 曹世江^{2,3,*}

(1.福建农林大学计算与信息学院 福州 350002; 2.福建农林大学林学院 福州 350002; 3.林木逆境生理生态及分子生物学福建省高校重点实验室 福州 350002; 4.福建农林大学生命科学学院 福州 350002; 5.北京林业大学生物科学与技术学院 树木遗传育种国家重点实验室 北京 100083)

摘 要:【目的】明确闽楠中 Dof 转录因子基因家族成员, 并且分析得出闽楠 Dof 基因家族在响应非生物胁迫中起的作用。【方法】本研究在全基因组尺度上对闽楠 *Dof* 基因家族进行了综合测定和分析, 包括其系统发育关系、基因结构、蛋白质的理化性质、顺式作用元件、共线性和共线分析、Ka (非同义替换率)、Ks (同义替换率) 和 Ka/Ks (ω) 值、组织表达谱、SSR 位点预测和非生物下实时定量 PCR 测定基因相对表达水平。【结果】在这项研究中, 我们在全基因组水平上鉴定并分析了 34 个 *PbDof* 基因成员。结果表明, 34 个 *PbDof* 基因在 12 条染色体上分布不均匀。我们利用来自闽楠和拟南芥的 *Dof* 基因构建了系统发育树, 并将这些基因分为 8 个亚组。在种间共线性分析中, *AtDof* 和 *PbDof* 之间存在 16 个同源基因对, *ZmDof* 和 *PbDof* 之间存在 9 个同源基因对。我们还进行了顺式作用元件分析, 发现参与光响应的顺式作用元件在 *PbDof* 基因中最丰富。通过 SSR 位点预测, 我们根据结果得出闽楠 *Dof* 基因的进化水平较低。此外, 我们进行 qRT-PCR 实验评估了 8 个 *PbDof* 基因在高温、干旱和光照胁迫下的表达谱。特别是, *PbDof08* 和 *PbDof16* 在 3 种胁迫下显著上调。【结论】闽楠是中国特有的二级濒危保护物种, 具有重要的生态和经济价值。DNA 结合单锌指 (Dof) 转录因子是植物特异性调节因子。大量研究表明, Dof 基因参与植物的生长、发育和对非生物胁迫的反应。我们通过系统发育分析, 发现 *PbDof11* 与 *AT5G60850.1* 表现出高度同源性, 而 *PbDof07* 与 *AT3G50410.1* 表现出高度同源性。基因共线性分析结果表明, 34 个 *PbDof* 基因形成了 24 对同源基因对。在干旱、高温和光照处理下, 分析 7 个 *PbDof* 基因的表达模式。推测 *PbDof08* 和 *PbDof16* 是参与光响应的主要基因。此外, 还讨论了植物处于非生物胁迫下 *Dof* 基因的作用机制。本研究为 *PbDof* 基因研究提供了基础信息, 并为进一步研究 Dof 转录因子响应逆境的机制以及闽楠 *Dof* 基因家族对环境变化的适应提供了新的见解。

Identification and characterization of the *DOF* gene family in *Phoebe bournei* and its role in abiotic stress—Drought, Heat and Light stress

Kehui Zheng¹ Mengmeng Lv² Jiaying Qian³ Yiran Lian⁴ Xiaomin Liu^{5,*} and Shijiang Cao^{2,3,*}

(1. College of Computer and Information Sciences, Fujian Agriculture and Forestry University, Fuzhou 350002; 2. College of Forestry, Fujian Agriculture and Forestry University, Fuzhou 350002; 3. University Key Laboratory of Forest Stress

Physiology, Ecology and Molecular Biology of Fujian Province, Fuzhou 350002; 4. College of Life Sciences, Fujian Agriculture and Forestry University, Fuzhou 350002; 5. State Key Laboratory of Tree Genetics and Breeding, College of Biological Sciences and Technology, Beijing Forestry University, Beijing 100083)

Abstract: 【Objective】 The members of the *Dof* transcription factor gene family in *Phoebe bournei* were clarified, and the role of *Dof* gene family in response to abiotic stress was analyzed. 【Method】 In this study, the *Dof* gene family was comprehensively determined and analyzed at the genome-wide scale, including its phylogenetic relationship, gene structure, physicochemical properties of proteins, *cis*-acting elements, collinearity and collinear analysis, *Ka* (non-synonymous replacement rate), *Ks* (synonymous replacement rate) and *Ka/Ks* (ω) values, tissue expression profile, SSR locus prediction, and real-time quantitative PCR to determine the relative expression levels of genes. In this study, we identified and analyzed 34 *PbDof* gene members at the whole-genome level. 【Result】 The results indicated that the 34 *PbDof* genes were unevenly distributed across 12 chromosomes. We utilized the *Dof* genes from *Arabidopsis thaliana* and *P. bournei* to construct a phylogenetic tree and categorized these genes into eight subgroups. In the collinearity analysis, there were 16 homologous gene pairs between *AtDof* and *PbDof* and nine homologous gene pairs between *ZmDof* and *PbDof*. We conducted a *cis*-acting element analysis and found that *cis*-acting elements involved in light response were the most abundant in *PbDof* genes. Through SSR site prediction, we analyzed that the evolution level of *Dof* genes is low. Additionally, we assessed the expression profiles of eight *PbDof* genes under high temperature, drought, and light stress using qRT-PCR. In particular, *PbDof08* and *PbDof16* are significantly upregulated under the three stresses. 【Conclusion】 *Phoebe bournei* is a second-class endangered and protected species unique to China, and it holds significant ecological and economic value. DNA binding one zinc finger (*Dof*) transcription factors are plant-specific regulators. Numerous studies have demonstrated that *Dof* genes are involved in plant growth, development and responses to abiotic stress. Through phylogenetic analysis, it was found that *PbDof11* exhibits high homology with *AT5G60850.1* and *PbDof07* shows high homology with *AT3G50410.1*. The results of collinearity analysis of genes indicated that 34 *PbDof* genes formed 24 pairs of homologous gene pairs. Under drought, high temperature, and light treatments, the expression patterns of seven *PbDof* genes were analyzed. It is speculated that *PbDof08* and *PbDof16* are the main genes involved in light response. Additionally, the mechanism of action of *Dof* genes when plants are under abiotic stress was also discussed. This study provides foundational information for *PbDof* genes and offers new insights for further research on the mechanism of *Dof* transcription factors responding to stress, as well as the adaptation of *P. bournei* to environmental changes.