

马尾松顶芽的转录组和JAZ基因家族分析表明茉莉酸途径积极响应了异胚性叶的发育*

尤素洁^{1,2} 吴峰^{1,2,*}

(1.贵州大学林业学院 贵阳 550025; 2.贵州大学森林资源与环境研究所 贵阳 550025)

摘 要:为明确马尾松顶芽如何调控腋芽的生长以及对异胚性叶发育的响应,以马尾松 PN 幼苗以及 SNB 幼苗的顶芽为材料,使用转录组分析、GO、KEGG 富集分析、基因家族鉴定和生信分析等方法,共同探讨了顶芽如何响应异胚性叶的发育。在两种类型幼苗的顶芽中共有 967 个基因(其中包括 88 个 TFs) 差异表达,研究通过 KEGG 和 GO 分析发现植物激素信号转导途径以及 ABC 转运蛋白途径在 PN 和 SNB 的顶芽中显著富集,且植物激素信号转导途径的连通度最高。差异表达基因(DEGs)与差异表达转录因子(DETFs)的相关性分析发现,茉莉酸负调控因子 *PmJAZs* 与 DETFs 有显著的相关性。使用生信分析的方法从马尾松幼苗全长转录组中鉴定出 30 个 *PmJAZs* 家族成员,分为 3 个亚家族,该蛋白家族为碱性不稳定亲水蛋白,无跨膜结构。系统进化分析表明 JAZ 家族基因进化较保守,*PmJAZs* 和油松 JAZ 家族(*PtJAZs*) 的亲缘关系近,且 JAZ 成员多于其它植物,针叶数 JAZ 基因的扩增可能与针叶树的全基因组复制事件有关。不同组织的表达谱显示,*PmJAZs* 在根茎中的表达量高于针叶和顶芽,在 PN 顶芽中的表达量高于针叶,而在 SNB 针叶中的表达量高于顶芽。*PmJAZs* 作为茉莉酸(JA)信号转导途径中的负调控因子,在马尾松异胚性叶发育过程中发挥着重要作用。以上结果可为深入揭示 *PmJAZs* 基因家族功能、系统进化关系及其对马尾松顶芽响应异胚性叶发育的机制提供理论依据。

Transcriptome and JAZ gene family analysis in *Pinus massoniana* reveals the jasmonate pathway responds to the development of Heteroblastic foliage positively

Sujie You^{1,2}, Feng Wu^{1,2,*}

(¹College of Forestry, Guizhou University, Guiyang 550025, China; ²Institute for Forest Resources and Environment of Guizhou, Guizhou University, Guiyang, 550025, China)

Abstract: *P.massoniana* seedlings develop primary needles (PN) and secondary needles (SN) that are structurally and functionally different from each other, a phenomenon known as heteroblastic foliage. Previous studies have shown that SNs develop from axillary buds of *P.massoniana* (SNB) and that they arise from the differentiation of terminal buds. However, the mechanism of action of how the terminal buds regulate axillary bud growth and respond to the development of heteroblastic foliage is unknown. In this study, comparative transcriptomic analyses of the terminal buds of PN and SNB were conducted, along with the identification and analysis of the *P.massoniana* JAZ gene family (*PmJAZs*). The plant hormone signal transduction pathway and the ABC transporter pathway were significantly enriched in the terminal buds of PN and SNB by KEGG and GO

analysis, and that the plant hormone signal transduction pathway had the highest degree of connectivity. Correlation analysis of differentially expressed genes (DEGs) with differentially expressed transcription factors (DETFs) revealed a significant correlation between *PmJAZs* and DETFs. 30 *PmJAZ* genes were identified by bioinformatics analysis, Phylogenetic analyses suggest that *PmJAZs* and *Pinus tabulaeformis JAZs* (*PtJAZs*) are closely related and have more members than other species, and that the amplification of JAZs in *Pinus* may be associated with a genome-wide duplication event in *Pinus*. Expression profiles of different tissues showed that *PmJAZs* were more abundant in rhizomes than in needles and terminal buds, in PN terminal buds than in needles, and in SNB needles than in terminal buds. *PmJAZs* predictions of protein-interaction networks predictive and expression pattern analyses suggest that these genes play vital roles in heteroblastic foliage development in *P. massoniana* as negative regulators in the jasmonic acid (JA) signal transduction pathway. The above results may provide a theoretical basis for an in-depth understanding of the function of the *PmJAZs*, and its mechanism on the development of terminal buds in response to development of heteroblastic foliage in *P. massoniana*.