

新疆野苹果 *PYL* 基因家族的全基因组鉴定与表达分析

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摘 要:【目的】植物激素脱落酸 (abscisic, ABA) 是调控植物生长和胁迫响应的关键激素, 在调控种子休眠与萌发和生长发育中起关键作用, ABA 受体 (Pyrabactin resistance-like, PYL) 作为 ABA 信号通路的核心成分之一, 在 ABA 信号通路中发挥功能。【方法】采用生物信息学方法和转录组测序对新疆野苹果 (*Malus sieversii*) PYL 家族成员进行全基因组鉴定, 分析了 PYL 成员的染色体位置、进化关系、基因结构、蛋白基序、共线性、顺式调控元件以及在不同组织中的表达模式和种子低温层积过程中的表达谱。【结果】在新疆野苹果全基因组中鉴定出 14 个 PYL 基因分布在 7 条染色体上, 且基因分布有成簇现象。系统发育分析将其分为 3 个亚组, MsiPYL3-5、MsiPYL10-12 和 MsiPYL14 属于 I 组, MsiPYL1-2 属于 II 组, MsiPYL6-9 和 MsiPYL13 属于 III 组。家族成员含有 0~4 个内含子和 1~5 个外显子, 所有亚家族存在 PYR-PYL-RCAR-like 保守结构, 鉴定出 5 个片段重复事件, 涉及 9 个 MsiPYL 基因。5 对基因 MsiPYL1-MsiPYL2, MsiPYL4-MsiPYL11, MsiPYL5-MsiPYL10, MsiPYL9-MsiPYL13 和 MsiPYL10-MsiPYL14 为在共线性区域的共线性基因。纯化选择主要驱动 MsiPYL 基因的进化动力学。顺式作用元件分析表明, 在新疆野苹果 PYL 基因上游 2000 bp 序列中, 普遍存在数目不等、种类不同的参与激素响应、生长发育响应、非生物和生物胁迫响应的顺式作用元件。基因本体富集表明, MsiPYL 基因主要参与脱落酸激活信号通路、调节磷酸酶活性和磷蛋白磷酸酶活性。KEGG 通路分析显示, 主要参与丝裂原活化蛋白激酶 (MAPK) 信号通路-植物和植物激素信号转导。MsiPYL 基因在 6 个不同组织中均呈组成型表达, 生殖器官 (花和果实) 的表达水平显著高于营养器官 (根和茎)。在 MsiPYL3、MsiPYL9 和 MsiPYL13 中, 生殖器官 (花、果实和种子) 和营养器官 (根、茎和叶) 的表达水平较高。MsiPYL12 在花、果实、种子和叶的表达水平显著高于种子和茎。在其它 MsiPYL 中, 花、果实和叶的表达水平显著高于种子、根和茎。低温层积 4 个时期 (30、60、90 和 120 d) 基因家族成员间表达模式存在一定差异。在种子不同低温层积处理下进行实时荧光定量 PCR 分析 MsiPYL8 (MsiPYR1) 的表达模式, 其整体表现出显著下调的趋势。【结论】在基因组水平上对新疆野苹果 PYL 基因家族进行鉴定和特征分析, 为揭示 MsiPYL8 (MsiPYR1) 基因在新疆野苹果种子休眠解除中的作用提供依据, 有助于未来研究 MsiPYL 基因的生物学功能及非生物胁迫响应。

Genome-wide identification and expression analysis of the *PYL* gene family in *Malus sieversii*

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基金项目: 新疆维吾尔自治区自然科学基金面上项目 (2023D01A28)。

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Abstract: 【Objective】 Absciscic acid (ABA), a key phytohormone that controls plant growth and stress responses, and plays a key role in the regulation of seed dormancy and germination and growth and development, and the ABA receptor (Pyrabactin resistance-like, PYL) functions as one of the core components of the ABA signaling pathway. 【Method】 Genome-wide identification of PYL family members in *Malus sieversii* was carried out using bioinformatics methods and transcriptome sequencing, and the chromosomal locations, evolutionary relationships, gene structures, protein motifs, collinearity, cis-regulatory elements, as well as expression patterns in different tissues and expression profiles of PYL members in the process of low-temperature seed stratification were analyzed. 【Result】 14 PYL genes were identified in the whole genome of *Malus sieversii*, and distributed on seven chromosomes, and the gene distribution had a clustering phenomenon. Phylogenetic analyses classified them into three subgroups, with MsiPYL3-5, MsiPYL10-12 and MsiPYL14 in group I, MsiPYL1-2 in group II, and MsiPYL6-9 and MsiPYL13 in group III. Family members contained 0-4 introns and 1-5 exons, and PYR-PYL-RCAR-like conserved structures were present in all subfamilies. 5 fragment duplication events were identified, involving 9 *MsiPYL* genes. 5 pairs of genes *MsiPYL1-MsiPYL2*, *MsiPYL4-MsiPYL11*, *MsiPYL5-MsiPYL10*, *MsiPYL9-MsiPYL13* and *MsiPYL10-MsiPYL14* were collinear genes in the collinear region. Cis-acting element analyzes showed that cis-acting elements involved in hormone response, growth and developmental response, abiotic and biotic stress response were prevalent in varying numbers and types in the 2000 bp upstream sequence of *PYL* gene in *Malus sieversii*. Gene ontology enrichment demonstrated that the *MsiPYL* gene was mainly involved in the absciscic acid activation signaling pathway, regulation of phosphatase activity and phosphoprotein phosphatase activity. KEGG pathway analysis showed that it was mainly involved in mitogen-activated protein kinase (MAPK) signaling pathway-plant and phytohormone signaling. *MsiPYL* gene was constitutively expressed in six different tissues, and the expression level was significantly higher in reproductive organs (flowers and fruits) than in nutrient organs (roots and stems). In *MsiPYL3*, *MsiPYL9* and *MsiPYL13*, the expression levels were higher in reproductive organs (flowers, fruits and seeds) and nutrient organs (roots, stems and leaves). *MsiPYL12* was expressed at significantly higher levels in flowers, fruits, seeds and leaves than in seeds and stems. In other *MsiPYL*, the expression levels were significantly higher in flowers, fruits and leaves than in seeds, roots and stems. There were some differences in expression patterns among gene family members during the four periods of low-temperature stratification (30, 60, 90, and 120 d). The expression pattern of *MsiPYL8* (*MsiPYR1*) was analyzed by real-time fluorescence quantitative PCR under different low-temperature stratification treatments in seeds, and its overall expression showed a significant down-regulation trend. 【Conclusion】 The identification and characterization of the *PYL* gene family in *Malus sieversii* at the genome level provides a basis for revealing the role of the *MsiPYL8* (*MsiPYR1*) gene in seed dormancy lifting in *Malus sieversii*, and contributes to the future study of the biological function and abiotic stress response of *MsiPYL* genes.