

miRNA 在麻竹从头芽再生过程中的作用机制

王楠楠¹, 朱强¹

(福建农林大学, 福建省福州市 350002)

摘要: 竹子作为我国非常重要的一种非木制森林资源。竹子的克隆和繁殖一直是其研究的难点与热点。近期, 高效稳定的麻竹遗传再生体系虽然已经建立, 但是其再生过程中分子机制尚未明确。本课题组前期对麻竹从头芽再生过程中的转录组测序数据揭示了 microRNAs (miRNAs) 可能在此过程中发挥潜在作用。然而, miRNAs 如何调节竹子的再生仍不为人所知。于是, 本研究结合小 RNA 组学、降解组学以及转录组学技术对麻竹从头芽再生过程的 4 个阶段的样本进行综合分析, 揭示了竹子再生的核心“miRNA-mRNA”介导的调节网络。结果显示, 共鉴定出 667 个在竹子再生过程中差异性表达的 miRNAs。通过降解组学分析鉴定出涉及 167 个 miRNAs 和 376 个靶基因的 miRNA-mRNA 配对, 并以此构建了核心的“miRNA-mRNA”转录调控网络。通过进一步细致的分析发现 miR156 的显著表达, 因此 miR156 被选择用于进一步分析其在竹子器官发生中的潜在作用。我们构建了表达 miRNA156 基因的转基因竹子, 并发现它们的再生效率有所提高。与此相反, 降低竹子中 miRNA156 的水平则导致其再生效率下降。总的来说, 本研究揭示了 miRNA 介导的调控途径对竹子再生过程非常重要。这些调节网络将有助于我们更全面地了解植物器官发生的分子机制, 并为竹子的遗传改良提供了基础。该研究对于竹子的再生和利用提供了新的思路和方法, 有望促进竹子产业的发展。

关键词: 竹子; miRNA; miR156; 芽再生

Uncovering the miRNA-mediated regulatory network involved in Ma bamboo (*Dendrocalamus latiflorus*) de novo shoot organogenesis

Nannan Wang¹

(Fujian Agriculture and Forestry University, Fuzhou, 350002, Fujian, China)

Abstract: Bamboo is an important non-timber forest product. The study of bamboo clonal regeneration has always been a difficult problem and attention-getting focus in bamboo research. Recently, we have established a de novo organogenesis (DNSO) protocol in Ma bamboo and revealed the transcriptomic dynamics during Ma bamboo regeneration, which suggested the potential roles of microRNAs (miRNAs) in this process. However, how miRNAs regulate bamboo regeneration is poorly understood. Here we performed integrated analysis with small RNA, degradome and transcriptome sequencing by using samples covering the 4 stages of bamboo regeneration process, to reveal core “miRNA-mRNA” mediated regulatory networks for bamboo regeneration. A total of 667 miRNAs showed differential expression during the process of bamboo regeneration. miRNA-mRNA pairs involving 167 miRNAs and 376 target genes were identified through degradomes analysis. The core “miRNA-mRNA” transcriptional regulatory network was constructed, and miR156 was selected for further analysis based on the above analysis. We engineered transgenic bamboos with increased levels of miRNA156, leading to an enhancement in their regeneration efficiency. Conversely, when miRNA156 levels were down-regulated in bamboo, the regeneration efficiencies decreased. Our findings showed that the miRNA-mediated regulatory pathways are significant in the process of bamboo regeneration and will contribute to our understanding of the molecular mechanisms governing plant organogenesis in a more comprehensive manner.

Key words: Bamboo, miRNA, miRNA156, shoot organogenesis