枣 Dicer-like 蛋白基因家族鉴定与表达分析

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摘要：枣是重要的经济树种，枣疯病是植原体引起的传染性病害，威胁枣产业健康发展。植物 Dicer-like (DCL)蛋白是核糖核酸酶 III (RNase III)家族成员之一，参与 RNAi 途径，可以将病毒核酸转变为 siRNA，在植物 RNA 的降解、转录后调控以及抗病毒侵染等方面具有关键的作用。植原体能够通过 RNA 沉默抑制导致寄主植物病症发生。本文旨在通过对枣 DCL 蛋白基因家族的鉴定和在发病过程中的表达分析，探究 DCL 蛋白在枣疯病发生过程中的作用，并筛选出与病症发生密切相关的基因。利用枣全基因组的测序数据鉴定枣 DCL 家族成员，并对得到的基因进行生物信息学分析；根据枣 ZjDCLs 与拟南芥 AtDCLs 蛋白的序列比对，构建出系统进化树；根据转录本的全长测序数据分析枣感病不同时期的基因表达谱，并通过 qRT-PCR 分析 ZjDCLs 的表达模式。鉴定出了 11 个枣 DCL（ZjDCLs）蛋白，并根据其在染色体上的位置命名为 ZjDCL1-ZjDCL11。枣 DCL 分为 4 类，分别是 DCL1,DCL2,DCL3,DCL4。枣 DCL 蛋白分子量范围分布于 15217.48～225623.49 Da 之间，等电点介于 5.82（ZjDCL11）～（ZjDCL2）9.05 之间。11 个枣 DCL 基因不均匀分布在 6 条枣染色体上，其中 1 号染色体上的最多。枣 DCL 蛋白在枣疯病发生过程中表达谱发生明显变化，ZjDCL4 响应植原体侵染时显著上调，ZjDCL3,6,7,9,10 先显著上调再显著下调，ZjDCL5 和 11 先显著下调再显著上调。鉴定出了枣 11 个 DCL 蛋白基因家族成员，在感染枣疯病植原体后，枣 DCL 基因的表达模式发生变化，ZjDCL6 和 ZjDCL10 在枣响应枣疯病植原体的入侵过程中扮演着重要的角色。

Identification and Expression Analysis of the Dicer-like Protein Gene Family in Jujube

Abstract: Juvenile jujube witches' broom disease (JWBD) is a severe phytopathogenic disorder that has exhibited an escalating incidence in recent years, posing significant constraints on the development of the jujube industry. The plant Dicer-like (DCL) protein, belonging to the Ribonuclease III (RNase III) enzyme family, represents an indispensable component in plant defense against viral infections. Functioning within the RNA interference (RNAi) pathway, the DCL protein facilitates the conversion of viral nucleic acids into small interfering RNA (siRNA), exerting critical roles in various aspects such as RNA degradation, post-transcriptional gene expression modulation, and antiviral responses.Pathogens have evolved mechanisms to antagonize RNA silencing, thereby subverting the host plant's antiviral defense machinery and promoting the manifestation of disease symptoms. The present study aims to elucidate the involvement of DCL proteins in the pathogenesis of JWBD through comprehensive identification and expression analysis of the jujube DCL gene family. By uncovering the pivotal genes closely associated with disease development, this research endeavors to enhance our understanding of the underlying molecular mechanisms driving JWBD. The findings of this investigation hold the potential to provide valuable scientific insights for the effective management of JWBD in jujube trees, ultimately fostering the sustainable advancement of the jujube industry.The jujube DCL gene family members were identified utilizing high-throughput whole-genome sequencing data of jujube. Subsequently, comprehensive bioinformatics analyses were performed on the acquired gene set. Alignment of the jujube ZjDCLs protein sequences with the homologous counterparts from Arabidopsis (AtDCLs) facilitated the construction of a robust phylogenetic tree, enabling the inference of their evolutionary relationships. Moreover, leveraging transcriptome-wide sequencing data, a

comprehensive examination of the temporal gene expression profiles during distinct stages of jujube pathogen infection was conducted. The expression patterns of ZjDCLs were further validated through quantitative real-time polymerase chain reaction (qRT-PCR) analysis, providing valuable insights into their transcriptional dynamics.A total of 11 jujube DCL genes (ZjDCLs) were identified and named based on their sequential positions on the jujube chromosomes, ranging from ZjDCL1 to ZjDCL11. The ZjDCLs were categorized into four classes, namely DCL1, DCL2, DCL3, and DCL4. Physicochemical property analysis revealed that the molecular weight of ZjDCL proteins ranged from 15,217.48 to 225,623.49 Da, while the isoelectric points varied from 5.82 (ZjDCL11) to 9.05 (ZjDCL2). Chromosomal localization analysis of the ZjDCL genes illustrated their non-uniform distribution across the six jujube chromosomes, with the highest representation observed on chromosome 1.After infection with Jujube Phytoplasma, the expression pattern of Jujube DCL protein changed, indicating that it played a very important role in the response of Jujube to the invasion of Jujube Phytoplasma.