

多组学揭示松材线虫的抗逆性和致病性

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摘要:【目的】松材线虫 (*Bursaphelenchus xylophilus*) 是全球森林生态系统中最具危险性和破坏性的害虫之一。其抗逆性和致病性的遗传基础尚未阐明。了解松材线虫的环境适应性和致病性的分子机制有助于预防和控制松材线虫病。【方法】本研究比较了 9 个线虫物种的基因组, 包括松材线虫 (*B. xylophilus*) 和拟松材线虫 (*B. mucronatus*) 的两个全新基因组组装和分析, 结合多个转录组筛选松材线虫关键的环境适应性和致病性的基因。通过分子生物学技术验证了三个家族基因 (BoIA, DGAT 和 PLCP) 的功能验证。【结果】研究表明, 松材线虫起源于约 2 900 万年前。在松材线虫中, 一系列基因家族迅速扩展, 包括类 BoIA 超家族、二酰甘油酰基转移酶 a 和木瓜蛋白酶样半胱氨酸肽酶。编码松材线虫的三个 BoIA 样基因已被确定为应激反应基因, 能在不利的生长条件下适应生存。分子生物学结果证明, 两个 DGAT 基因对松材线虫的脂质合成至关重要, 在抵抗饥饿和寒冷方面发挥着重要作用。此外, 松材线虫的三个 PLCP 基因能抑制松树的免疫反应, 促进线虫感染松树。【结论】松材线虫 BoIA, DGAT 和 PLCP 三个家族的基因对松材线虫的环境适应性和致病性起着非常重要的作用。

关键词: 松材线虫; Bxy-mix-1; 性别决定; RNAi; 原位杂交

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Integrated analysis of genomics and transcriptomics provides novel insights into the stress resistance and pathogenicity of *Bursaphelenchus xylophilus*

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Abstract: 【Objective】The pine wood nematode (PWN) *Bursaphelenchus xylophilus* is one of the most dangerous and destructive pests in global forest ecosystems. The genetic basis for its stress resistance and pathogenicity has not been elucidated. This work provides valuable information for better understanding the molecular mechanisms of environmental adaptability and pathogenicity of *B. xylophilus* and facilitates the prevention and control of pine wilt disease. 【Method】Here, we compare the genomes of 9 nematode species, including two de novo genome assemblies for *B. xylophilus* and *B. mucronatus*. Our results show that *B. xylophilus* originated ~29 million years ago. Functional validation of three family genes (BoIA, DGAT and PLCP) was verified by molecular biology techniques. 【Results】Within *B. xylophilus*, a wide range of gene families rapidly expanded, including BoIA-like superfamily, diacylglycerol acyltransferase and papain-like cysteine peptidase. The three BoIA-like genes encoding *B. xylophilus* have been identified as stress response genes, enabling adaptation to survive under adverse growth

conditions. And we demonstrate that two DGAT genes are crucial for lipid synthesis in *B. xylophilus*, playing an important role in resisting starvation and cold. Additionally, three PLCP genes in *B. xylophilus* can suppress the immune response of pine trees, facilitating the nematode's infection of pine trees.【Conclusion】*The three families of genes, Bola, DGAT and PLCP, play very important roles in the environmental adaptation and pathogenicity of B. xylophilus.*

Key words: *Bursaphelenchus xylophilus*, comparative genomics, stress resistance, pathogenicity