基于转录组和代谢组揭示 *Coniochaeta velutina* 对胶孢炭疽菌的生防机制

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摘要:【目的】胶孢炭疽菌可以侵染多种植物引起炭疽病，给农林业生产造成巨大的经济损失。本研究发现 *Coniochaeta velutina* 与胶孢炭疽菌在 PDA 培养基上对峙培养后，前者对后者有显著的抑制生长现象。【方法】为了探究 *C. velutina* 对胶孢炭疽菌的作用机制，本研究用 PDA 培养基上纯培养的胶孢炭疽菌作为对照（CK），与 *C. velutina* 对峙培养的胶孢炭疽菌作为处理（T），用转录组学和代谢组学联合分析的方法揭示被抑制生长的胶孢炭疽菌与正常生长的胶孢炭疽菌在基因表达量和代谢物含量方面的差异。【结果】转录组学结果显示每个样品平均产出 6.46 Gb 数据。样品比对基因组的平均比对率为 91.00%，预测的新基因 109 个；共检测到表达的基因数为 15310。两组样品检测到的显著差异表达基因 3938 个（$p<0.05$），其中上调基因 2093 个，下调基因 1845 个。所有显著差异表达基因主要富集在 MAPK 信号通路、抗生素生物合成通路、氨基酸代谢通路、碳代谢通路和过氧化物酶通路。两组样品共鉴定到 452 种代谢物，其中差异代谢物有 138 种。差异代谢物主要富集在次级代谢物生物合成、氨基酸生物合成和 α 亚麻酸代谢等通路。【结论】转录组和代谢组关联分析以及 qPCR 结果证明胶孢炭疽菌与 *C. velutina* 对峙培养过程中，前者细胞内 MAPK 信号发生异常，并且维持细胞正常生长的氨基酸生物合成减少，特别是萜类化合物的减少是生防真菌 *C. velutina* 抑制胶孢炭疽菌生长的主要原因。

The biocontrol mechanism of Coniochaeta velutina against Colletotrichum gloeosporioides was revealed based on transcriptome and metabolome

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Abstract: [Objective]*Colletotrichum gloeosporioides* can infect a variety of plants and cause anthracnose, which causes huge economic losses to agriculture and forestry production. In this study, it was found that *Coniochaeta velutina* inhibited the growth of *C. gloeosporioides* on PDA medium. [Method]In order to explore the mechanism of action of *C. velutina* on *C. gloeosporioides*, this study used pure cultured *C. gloeosporioides* on PDA medium as the control (CK), and *C. gloeosporioides* confrontation cultured with *C. velutina* as the treatment (T). The combination of transcriptomics and metabolomics analysis was used to reveal the differences in gene expression and metabolite content between the inhibited growth of *C. gloeosporioides* and normal growth of *C. gloeosporioides*. [Result]The transcriptomic results showed that each sample produced an average of 6.46 Gb of data. The average alignment rate of the samples to the reference genome was 91.00%, and 109 novel genes were predicted. A total of 15,310 expressed genes were detected in both groups of samples. Among them, 3,938 genes showed significant differential expression ($p<0.05$), with 2,093 up-regulated genes and 1,845 down-regulated genes. All differentially expressed genes were mainly enriched in the MAPK signaling pathway, antibiotic biosynthesis pathway, amino acid metabolism pathway, carbon metabolism pathway, and peroxidase pathway. A total of 452 metabolites were identified in the two groups of samples, of which 138 were different. Differential metabolites are mainly enriched in secondary metabolite biosynthesis, amino acid biosynthesis and α linolenic acid metabolism. [Conclusion]Transcriptome and metabolome association analysis and qPCR results showed that during the confrontation culture between *C. gloeosporioides* and *C. velutina*, the former's intracellular MAPK signaling was abnormal, and the biosynthesis of amino acid that maintained normal cell growth was decreased. In particular, the reduction of terpenoid compounds was the main reason for the inhibition of *C. gloeosporioides* by the biocontrol fungus *C. velutina*.