

Transcriptome analysis of *Neofusicoccum luteum* during avocado branch and fruit infection.

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The most important aerial diseases affecting avocado orchards on the Andalusian coast (Spain) are caused by species of fungi belonging to the Botryosphaeriaceae family, one of the most common being *Neofusicoccum luteum*. The symptoms produced by this fungus are branch dieback and fruit rot. Currently, it is essential to develop strategies to control this disease. In this line, knowledge of the infection mechanisms of the pathogen is considered an essential objective. Therefore, a transcriptomic study was carried out by RNAseq of *N. luteum* growing on avocado branch and fruit in comparison with its *in vitro* growth in PDA medium. Transcriptome analysis revealed a total of 903 and 1271 genes significantly downregulated ($-2 > \text{fold change} > 2$) during growth on branch and fruit compared to growth on PDA, respectively. Among the genes overexpressed in the *N. luteum*/branch/fruit interaction, genes related to mycotoxin production, wall degradation, detoxification of harmful compounds, protein degradation and candidate effector proteins were identified, three of which showed 100% probability (Effector P3) and apoplasmic localization. The analysis of *N. luteum* transcriptome during the infection process will be a very useful tool to better understand the biology and virulence of this emerging pathogen and will help in the development of strategies for its control.