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Abstract Book

P26: Comparative untargeted metabolomic analysis of Alternaria strains to uncover phytotoxic compounds

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Abstract text

Alternaria fungi are major contributors to apple spoilage, causing small brown spots on the fruit's surface as well as leaf blotches, primarily due to the production of a wide range of mycotoxins. Despite their agricultural impact, the complexity of the Alternaria's genetic diversity, the virulence of the strains and the related phytotoxins responsible for Alternaria's symptoms remains poorly understood. This study aims to apply an untargeted metabolomics workflow to investigate the chemical composition of Alternaria spp. and identify the compounds associated with plant damage. The metabolome of different pathogenic and non-pathogenic strains of Alternaria alternata subspecies tenuissima and arborescens was chemically characterized using untargeted mass spectrometry coupled to liquid chromatography (LC-MS), and potential markers features were highlighted by applying multivariate and univariate statistical approaches. Preliminary annotations of the most prominent signals were performed by using SIRIUS platform and a tailored feature-based molecular network (FBMN) approach.

Unsupervised PCA analysis grouped pathogenic and non-pathogenic Alternaria spp. into distinct clusters, indicating that the pathogenicity of the strains is the main source of variability and that its metabolic fingerprint is generally shared among the different strains. Multiple ions characteristic of pathogenic strains were identified: 9% and 16% of the detected features, in positive and negative ionization respectively, were identified as characteristic of pathogenic strains. FBMN analysis indicates that the most intense ions characteristic of pathogenic isolates are grouped together, suggesting the structural similarity of the compounds. As far as their chemical identification is concerned, SIRIUS analysis revealed that most of them could be related to the terpenoid pathway. Identifying these compounds could provide a deeper understanding of the biochemical mechanisms underlying apple spoilage by Alternaria. Further work is necessary to explore and annotate all compounds responsible for Alternaria fruit spots.