

Untargeted metabolomics analysis reveals dynamic changes in azelaic acid- and salicylic acid derivatives in LPS-treated *Nicotiana tabacum* cells

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ABSTRACT:

To counteract biotic stress factors, plants employ multilayered defense mechanisms responsive to pathogen-derived elicitor molecules, and regulated by different phytohormones and signaling molecules. Here, lipopolysaccharide (LPS), a microbe-associated molecular pattern (MAMP) molecule, was used to induce defense responses in *Nicotiana tabacum* cell suspensions. Intracellular metabolites were extracted with methanol and analyzed using a liquid chromatography-mass spectrometry (UHPLC-qTOF-MS/MS) platform. The generated data were processed and examined with multivariate and univariate statistical tools. The results show time-dependent dynamic changes and accumulation of glycosylated signaling molecules, specifically those of azelaic acid, salicylic acid and methyl-salicylate as contributors to the altered metabolomic state in LPS-treated cells.