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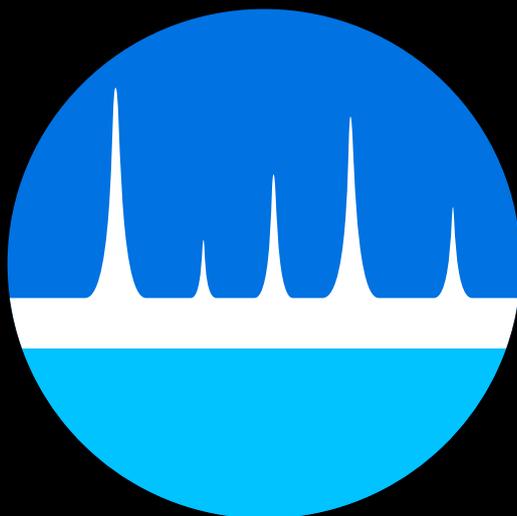
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LIVRO DE RESUMOS
BOOK OF ABSTRACTS

UHPLC-Q-TOF-MS/MS-Based Metabolomics for the Study of Plant-Insect Interactions in Soybean

Josicleia Oliveira Costa*[1], Fernando Mauro Lanças[1], Victoria Patricia Peña Arroyo[2], Felipe Christoff Wouters[2]

[1]Instituto de Química, Universidade de São Paulo, São Carlos, São Paulo, Brazil
[2]Universidade Federal de São Carlos, São Carlos, São Paulo, Brazil

* Corresponding author: cleia.95oliveira@gmail.com

Metabolomics, combined with liquid chromatography coupled to mass spectrometry (LC-MS), has proven to be an effective approach for analyzing complex metabolic changes in plants under biotic stress. This technique allows the identification and quantification of metabolites, providing insights into the metabolic dynamics related to plant defense. Advances in high-resolution mass spectrometry, such as UHPLC-Q-TOF-MS/MS, have expanded the capacity for detecting and annotating a wide range of compounds, increasing the sensitivity and selectivity of the analyses. Soybean (Glycine max L. Merrill), a crop of great economic relevance, is susceptible to herbivory by Spodoptera frugiperda (Lepidoptera: Noctuidae), which impacts productivity. This caterpillar stands out due to its high adaptability and resistance to traditional control methods, such as the use of insecticides, motivating the investigation of plants' natural resistance. The present study evaluated the natural resistance of soybean by assessing the induction of metabolites in young and mature leaves at vegetative stages VC, V2, and V5. For this purpose, UHPLC-Q-TOF-MS/MS was employed in an untargeted metabolomic approach, allowing broad metabolic coverage and annotation of compounds from different chemical classes, including fatty acids, phenolics, and terpenoids. The results showed that stages VC and V2 were the most responsive to herbivory-induced stress, presenting greater metabolic alterations. In contrast, stage V5 exhibited lower metabolic induction, with compounds exclusively related to primary metabolism. Fatty acids, phenolic acids, and terpenoids were the main metabolites detected during the vegetative phase, but their accumulation differed between young and old leaves, with young tissues appearing more inducible than older ones. These findings reinforce that leaf age and plant developmental stage directly influence the magnitude of metabolic induction. Furthermore, they highlight UHPLC-Q-TOF-MS/MS as a robust tool to investigate plant defense mechanisms and characterize herbivory-induced metabolic changes, providing insights into natural resistance in soybean and the importance of this technique in studying plant-insect interactions.