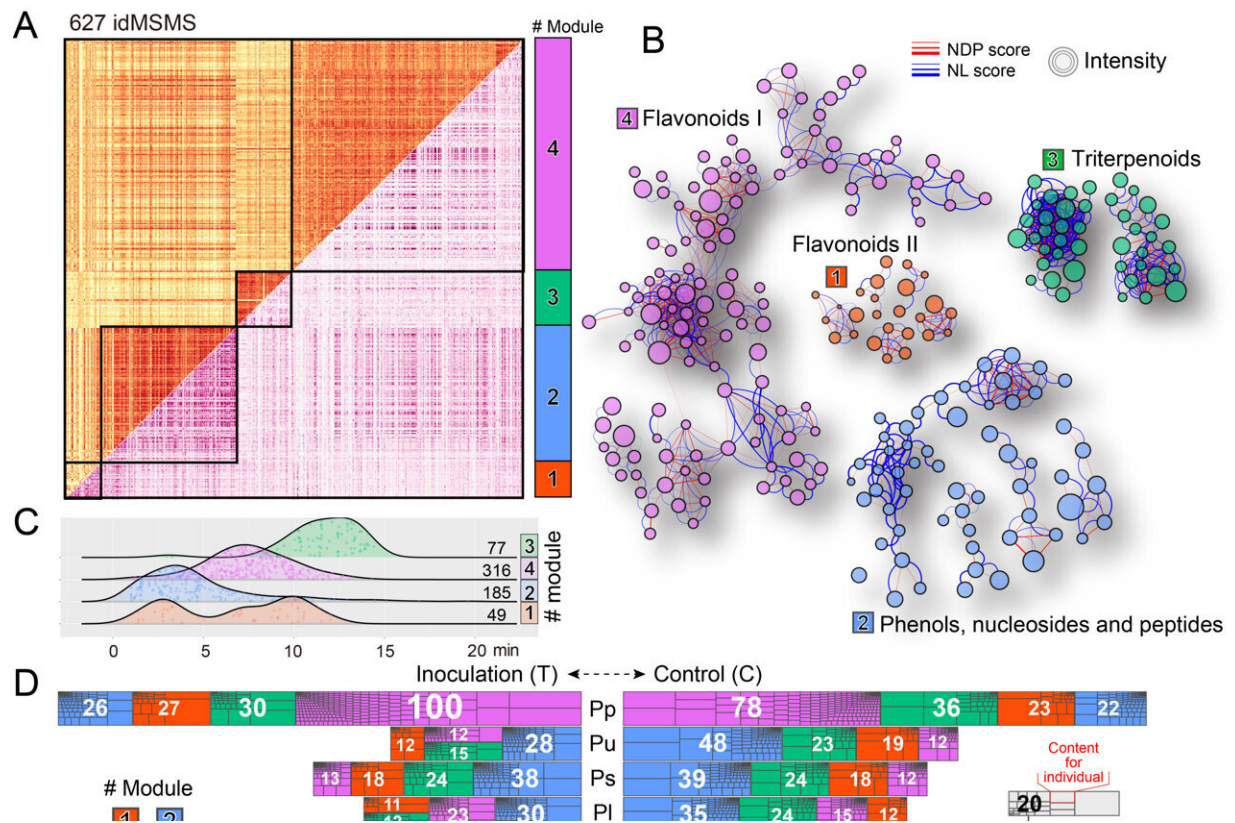


# Metabolomic insights into soybean defense strategies against diverse pathogens

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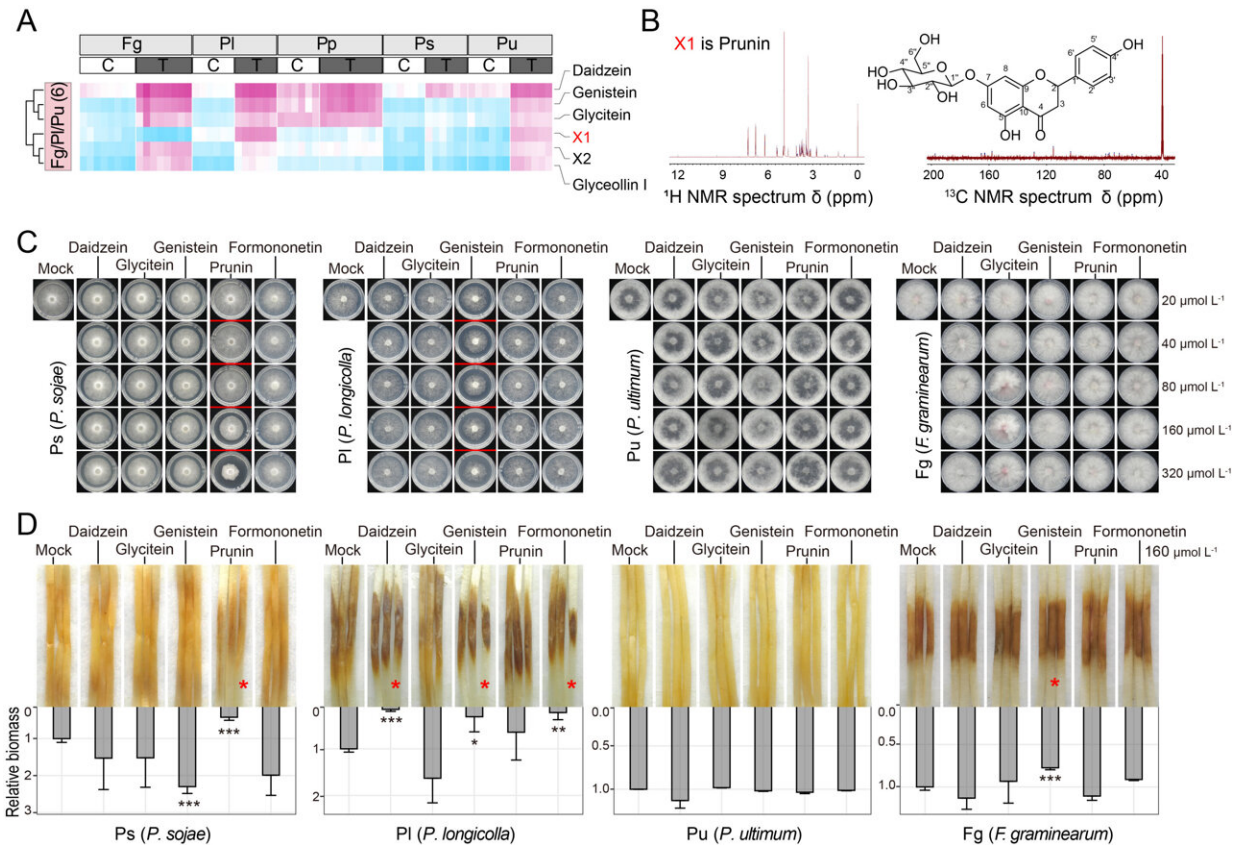
In soybean, the structural elucidation infers four main metabolic modules and their differential distributions in response to five pathogens. Credit: Science China Press

Soybean, as a globally critical leguminous crop, faces continuous threats from different pathogens, which profoundly affect global production.

Although the genetic interactions between soybean and pathogens have attracted extensive attention and research, the complex biochemical responses remain poorly understood. Qiu Min and colleagues decided to use targeted and untargeted liquid chromatography-mass spectrometry (LC-MS) metabolomics to dissect the intricate interactions between soybean and various pathogens.

The team identified a total of 627 featured metabolites in infected [soybean](#) samples, which were clustered into four modules covering [flavonoids](#), isoflavonoids, triterpenes, [amino acids](#) and peptides, and other compounds such as phenols. Researchers found significant changes in both primary and secondary metabolism in response to pathogen invasion.

The bidirectional changes in total flavonoids across diverse pathogenic inoculations were particularly notable. Noteworthy among the highly inducible total flavonoids were known representative anti-pathogen compounds (glyceollin I), backbone forms of isoflavonoids (daidzein, genistein, glycitein, formononetin), and newly purified compounds in this study (prunin).



The functional validation of five inducible compounds. Credit: Science China Press

Subsequently, the authors further demonstrated the biological roles of these five compounds, validating their diverse functions against pathogens: prunin significantly inhibited the vegetative growth and virulence of *Phytophthora sojae*; genistein exhibited a pronounced inhibitory effect on the vegetative growth and virulence of *Phomopsis longicolla*; daidzein and formononetin displayed significant repressive effects on the virulence of *P. longicolla*.

This study underscores the potent utility of metabolomic tools, providing in-depth insights into plant-pathogen interactions from a biochemical

perspective. The findings not only contribute to plant pathology but also offer strategic pathways for bolstering plant resistance against diseases at a broader scale.

The work is [published](#) in the journal *Science China Life Sciences*. This study was reported by Professor Wang Ming's research team from Nanjing Agricultural University, led by Professor Wang Yuanchao.

**More information:** Min Qiu et al, Decoding the biochemical dialogue: metabolomic insights into soybean defense strategies against diverse pathogens, *Science China Life Sciences* (2024). [DOI: 10.1007/s11427-023-2596-1](#)

Provided by Science China Press

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