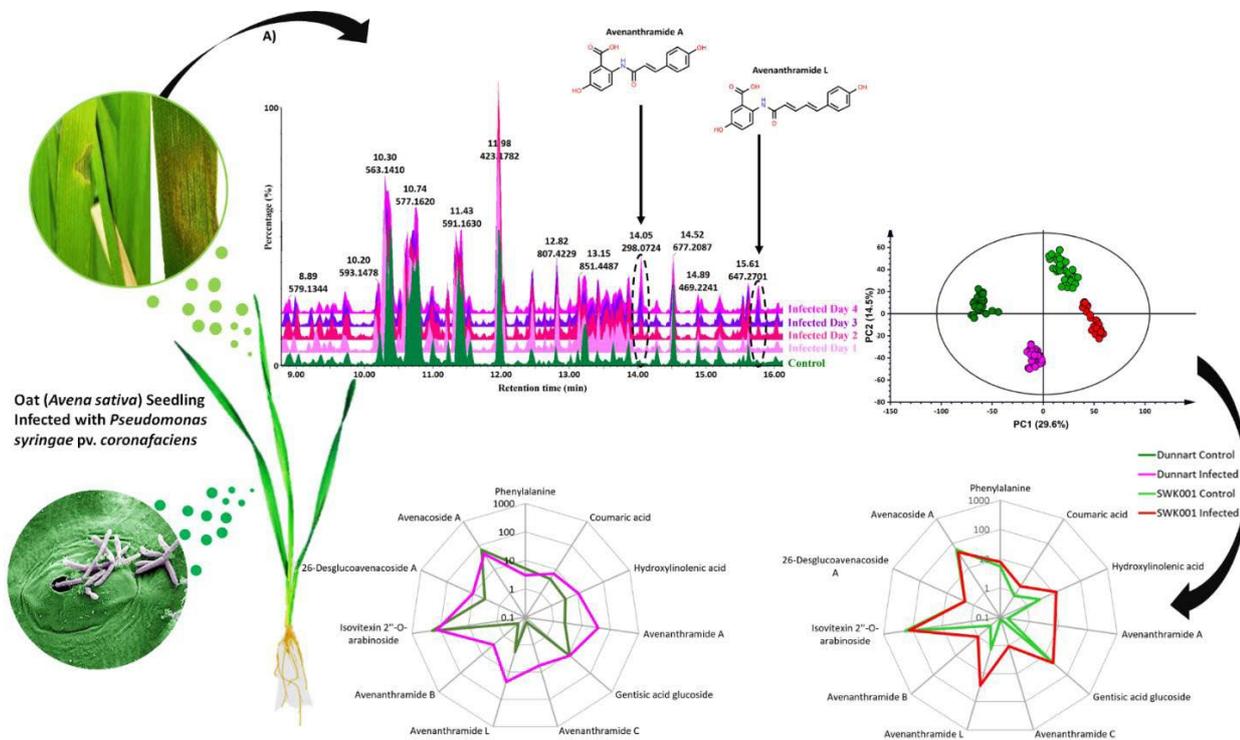


# Metabolomics of Plant Defense : The *Pseudomonas coronafaciens* – *Avena sativa* Interaction

CJ Pretorius, F Tugizimana, P Steenkamp, L Piater, I Dubery\*

Research Centre for Plant Metabolomics, Department of Biochemistry, University of Johannesburg, South Africa



Metabolomic characterisation of halo blight disease in oat plants

**Introduction:** The metabolome is the underlying biochemical layer of the phenotype and offers a functional readout of the cellular mechanisms involved in a biological system. Since metabolites are considered the end-products of regulatory processes at a cellular level, their levels are regarded as the ultimate response of the biological system to genetic or environmental changes. Hence, the metabolome serves as a metabolic fingerprint of the biochemical events that occur in a biological system under specific conditions.

**Methodology:** In this study, an untargeted metabolomics approach was applied to elucidate biochemical processes implicated in oat plant responses to *Pseudomonas syringae* pv. *coronafaciens* (Ps-c) infection and to identify signatory markers related to defence responses and disease resistance against halo blight. Metabolic changes in two oat cultivars (Dunnart and SWK001) responding to Ps-c, were investigated at the 3-leaf growth stage and metabolome changes monitored over a 4-day post-inoculation period. Metabolites were extracted using an 80% methanol extraction method. The extracts were analysed using an ultra-high-performance liquid chromatography (UHPLC) system coupled to a high-definition mass spectrometer analytical platform. The acquired multi-dimensional data were processed using multivariate statistical analysis and chemometric modelling.

**Results:** The demonstrated chemometric models indicated time- and cultivar-related metabolic changes, defining the host response to the bacterial inoculation. Further multivariate analyses of the data were performed to profile differential signatory markers, which included amino acids, phenolics, phenolic amides, fatty acids, flavonoids, alkaloids, terpenoids, lipids, saponins and plant hormones.

**Conclusion:** Based on the results, metabolic alterations involved in oat defence responses to Ps-c were elucidated and key signatory metabolic markers defining the defence metabolome were identified. The study thus contributes toward a more holistic view of the oat metabolism under biotic stress.

**Keywords:** *Avena sativa*; LC-MS; metabolomics; multivariate data analysis; Oat; *Pseudomonas syringae* pv. *coronafaciens*; secondary metabolites.