Summary of scientific achievement

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Climate change and caused by it environmental stresses are leading to a decline in global crop production. In order to maintain food security, it is important to introduce new plant varieties that are able to survive adverse conditions. One element in the acclimatisation of plants to changing environmental conditions is the biosynthesis of low-molecular compounds that have multiple functions in their metabolism and defence against stresses. Metabolomics, the comprehensive analysis of these compounds present in biological systems, has become a powerful tool for studying the complex interactions between plants and the environment. Techniques such as liquid chromatography (LC) or its combination with mass spectrometry (LC-MS) have been successfully used in the search for molecular markers of plant tolerance to environmental stresses. The primary objective of my research has been to identify elements of the metabolomic response of plants to environmental stresses, both abiotic and biotic. My research achievements include the development and optimisation of methodologies for comparative metabolomics to search for biomarkers of tolerance to drought and resistance to fungal pathogens in plants. I have conducted research on the identification of metabolomic biomarkers of drought tolerance as well as phenomena related to plant acclimatisation to the effects of drought. Based on mass spectra, I identified a number of metabolites that significantly alter their accumulation under water deficit conditions. Flavonoids, hydroxycinnamic acids and apocarotenoids predominated among them. Correlations of metabolites with quantitative trait loci (QTL) have shown that these metabolites in drought are associated with antioxidant processes, regulation of gene expression and modulation of protein function in barley plants. On the other hand, acclimatisation processes influenced metabolomic profile in correlation to yield physiological parameters.

Metabolomic studies play a key role in understanding the immune response of plants to pathogenic fungal infections. *Fusarium* spp., including *F. culmorum*, are the cause of cereal diseases, leading to a dramatic reduction in yield and mycotoxin production. I have identified both common and genotype-specific metabolites with altered accumulation in response to the pathogen. Metabolites correlating with increased resistance to the pathogen belonged to different structural classes, including tryptophan derivatives, pyrimidines, proline and serine amino acids, and jasmonic acid. Description of the metabolome in different organs of *Brachypodium distachyon*, allowed me to compare the immunological response in model plant to barley and wheat. I have identified numerous threonic acid derivatives, characteristic of this species, which are absent in barley and wheat, and which may be important in the context of using *B. distachyon* as a model plant for genomic studies in the Poaceae family. I have also been interested in questions of the evolution of pattern-triggered resistance (PTI) in plants of the Brassica family. The results show that PTI variation at the transcriptome and metabolome level in different Brassicaceae species is not consistent with their phylogenetic similarity. This issue was extended to a comparative analysis of the biosynthesis of glucosinolates, specialised metabolites with immunological functions in the cabbage family. The results suggest an adaptive advantage of long-chain aliphatic glucosinolates in the tribe *Camelineae* over short-chain structures found in abundance in the model plant *Arabidopsis thaliana* .

Findings from my research may contribute to the development of new breeding strategies to increase plant resistance to environmental stresses and pathogen infections. The development of an advanced approach for functional integration and correlation of multiomics data jets a great contribution to the creation of a comprehensive model platform to study the mechanisms of plant responses to environmental stresses.