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Analysis of cereal response to abiotic stress using gel-based proteomics

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Plant exposure to stress induces a dynamic proteome response aimed at a damage recovery and an adaptation to the stress condition. The two-dimensional differential gel electrophoresis (2D-DIGE) analysis enables protein relative quantification leading to an identification of the protein spots revealing an enhanced abundance in stress-treated or stress-tolerant varieties which could be further tested as potential markers of stress tolerance. Proteomic experiments aimed at crop (wheat, barley, melon) proteome response to cold, drought and/or salinity were analyzed. The aim of these analyses was to identify protein spots revealing differential abundance between different stress treatments or differently tolerant genotypes that could be potentially used for abiotic stress phenotyping. Unsurprisingly, the majority of potential proteins for phenotyping belong into stress- and defense-related proteins. The results of proteomic analyses were interpreted with respect to other physiological data such as parameters related to stress tolerance (membrane stability, LT50), water regime-related characteristics (water saturation deficit, osmotic potential) and others. The role of gel-based proteomic analysis in understanding plant stress response and acquisition of plant stress tolerance is discussed.

Biography

Pavel Vítámvás completed his PhD study on Anatomy and Plant Physiology at Charles University, Prague. He is Senior Scientist and the Head of Laboratory of Plant Proteomics in Crop Research Institute in Prague. He has published 30 papers in journals with impact factor (WoS: H-index 13). He is interested in the study of plant response to abiotic and biotic stresses on protein level.

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