Exploring the Plant–Microbe Interface by Profiling the Surface-Associated Proteins of Barley Grains

Cereal grains are colonized by a microbial community that actively interacts with the plant via secretion of various enzymes, hormones, and metabolites. Microorganisms decompose plant tissues by a collection of depolymerizing enzymes, including β-1,4-xylanases, that are in turn inhibited by plant xylanase inhibitors. To gain insight into the importance of the microbial consortia and their interaction with barley grains, we used a combined gel-based (2-DE coupled to MALDI-TOF-TOF MS) and gel-free (LC–MS/MS) proteomics approach complemented with enzyme activity assays to profile the surface-associated proteins and xylanolytic activities of two barley cultivars. The surface-associated proteome was dominated by plant proteins with roles in defense and stress-responses, while the relatively less abundant microbial (bacterial and fungal) proteins were involved in cell-wall and polysaccharide degradation and included xylanases. The surface-associated proteomes showed elevated xylanolytic activity and contained several xylanases. Integration of proteomics with enzyme assays is a powerful tool for analysis and characterization of the interaction between microbial consortia and plants in their natural environment.
Original language: English

Keywords: Cereal proteins, Mass spectrometry, Proteome analysis, Xylanase activity, Metaproteome, Microbial communities, Environmental proteomics

DOIs: 10.1021/acs.jproteome.5b01042

Source: FindIt

Source-ID: 2292502925

Research output: Research - peer-review; Journal article – Annual report year: 2016