

Barley germination - DTU Orbit (09/11/2017)

Barley germination: Spatio-temporal considerations for designing and interpreting 'omics' experiments

Germination of barley grain is central to the malting industry and is a valuable model for cereal grain germination. Our current understanding of the complexity of germination at the molecular level is facilitated by access to genomic, transcriptomic, proteomic and metabolomic data. Here we review recent progress in barley germination research and discuss the factors to be considered when designing 'omics' experiments and interpreting the results. These factors include the structural and functional relationships between the various tissues of the barley caryopsis and the timing of the events of germination in the context of industrial malting. For transcriptomics, recent advances in sequencing the barley genome allow next-generation sequencing approaches to reveal novel effects of variety and environment on germination. For proteomics, selection of the source tissue(s) and the protein extraction conditions continue to be key to discovering the roles of individual protein forms and posttranslational modifications, such as glycosylation. Activity-based proteomics, particularly in combination with new gene editing technologies, has great potential to elucidate the network of enzymes in barley germination. Lastly, the application of metabolomics to barley grain germination provides essential data on biochemical processes, including insights into the formation of compounds that contribute to malt quality. To maximize the benefits of the 'omics' revolution to the malting industry, there is a need to integrate these data, taking into account barley variety, time, tissue, and specific physiological processes.

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Organisations: Department of Systems Biology, Enzyme and Protein Chemistry, University of Sydney

Authors: Daneri-Castro, S. N. (Ekstern), Svensson, B. (Intern), Roberts, T. H. (Ekstern)

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