

High-throughput Phenotyping – a Boost for Genomics in the 21st Century

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Due to the development of highly automated genetic analysis, plant genomics has immensely enlarged our understanding of the genetic structure of plants over the last two decades.

The fast evolving need to identify interactions between genes and environmental factors (biotic and abiotic) that brings about a certain plant phenome made it necessary to develop quantitative, reproducible and highly automated plant phenotyping systems for large plant numbers.

Phenotyping systems such as these have to integrate reproducible plant management (randomization, watering) and comprehensive imaging of root and shoot far beyond human vision (visible light, fluorescence, near infrared, infrared, X-rays, THz) as well additional chemical analysis methods. Immediate and automated image analysis of the stored images and further data transformation using plant shape and plant growth models are the important intermediate steps before undertaking statistical data analysis of the phenotyping results to characterize plant phenotypes quantitatively. Such quantitative data contributes in a decisive way to the further analysis of gene functions (tilling, QTL etc.), especially under fluctuating or stress-induced environmental conditions with a special focus on complex traits like yield or drought tolerance. This presentation will provide a survey on phenotyping technology and the close interaction between phenotyping technologies, modeling approaches and the new opportunities of fast and automated high-throughput genomics.