

FORWARD AND REVERSE GENETICS APPROACHES FOR THE CHARACTERIZATION OF BARLEY PLANT ARCHITECTURE GENES

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With its diploid genome fully sequenced, and availability of extensive mutant collections, barley is not only a major global crop but also an established model for genetic analysis in the Triticeae tribe. In cereals, tiller number, leaf size and orientation have direct implications for plant productivity and adaptation to the environment. Thus, knowledge of their genetic basis is an important prerequisite for breeding of improved varieties. In order to discover/characterize genes underpinning these traits in barley, our group is applying forward and reverse genetic screens on TILLING populations such as HorTILLUS, obtained by chemical mutagenesis of the two-row spring cultivar Sebastian.

Starting from two rounds of screening under field conditions in two different environments, we identified two lines exhibiting more erect leaf angle compared to the Sebastian background. Mapping-by-exome-sequencing

placed the first locus on chromosome 5H and uncovered a splice-junction mutation in the barley *HvDEP1* gene as the causative variant for erect habit and short stature, as also supported by allelism with the *ari-e.GP* mutant. Positioning of the second locus on telomere of chromosome 7HL via SNP array Bulk Segregant Analysis provides an ideal starting point for fine mapping and candidate gene searches.

In parallel, we are characterizing mutants altered in the pathway of strigolactones, a class of phytohormones playing a key role in plant architecture and abiotic stress responses. Allelic variants of a barley strigolactone biosynthesis gene were isolated from reverse screens of the HorTILLUS population, and phenotypic analyses suggest a role for this gene in shoot and root architecture. The performance of these lines under different water availabilities is under investigation at the PlantArray physiological phenotyping platform and complementation of the corresponding Arabidopsis mutant is used to test for functional conservation between the two species.

The selected mutants represent interesting materials to better understand the molecular mechanisms controlling plant architecture in barley.

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