Research interest

Our research group has a strong focus on identification and utilization of genes regulating quantitative traits (QTLs) in barley and wheat. For this reason, we study the genetic diversity present in wild barley and wild wheat species by means of advanced backcross (AB) QTL analyses. So far, we identified numerous QTLs for the trait complexes yield, pathogen resistance, abiotic stress tolerance and grain quality. Quite often, the exotic QTL allele is associated with the improvement of the trait under investigation.

Currently, we are setting up a representative introgression library for barley (see picture). Each introgression line (IL) contains a single chromosomal segment from wild barley in the genetic background of the elite cultivar Scarlett. In addition, we produce segregating high resolution populations, multi-cross populations and double introgression libraries, all originating from crosses with exotic barley. These genetic resources are used to study the exotic variability present in barley and epistatic interactions between QTLs. The established ILs are used in collaboration with extra-mural partners, to identify and verify QTLs and to explain QTL effects on different expression levels. These are the genome, transcriptome, proteome, metabolome and the phenotype.

In collaboration with breeders, useful ILs, which improve relevant traits for agriculture, are crossed with modern elite lines and employed through marker–assisted selection (MAS) in order to develop new elite cultivars. Simultaneously, promising QTLs are subjected to map-based cloning. In the long run, the isolated genes will allow us to study their molecular effects on the regulation of defined phenotypes of agronomic importance for barley and wheat cultivation.

Selected publications