

## IDENTIFICATION AND CHARACTERIZATION OF MAJOR QTLs FOR CULM DIAMETER IN BARLEY

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Barley (*Hordeum vulgare* L.) is one of the most important cereal crops and it has been extensively used as a model for plant genetic analyses and breeding. Stem lodging in barley can cause a reduction in grain yield and quality. The morphology and the composition of the culm has been associated with lodging resistance in cereals. However, the genetic and molecular bases underlying culm architecture traits are poorly understood in barley.

Multi-Environment GWAS analysis for culm morphology on a panel of European spring two-row barleys led to the identification of three stable QTLs across environments. For estimating the QTL effects, six lines were selected as parents based on their contrasting phenotypes for culm diameter and different alleles at the selected QTLs to make three different crosses. Further evaluation of selected parents confirmed their contrasting phenotypes for the culm diameter. For each cross, BC1F1 segregating populations were obtained by crossing the F1 plants to the respective small culm parent. In collaboration with the University of Silesia, the development of Double Haploids (DH) lines carrying different allele combinations for the target QTL(s) from the BC1F1 plants is underway. At the same time, candidate genes at the QTL regions are being targeted for identification of allelic variants by screening of the *HorTILLUS* mutagenized population developed by University of Silesia.

A further goal of our research is the identification of mutants for culm morphology traits in the six-row barley mutagenized population TILLMore, developed by University of Bologna. In a preliminary field screening, we selected 57 lines that were subsequently grown in the greenhouse in completely randomized blocks with 10 replicates. Mutants with increased/decreased culm diameter compared to the wild type Morex background were identified through the analysis of phenotypic data.

This work is expected to put the basis for the advancement of lines carrying favourable alleles for culm diameter and identifying the underlying genes controlling this trait.

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