

EXPLORING NATURAL AND INDUCED VARIATIONS FOR THE GENETIC IMPROVEMENT OF BARLEY BIOMASS AND YIELD

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With the increasing demands for renewable energy sources, plant biomass such as cereal straw is becoming more attractive. The BarPLUS project aims at finding genes, alleles, and candidate lines related to barley architecture and photosynthesis to maximize barley biomass and yield (<https://barplus.wordpress.com/>). The major focus of our research group is to identify genes and alleles controlling tillering, leaf size and angle exploiting both induced and natural allelic variation. Using a forward genetics approach, we screened the *Hor*Tillus population derived from chemical mutagenesis of the barley cultivar “Sebastian” under both field and controlled conditions and identified mutants with increased tillering and/or erect leaves. The selected candidate lines were crossed with two reference cultivars and the mapping populations are being targeted for mapping-by-sequencing to isolate the underlying genes. We also utilized genome wide association on a set of 240 diverse barley accessions with exome capture data provided by the WHEALBI consortium (<http://www.whealbi.eu/>) in order to dissect natural allelic variation in leaf size and angle. Data were collected from the WHEALBI field trial for precision phenotyping of canopy development (Fiorenzuola d'Arda, Italy). High-throughput protocols based on the PocketPlant3D smartphone app for leaf angle and quantitative image-analysis for leaf size were exploited. Strong positive correlations were observed between leaf size parameters. In addition, leaf width and area had moderate to weak negative correlations with leaf angle, respectively. Noteworthy, 6-row barleys had higher values than 2-row barleys for leaf size parameters whereas leaf angle was higher in 2-row barleys, indicating the effect of row-type on the traits. High heritability values supported the existence of genetic factors for both traits, and several markers potentially associated with leaf size and angle were detected and are under evaluation for validation and analysis of potential candidate genes. In parallel, based on previous knowledge in model plants, a total of 48 candidate genes involved in canopy architecture and photosynthesis were selected for allele mining analyses. Taking advantage of WHEALBI exome capture data, in silico analysis of the corresponding sequences

revealed the presence of several variants with potential effects on protein function. Finally, using reverse genetics approach, we targeted a subset of candidate genes for TILLING and identified several interesting mutations: the candidate lines are currently growing under controlled condition to confirm their phenotypes. Together, this research will provide valuable knowledge and resources for potential improvement of barley biomass and yield.