

## QUEST FOR BARLEY CANOPY ARCHITECTURE GENES IN THE HORTILLUS POPULATION AND WHEALBI GERMPLASM COLLECTION

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Barley grains are predominantly used for animal feed and malting, and breeding traditionally focused on increase of grain yield by partitioning biomass from straw to grains. The increasing demand for renewable energy sources makes straw, and specially barley straw characterized by the largest content of carbohydrates among the cereals, a valuable product for its potential conversion into biofuels and other products. The BarPLUS project aims at finding genes, alleles and candidate lines related to barley canopy architecture and photosynthesis, to maximize barley biomass and yield (<https://barplus.wordpress.com/>). In this framework, our research group focuses on identifying genes and alleles controlling tillering, leaf size and leaf angle traits in barley by exploiting both induced and natural allelic variation. Using a forward genetics approach, we screened the *HorTILLUS* population (Szurman-Zubrzycka et al., 2018) under both field and controlled conditions, identifying 5 mutants with increased tillering and/or erect leaves. After crossing with four reference cultivars, pools of F2 wild-type and mutant plants were selected to map and identify the underlying genes by exome sequencing (Mascher et al., 2014). In parallel, TILLING of the *HorTILLUS* population identified four lines carrying mutations in the LBO (Lateral branching oxidoreductase) gene involved in tiller number. In order to explore also natural genetic variation, we are taking advantage of the 'WHEALBI' germplasm collection, which includes 403 exome-sequenced diverse accessions (Bustos-Korts et al., 2019): a field trial on a subset of 240 lines (Fiorenzuola d'Arda, Italy) allowed us to conduct a preliminary genome wide association study based on high-throughput phenotyping for leaf angle (PocketPlant3D smartphone app) and quantitative image-analysis for leaf size. Results will be compared with those from a greenhouse experiment on the same 240 accessions to analyze a wide range of morphological traits and identify associated markers and genomic regions.