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GENETIC DISSECTION OF NATURAL VARIATION FOR CULM MORPHOLOGICAL TRAITS IN BARLEY

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Barley (*Hordeum vulgare* L.) ranks fourth among cereals for worldwide production. Despite the introduction of semi-dwarfing genes to improve stem sturdiness and harvest index, extreme climatic events associated to climate change are causing lodging and yield losses. Culm morphological and anatomical features have been linked to lodging resistance in rice and wheat, but information is very scarce for the genetic basis of such traits in barley. As part of the ClimBar project, the objective of our studies is to explore and dissect natural genetic variation for culm traits in barley, using a diverse germplasm collection including more than 240 barley accessions previously genotyped with the 9k iSelect SNP chip. In particular, we are mainly focusing on analysis of the second (basal) internode, as a critical site for lodging in barley. Phenotypic data were collected from field-grown plants in three different locations in Italy, Spain and UK at pre-harvest growth stage. Straw samples were dissected and subjected to image analysis to extract quantitative data for culm diameter and culm wall thickness. Statistical analyses indicated the existence of significant genetic variation for the studied traits, as supported by high heritability values. For GWAS, 3661 markers were considered, applying minor allele frequency ≥ 0.1. Marker-based Principal Components Analysis indicated the presence of population structure due to spike row-type (2-rowed vs. 6-rowed), an important trait associated with domestication in barley. Significant marker-trait associations for both culm diameter and culm wall-thickness were identified across trials (FDR significant threshold values <0.01). In addition, trial-dependent associations were detected, possibly due to the existence of QTL-environment interactions for the studied traits. To gain further insight into the genetic control of culm morphology, hand sections from internodes collected at dough stage (Italy field trial) were stained to allow measurement of culm diameter, as well as counting of vascular bundles. The analysis of green culm data indicated high heritability values for the studied traits and GWAS identified numerous associated markers, including some shared with those identified from straw culm data. This is in agreement with correlation of culm diameter between straw and green culm samples ($r=0.716$). SNP variants identified from exome resequencing of the studied accessions will be used to refine these results, identify putative candidate genes and carry out allelic diversity studies.

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http://plen.ku.dk/english/research/plant_soil/breeding/quality/climbar/