

MONITORING DROUGHT RESPONSES OF BARLEY GENOTYPES WITH SEMI-ROBOTIC PHENOTYPING PLATFORM AND ASSOCIATION ANALYSIS BETWEEN RECORDED TRAITS AND ALLELIC VARIANTS OF SOME STRESS GENES

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Genetic improvement of complex traits such as drought adaptation can be advanced by the combination of genomic and phenomic approaches. Semi-robotic phenotyping platform was used for computer-controlled watering, digital and thermal imaging of barley plants grown in greenhouse. In soil with 20% water capacity the reduction in green pixel-based shoot surface area of tested barley variants ranged from 0% to 76% as compared to control plants grown with 60% water capacity. The EcoTILLING and the subsequent DNA sequencing have defined four (A-D) haplotypes of the HvA1 gene encoding the group 3 LEA protein. The green pixel mean value of genotypes with haplotype D was higher than the mean value of the remaining haplotypes under drought. Thermal images indicated genotype-dependent variation in elevation of the canopy temperature of drought-exposed plants. The drought-induced changes in leaf temperature showed low correlation with the water use efficiency ($r^2 = 0.431$). The haplotype/trait association analysis based on the t-test has revealed a positive effect of the haplotype B of the gene encoding the barley fungal pathogen induced mRNA for pathogen-related protein (HvPPRPX) on harvest index, thousand grain weight, water use efficiency and grain yield. The presented pilot study establishes basic methodology for the integrated use of phenotyping and haplotyping data in characterization of genotype-dependent drought responses in barley.