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Whole Genome Association Mapping And Exploitation Of Marker Trait Associations In Barley Breeding

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In a genome-wide approach to associate genetic diversity to agronomically important traits in barley (*Hordeum vulgare* L.) a set of 113 German winter barley cultivars representing breeding progress within the period 1959-2003 was genotyped using the Illumina GoldenGate BeadArray. Phenotypic data were obtained from field trials carried out at 12 locations in three years. In summary, 221 significant associations regarding all traits analyzed corresponding to 128 different SNPs were detected based on primary phenotypic data. In addition to this, existing data records (secondary data) available from German VCU trials were used to calculate marker-trait associations. Phenotypic data were corrected for all site and weather parameters that proved to influence the traits significantly. A total of 79 loci were found to be significantly associated with yield, crop density, kernels per spike and thousand grain weight. About one third of these loci (26) corresponded to those identified based on data obtained from the exact field trials. In order to prove whether the marker-trait associations detected can be efficiently applied in barley breeding verification in bi-parental populations was conducted by analyzing segregating doubled haploid (DH) populations derived from intercrosses of these cultivars. Seven populations comprising 600 DH-lines have been phenotyped in one-year field trials at two locations each. Genotyping of these populations was done with the respective SNPs linked to the trait of interest using an Illumina VeraCode GoldenGate custom 144plex SNP genotyping assay. The use of verified markers associated to the detected QTLs will facilitate efficient selection of parental lines and marker assisted selection procedures in allele based barley breeding.