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Detection of significant loci associated with agronomical important traits in Serbian barley core collection

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Barley (*Hordeum vulgare* L. subsp. *vulgare*) is the second most important cereal crop widely grown in a range of various climate and environmental conditions, primarily used for livestock feed, in alcohol production and human consumption. The main objective of this study was to assess genetic diversity and to reveal the genomic regions, which control the most valuable breeder's traits, important for Serbian barley breeding programme. A set of 71 diverse elite lines and well-adapted commercial barley cultivars was used for genotypic and phenotypic evaluation. The field trial was conducted near Novi Sad, at Rimski šančevi, Serbia, while the following agronomic traits were measured during the three growing seasons: heading and flowering time, stem height, yield, thousand grain weight, hectolitre mass and spike length. A set of 15 microsatellites, covering all linkage groups, was used to detect 83 polymorphic alleles with an average of 5.53 alleles per locus. A satisfying level of differentiation and informativeness in almost all genomic loci were found. The PIC values ranged from 0.108 (GMS001) to 0.740 (Bmac0067). Population structure distributed the genotypes into two clusters primarily corresponding with row type. A total number of 18 marker-trait associations was detected in two and/or three years by applying general linear model, whereas mixed linear model confirmed presence of stable associations for 5 QTLs. Flowering time and spike length were associated with 5 analysed markers, whereas hectolitre weight did not show significant associations with the analysed markers. The stable and significant QTLs could be of the great importance for further improvement of barley varieties during the selection of the parents, which carry desirable alleles and could be valuable preliminary groundwork for further genomic selection with fine-tuning refinement.

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