

عنوان مقاله:

Genetic architecture of traits affected barley lodging by GWAS

محل انتشار:

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خلاصه مقاله:

Association analysis based on the evaluation of unrelated accessions provided an additional option to identify the loci (genes and/or QTLs) for traits. To determine marker/trait association, 148 modern European spring barley cultivars were evaluated. Traits caused lodging such as plant height (PH), internode length (IL) and number of main stem nodes (MSN) were measured. Associations of morphological traits with AFLP/SSR markers were investigated based on the mixed linear model using the TASSEL3.0. Linkage disequilibrium analysis showed that by increasing genetic distance, LD decreases. A total of 56 significant associated markers for traits were identified in both treatments. Six markers displayed significant associations with plant height (PH) in 90% fc treatment and seven markers in 40% fc treatment. A stable significant associated marker (E35M54-163) for Plant Height was detected in 40% fc treatment. Twenty-four markers were found to be significantly associated with the trait, Internode Length (IL), in both treatments in the two years. In 90% fc treatment, QTLs were found on 5H, 4H (2016) and 1H, 2H (2017), while in 40% fc treatment, they were observed on 5H, 4H, 2H and 7H. A stable QTL was detected on 5H (Bmag0223) for Internode Length in 40% fc treatment. Total number of markers associated with number of main stem nodes (MSN) was nineteen. In 90% fc treatment, a QTL region was detected on 2H at 88.013, which was previously reported as 'Zeo' QTL for 'Zeocriton dwarf' trait. Several significant markers were found to be co-localized with previously mapped QTLs for traits together. Results of this study provide an insight into the genetic architecture of important morphological traits in barley affected lodging.

کلمات کلیدی:

Lodging; Barley; GWAS; QTLs

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