

Identification of new QTLs for dietary fibre content in an *Aegilops biuncialis* collection through a GWAS approach

Supplementary Material

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Table S1.

Phenotypic data of grain quality traits (β -glucan, total and water-extractable pentosans, and protein content) measured in a collection of 83 *Aegilops biuncialis* accessions and the Mv9kr1 wheat genotype for two years.

Table S2.

Results of the BLASTn search of SNP-DaT markers associated with grain quality traits against the draft sequence assemblies of M and U genome chromosomes of *Ae. comosa* and *Ae. umbellulata*, respectively, and the reference sequences of hexaploid wheat chromosomes (Ensembl Plants, release-46).

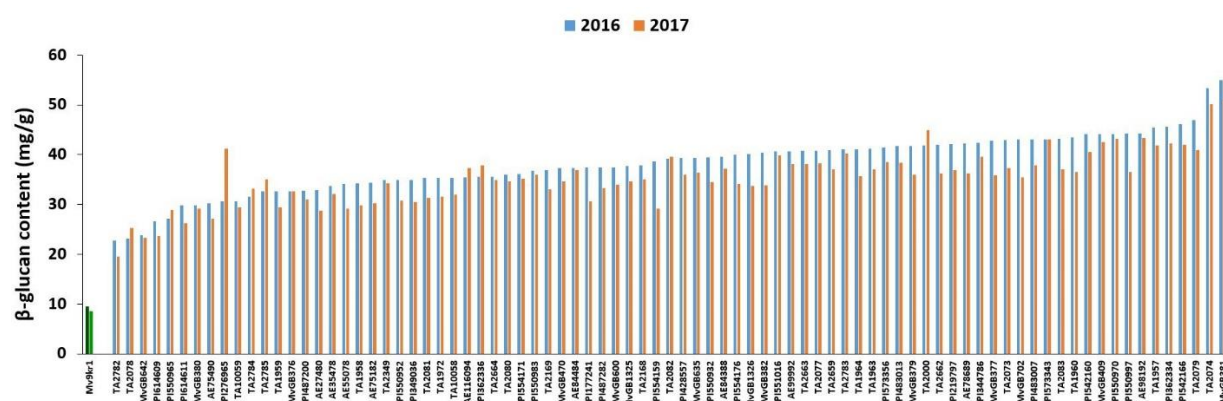


Figure S1. Intraspecific variation of β -glucan content in the *Ae. biuncialis* collection (2016, 2017, n=83). The β -glucan content of the Mv9kr1 wheat genotype was labeled with green (2016: dark-green, 2017: pale-green).

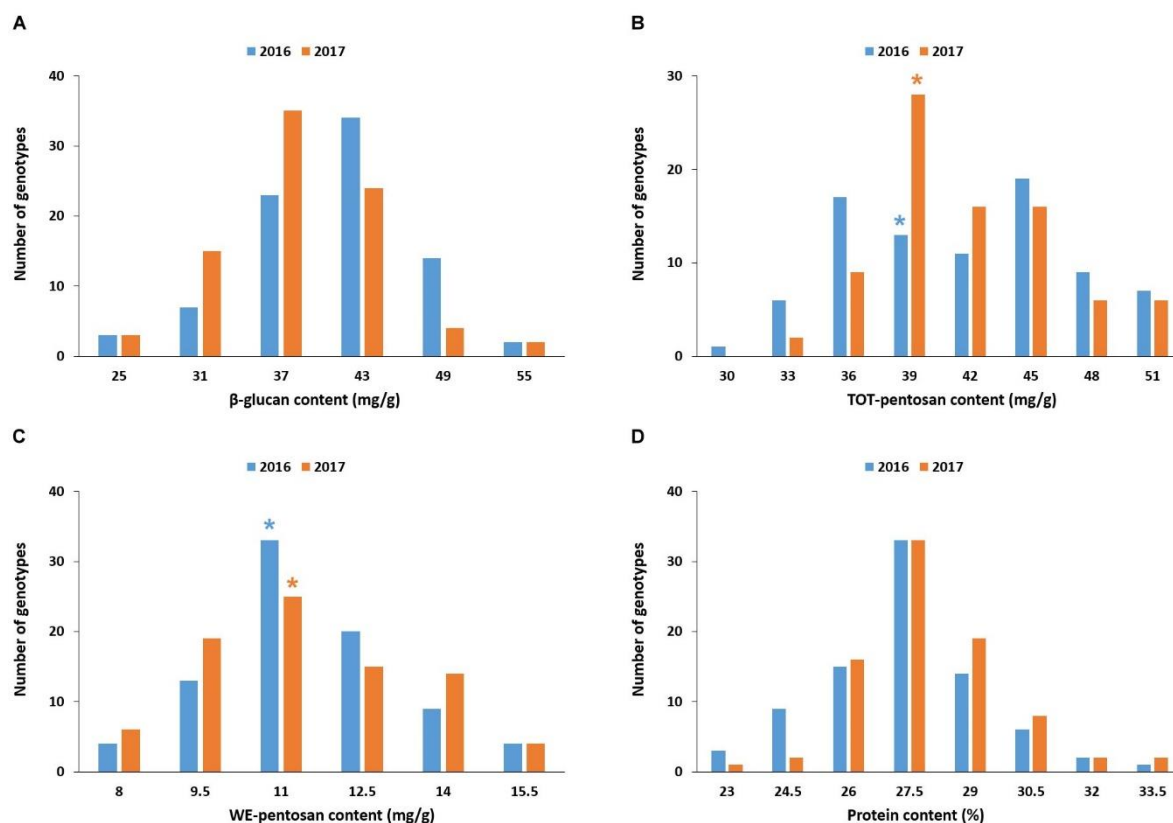


Figure S2. Frequency distribution of grain quality parameters in the *Ae. biuncialis* collection grown in Martonvásár (2016, 2017). For pentosan fractions, the location of the Mv9kr1 control wheat line has been indicated by stars on the relevant plots. The location of Mv9kr1 was not labeled for β -glucan and protein because of their extremely low values (β -glucan: 9.44 and 8.62 mg/g, protein: 12.91 and 13.01%).

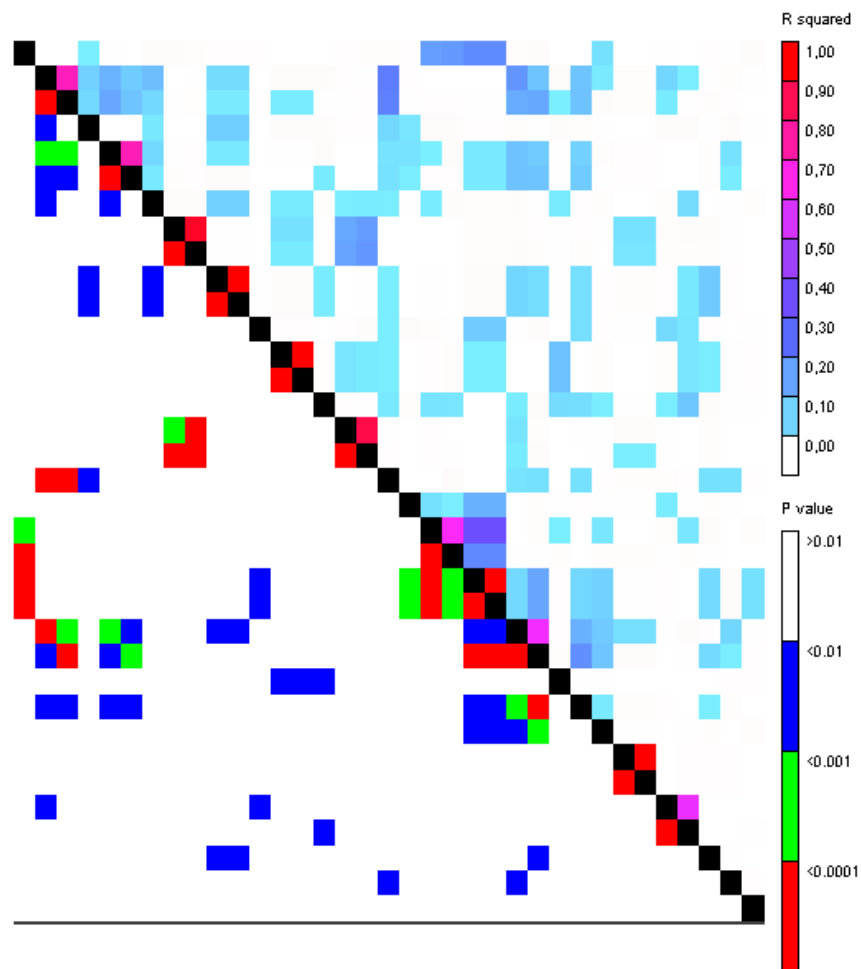


Figure S3. Linkage disequilibrium revealed by DArTSeq derived SNP markers in *Ae. biuncialis* population.

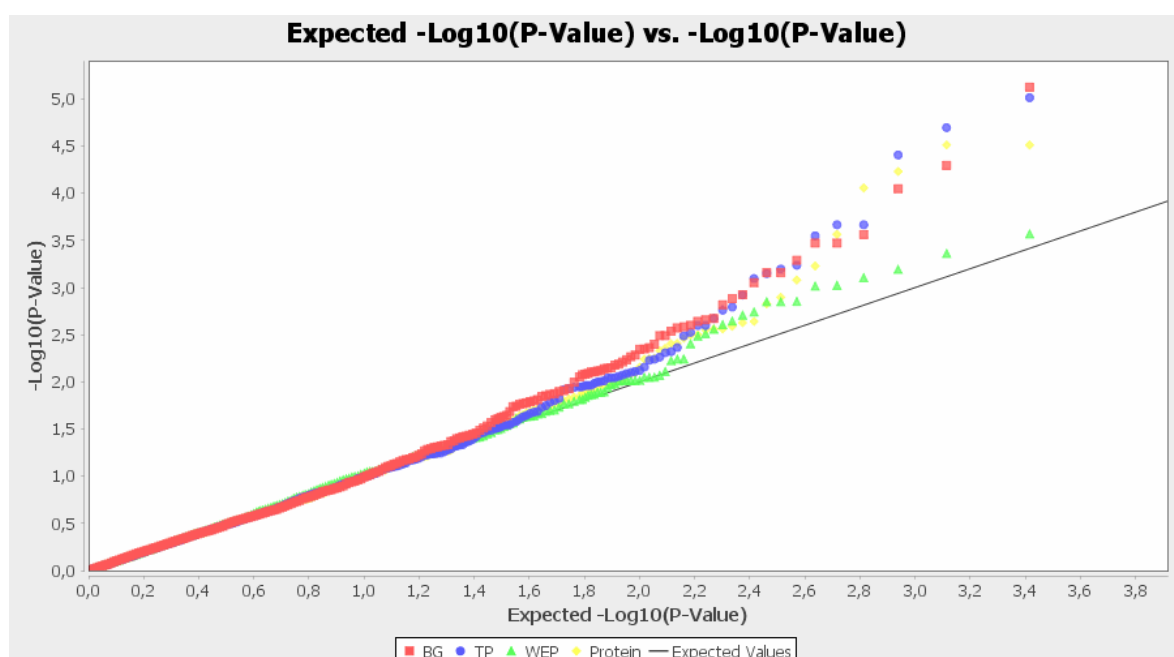


Figure S4. Q-Q plots generated for the four traits analyzed using the 83 *Ae. biuncialis* accessions.

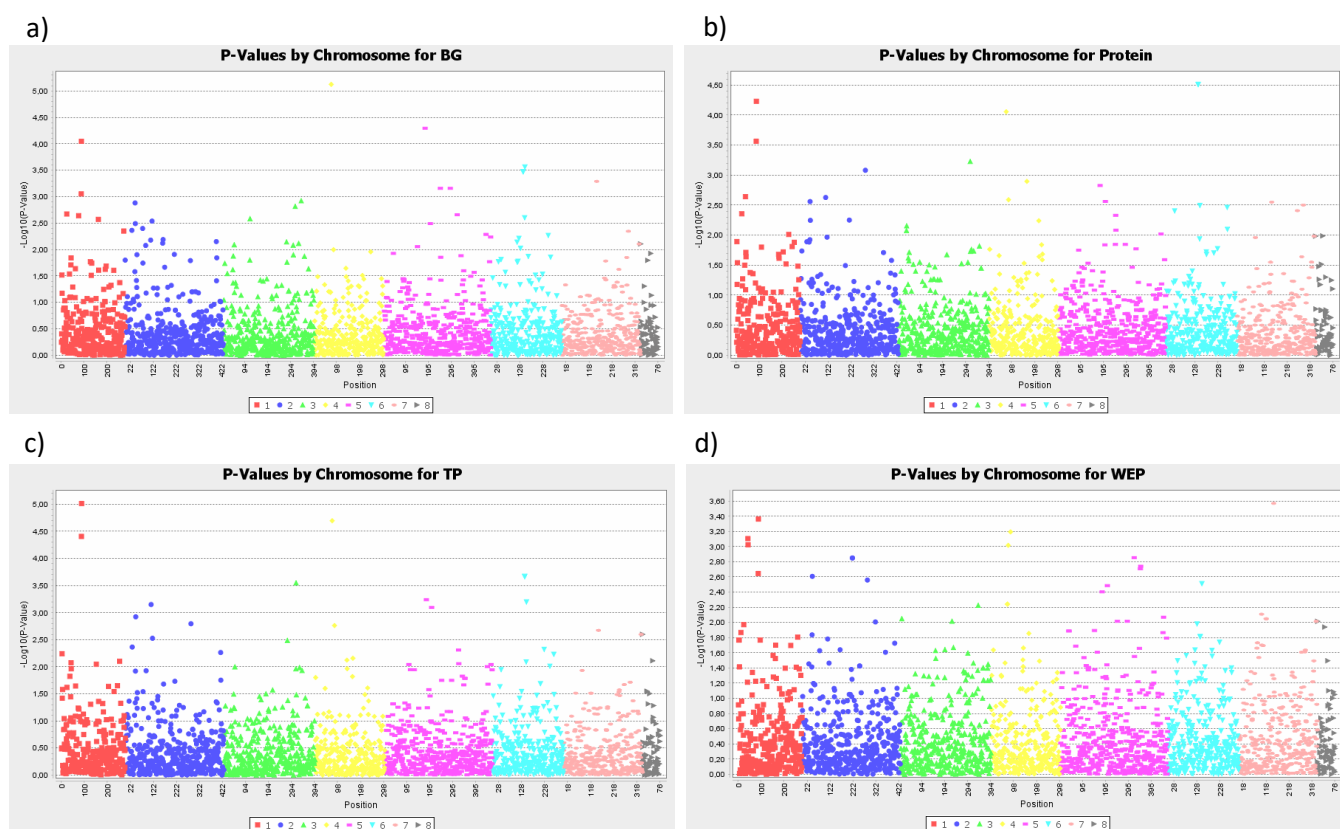


Figure S5. Manhattan plot represented the association of DArTSeq derived SNP markers with a) β -glucan (BG), b) protein, c) total-pentosan (TP) and d) water-extractable pentosan (WEP) traits in *Ae. biuncialis* population from mixed linear model (MLM).