

Common wheat introgression lines with genetic material of the tribe Triticeae as a source of diversity for quality traits

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Wild and cultivated wheat relatives have a high potential for expanding the genetic diversity of common wheat for grain quality traits. The aim of the study was identification and chromosomal localization of loci associated with gluten and mineral element contents. A wheat panel consisted of cultivars and introgression lines developed on the base wild relatives was characterized by gluten content, glutenin alleles and seven mineral elements. Phenotypic evaluation showed that introgression lines exceeded commercial wheat varieties in gluten content and concentration of Ca, Fe, K, Mn and Zn. Genome wide association study revealed 13 significant QTNs contributed to the gluten content on chromosomes 1D, 2A, 2B, 5A, 6A, 6D, and 7B. Among them, the locus on chromosome 2A inherited from *Triticum timopheevii* is of the greatest importance. Four QTLs located on the 5B, 6A, and 7A chromosomes were associated with the mineral elements, of which two loci have a significant effect on the content of both Fe and Mn. Genotypes containing putative QTLs can be used as prospective material for breeding.

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The main publications of authors on the subject of the abstract:

Leonova I.N. et al. Identification of QTLs for grain protein content in Russian spring wheat varieties (2022) *Plants* 11, 437. doi:10.3390/plants11030437

Leonova et al. Detection of genomic regions associated with resistance to stem rust in Russian spring wheat varieties and breeding germplasm (2020) *Int. J. Mol. Sci.* 21, 4706; doi:10.3390/ijms21134706