

QTL analysis for heading time and grain-filling period in *Triticum aestivum* L.

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The study of the heading time and maturity in wheat is a topic of pivotal importance because these traits influence the adaptability and yield of the crop. The aim of the present study was to apply the QTL analysis to map the loci underlying the heading time, grain-filling period and maturity. The F2 mapping population was created from a cross between late wheat line 124-1 and early wheat cultivar Novosibirskaya 31 and evaluated in glasshouse. The experiment was then repeated in field conditions in two years using the F2:3 population. The F2 population was genotyped using the Illumina Infinium 25k Wheat array and the linkage map was constructed. A total of 17 QTLs were mapped on 10 wheat chromosomes. The QTL found on the 7B chromosome was detected in both glasshouse and field and it most likely corresponded to the VRN-B3 gene (*FLOWERING LOCUS T*). The studied population segregated for the SNP G/C within the first exon of this gene, resulting in 2.2 days difference ($p < 0.001$). The other probable candidate genes are an SPL family gene and an ortholog of the CHE transcription factor.

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Take-home message:

The heading QTL corresponding to the VRN3 gene is defined by a non-synonymous SNP.

17 QTLs were mapped on 10 chromosomes. The probable candidate genes for the most environmentally stable QTLs are a SPL family gene and a CHE transcription factor.