

QTLs associated with the duration of the developmental phases in wheat

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Motivation and Aim: The adaptability and yield of wheat is strongly dependent on the flowering and maturity times. Flowering time has been shown to be affected by three major genetic systems: vernalization response (*Vrn*) loci, photoperiod response (*Ppd*) genes, and some other loci [1]. Meanwhile, knowledge about specific genetic factors controlling maturity time in wheat is limited. The aim of the study was to identify QTLs associated with the duration of the developmental phases in wheat using SNP markers.

Methods and Algorithms: The study was conducted on a F₂ mapping population developed from a cross between two spring wheat varieties – Novosibirskaya 31 and 124-1 line. A mapping population of 80 F₂ progenies and the two parents were genotyped at the TraitGenetics GmbH, Germany, with the the Illumina Infinium 25k Wheat array. The F₂ progenies along with the parental lines were phenotyped for the time of heading and maturity in the glasshouse. The F₃ progenies were divided into 2 groups and evaluated separately for flowering and maturity times under field conditions during 2020 and 2021 growing seasons. MultiPoint UltraDense was employed to construct the linkage map. Kosambi mapping function was used to convert recombination fractions to centimorgans [2]. QTL analyses were performed using the software package MultiQTL.

Results: In both environments parent 124-1 headed and matured later compared to parent Novosibirskaya 31: there was 8 days difference in the first experimental year and 13 days in the second. The F₃ progenies required 42-49 days to flowering and 81–95 days to maturity. Shapiro–Wilk tests confirmed normal distributions of all investigated traits in both environments. Heritability estimates were low for days to maturity (0.32) and moderate for days to heading (0.6) and vegetation period (0.57).

Traits	Parents		F ₂ 2019		F ₃ 2020		F ₃ 2021		H ²
	N31	L124-1	Avera-ge	Range	Avera-ge	Range	Avera-ge	Range	
Days to heading	34.3 ± 0.2	35.1 ± 0.3	31.8 ± 0.2	27.0–37.0	47.4 ± 0.2	43.1–52.9	46.3 ± 0.21	42.0–51.2	0.60
Days from heading to maturity	34.8 ± 0.2	41.5 ± 0.2	37.7 ± 0.3	32.0–47.0	37.8 ± 0.23	33.8–44.0	42.8 ± 0.24	38.7–49.0	0.32
Vegeta-tion period	69.1 ± 0.3	76.6 ± 0.3	69.5 ± 0.4	63.0–78.0	85.2 ± 0.35	48.8–94.0	88.8 ± 0.35	82.8–95.9	0.57

No correlation was detected between days to heading and days to maturity.

A genetic map was constructed based on 4774 marker loci, including 814 skeletal markers, and spanned 2368 cM. The average distance between markers was 3.1 cM. Chromosome size ranged from 8.5 cM (chromosome 5D) to 212.9 cM (chromosome 5A). During the linkage map construction 25 linkage groups were developed. This linkage map did not represent 3D, 4D, 6D chromosomes, which is probably due to the lack of SNP polymorphism on the D genome. QTL analysis was performed using both composite interval mapping and multiple interval mapping.

We identified a total of 15 QTLs. Six QTLs were identified to control time to heading. The most significant QTLs were QHD.icg-7D and QHD.icg-2A, which had a LOD score > 3 , and explained 20 and 19 % of the phenotypic variation respectively. Three QTLs on 5B, 6A, and 6B were associated with maturity time. The strongest QTL was QMT.icg-6A, which explained 21 % of the variance. The LOD score peak was in the *AX-158527841 – AX-109855005* interval (LOD = 3.5). Another six QTLs were associated with vegetation period. The most significant QTLs were located on chromosomes 1D, 5A, and 6B. QTL on 5B associated with maturity, and another two QTLs on 1D and 7B associated with vegetation period. These were moderate effect QTLs, which individually explained 14–18 % of the phenotypic variance.

Conclusion: The present study revealed several QTLs associated with the duration of developmental phases of wheat. The identified QTLs can be used in further studies on the genetic control of heading and maturity time.

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References

1. Snape J.W., Butterworth K., Whitechurch E. et al. Waiting for fine times: genetics of flowering time in wheat. *Euphytica*. 2001;119(1-2):185-90.
2. Kosambi D.D. The estimation of map distances from recombination values. *Ann Eugen*. 1944;12:172-175.