Mapping of agronomically important traits in *Triticum monococcum* L.

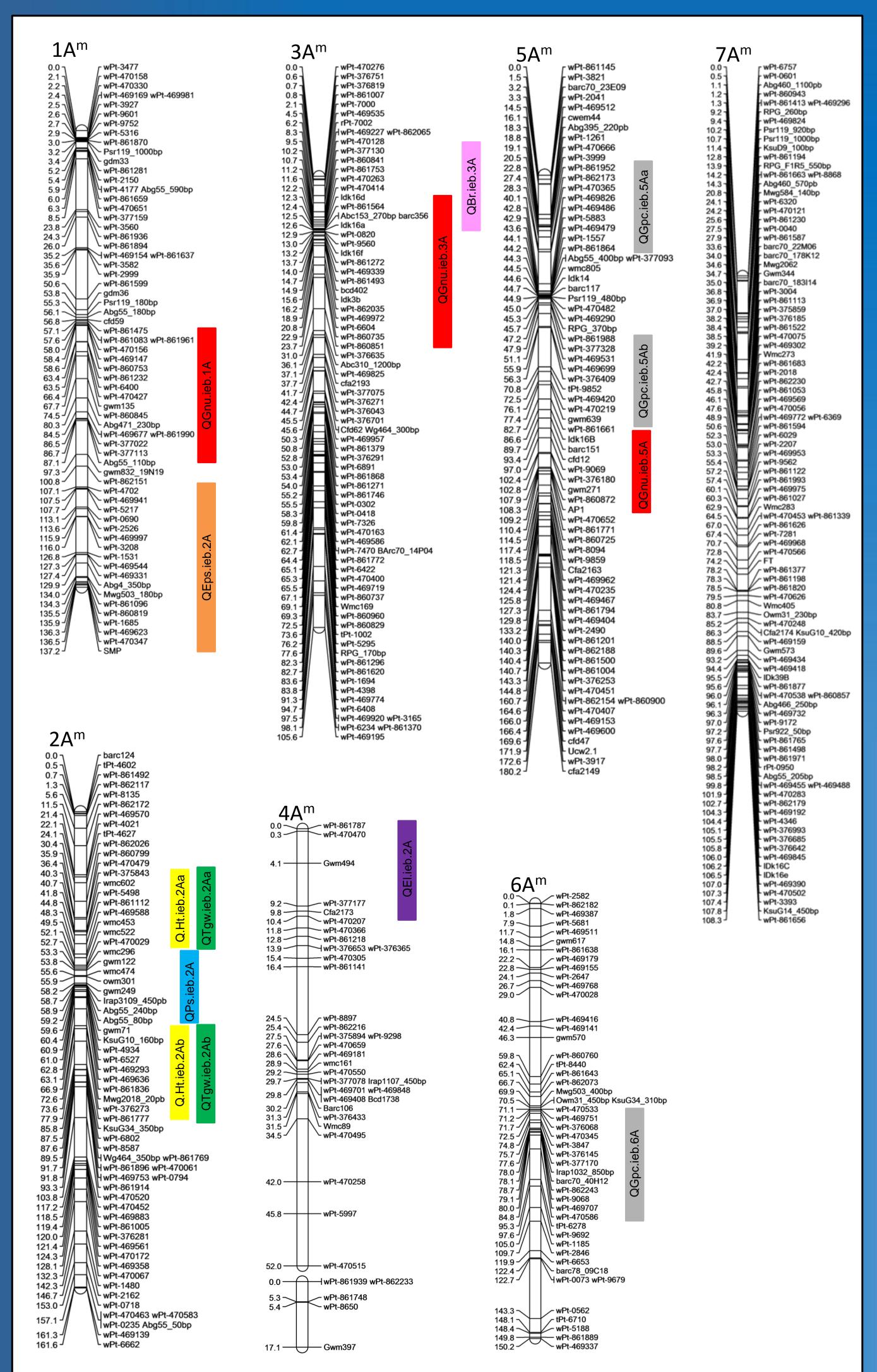






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Genetic map of *T. monococcum* L. and newly identified QTLs

The map contains 475 molecular markers. Identified QTLs are marked as color bars according to table "Traits and the newly identified QTLs".

Note: The chromosome 7A^m is the longest and the most populated with molecular markers. On the other hand,

the highest number of QTLs were identified on chromosome 2A^m.

Traits and the newly identified QTLs Trait QTL Chromosome $1A^{m}$, $3A^{m}$, $5A^{m}$ Grain per spikelet QGnu.ieb. 2A^m Grain weight QTgw.ieb. 4A^m Earn length QEl.ieb. Plant height QHt.ieb. 2A^m Plant shape QPsh.ieb. 2A^m 5A^m, 6A^m Grain protein content QGpc.ieb. QBr.ieb. 3A^m Brittle rachis 1A^m Flowering time QEps.ieb.

Goals of project

The main goal was to identify QTLs (Quantitative Traits Loci) for agronomically important quantitative traits in wheat to support MAS (Marker Assisted Selection) and positional cloning of this genes.

Introduction

Bread wheat is allohexaploid species (2n=6x=42, AABBDD) with large genome (~17 Gb), which makes it one of the most complex crop genomes. Moreover, the genome is composed of three homoeologous genomes A, B and D. All of this make gene mapping and cloning a difficult task. The use of diploid ancestors of wheat for gene mapping and cloning is one of possible approaches to overcome these difficulties.

Einkorn wheat *T. monococcum* is a diploid wheat species (2n=2x=14) closely related to the A genome of the bread wheat. The diploid genome and availability of wild and domesticated cultivars is source of great variability incomparable with the hexaploid wheat. This makes *T. monococcum* an ideal target for QTL mapping and positional cloning.

Results

Genetic map

A high density linkage map of diploid wheat *T. monococcum* was constructed using a mapping population derived from a cross of cultivated *T. monococcum* ssp. *monococcum* cv. Dv92 and wild *T. monococcum* ssp. *aegilopoides* cv. G3116. A set of 475 markers comprising 367 DArTs, 50 SSR, 42 STS, 9 markers derived from BAC-ends sequences, four wheat genes (*Vrn1,2,3*, and *Br-A1*) and tree IRAP markers were mapped on 93 lines of the F9 RIL mapping population. The length of the map was 913 cM. Chromosome 7A^m was the most densely populated with markers. Linkage groups without gaps were identified for all chromosomes except chromosome 4A^m which was also the shortest with lowest number of markers mapped.

Map length and number of markers

Chromosome	1A ^m	2A ^m	3A ^m	4A ^m	5A ^m	6A ^m	7A ^m	Total
Length [cM]	137,2	161,6	105,6	69.8	180,2	150,2	108,3	912,9
Number of markers	68	66	79	38	73	48	103	475

QTL mapping

The mapping population was used for mapping of QTLs influencing a set of agronomically important traits, including QTLs affecting yield components, plant height, plant shape, flowering time, nitrogen content and brittle rachis. These traits were mapped during tree seasons at two different treatments and locations. In total 14 QTLs were identified. Most of the QTLs (6) were identified for yield components. The highest number (5) of QTLs were identified on chromosome 2A^m. Interestingly, no QTL were found on chromosome 7A^m.

Conclusion

All new identified QTLs for agronomically important traits will be validated by using new verification mapping population.