Molecular mapping of the sterility QTLs regions for Timopheevii cytoplasmic male sterility in triticale.

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INTRODUCTION

Triticale (x Triticosecale Wittmack) is a relatively young synthetic allopolyploid created by hybridization of wheat and rye about 150 years ago. There is a growing interest in its breeding due to, i.e., high yield potential demonstrated under marginal growing conditions, the opportunity of raising cereal production globally and also being considered for hybrid breeding based on cytoplasmic male sterility (CMS). The CMS in plants is characterized by impaired development of fertile pollen and is the result of the incompatibility of the mitochondrial and nuclear genome. Many hypotheses explain CMS; however, the molecular mechanism of male sterility and pollen fertility restoration in many crop species remains uncovered.

MATERIAL AND METHODS

The phenotypes of the RIL6 lines were evaluated based on BC1F6: DB2 x [RIL8: DB2xRB2] where the number of seed per spike was determined. Distribution of the trait was tested in XlStat software. One hundred eighty-four RIL6: DB2 x RB2 plants were genotyped with DArTseq and silicoDArT markers. A genetic map was constructed using MultiPoint UltraDense software. Composite interval mapping (CIM) was performed in WinQTL Cartographer. The following settings were used: Walk Speed' – 2, ‚Window Size' – 2, ‚Markers' – 10. QTL significance was determind based on 1000 permutations.

AIMS

Identification of the QTLs and candidate markers linked to pollen sterility in Triticale with cms Tt for MAS purposes via composite interval mapping approaches.

RESULT

Based on normality test the trait (number of seed per spike) confirmed to follow the normal distribution (Table 1).

In total, 849 DArT skeleton markers and 1220 redundant were mapped. Twenty-one linkage groups, covering 2270.72 cM, were evaluated. On average, a marker was present every 2.67 cM. The groups were 35.72 to 174.77 cM long and included from 15 (LG12) to 81 (LG9) skeleton markers (Figure 1). Based on available data on the wheat reference genome and the genetic map of rye, all linkage groups of the triticale genome were allocated to the corresponding chromosomes of the species. Similarly, the S-L orientation was evaluated. CIM analysis (cut-off value 3.7) showed the presence of at least four QTLs reflecting pollen sterility gene/s acting in CMS Tt system. The QTLs located on chromosomes 1B, 3B, 5B, and 6A (Figure 2, Table 2).

Figure 1. Arrangement of linkage groups evaluated for the RIL6 mapping population of DArTseq and silicoDArT markers.

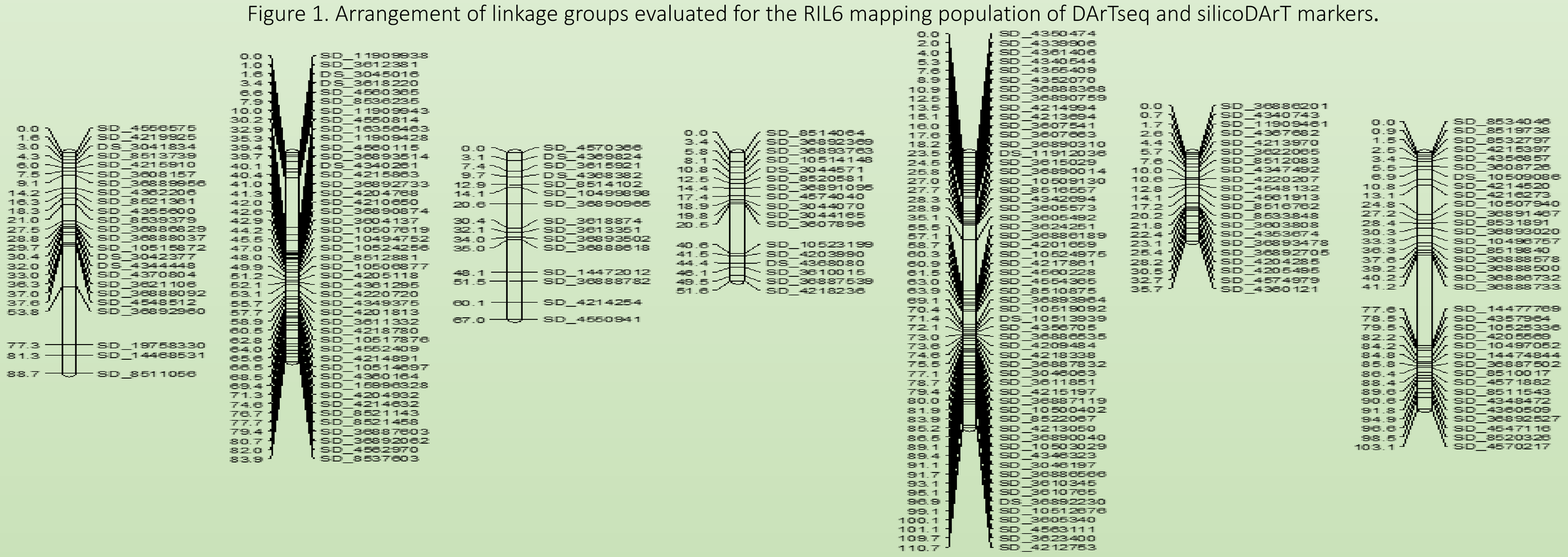


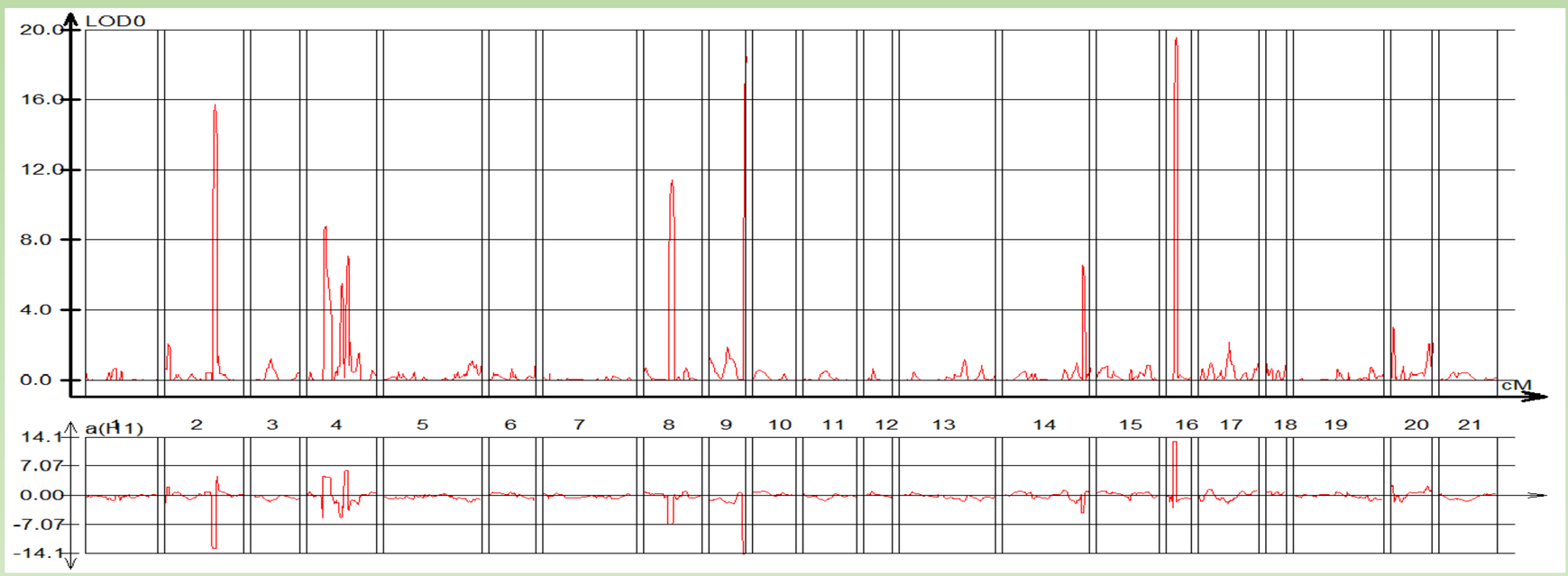
Table 1. Results of the Shapiro-Wilk and Anderson-Darling normality tests performer on the number of seeds per spike for the BC1F6 : DB2 x [DB2 x RB2].

Trait\Test	Shapiro-Wilk	Anderson-Darling
Number of seeds per spike	0.009	0.019

Table 2. Arrangement of markers data mapped within QTL regions.

QTL	Linkage group (chromosome)	Marker within QTL maximum	QTL maximum	Marker position (cM)	Skeleton markers within QTL	QTL range (cM)	Additive value	R2	RecL	RecR
QTL 1	LG7 (1B)	DS_3045331	15.76	88.2	SD_10501730 DS_3045331 SD_4369121	84.2 - 92.9	-12.8	0.29	0	0.05
QTL 2	LG10 (3B)	SD_36887874	11.46	49.1	SD_4565257 SD_36887874 SD_4200724	42.9 - 53.2	-7.02	0.11	0	0.04
QTL 3	LG20 (5B)	SD_10520104	6.6	141.2	SD_4203927 SD_10520104 SD_36894840	141 - 146.3	4.18	0.04	0	0.02
QTL 4	LG6 (6A)	SD_4205623	19.63	16.2	DS_3043978 SD_4205623 SD_3604165	12.4 - 18.5	13.1	0.41	0	0.02

Figure 2. QTLs identified based on the genetic map (RIL8 mapping population RIL8: DB2 x RB2), and pollen sterility expressed as the number of seeds per spike per each line.



CONCLUSION

1. Genetic map of triticale encompassing 21 linkage groups representing each chromosome of the species was evaluated.2. BC1F6 (pollen sterile line on CMS Tt was crossed to the RILF6) used to determine the number of seed per spike showed that the RILF6 mapping population has pollen sterility genes as the trait varied among materials. 3. 3. The trait distribution was close to normality and thus, could be used in composite interval mapping analysis.4. Genetic mapping combined with composite mapping (CIM) enabled the identification of markers strongly linked to the QTLs of the examined trait.