Markers towards pollen sterility genes in triticale with CMS Tt.

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INTRODUCTION

Cytoplasmic male sterility (CMS) is widespread among higher plants and results from an interaction between nuclear and mitochondrial genomes leading to impairment of pollen production. The phenomenon facilitates the production of hybrid seed (i.e. in rye, maize, or rapeseed) [1]. The CMS from *Triticum timopheevii* (cms Tt) is the most promising system for hybrid breeding in triticale. However, currently little is known about the genes responsible for pollen fertility restoration and maintenance of pollen sterility in the species [2]. Nevertheless, analysis of F2 mapping population [3] unveiled that several nuclear genes with relatively weak phenotypic effects code for the trait. The genes conferring pollen fertility mapped to the chromosomes 6A, 6B and 6R [3] with additional ones on the chromosomes 1B, 3A, and 3B [3], respectively. Moreover, our unpublished data using RIL4: MS 114(5)-2-1 x Borwo mapping population showed that putative genes responsible for pollen sterility mapped to the chromosomes 3A, 5B, and 7B.

MATERIALS AND METHODS

RIL5 [DB1 x RB1] mapping population and phenotypic data were employed for the identification of a pollen sterility QTL as well as molecular markers linked to the trait. One hundred seventy RIL5 plants were genotyped with DArTseq markers. The phenotype of the RIL5 lines was evaluated based on BC1F5: DB1 x [RIL5: DB1 x RB1] where the number of seed per spike was determined. A genetic map was built in MultiPoint Ultra Dense software. Composite interval mapping (CIM) was performed in WinQTL Cartographer whereas association mapping in TASSEL.

RESULTS

A total of 637 skeletons and 2705 redundant markers felt into 22 linkage groups. The groups were 4.3 to 182 cM long and included from 19 (LG21) to 327 (LG9) markers. Based on the known map positions of wheat DArTseq's, eight and seven linkage groups were allocated to the A and B genomes, respectively. Assignment of remaining seven linkage groups to the chromosomes was difficult due to the lack of information about DArTseq markers localization. CIM allowed the identification of a single QTL most probably reflecting pollen sterility gene/s acting in cms Tt system. The QTL mapped to the chromosome 4A. The maximum of the LOD function equaled to 6.2 with LOD cut-off values equal to 2.5. The DS3610112TC11 marker was 0.2cM away from the QTL maximum. This marker has two redundant counterparts: DS3604977AG23 and DS4348966GC15. The QTL explained 32% of the phenotypic variance of the trait. Association mapping identified numerous markers responsible for pollen sterility. The markers were assigned to 4A, 1B, and 3B chromosomes but they failed to pass Bonferroni test.

Figure 2. Composite interval mapping of male sterility of pollen in triticale with cms Tt for population RIL5: DB1xRB1.

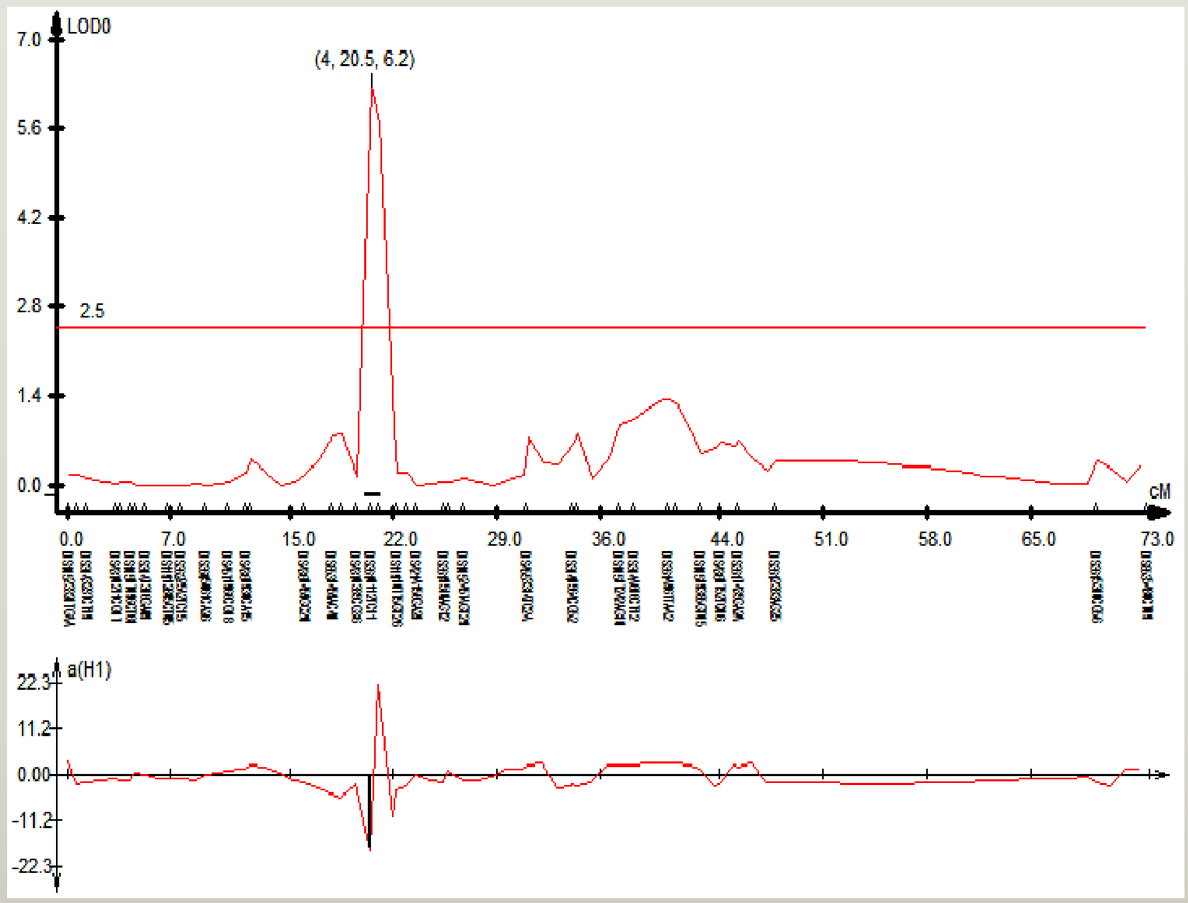
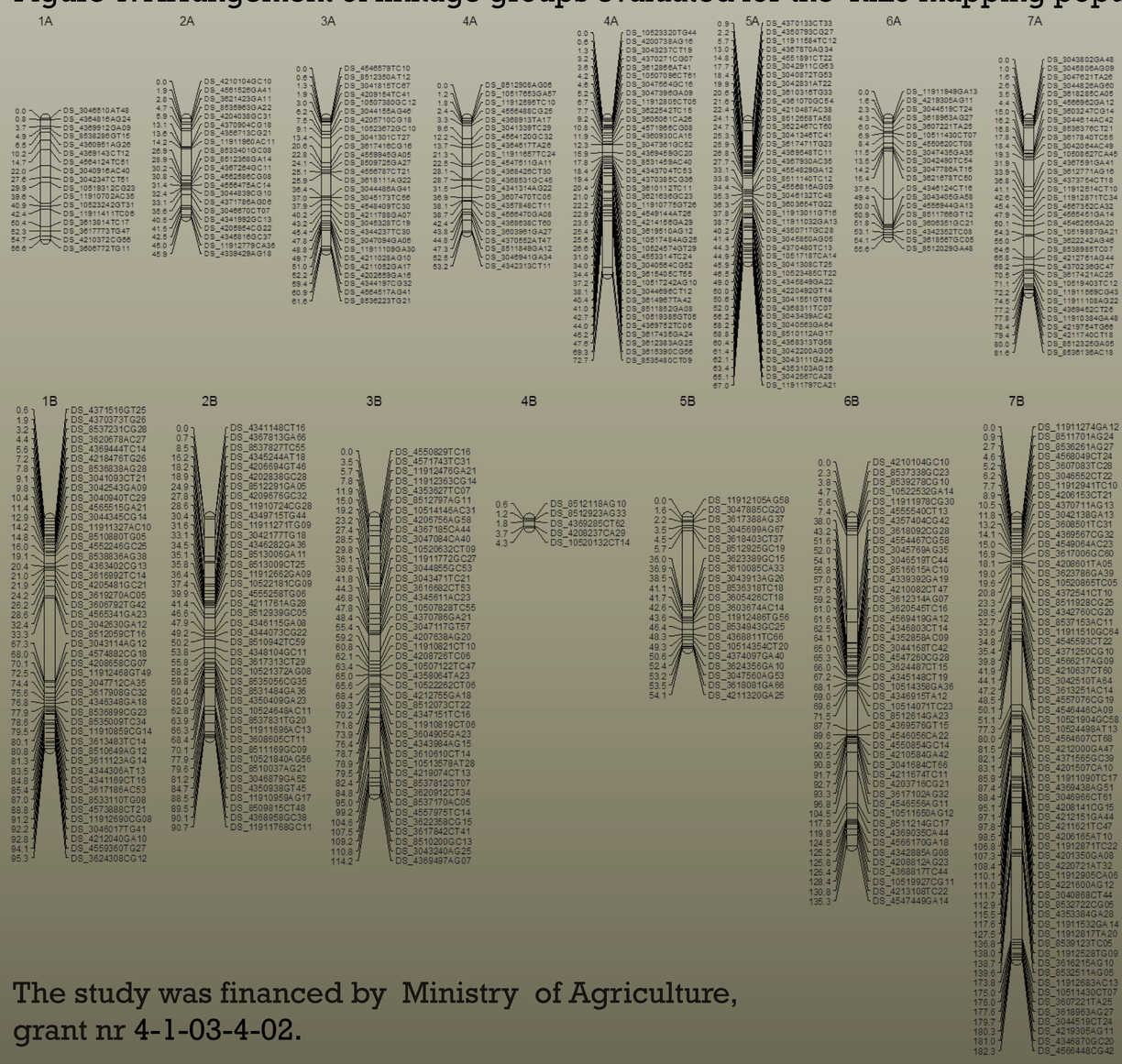
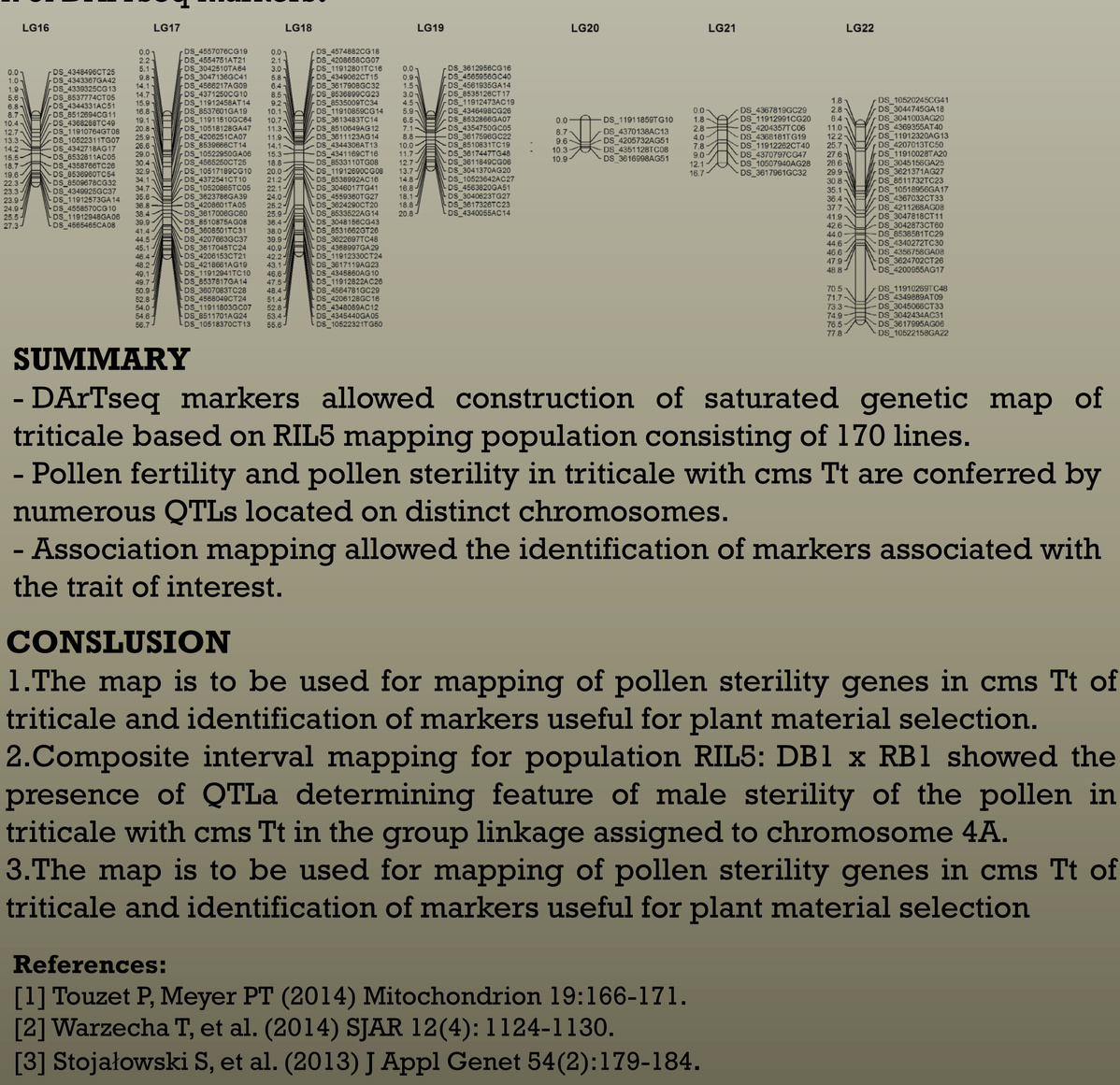


Table 1. Arrangement of mapping data evaluated for the RIL5 mapping population (*n.a. – linkage group (LG) not assigned to the chromosome).

Group	LG1	LG2	LG3	LG4	LG5	LG6	LG7	LG8	LG9	LG10	LG11	LG12	LG13	LG14	LG15	LG16	LG17	LG18	LG19	LG20	LG21	LG22
Length (cM)	56,7	45,9	61,6	53,2	72,7	66,1	55,6	81,6	94,7	90,7	114	4,32	54,2	135	182	27,3	56,7	55,6	20,8	10,9	16,7	76
No. of markers (total)	71	194	108	66	202	163	89	137	327	219	193	53	72	311	305	93	246	266	100	20	19	88
Density (cM)	3,33	2,19	2,2	2,42	1,86	1,54	2,93	2,33	2,01	2,16	2,65	0,73	2,46	2,88	2,8	1,44	1,72	1,69	1,15	2,17	2,09	2,92
Longest gap (cM)	9,69	12,7	10,4	6,29	21,7	7,3	22,2	12,6	34	7,79	10,1	1,83	30,3	30,6	34,2	3,67	5,09	10,5	2,03	8,65	4,66	21,7
Localization	1A	2A	3A	4A	4A	5A	6A	7A	1B	2B	3B	4B	5B	6B	7B	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

Figure 1. Arrangement of linkage groups evaluated for the RIL5 mapping population of DArTseq markers.





SUMMARY

- DArTseq markers allowed construction of saturated genetic map of triticale based on RIL5 mapping population consisting of 170 lines.
- Pollen fertility and pollen sterility in triticale with cms Tt are conferred by numerous QTLs located on distinct chromosomes.
- Association mapping allowed the identification of markers associated with the trait of interest.

CONSLUSION

1.The map is to be used for mapping of pollen sterility genes in cms Tt of triticale and identification of markers useful for plant material selection.
2.Composite interval mapping for population RIL5: DB1 x RB1 showed the presence of QTLa determining feature of male sterility of the pollen in triticale with cms Tt in the group linkage assigned to chromosome 4A.
3.The map is to be used for mapping of pollen sterility genes in cms Tt of triticale and identification of markers useful for plant material selection

The study was financed by Ministry of Agriculture, grant nr 4-1-03-4-02.

References:
[1] Touzet P, Meyer PT (2014) Mitochondrion 19:166-171.
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[3] Stojałowski S, et al. (2013) J Appl Genet 54(2):179-184.