Genetic map of triticale based on DArTseq markers

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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 and the opportunity of raising cereal production globally [1]. It is also being considered for hybrid breeding based on cytoplasmic male sterility (cms) Tt or Pampa [2]. Some hybrids were recently released in France (personal communication). However, there is a gap in understanding of the genetic background of cms in triticale. It is not known how many genes participate in pollen sterility preservation and pollen fertility restoration in both cms systems, as well as their precise location, and putative function is not evident. Thus, genetic maps based on specially designed mapping populations are required to identify QTLs responsible for the trait and allowing the identification of molecular markers useful for MAS.

The first genetic map of triticale-based on DArT, SSR and AFLP markers was described by Tyrka et al. [2011]. Later Alheit et al. (2011) presented triticale map based exclusively on DArT markers. Nevertheless, any of the maps were based on hybrid materials and could not be applied for studies of genes conferring pollen sterility/fertility trait in cms Tt. with the development of Next Generation Sequencing technologies highly saturated genetic maps based on RILs could be evaluated.

MATERIALS AND METHODS

HT352 x Borwo RIL6 mapping population encompassing 182 individuals was genotyped with DArTseq. The genetic map was constructed using MultiPoint UltraDense commercial software.

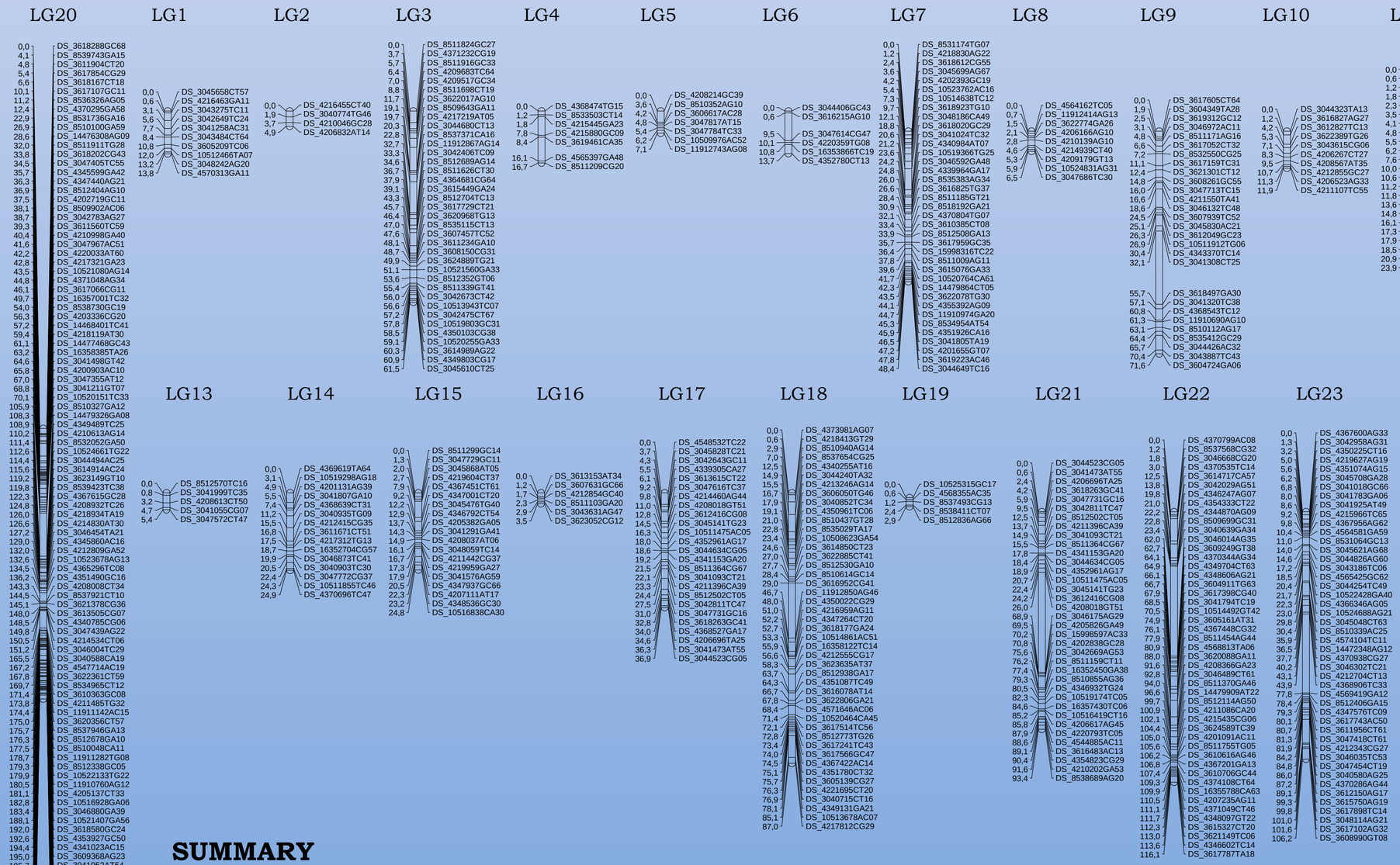
RESULTS

There were 563 (6446) DArTseq skeleton (total) markers on the map. It has 23 linkage groups with the shortest spanning over 2,93 and the longest over 224,28 cM. On average, the markers were distributed every 1,82 cM. Despite the high saturation of the maps, some gaps were also present. The largest one was detected in the LG21 and was 42,93 cM long.

Table 1. Arrangement of mapping data evaluated for the RIL6 mapping population.

Group	LG1	LG2	LG3	LG4	LG5	LG6	LG7	LG8	LG9	LG10	LG11	LG12	LG13	LG14	LG15	LG16	LG17	LG18	LG19	LG20	LG21	LG22	LG23	total
Length (cM)	13,75	4,85	61,49	16,73	7,08	13,71	48,39	6,49	71,61	11,85	23,87	17,7	5,37	24,87	24,77	3,49	36,92	86,97	2,93	224,3	93,37	116,1	106,2	1023
No. of total markers	62	52	550	39	56	96	595	79	264	75	477	279	108	131	214	52	216	527	61	1187	497	324	505	6446
No. of skeleton markers	10	4	37	7	7	6	37	9	28	10	23	20	5	15	19	6	25	45	5	116	36	47	46	563
Density (cM)	1,38	1,21	1,66	2,39	1,01	2,29	1,31	0,72	2,56	1,19	1,04	0,89	1,07	1,66	1,30	0,58	1,48	1,93	0,59	1,93	2,59	2,47	2,31	1,82
Longest gap (cM)	2,58	1,86	9,84	7,75	3,56	8,89	6,65	1,84	23,61	2,97	2,99	1,82	2,4	4,3	5,24	1,16	3,66	17,73	1,17	35,76	42,93	38,61	33,94	11,36
Shortest gap (cM)	0,58	1,19	0,59	0,59	0,6	0,59	0,58	0,61	0,59	0,59	0,58	0,6	0,71	0,6	0,6	0,58	0,57	0,57	0,58	0,57	0,57	0,59	0,58	0,62

Figure 1. Genetic map of the population RIL 6: HT352 x Borwo constructed based on DArTseq markers.



SUMMARY

1. Genetic map developed for RIL6: HT352 x Borwo is characterized by a relatively high density of molecular markers, as evidenced by an average genetic distance between them, which amounts to 1.82 cM.
2. Despite sufficient saturation of the map with DArTseq markers, there were some regions missing markers. The largest gap reached circa 43 cM.

CONCLUSION

1. Highly saturated genetic map of triticale with 23 linkage groups spanning over 1023 cM.
2. DArTseq markers formed groups of redundant markers (6446 out of 5883 were redundant).
3. Despite the fact that the mapping population was based on RIL6 still significant gaps were present.
4. The map is to be used for the identification of pollen fertility/sterility QTLs as soon as the phenotypic data concerning the trait will be available.

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References
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