1. ***Construction of Saturated Genetic Map:*** The first version of genetic map was constructed using the T-population (Tifrunner × GT-C20) with 239 mapped loci which was then improved to 378 marker loci. In the present study, genotyping data was generated for additional 45 loci and 40 marker loci were successfully integrated to the existing genetic map. The current saturated genetic map has now 418 marker loci distributed onto 20 linkage groups (LGs) spanning a total genetic map length of 1935.4 cM with map density of 5.3 cM per loci. The mapped marker loci per LG varied from 6 (B09) to 36 (A03 and A08) with the mean of 19 loci per LG. Of the total 418 mapped markers, 250 marker loci were mapped onto the 10 LGs of A sub-genome with a total map distance of 1041.6 cM and 4.45 cM inter marker distance while 168 marker loci onto the 10 LGs of B sub-genome with total map distance of 893.8 cM and 6.25 cM inter marker distance **(Table 1)**.

Table 1: Map features of the saturated genetic linkage map with 418 mapped loci for the T-population

Linkage group	**Mapped loci**	**Length of LG (cM)**	**Map density (cM/loci)**	**Linkage group**	**Mapped loci**	**Length of LG (cM)**	**Map density (cM/loci)**
A sub-genome				***B sub-genome***			
A01	18	133.4	7.4	B01	18	92.2	5.1
A02	11	96.0	8.7	B02	23	68.2	3.0
A03	36	176.0	4.9	B03	7	81.2	11.6
A04	42	127.2	3.0	B04	21	244.3	11.6
A05	24	56.6	2.4	B05	12	50.7	4.2
A06	30	151.9	5.1	B06	15	59.4	4.0
A07	15	50.0	3.3	B07	22	100.4	4.6
A08	36	143.4	4.0	B08	27	50.4	1.9
A09	19	66.1	3.5	B09	6	73.2	12.2
A10	19	41.0	2.2	B10	17	73.8	4.3
Total	250	1041.6	4.45		168	893.8	6.25
Grand Total	418	1935.4	5.3				