Molecular, genetic and evolutionary analysis of a paracentric inversion in Arabidopsis thaliana

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S5 Table. Patterns of 250K Chip SNP variation in the inversion region and in a "Control" region, 13.214 - 15.097 Mb on Chromosome 4.

Chromo-somal region	Col-0 vs Ws-2 SNP differences	Total accessions	Inferred inversion accessions	#SNPs fixed in inversion class, polymorphic in remainder	#SNPs polymorphic in inversion class, fixed in remainder	#SNPs polymorphic in both classes
Inversion	55 of 2653	1201	159	**534**	**7**	**2112**
			150	**1265**	**0**	**1388**
		1018 (US removed)	51	**854**	**10**	**1788**
			46	**1672**	**2**	**978**
Control	392 of 2954	1201	159	**81**	**0**	**2873**
			150	**99**	**0**	**2855**
		1018 (US removed)	51	**182**	**0**	**2772**
			46	**202**	**0**	**2752**

For each region, subset of accessions, and threshold for designating an accession as carrying the inversion, the last 3 columns of the table give the number of SNPs that are: 1) fixed in the inversion class but polymorphic in the non-inversion accessions; 2) polymorphic in the inversion class but fixed in the non-inversion accessions; and 3) polymorphic in both classes. No fixed differences were found between the inversion and non-inversion classes. A total of 1201 of the RegMap accessions were used for these analyses, after dropping all accessions with a high likelihood of representing contamination, sample mislabeling, or recent migration (the 'red list' from Anastasio et al. 2011) but retaining Col-0 and Ws-2. Because the RegMap USA samples are characterized by low diversity, analyses were repeated with a set of 1018 accessions (the previous 1201 with the remaining USA accessions removed). Additionally, for each set of accessions two separate thresholds were used to infer whether an accession carried the inversion or not, resulting in either 159 or 150 inversion accessions in the set of 1201, or in either 51 or 46 inversion accessions in the set of 1018. In all cases, the proportion of SNPs *from the inversion region* that are fixed in the inversion class is always much higher than the parallel proportion *from the control region*, providing support for the inference that all of these accessions carry the inversion. However, the large proportion of SNPs from the inversion region that are polymorphic in both inversion and non-inversion classes also provides clear evidence for some type of recombination (gene conversion or double crossovers) in this region, because such a high rate of recurrent mutation occurring independently in both classes is implausible.