

Six new recombinant inbred populations for the study of quantitative traits in *Arabidopsis thaliana*

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Published online: 27 March 2008
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Erratum to: Theor Appl Genet (2008) 116:623–634 DOI 10.1007/s00122-007-0696-9

The locus genotyping file used for the analysis of the NG population reported in the manuscript contained the incorrect assignment of maternal and paternal alleles. Consequently:

The proportion of maternal alleles in this population (Table 3) should be 54.4%, not 45.6%.

The parental assignment of genome representation for this population (Fig. 1) shows male alleles expressed as a percentage of male and female alleles combined, not female

alleles expressed as a percentage of male and female alleles combined. Nok-3 alleles are thus over-represented in regions of chromosomes 1 and 2, and under-represented in a region of chromosome 4.

For each of the three flowering time QTL identified in this population (Fig. 2; Table 4), the increasing allele is from Nok-3, not Ga-0.

The correct versions are given here.

The online version of the original article can be found under
doi:10.1007/s00122-007-0696-9.

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Table 3 Genetic analysis of the recombinant populations at the F8 generation

Population	Total Mb	Total cM	Average distance between markers (cM)	Numbers of markers used in the maps	kb/cM	Residual heterozygosity (%)	Maternal alleles in the populations (%)
NG	114	448	7.7	58	255	1.0	54.4
TJ	108	386	7.3	53	280	0.8	49.2
CA	107	453	9.6	47	236	0.65	40.5
KB	104	351	6.8	52	296	1.0	41.4
SG	97	297	6.2	48	326	0.8	43.9
WC	112	470	8.2	57	238	0.6	52.8

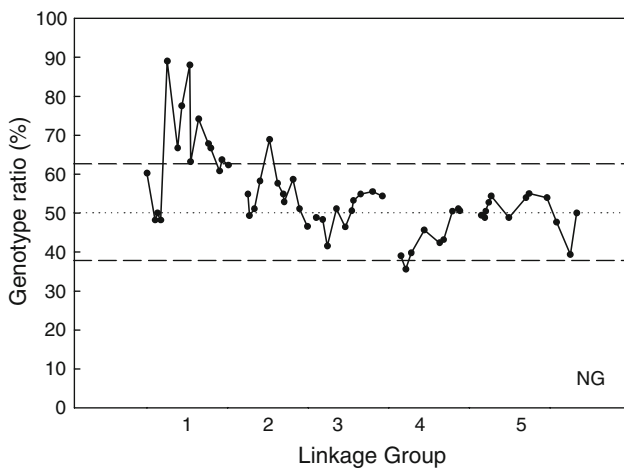
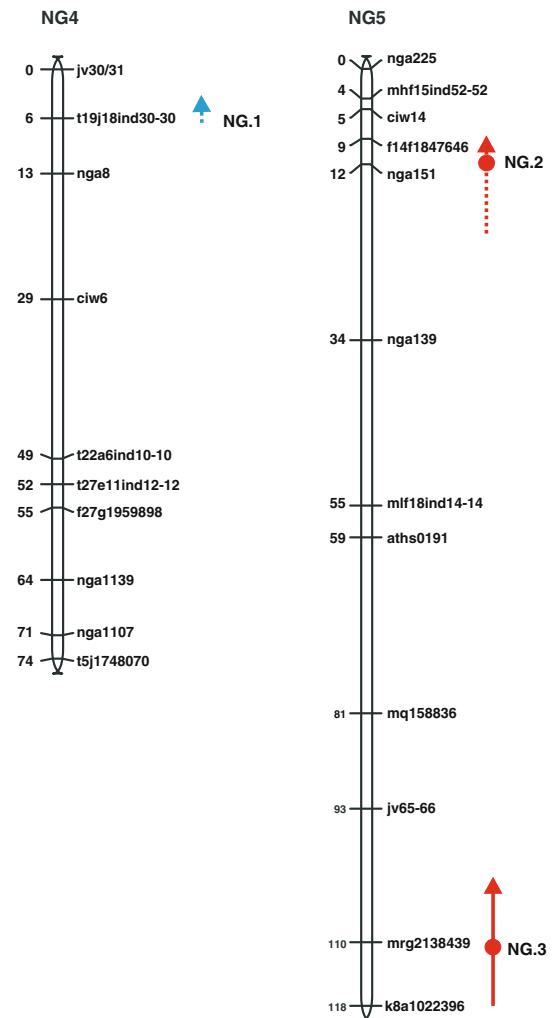
**Fig. 1** Allele segregation ratios for the six populations. The female alleles are expressed as a percentage of the male and female alleles combined. The significance threshold $P < 0.001$ (i.e. between 38 and 62%) is indicated by the horizontal *dashed lines***Fig. 2** QTL for flowering time for 6 RIL *Arabidopsis* populations. The position of the QTL are represented as 2 LOD intervals where sufficiently large, *solid lines*, otherwise the 5% significance LOD threshold is used, *dashed lines*. The position of peak LOD scores are indicated by *closed circles*. QTL detected by interval mapping are indicated in *red*, while QTL detected only by CIM mapping are indicated in *blue*. *Upward arrows* indicate the maternal parent as the source of the increasing allele, *downward arrows* indicate the paternal parent as the source of the increasing allele

Table 4 QTL affecting flowering time in the six populations and heritability in the individual populations

Population	Heritability (h_b^2)	QTL analysis						
		QTL	Chr	LOD max	QTL position (cM)	Peak max (cM)	Variation explained (%)	Increasing allele
KB ^a	0.69	KB.1	C2	13	26.5–34	30.7	58	Kondara
NG ^b	0.65	NG.1 ^c	C4	2.5	6	6	10	Nok-3
		NG.2	C5	4	7.7–20	11	19	Nok-3
		NG.3	C5	4.7	101–117	110	22	Nok-3
TJ ^a	0.63	TJ.1 ^c	C4	2.9	0–2	0	9	Ts-5
		TJ.2	C5	3.1	13.7–26	19.7	18	Ts-5
		TJ.3	C5	7.4	74–97	89.9	37	240#14
CA ^b	0.2	CA.1	C4	7.4	0.5–14	4	38	Ag-0
SG ^a	0.82	SG.1	C1	3.8	68–74.5	74.5	14	Gy-0
		SG.2	C4	3.4	0–6	1.4	16	Sorbo
		SG.3 ^c	C4	3.8	16–38	30.5	15	Sorbo
		SG.4	C5	4.3	10–32	21.3	20	Gy-0
		SG.5	C5	5.1	45.6–63.8	63.8	23	Gy-0
WC ^b	0.6	WC.1	C5	8.9	93–103	96.8	37	Wt-5
		WC.2	C5	10.2	107–end	112.2	41	Wt-5

^a Population grown in a glasshouse

^b Population grown in a controlled environment room

^c QTL detected only in the MQM analysis