THE gi LOCUS SHOWS LINKAGE WITH gp, r AND tl

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The recessive allele gi (gigas) delays flowering (7,8). To test for linkage of the gi locus, Hobart lines 158 (Vassileva mutant III/83; gi Bt R Tl Gp Cp Te) and 111 (Marx A875-55-0; Gi bt r tl gp cp te) were crossed and the F_2 grown in the phytotron at Hobart under a 12 h photoperiod (12 h daylight/12 h dark). Night temperature was 16°C and day temperature was usually within the range 22-25°C. On day 65, any plants still without visible flower buds were transferred to a 14 h photoperiod. These plants had between 31 and 33 expanded leaves at the time of transfer. Lateral shoots were excised regularly. Node counts commenced from the first scale leaf as node 1. The joint segregation chi-squared was obtained using a 2 x 2 contingency table and the recombination fraction was estimated using the product ratio method.

Under the above conditions, Gi/- segregates commenced flowering at nodes 14-26 and _gi/gi segregates at nodes 28-48. Parental lines 111 (Gi) and 158 (gi) flowered at nodes 17-18 and 44, respectively. Consistent with previous results (7), there was a significant deficiency of gigas segregates {Table 1). It is not presently known whether the deficiency of plants with a gigas phenotype results from a deficiency of segregates with genotype gi/gi or because some plants with this genotype escape detection at the phenotypic level. That is, the problem may be caused by a factor such as gametic selection or it may result from gi having incomplete penetrance.

The joint segregation data in Table 2 show evidence of linkage between gi and markers gp, tl and r. Moreover, in this cross significant linkage also occurred for tl-gp (27.2 units, P <0.001) and r-gp (28.6 units, P <0.001). These results are consistent with claims (2-4, 10-12) that the loci r_, tl and gp form part of one linkage group (group 5) and are further evidence against the long standing map of Lamprecht (1,6) which placed r and tl in linkage group 7 and gp in linkage group 5.

Table 1. Individual segregation data for gi and several markers in the F_2 of cross 111 x 158

Phenotype/numbers		Chi-squared (3:1)
Bt/98	bt/30	0.17
Cp/103	cp/25	2.04
Gi/107	gi/21	10.34**
Gp/97	gp/31	0.04
R/93	r/35	0.38
Tl/92	tl/36	0.67
Te/90	te/38	1.50

**P <0.01

Table 2. Joint segregation data for gi and several markers in the F_2 of cross 111 x 158. Progeny size 128

Phenotype/numbers				Joint seg.χ^2_1	Recomb. fract.	SE	Phase
Gi Bt 82	Gi bt 25	gi Bt 16	gi bt 5	0.00	50.4	6.6	R
Gi R 74	Gi r 33	gi R 19	gi r 2	4.01*	30.5	7.9	R
Gi Tl 73	Gi tl 34	gi Tl 19	gi tl 2	4.30*	29.9	7.9	R
Gi Gp 76	Gi gp 31	gi Gp 21	gi gp 0	8.04**	<22.6	8.3	R
Gi Cp 85	Gi cp 22	gi Cp 18	gi cp 3	0.44	43.8	7.1	R
Gi Te 77	Gi te 30	gi Te 13	gi te 8	0.85	56.4	6.2	R
Bt R 75	Bt r 23	bt R 18	bt r 12	3.16	39.4	5.8	C
Bt Tl 74	Bt tl *24*	bt Tl 18	bt tl 12	2.73	40.1	5.9	C
R Tl 91	R tl 2	r Tl 1	r tl 34	113.51***	1.7	1.2	C
R Gp 79	R gp 14	r Gp 18	r gp 17	15.57***	28.6	4.9	C
R Cp 81	R cp 12	r Cp 22	r cp 13	9.51**	31.9	5.2	C
R Te 66	R te 27	r Te 24	r te 11	0.07	48.4	6.5	C
Tl Gp 79	Tl gp 13	tl Gp 18	tl gp 18	18.14***	27.2	4.8	C
Tl Cp 81	Tl cp 11	tl Cp 22	tl cp 14	11.94***	30.0	5.0	C
Tl Te 66	Tl te 26	tl Te 25	tl te 11	0.07	48.5	6.5	C
Gp Cp 86	Gp cp 11	gp Cp 17	gp cp 14	17.10***	26.6	4.7	C
Gp Te 73	Gp te 24	gp Te 17	gp te 14	4.67*	37.6	5.7	C
Cp Te 84	Cp te 19	cp Te 6	cp te 19	31.92***	19.4	4.0	C

*,**,*** P <0.05, 0.01 and 0.001, respectively

The results in Table 2 generate the following map.

bt --- 39 ------ r -- 2 - tl ----- 30 --- gi --- 23 ---- gp ---- 27 ---- cp --- 19 -- te

This map places gi toward the middle of the tl-gp segment. Loci het (10) and coch (2,12) also appear to be in this general area. The order bt-r-tl-gp is consistent with the data of Swiecicki (10) and the sequence proposed by Lamm and Miravalle (4) and Folkeson (2) but tl is generally shown as lying between r_ and bt (1,6,11). Contrary to the above map, gp is usually considered as lying between cp and te. The recombination fraction of 29% obtained for r-gp in cross 111 x 158 is below the value usually observed (5,6). Nevertheless, statistically significant deviations from independent assortment for r-gp_ have now been reported on several occasions (e.g. 2,10, Table 2) and this point is noteworthy since r_ and gp were without doubt two of the seven genes studied by Mendel. Nevertheless, the linkage between r and gp seems sufficiently weak to escape detection on many occasions. Genes le and v also do not assort independently but some doubt remains as to whether the non-parchmented pods in Mendel's crosses were determined by v or by p which shows no linkage with le or the other five genes used by Mendel (9).

In summary, the data in Table 2 suffer from the fairly small progeny size (n=128), the deficiency of gi segregates and the difficulty of scoring cp and te unequivocably but have the advantage that seven linked genes are segregating in a single progeny. The results clearly indicate that gi is in linkage group 5 and they support the view that loci r, tl and gp reside in one linkage group.

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