OBSERVATION OF LINKAGE BETWEEN rui AND LOCI ON CHROMOSOME 6

Wolko, B. Plant Breeding Station, Wiatrowo, 62100 Wagrowiec, Poland

The gene ruinous (rui) belongs to the group of mutants characterized as complex genes with extensive pleiotropic effects (2). The general habit of the mutant plant is drastically changed. Rachitic rui plants show extremely reduced stem and petiole length, the vestigial, deformed leaflets dry up on the tip and the mutant plants are completely sterile as a result of abortion of the generative organs.

Mapping of complex, sterile mutants of this type presents difficulties. The sterility of homozygous plants makes it a necessity to use heterozygotes in crossing experiments. A deficiency of mutant segregants, and difficulties with observation of the phenotype of many morphological markers, is also a problem. The use of isozymic markers can help to resolve this puzzle.

The electrophoresis of isozymes was carried out on horizontal starch gels. The isozymes were visualized by assays as described by Weeden and Marx (3,4).

Three of the F2 populations were segregating for a considerable number of known marker loci. Only progenies of F1 plants which showed segregation for rui were used for mapping studies of this gene. The cross Wt15046 x Wt11238 segregated at loci i, le, r, tl, wsp, Aat-2, Aat-3, Acp-1, Aldo, Est-2, Fum, Gal-2, Gal-3, Idh, Lap-1, Lap-2, 6pgd-1, Px-1. The Wt15046 x Wt11143 progeny segregated for many of the above markers plus Dia-1, Nag-1, Pgm-2, Prx-3. The Wt15046 x Wt10345 progeny segregated additionally for wlo, Acp-5, 6pgd-2.

An undisturbed Mendelian segregation of phenotypes in F_2 progenies was observed for rui, wlo and Prx-3. A 3:1 segregation for rui and wlo was obtained. For Prx-3 a codominant type of inheritance of 1:2:1 was observed (Table 1). Significant deviation from random assortment was obtained between rui and Prx-3 in two F_2 progenies (Table 2). None of the other markers showed linkage with rui.

These results indicate that rui is located near Prx-3 on chromosome 6. The calculated map distance differed slightly between the two crosses. The close linkage between Prx-3 and wlo is worth emphasizing, since at the same time there was a lack of linkage between rui and wlo in the cross Wt15046 x Wt10345 (Table 2). This suggests that the rui locus is more distal from the centromere than Prx-3.

More precise localization of the rui locus has not yet been possible. There are no more isozyme markers on chromosome 6 and good morphological markers are difficult to observe on sterile, strongly changed plants of the rui mutant. Because of this situation a recent report of the localization of the sbm gene in the Pl end of chromosome 6 is especially interesting (1). The sbm and Arg genes may allow the location of the rui gene to be determined more precisely.

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Table 1. Phenotypic distribution and Chi-square analysis in three F2 populations segregating for genes on chromosome 6.

Cross	Locus	N	Number of progeny with designated phenotype* a	ab	b	Expect, ratio	X^2
Wt15046 x Wt11238	rui	30	27	-	3	3:1	3.60
Wt15046 x Wt11143	rui	30	23	-	7	3:1	0.04
	Prx-3	30	8	15	7	1:2:1	0.07
Wt15046 x Wt10345	rui	61	43	-	18	3:1	0.66
	wlo	134	101	-	33	3:1	0.01
	Prx-3	136	27	78	31	1:2:1.	3.18

Table 2. Joint segregation analysis of loci on chromosome 6.

Cross/Loci	Number of progeny with designated phenotype* a/a	a/ab	a/b	b/a	b/ab	b/b	X^2	Recomb. Fract.	S.E.
Wt15046 x Wt11143									
rui - Prx-3	8	13	2	0	2	5	12.3	14	7
Wt15046 x Wt10345									
rui - Prx-3	11	27	5	0	7	11	17.8	19	6
wlo - Prx-3	2	70	29	25	7	1	84.5	8	2

* Designations: a = dominant phenotype or faster migrating isozyme variant
ab = two banded isozyme phenotype
b = recessive phenotype or slower migrating isozyme variant

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