GOLD NECROSIS (gn): A NEW GENE ON CHROMOSOME 5

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Another new mutant has been isolated from an experiment on induced mutations (1,2). Mutant Wt 16129, selected in an M2 population after seed treatment of cv. 'Paloma' by 200rNf + 0.014%NEU, is characterized by gold-orange color of the lower surface of leaves. Because mutant expression is somewhat intermediate between the phenotypes of nec and/or py, orl, locus identity tests were performed. Wt.16129 was used in diallel crosses with type lines for genes in the necrotic group, viz. nec, dgl (3) and also with type lines for py, o, and orl. Normal plants were obtained in all cases. Mutant Wt.16129 was therefore regarded as new and was named gold necrosis; the symbol gn is suggested.

For the linkage test Wt.16129 (gn) was crossed with WL. 1238 (testerline). The F1 plants grown in the greenhouse in 1983 were normal and fully fertile. The F2 generation (495 plants) was grown in the field in 1984. Table 1A shows the segregation ratios for gn and also for the marker genes. Despite strong deviations from 3:1, the cp segregation data was included into the linkage calculations because the product-ratio method was used. Linkage was detected between Gn and genes in chromosome 5, viz. Cp, Te, and Gp (Table IB). Gn, together with nec and art-2 (3,4), extends the number of available loci on this chromosome. For more precise mapping better markers than cp and te are needed, and a multi-point analysis should be used.

1. Swiecicki, W. K. 1984. PNL 16:70-72.
2. Swiecicki, W. K. 1985a. PNL 17:72-74.
3. Swiecicki, W. K. 1985b. Gen. Pol. 26(3):351-359.
4. Swiecicki, W. K. 1986. Gen. Pol. 27:1-2.

Table 1. Phenotypic distribution in F2 population segregating for gold necrosis from the cross WT 16129 (mutant) x WL 1238 (testerline).

A. Monohybrid F2 segregation

Cp	cp	Total	Chi square (3:1)
397	49	446	46.72**
Te	te		
335	111	446	0.00
Gp	gp		
371	103	474	2.70
Gn	gn		
349	121	470	0.14

B. Joint segregation of gold necrosis with cp, te, and gp

Cp Te	Cp te	cp Te	cp te	Total	Joint chi square	Recomb. fract.	S.E.
330	59	0	49	438	170.02**	5.0	1.1
Cp Gp	Cp gp	cp Gp	cp gp				
347	50	1	48	446	180.63**	4.6	1.0
Cp Gn	Cp gn	cp Gn	cp gn				
286	111	46	3	446	11.80**	26.5	4.4
Te Gp	Te gp	te Gp	te gp				
333	2	12	99	446	375.91**	2.3	0.7
Te Gn	Te gn	te Gn	te gn				
225	109	105	6	445	32.98**	22.7	4.4
Gp Gn	Gp gn	gp Gn	gp gn				
250	117	99	4	470	34.12**	19.8	4.4

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