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Linkage Test of Necrotic Root (*Rn₁*) with Chlorophyll-deficient (*Y₁₈*)

The necrotic root mutant locus (*Rn₁*) has been tested for linkage with *Fr₁* root fluorescence, classical linkage group 1, (LG1), *Pgm1* phosphoglucomutase, (LG15), *Mdh1* malate dehydrogenase, *Idh1* isocitrate dehydrogenase, (LG11), *Ep* seed coat peroxidase, (LG12), *W₄* flower color, and CD-5 chlorophyll deficient (Kosslak et al., 1996; Wubben and Palmer 1998; Palmer 2005). No linkage was detected.

The necrotic root mutants descended from germinal revertants in the *w₄*-mutable line (Palmer et al. 1989). The chlorophyll-deficient mutant *y₁₈* is descended from *Y_{18-m}*, T225M (Sheridan and Palmer 1975). The *Y₁₈* mutant is a duplicate factor mutant. *Y₁₈₋₁* and *Y₁₈₋₂* are located on the USDA/ISU molecular map on linkage groups B2 and D2, respectively (Kato and Palmer, 2004).

Our objective was to test for linkage between the necrotic root mutant locus, *Rn₁*, and the duplicate chlorophyll-deficient mutant locus, *Y₁₈*.

Materials and Methods

Normal plants from families segregating normal and necrotic root phenotypes were crossed to green plants from families segregating green and yellow (lethal) plants. The male and female parent plants were assigned identification numbers and progeny tested. Only F₁ seeds that originated from the crosses of heterozygote X heterozygote were advanced to the F₂.

One F₂ family that segregated for normal: necrotic roots and green: yellow lethal seedlings was used for the linkage study. The F₂ seed were scarified and placed on germination paper. The F₂ seedlings were scored for root necrosis after seven days. Plant color was scored after 10 days.

Results and Discussion

The segregation of normal: necrotic root fit the expected ratio, $\chi^2(3:1) = 0.01$, $P = 0.93$; data obtained from Table 1. The segregation of green: yellow lethal fit the expected ratio, $\chi^2(15:1) = 0.07$, $P = 0.80$; data obtained from Table 1. Three allelic lethal yellow mutants have been identified in soybean and assigned genetic type collection numbers T218H, T225H, and T362H. In certain genetic crosses, duplicate factor inheritance in the F₂ generation was observed with these three mutants, (Palmer et al., 2000; Kato and Palmer, 2004). Thus the 15:1 ratio was not unexpected.

Our linkage data show that the Rn_1 locus is not linked to the Y_{18} locus (Table 1). A total of eight mutants have been tested for linkage with the Rn_1 locus and linkage has not been identified.

Table 1. Linkage test of necrotic root, Rn_1 with chlorophyll-deficient, Y_{18} in soybean. F_2 data.

Phenotype	No. F_2 plants	χ^2 (45:3:15:1)	P
Normal root, green leaves	138	0.02	
Normal root, yellow leaves	8	0.13	
Necrotic root, green leaves	43	0.13	
Necrotic root, yellow leaves	5	1.28	
Total	194	1.56	0.67

References

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