A more precise location for the bronze mutation on LG IV

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The line E107 was obtained by EMS mutagenesis of pea cultivar 'Sparkle' (2). This line was originally isolated as a mutant that nodulated poorly, but the altered nodulation phenotype appears to be a pleiotropic effect of a modification in iron uptake that leads to high accumulation of iron in leaf cells, causing an initial chlorosis and later development of bronze colored lesions on the leaflets. Kneen et al. (3) characterized this mutation and called the affected gene *brz (bronze)* after the lesion color and general tint of some of the leaflets. The gene was located on LG IV, 0.1 $\pm$ 12 cM from *Was* on the basis of a single cross with the two dominant genes in repulsion phase linkage (3). Although experimental data were not presented, Ellis and Poyser (1) show *Brz* located approximately 10 cM distal to *Was* on LG IV.

When growing populations in the artificial soil mix at Cornell, the appearance of the BRONZE phenol-type was not consistent, and mapping experiments had to be performed growing plants in vermiculite with supplemental chelated Fe^{2+} (3). At Montana State University I have been able to obtain the phenotype reliably in glasshouse-grown plants, the bronze lesions of the *brz/brz* homozygote being easily observed after 3 weeks growth.

A *brz, was* line (C03-6c-6) was developed by crossing the original E107 line with a derivative of A583-139 (*was/was*). This line was crossed with a homozygous *Brz, Was* line (A04-12) and the F_1 grown in the field to maximize seed production. An F_2 of 221 seed was scored for recombinant phenotypes. The joint segregation data are presented in Table 1. Each mutant gave a segregation pattern close to the expected 3:1 ratio. Joint segregation analysis of either *Brz* or *Was* with *St* gave ratios consistent with independent assortment. However, joint segregation analysis of *Brz* and *Was* gave significant deviation from independent assortment, indicating that the two loci were separated by about 9 cM (Table 1). These results are consistent with the two previous mapping studies and provide a more precise estimate of the linkage intensity between two loci on LG IV.

Table 1. Genetic analysis of segregation patterns in the cross E107(*brz*) x A583-139 (*was*)

		Single locus		Joint segregation analysis *(Brz/Was)*					
Locus (loci)	n	Domin	Recess	*Brz/Was*	*Brz/was*	*brz/Was*	*brz/was*	χ^2	R $\pm$ S.E.
Brz	221	162	59						
Was	221	156	65						
St	221	158	63						
Brz/Was	221			149	13	7	52	134***	9.1 $\pm$ 6.7

*** P < 0.001

1. Ellis, T.H.N. and Poyser, S.J. 2002. New Phytol. 153: 17-25.
2. Kneen, B.E. and LaRue, T.A. 1988. Plant Sci. 58: 177-182.
3. Kneen, B.E., LaRue, T.A., Welch, R.M. and Weeden, N.F. 1990. Plant Physiol. 93: 717-722.