Linkage between *Brac* and *Idh* on linkage group I of *Pisum sativum*

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Gottschalk (1) reported the recessive mutation *brac*, which was induced by mutagenic treatment of seeds. The *brac* plants produce large bracts on the inflorescence. Recently, Rozov *et al.* (2) also isolated a similar mutation in an M_2 progeny of an EMS treated SG line. The mutant plants had large bracts on the inflorescence and open flowers. Complementation tests revealed that their mutation is allelic to the Gottschalk's *brac* mutation. The respective locus, *Brac*, showed linkage to *D* on linkage group I.

A phenotypically similar spontaneous mutation was isolated from variety 'Hans' (L 116) in the experimental fields of I.A.R.I., Delhi. The variety 'Hans' itself is a mutant derivative of the old Swedish variety 'Weitor.' The mutant line, designated P 1440 (*a, I*) was crossed with the bractless line P 1297 (*A, D*) earlier by Dr. Y.C. Kala. The F_1 plants were structurally normal and the peduncles did not have bracts, confirming the recessive nature of this new *brac* mutation. The line P 2329 (*A, D, brac*) was isolated from an F_2 population of this cross, which had normal flowers, bracts on peduncles, and the slow allozyme of isocitrate dehydrogenase (*Idh*). These results indicate that the genetic elements for flower structure and bract formation, although both appearing in the same mutant, are separable by recombination. The line P 2329 was crossed with P 1865 (*A, d, Brac*) having a fast variant at *Idh*. The F_1 plants were fertile, and their hybridity was confirmed by isozyme assay (codominant expression). The IDH assay was carried out by the method of Shaw and Prasad (3) using Tris-citrate system at pH 7.1. The enzyme was extracted from leaves of young seedlings using a 0.5 M Tris-HCl, pH 7.5 extraction buffer containing 0.6% 2-mercaptoethanol.

The F_2 data were analyzed by the computer program CROS, developed by Dr. S.M. Rozov. Table 1 shows monohybrid and dihybrid segregation for *Brac*, *Idh* and *D.* Segregation at all loci did not differ significantly from a 3:1 ratio. The results showed significant linkage between *Brac* and *D* (χ^2_L = 11.6; P < 0.001). The recombination fraction was estimated as 25.6 $\pm$ 6.1. a similar distance (27.5) was reported by Rozov *et al.* (2).

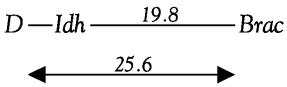
Table 1. Joint segregation in F_2 progeny for the markers *brac*, *D* and *Idh*.

								Chi-square					
Gene A	**Gene B**	**Phase**	**A/B**	**A/b**	**a/B**	**a/b**	**Total**	**Locus A**	**Locus B**	**joint**	**Linkage**	**SE**	**P**
brac	***D***	**Rep[1]**	**124**	**54**	**45**	**3**	**226**	**1.70**	**0.005**	**11.6**	**25.6**	**6.1**	**<0.001**
brac	***Idh***	**Rep.**	**119**	**59**	**46**	**2**	**226**	**1.70**	**0.477**	**16.1**	**19.8**	**6.3**	**<0.0001**

[1]Rep. = repulsion phase

Note: Because of codominant inheritance of the isozyme marker, the fast variant has been added to heterozygotes to obtain 3:1 ratio.

The linkage between *Brac* and *Idh* was also highly significant (χ^2. = 16.1; P < 0.0001). The recombination fraction between these two loci was estimated to be 19.8 $\pm$ 6.3. Considering the position of *Idh* with respect to the *D* locus in the pea linkage map (4) and our results, the order of these three genes can be proposed as



The allelism of the spontaneous *brac* mutation with the *brac* mutation of Gottschalk (1) and Rozov *et al.* (2) remains to be confirmed directly by crossing all three strains.

1. Gottschalk, W. 1961. Planta 57: 313-330.
2. Rozov, S.M., Gorel, F.L. and Berdnikov, V.A. 1997. Pisum Genetics 29: 26.

3. Shaw, C.R. and Prasad, R. 1970. Biochem. Genet. 4: 297-320.
4. Weeden, N.F., Ellis, T.H.N., Timmerman-Vaughan, G.M., Święcicki, W.K., Rozov, S.M., Rozov, S.M. and Bernikov, V.A. 1998. Pisum Genetics 30: 1-4.