

## Further confirmation of the integrity of linkage group III

Tonguc, M.

Dept. Horticultural Sciences

Cornell University, Geneva, NY 14456

Weeden, N.F.

Dept. Plant Sciences and Plant Pathology

Montana State University, Bozeman, MT 59717

Several recent studies (1, 2, 6) have reported the synteny of markers on what was earlier assumed to be the *B-Chi6* end of linkage group (LG) III and markers on the linkage group identified as LG IVB in (8). Here we provide additional evidence that LG IVB is actually one end of LG III. We used the morphological marker *bulf*, originally described by Sharma (7) and mapped to a position near *Chi6* by Marx and others (3, 4, 5). Although *bulf* is not commonly used in mapping studies, its phenotype (burnt leaf) is clear, and the position of the locus (approximately 20 cM from *B*) makes it an excellent marker to use for testing the integrity of the redefined LG III.

We examined an F<sub>2</sub> derived from the cross Marx 19051 (*bulf*, *Lap1-s*) x A98-38-5 (*Td*, *Lap1-f*). The 25 F<sub>2</sub> plants were grown in the greenhouse and scored for segregation at *Lap1*, *Bulf* and *Td*, the latter locus usually associated with the previous LG IVB. Phenotypes were clearly expressed, and segregation for all three loci gave normal Mendelian ratios (*Lap1*= 7:13:5; *Bulf*=19:6; *Td*=19:6). Joint segregation analysis is presented in Table 1. The linkage and order of the loci are unambiguous. Only one plant displayed recombination both between *Lap1* and *Bulf* and between *Bulf* and *Td*. The linkage value between *Lap1* and *Bulf* (21 cM) agrees well with the value of 20 cM reported between *B* and *Bulf* (5). The 33 cM recombination value between *Lap1* and *Td* also compares satisfactorily with the 25 cM distance calculated between *B* and *Np* (6) (the latter locus known to be close to *Td*).

**Table 1. Joint segregation analysis of markers on linkage group III**

Loci	a/a*	a/b	h/a	h/b	b/a	b/b	$\chi^2$	% recomb.	Std. Er.
Lap1:Bulf	3	4	11	2	5	0	6.3	21	± 9
Lap1:Td	4	3	10	3	5	0	2.8	33	±11
Bulf:Td	17	2	—	—	2	4	7.9	18	+19

\*a=dominant or slow; h=heterozygous; b=recessive or fast

- Gilpin, B.J., McCallum, J.A., Frew, T.J. and Timmerman-Vaughan, G.M. 1997. *Theor. Appl. Genet.* 95: 1289-1299.
- Laucou, V., Haurogne, K., Ellis, N. and Rameau, C. 1998. *Theor. Appl. Genet.* 97: 905-915.
- Marx, G.A. 1980. *PNL* 12: 47-48.
- Marx, G.A. 1981. *PNL* 13: 29.
- Marx, G.A., Weeden, N.F. and Provvidenti, R. 1985. *PNL* 17: 57-60.
- Murfet, I.C. and Ellis, T.H.N. 1998. *Pisum Genetics* 30: 12-14.
- Sharma, B. 1973. *PNL* 5: 46.
- Weeden, N.F., Swiecicki, W.K., Timmerman-Vaughan, G.M., Ellis, T.H.N. and Ambrose, M. 1996. *Pisum Genetics* 28: 1-4.