Linkages of the *Aba* (*Albumin a*) locus with markers of the linkage group VI

Swiecicki, W.K., Przybylska, J., and Zimniak-Przybylska, Z.,

Institute of Plant Genetics, Polish Academy of Sciences
Poznan, 60-479 Strzeszynska 34, Poland

Investigations of seed proteins in the genus *Pisum* have identified the gene *Aba* for *Albumin a* and suggested a weak linkage with *Pl* on linkage group VI: joint chi square = 11.6; Cr-O = 39.3 (2). An electrophoretic screening of crude seed albumin extracts from over 500 *Pisum* accessions, representing a wide range of genetic and geographic variation, resulted in detection of 11 electrophoretic seed albumin patterns (3, 4). The patterns (phenotypes) were numbered from I to XI according to their sequence of discovery (1, 4). Using successive letters for the albumin alleles seems to be practical because differences in the phenotypes are due to the occurrence of seven bands forming different sets. For this reason it is not possible to designate the alleles according to electrophoretic mobility of respective electrophoretic variants as in the case of allozymes. Phenotypes V, X, XI were observed only in *P. fulvum* (3, 4). Phenotypes I to X are believed to be alleles of a single locus, with test crosses showing co-dominant inheritance.

In order to define the position of the locus more precisely, we performed another genetic analysis of *Aba*. The line Wt 11777 from the Polish *Pisum* Gene Bank was selected and used in the cross. It is the tester line for linkage group VI expressing the following markers: *Pl*, *Arg* (lower arm) and *wlo art*1 (upper arm) and the allele Aba^A controlling electrophoretic seed albumin pattern I. Line Wt 11777 was crossed to Wt 501 (albumin phenotype II and the suggested symbol Aba^C). Unfortunately, Wt 501 expresses, in common with Wt 11777, the dominant allele at *Pl*. As a consequence in the F_2 generation of K. 1880 (Wt 501 x Wt 11777) only the segregation of *Arg Wlo Art*1 and *Aba* were observed.

Table 1 shows undisturbed monohybrid segregation for *Aba* and the marker genes. Table 2 presents results of observations of a dihybrid segregation. *Arg* does not display significant linkage with *Aba* at the level of precision available in the experiment, thus indicating that Aba is not close to the *Pl*—*Arg* segment. Substantial deviations from independent assortment were found for gene pairs localized in an upper portion of the linkage group VI, i.e. *Art*1-*Wlo* but also *Art*1-*Aba* and *Wlo*-*Aba*. Calculated Cr-O values show clear linkages of the *Aba* with both markers. Comparison of linkage intensities suggests that *Aba* may be the most distal marker of those examined, but the data are not conclusive.

Table 1. Monohybrid segregation for genes from the linkage group VI in the linkage test cross K. 1880 (F_2 generation) – Wt 501 (*Aba-c*) x Wt 11777 (*Arg wlo art1 Aba-a*).

Gene	Allele		Total	Chi square (3:1)[1]
	Dominant	Recessive		
Arg	**104**	**34**	**138**	**0.01**
Art1	**99**	**39**	**138**	**0.78**
Wlo	**99**	**39**	**138**	**0.78**
Aba	**108**	**41**	**149**	**0.50**

[1]**Phenotypes of *Aba-c* were added to heterozygotes.**

Table 2. Distribution of phenotypes in F_2 generation and the linkage test for K. 1880 – Wt 501 (*Aba-c*) x Wt 11777 (*Arg wlo art*1 *Aba-a*).

Pair of genes	Phase	Phenotype				Total	Joint chi square	Cr-O value + SE (per cent)
		DD	Dr	rD	rr			
Arg-Art1	**R**	**69**	**35**	**30**	**4**	**138**	**6.82**	**31.8 ± 7.5**
Arg-Wlo	**R**	**68**	**36**	**31**	**3**	**138**	**9.28**	**27.4 ± 7.8**
Arg-Aba	**R**	**70**	**34**	**29**	**5**	**138**	**4.74**	**35.6 ± 7.3**
Art1-Wlo	**C**	**88**	**11**	**11**	**28**	**138**	**50.99**	**16.6 ± 3.5**
Art1-Aba	**C**	**88**	**11**	**11**	**28**	**138**	**50.99**	**16.6 ± 3.5**
Wlo-Aba	**C**	**82**	**17**	**17**	**22**	**138**	**21.35**	**26.9 ± 4.5**

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