LINKAGE OF AN AEROMACULATA MUTANT ON CHROMOSOME 1

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Aeromaculata mutants are so named because they cause epidermal layers of leaves to become separated from the subjacent cell layers, creating air spaces (1). White patches or flecks appear because light is differentially reflected and refracted (Fig. 1). Fl is one such mutant locus and Argis another; the former limits the expression to flecking whereas the latter results in near complete involvement. In 1982 Dr. Blixt sent me seeds of a series of aeromaculata lines from his collection. He designated them as "supaeromaculata" because many show a high degree of phenotypic expression. The set of lines contained the following numbers: WL-102 (fl), -581 (Fl-v), $-5120\,,\;\; -5136\,,\;\; -51\,57\,,\;\; -5287\,,\;\; -5289\,,\;\; -5349\,\,,\;\; -5401\,,\;\; -5534\,,\;\; -5360\,,\;\; -5727\,,$ -5987. Most of the mutants evidently were artificially induced. The lines differed in degree of expression, ranging from no flecking to moderate flecking to extreme expression (i.e. resembling Arg expression), and for that reason the lines were characterized on a basis of a scale from 1 to 10, with fl (no flecking) as 1 and strong expression as 10.

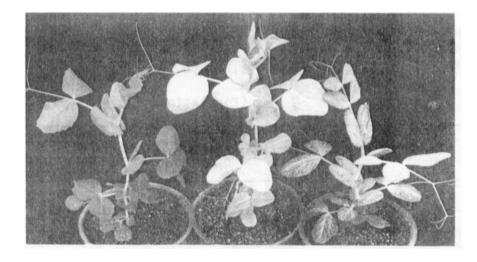


Fig. 1. Seedlings of jfj (left), $\underline{\text{Arg}}$ (middles, and $\underline{\text{aero}}$ (W1-5880). As the aero plants grow older they more nearly resemble the phenotype of Arg plants.

Although it was suggested previously (2) that the phenotypic differences in the above lines may result from genes located at loci other than Fl, as far as I am aware the matter has never been thoroughly investigated. Dr. Blixt had also informed me that the above mutant(s)show recessive inheritance, indeed recessive even to fl, a fact confirmed by the results of my own crosses. Initially, my principal interest in examining the material was to try to determine the relationship, if any, with Arg.

Of the WL lines listed above I used only three in crosses. WL-5837 and WL-5880 were used because they exhibited strong expression, approaching that of Arg. WL-102 was used as a source of $\underline{\text{f1}}$. Hereafter I will provisionally designate the gene derived from WL-5837 and WL-5880 as aero, pending official designation by Dr. Blixt.

Our attempts to determine whether or not $\underline{\operatorname{Arg}}$ and $\underline{\operatorname{aero}}$ are alleles at the same locus proved difficult not only because both mutants have similar phenotypes but also because $\underline{\operatorname{Arg}}$ shows a certain amount of phenotypic instability. Moreover, except for the $\underline{\operatorname{aero}}$ x f1 crosses, all the original crosses were between $\underline{\operatorname{aero}}$ and $\underline{\operatorname{Arg}}$, so it was difficult to establish linkage patterns even if $\underline{\operatorname{aero}}$ did not prove to be an allele of F1 or of $\underline{\operatorname{Arg}}$. Numerous populations derived from $\underline{\operatorname{Arg}}$ x $\underline{\operatorname{aero}}$ crosses gave no indication that aero was an allele of $\underline{\operatorname{Arg}}$ (data not shown).

It was not until two small populations were analyzed in 1985 that evidence was obtained suggesting that <u>aero</u> is situated on chromosome 1 near I and Af (Table 1). The <u>aero</u> parent in these crosses, an F6, descended from an earlier cross with WL-5837. Though the population sizes are undesirably small and the genes are in the repulsion phase, the data seem to support the claim of linkage. Since the <u>aero</u> gene derived from only one (WL-5837) of several <u>aero</u> lines, it cannot be concluded that the same linkage relationship applies to all aeromaculata lines in the set. To ascertain if different degrees of expression among the WL lines reflect the presence of a series of alleles would require crossing the lines <u>inter se</u> as well as to a common fl line. Otherwise the wide variation in flecking which prevails in the gene pool would confound the analysis.

Data in Table 2 show the results of joint segregation between $\underline{\text{aero}}$ and $\underline{\text{sil}}$. Although there was no evidence of linkage between the two mutants, the data are included to show that $\underline{\text{aero}}$ segregated with a good fit to a 3:1. Earlier crosses between aero and fl also gave good monogenic segregation (data not shown).

 $\underline{\text{Aero}}$ is another valuable seedling marker which should help to extend our knowledge of chromosome 1. How the various aeromaculata genes act to cause their effect remains an intriguing, unstudied question.

- 1. Blixt, S. 1962. Agri Hort. Genet. 20:95-110.
- 2. Blixt, S. 1972. Agri Hort. Genet. 30:1-293.

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Table 1. Joint segregation analysis between an $\underline{\text{aeromaculata}}$ mutant derived from WL-5837 and two marker lines.

Gene						(Chi-squ	are	Recomb.	
pair	XY	Xy	XY	ху	N	X		Linkage	fract.	S.E.
Aero I	72	28		0	142	1.59	2.11	14.90**	<16.9	8.1
Af Aero	45	24	13	0	82	3.66	0.80	5.90*		10.2
	uni es			ara e	128 57	325 10	o biblio		Economic pa e Bangang ras	
Table 2.	Joi	nt s	egre	gatio	n ana]	lysis be	tween Chi-so	aero and		
							Chi-so		Recomb.	
Gene	_X	<u>Y</u> <u>X</u>	<u>y</u> <u>x</u>	<u>Y</u> <u>xy</u>	N	X	Chi-sc	quare	Recomb.	
