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BRIEF COMMUNICATION

ON THE INTERRELATIONSHIPS OF CERTAIN SPECIES OF PETUNIA. V. INHERITANCE OF FLOWER MORPHOLOGY.

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The hybrid varieties known under the collective vernacular name of Petunia (*Stimoryne hybrida* (Hook.) Wijsman) have been derived from crossing two ancestral species, *S. axillaris* and *S. integrifolia*. Formerly the two species and their hybrid were included into the genus *Petunia* Juss., but recently they have been transferred to *Stimoryne* Rafin. (WIJSMAN & DE JONG 1985). The difference between *S. axillaris* with large white flowers with a slender long flower tube, and *S. integrifolia* with smaller, purple flowers so wide as to obscure the border between limb and tube have been described (WIJSMAN 1982, 1983) and can be seen in *fig. 1*. Because a considerable number of genes has been characterized in the hybrid (DE VLAMING et al. 1984), it seemed of interest to investigate whether in addition to the genetic basis of the difference in flower colour (WIJSMAN 1983), the genetics of the difference in flower morphology between the two species could be understood.

Two lines have been crossed, S2 (*S. axillaris* ssp. *axillaris*) and S6 (*S. integrifolia* ssp. *inflata*), differing in several factors located in most linkage groups. Some of the genetic differences (see DE VLAMING et al. 1984) can be determined visually, like *Fl* (on chromosome II), *Po* (V), *An2* (VI), others by chromatography like *F1*. The difference as to *F1* is blurred by the presence of modifiers in S6, which has relatively much flavonol. The genes *prxB* (I), *prxA* (III), and *prxF* (VII) concern electrophoretic differences in isoperoxidases. Line S6 was formerly heterozygous for *prxC*; unfortunately no F1 heterozygous for *prxC* could be found, and no other marker on chromosome IV segregated.

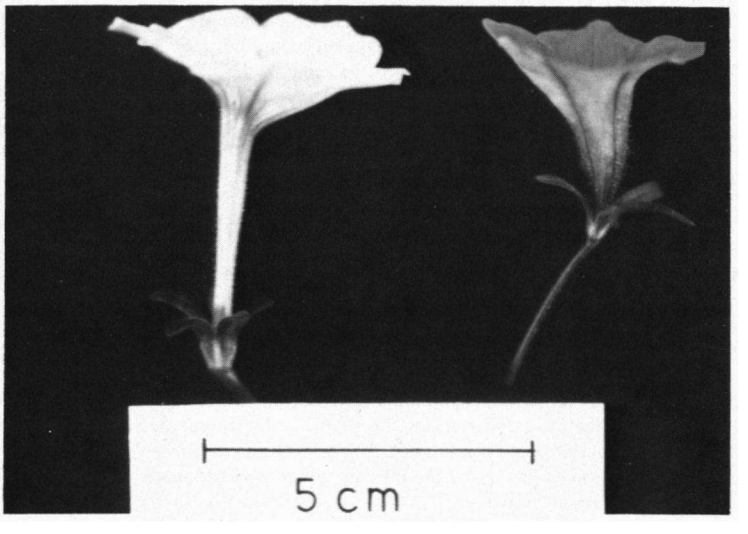

Fig. 1. Flowers of *S. axillaris* (left) and *S. integrifolia* (right).

Table 1. Distribution of flower shape in the F2 (S2 × S6) among markers fom every linkage group except IV. Flower shape was expressed in one figure by measuring the ratio of greatest length of the flower and widest width of the flower tube. None of the differences is significant except for the case of *Fl* (*, $P < 0.01$).

Genotypic formula for the homozygous lines:

S2: *prxB2* *Fl*$^+$ *prxA1* *po*$^-$ *an2*$^-$ *prxF1*
S6: *prxB3* *fl*$^-$ *prxA2* *Po*$^+$ *An2*$^+$ *prxF2* (null)

linkage group	locus	phenotype	No.	flower shape	
				Mean	SD
I	*prxB*	B2B2	32	4.1	0.73
		B2B3	41	4.4	0.44
		B3B3	8	4.2	0.56
II	*Fl*	+	41	4.5	0.67*
		−	30	3.8	0.47*
III	*prxA*	A1A1	44	4.1	0.62
		A1A2	35	4.3	0.82
		A2A2	0	−	−
V	*Po*	+	49	4.1	0.69
		−	27	4.4	0.71
VI	*An2*	+	57	4.2	0.66
		−	20	4.1	0.77
VII	*prxF*	F1$^-$	48	4.1	0.96
		F2F2	26	4.2	0.59

The morphology of the flower was characterized by applying a flower shape index as described in the legend of *table 1*. In this respect, the F1 of the two species is intermediate between the parents (S2: 9.0 ± 0.85; F1: 4.0 ± 0.75; S6: 2.4 ± 0.69). The amplitude of variation in the F2 (index 4.2 ± 0.67) suggests polyfactorial determination of the difference between the species, because no discrete flower shape types could be distinguished. In general, the F2 shows considerable variation for other phenotypes because of the many markers segregating with in addition some blending by the apparent occurrence of modifiers in the parental species. Unfortunately, there occurred much lethality, late germination, and late flowering, as well as many a much shorter lifespan than normal (under standard conditions). From about 250 seeds sown, only about 80 plants could be used for the analysis.

For most markers the means of the morphology indices of the F2 flowers (*table 1*) show no significant difference among the alternative genotypes. The only exception is the case of the factor *Fl*. Even though distinction of *Fl*$^+$ and *fl*$^-$ types is difficult in the present cross, the average shape indices differ highly significantly, which can be ascribed to linkage of factors relating to flower morphology to the gene *Fl* on chromosome II. However, the absence of Mendelian segregation is evidence for the fact that other chromosomes must necessarily share some of the other factors involved. Most segregations of the markers screened differ significantly from simple Mendelian ratios; this is the normal situation in petunia and it can be ascribed to certation between pollen tubes as well as to differential viability of the various alleles. In general the S6 marker is underrepresented. However, the underrepresentation of S2 types both for *Fl* as well as for the flower shape index supports the notion of linkage of the relevant genes. Unfortunately, chromosome IV could not be screened in the present analysis.

Several recent investigations (e.g. TANKSLEY et al. 1982, VALLEJOS & TANKSLEY 1983, BACHMANN et al. 1982) found linkage of major determinants of polygenic inheritance to specific isozyme

markers. VAN DIJK (1984) analyzed several polygenically determined differences in *Plantago* and in all cases at least one (in some cases two) linkage groups were implied. Several factors involved resided in a complex of loci in one linkage group involved in ecotypic differentiation. This suggests that differences of adaptive value, be they composite in nature, may be inherited as a complex. The same may apply to factors determinative of the reproductive barrier between species, as in our case, because the flower selects the pollinating insect. The gene *Fl* may be part of such a complex together with the flower shape determining factor because it is tempting to consider the presence of much flavonol (by the action of *Fl*), with its strong fluorescence, as an adaptation to pollination by moths in the case of *S. axillaris*. By contrast, *S. integrifolia* is pollinated by bees and bumble-bees. Further genes tightly linked to *Fl* are the flower morphology markers *Cr* and *Px* (DE VLAMING et al. 1984) and it may well be that the two wild species carry different alleles at these loci, contributing to flower shape differentiation. In petunia on the one hand the distribution of genes over the length available is far from random on the genetic map, while on the other hand in different genetic backgrounds differences in local recombination on the chromosome are very apparent (cf. GERATS et al. 1984; MAIZONNIER et al. 1984). Possibly this phenomenon of apparent gene clustering reflects selective forces limiting recombination in regions carrying co-adapted alleles.

Interestingly, the number of genes involved in reproductive barriers between both present species may be low, just as was the case for flower colour (WIJSMAN 1983). This further stresses the close relationship of both species.

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