

INHERITANCE OF PIGMENTATION AND POD SHAPE IN WINGED BEAN

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INDEX WORDS

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SUMMARY

The inheritance of five qualitative character differences in winged bean was studied in two crosses. All five character pairs were based on a single gene difference with complete dominance of purple over green stem colour, purple over green calyx colour, purple over green pod wing colour, purple specks over green pod and rectangular over flat pod shape. Linkage was observed between stem and calyx colour and also pod wing colour and pod specks.

INTRODUCTION

The legume species, winged bean (*Psophocarpus tetragonolobus* (L.) DC.) is a rich source of protein (MASEFIELD, 1973). Almost all parts of the plant including green pods, leaves, flowers, root tubers and dry seeds are edible. Its potential has recently been recognized (ANON., 1975). SASTRAPRADJA & AMINAH-LUBIS (1975) and KHAN (1976) have reported a wealth of genetic diversity in material indigenous to Indonesia and Papua New Guinea, respectively. This note reports the inheritance of five qualitative characters in winged bean which may be useful as markers in further genetic studies and also in varietal identification.

MATERIALS AND METHODS

Two crosses involving five character differences amongst three pure lines were made in 1974 (Table 1). F₁ plants were allowed to self pollinate. During 1976, F₂ plants were individually studied. Data on the pigmentation of stem and calyx were recorded at flowering and all pod characters were scored once pods were > 10 cm long. There was considerable variation in the intensity of pigmentation and only the presence or absence of pigmentation was recorded. Pod shape was defined as seen in the cross section (KHAN, 1976). F₂ data from both crosses were analyzed simultaneously according to MATHER (1951). The method of maximum likelihood was used for recombination estimation. It was assumed that recombination in both male and female F₁ gametes was similar.

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Table 1. Parental characteristics.

Pure line	Stem colour	Calyx colour	Pod wing colour	Pod speck colour	Pod shape as seen in cross section
UPS 31	purple	purple	purple	green	rectangular
4F 1054	green	green	green	specks	flat
4F 1061	green	green	green	specks	flat

RESULTS AND DISCUSSION

All five pairs of characters were found to be based on single gene difference with complete dominance of purple over green stem colour, purple over green calyx colour, purple over green pod colour, purple speck over green pod, and rectangular over flat pod shape (Table 2). In all cases the results from both families were homogeneous.

There was significant linkage between stem and calyx colour in the coupling phase. In addition, wing colour was found linked to pod specks in the repulsion phase (Table 3).

These results are the first reported inheritance studies on winged bean. Amongst the characters studied stem colour is of particular importance to future crop improvement as a genetic marker since it displays simple inheritance and can also be readily observed at the seedling stage. The stem colour marker is now being

Table 2. F₂ results.

Character	Cross	Result	Deviation from 3:1 ratio (P)	Heterogeneity between families (P)
Purple: green stem	31 × 1054	111:32	0.3 - 0.5	0.8 - 0.9
	31 × 1061	105:32		
Purple: green calyx	31 × 1054	102:32	0.5 - 0.7	0.95
	31 × 1061	98:31		
Purple: green wing	31 × 1054	99:29	0.5 - 0.7	0.1 - 0.2
	31 × 1061	95:40		
Speckled: green pod	31 × 1054	104:24	0.3 - 0.5	0.1 - 0.2
	31 × 1061	100:35		
Rectangular: flat pod	31 × 1054	101:31	0.7 - 0.8	0.3 - 0.5
	31 × 1061	92:36		

Table 3. Linkage statistics.

Linked characters	P	Standard deviation	Phase
Stem and calyx colour	0.131	0.060	coupling
Wing colour and specks	0.266	0.033	repulsion

extensively used to estimate the extent of outcrossing in winged bean over a wide range of environments.

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BOOK ANNOUNCEMENTS

R. RIEGER, A. MICHAELIS & M. M. GREEN, 1976. *Glossary of genetics and cytogenetics*. 4th completely revised edition. Springer Verlag, Berlin. 647 p. DM 36, US \$ 14.80.

According to the authors, about 50% of the old text has been completely rewritten. The most important new terms have been included to bring the glossary up-to-date. The 3rd edition with its 507 pages of text has, as a result of the revision, evolved into a new volume with a total of 647 pages. There has thus been an increase of some 28%.

Taking p. 110 and 111 of the new edition in a random choice to compare them with the same part of the 3rd edition, we find new items as cloning, closed regulatory loop, coancestry, coated visicle, co-conversion, coding ambiguity and codogenic. Using p. 384 and 385 for the purpose of such comparison we come across new items as neo-XY-system, nexus, N-formyl-methionyl transfer RNA, nick, non-diasmata, non-conservative, non-Darwinian evolution, nonhistone chromosomal protein. Deleted are: non-chromosomal and non criss-cross exception.

The glossary had made an extremely good reputation for itself and the same will hold for this 4th edition. (Extremely) good wine needs no brush.

The price is rather low and this will promote its wide spread and use.