

## GENETIC ARCHITECTURE OF GUM CONTENT IN CLUSTER BEAN UNDER DIFFERENT ENVIRONMENTS\*

B. S. JHORAR, K. R. SOLANKI AND D. S. JATASRA

Department of Plant Breeding, Haryana Agricultural University,  
Hisar-125 004, India

### ABSTRACT

Genetic architecture of gum content in cluster bean has been investigated using numerical and graphical analysis of a six-parent diallel cross under different environmental conditions. Environments exerted substantial effect on gene expression. The character was governed mostly by non-additive gene effects. The additive genetic component was stable whereas the dominance component significantly interacted with environments and was, thus, unstable. The mean degree of dominance invariably revealed overdominance in all the environments. Symmetry of positive and negative genes was observed in the parental population. One to four dominant genes governed inheritance of the gum content. Heritability estimates were low in all the environments. Graphical analysis revealed that cultivars HG 182, FS 277 and DPS possessed the maximum number of dominant genes and hence their exploitation in breeding programmes for developing varieties with high gum content has been suggested.

### INTRODUCTION

Gum content is an important quality trait in cluster bean [*Cyamopsis tetragonoloba* (L.) Taub.]. Dabas (1975) and Dabas *et al.* (1980) studied gene action in selected crosses of guar and found that gene action for gum content varies from cross to cross. Additive and non-additive components of genetic variance were equally important in the expression of the gum content (Nath, 1979). Non-additive gene effects were more important than additive gene effects for all the characters including quality

traits (Singh, 1981). These studies do not clearly bring out the genetic mechanism underlying the expression of gum content. Therefore, a multi-environmental approach has been adopted in this study for clear understanding of the genetics of gum content using component and graphical analysis for a six-parent diallel.

### MATERIAL AND METHODS

Six cluster bean cultivars (FS 277, Durgapura safed, HG 182, Pusa Naubahar, Agaita Guara 111 and KVS II) were

\*Part of Ph. D. dissertation submitted by the senior author to the Haryana Agricultural University, Hisar.

used to make a one-way diallel. The parents and  $F_1$ 's were grown in a thrice replicated randomized block design under four different environments (Table 1) at the Haryana Agricultural University Research Farm at Hisar and Bawal. Parents were sown in two rows with  $F_1$ 's in a single three meter row with 45 cm spacing between rows and 10 cm between plants. Five competitive plants from each row were selected at random for observations. Extraction and estimation of the gum was done as per Das *et al.* (1977). The data were subjected to diallel analysis (numerical and graphical) according to Hayman (1954). The genetic analysis was also done for the pooled data and the narrow sense heritability was worked out following Crumpacker and Allard (1962).

of genetic components of variation and their ratios are presented in Table 3. Non-significant  $t^2$  values revealed that assumptions of the diallel were generally fulfilled. The variance due to additive genetic effects (D) was significant in only one of the four environments whereas  $H_1$  which gives relative proportion of variance due to non-additive gene effects, was significant in all the environments. The  $H_1$  was greater than D in all the environments indicating a greater role for non-additive than additive gene effects in the inheritance of the gum content in cluster bean. Similar results have been reported by Chaudhary (1979) and Singh (1981) for the gum content in cluster bean. However, Dabas (1975), Nath (1979) and Dabas *et al.* (1980), reported that additive

Table 1. Details of four environments

Environment	Location	Date of sowing	Annual rainfall (mm)	Soil type
E 1	Hisar	19-7-1979	341	Sandy loam
E 2	Bawal	24-7-1979	174	Sandy
E 3	Hisar	17-7-1980	201	Sandy loam
E 4	Bawal	18-7-1980	601	Sandy

## RESULTS AND DISCUSSION

Analysis of variance for gum content in different environments as well as pooled analysis (Table 2) revealed highly significant differences between genotypes. The broad spectrum of genetic variability revealed by the analysis showed that the choice of the parents was appropriate. The estimates

and non-additive gene effects were equally important in the inheritance of the gum content. The degree of dominance in this study was consistent and more than one indicating over-dominance. The computed value of  $h^2/H_2$  ranged from 0.562 to 3.474 in different environments indicating one to four dominant genes or gene groups controlling this attribute.

Table 2. Analysis of variance for gum content under four environments and pooled data

Environment	Mean squares		C. V. %
	Genotype	Error	
	20 <sup>+</sup>	40 <sup>+</sup>	
E 1	5.82**	0.99	2.71
E 2	6.09**	0.78	2.80
E 3	6.94**	0.76	2.74
E 4	5.85**	0.97	3.11
Pooled	17.18**	0.87	1.70

\*\*Significant at P = 0.05

+ Degrees of freedom.

The ratio  $(4DH_1)^{1/2} + F / (4DH_1)^{1/2} - F$  was less than one in all the environments including pooled data. This shows that there was an equal proportion of dominant and recessive genes in the parents. The symmetry of positive and negative genes was evident from the non-significant ratios of  $H_2/4H_1$  in all the environments. The significant and negative value of the correlation coefficient (r) between the parental measurement ( $Y_r$ ) and parental order of dominance ( $W_r + V_r$ ) indicated that the positive genes for higher gum content were mostly dominant. The narrow sense heritability estimates were low in all the environments indicating that the character was highly influenced by the environmental factors. The low heritability estimates also confirmed the preponderance of non-additive gene effects governing gum content.

The widely scattered points of array means on the  $V_r$ - $W_r$  graphs for gum content in the four environments and pooled analysis revealed genetic diversity between parents (Fig. 1). The relative position of array points in different environments was not similar indicating that gene expression was influenced by the environmental conditions. The array points of the parents FS 277, DPS and HG 182 were near the origin in majority of the environments and thus, has maximum number of dominant genes for the gum content. Jhorar *et al.* (1983) have also reported these parents to have the maximum number of favourable genes for high gum content in cluster bean. On the contrary, AG 111 possessed the maximum number of recessive genes in all the environments.

Table 3. Estimates of the components of genetic variation under different environments in cluster bean

Component	E 1	E 2	E 3	E 4	Pooled
D	0.366 ±0.437	0.624 ±0.540	1.881* ±0.324	0.488 ±0.419	0.505* ±0.136
H <sub>1</sub>	4.727* ±1.110	4.218* ±1.372	5.550* ±0.824	4.985* ±1.063	0.716* ±0.346
H <sub>2</sub>	2.977* ±0.992	5.265* ±1.225	2.580* ±0.736	3.023* ±0.950	1.212* ±0.309
h <sup>2</sup>	1.673* ±0.667	5.615* ±0.825	7.291* ±0.495	13.527* ±0.639	6.377* ±0.208
F	-2.389* ±1.068	-0.171 ±1.320	-1.097 ±0.793	-0.250 ±1.023	-1.285 ±0.333
F	0.161 ±0.165	0.787* ±0.204	0.761* ±0.123	0.975* ±0.158	0.878 ±0.051
$(H_1/D)^{\frac{1}{2}}$	2.827	2.891	1.371	2.474	1.167
$H_2/4H_1$	0.250	0.250	0.249	0.250	0.243
$(4DH_1)^{\frac{1}{2}} + F /$ $(4DH_1)^{\frac{1}{2}} - F$	0.071	0.909	0.550	0.812	0.142
h <sup>2</sup> /H <sub>2</sub>	0.562	1.066	2.826	3.474	3.263
r (Y and W <sub>r</sub> + V <sub>r</sub> )	-0.148	-0.746	-0.572	-0.927**	-0.157
t <sup>2</sup>	2.742	1.257	1.050	5.372	0.039
heritability (%)	4.108	6.814	16.988	6.398	5.333

\*, \*\* Significant at 5% and 1% levels, respectively.

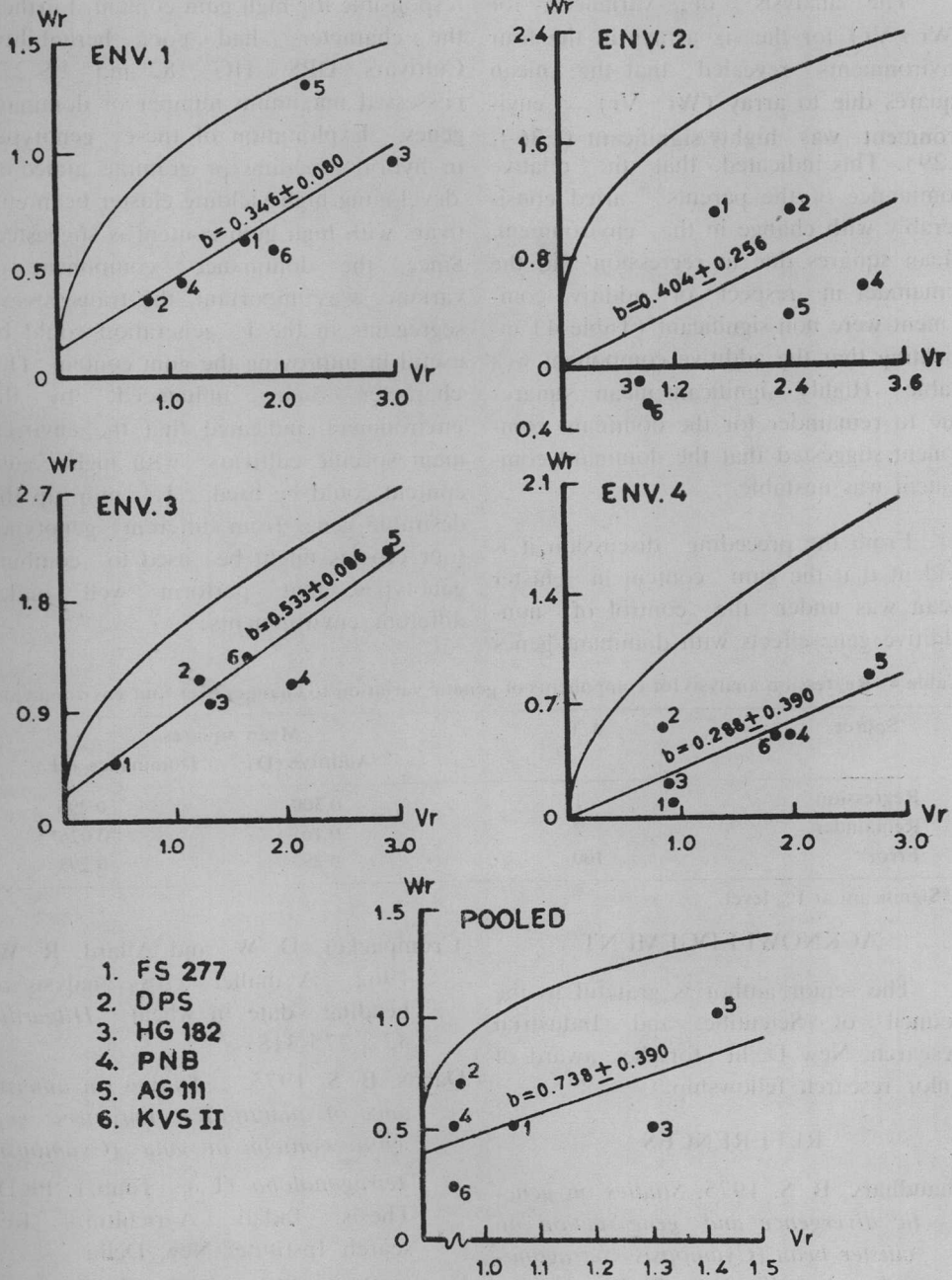


Fig. 1 Vr-Wr graphs for gum content in the four environments and pooled analysis

The analysis of variance for (Wr+Vr) for the six arrays in the four environments revealed that the mean squares due to array (Wr+Vr)  $\times$  environment was highly significant ( $1.36 \pm 0.29$ ). This indicated that the relative dominance of the parents varied considerably with change in the environment. Mean squares due to regression and the remainder in respect of additive component were non-significant (Table 4) indicating that the additive component was stable. Highly significant mean squares due to remainder for the dominant component suggested that the dominant component was unstable.

From the preceding discussion it is evident that the gum content in cluster bean was under the control of non-additive gene effects with dominant genes

responsible for high gum content. Further, the character had poor heritability. Cultivars DPS, HG 182 and FS 277 possessed maximum number of dominant genes. Exploitation of these genotypes in hybrid breeding programme aimed at developing high yielding cluster bean cultivars with high gum content is suggested. Since, the dominance component of variance was important, the transgressive segregants in the F<sub>2</sub> generation could be useful in improving the gum content. This character being influenced by the environment, indicated that the environment specific cultivars with higher gum content could be bred. To mop up the desirable genes from different genotypes four crosses might be used to combine genotypes that perform well under different environments.

Table 4 Regression analysis for components of genetic variation to changes over four environments

Source	d. f.	Mean squares	
		Additive (D)	Dominance (H)
Regression	1	0.300	0.296
Remainder	2	0.161	0.026**
Error	160	0.293	0.293

\*\*Significant at 1% level.

#### ACKNOWLEDGEMENT

The senior author is grateful to the Council of Scientific and Industrial Research, New Delhi for the award of senior research fellowship.

#### REFERENCES

- Chaudhary, B. S. 1975. *Studies on genetic divergence and gene action in cluster bean (Cyamopsis tetragonoloba (L.) Taub.)*. Ph.D. Thesis, Haryana Agricultural University, Hisar.
- Crumpacker, D. W. and Allard, R. W. 1962. A diallel cross analysis of heading date in wheat. *Hilgardia* 32 : 275-318.
- Dabas, B. S. 1975. *Studies on inheritance of quantitative characters and gum content in guar (Cyamopsis tetragonoloba (L.) Taub.)*. Ph.D. Thesis, Indian Agricultural Research Institute, New Delhi.
- Dabas, B. S., Mittal, S. P., Singh, H. B. and Swarup, V. 1980. Inheritance of endosperm percentage and gum

- content in guar. *Indian J. Genet.* 40 : 8-12
- Das, B., Arora, S. K. and Luthra, Y. P. 1977. A rapid method for determination of gum in guar (*Cyamopsis tetragonoloba* (L.) Taub.). First ICAR Guar Res. Workshop CAZRI, Jodhpur (India). p. 98-103.
- Hayman, B. I. 1954. The analysis of variance of diallel tables. *Biometrics* 10 :235-244.
- Jhorar, B. S., Solanki, K. R., Jatasra, D. S. and Grewal, R. P. S. 1983. Inheritance of gum content in clusterbean under different environments. *Indian J. Genet.* (In press).
- Nath, R. 1979. *Inheritance studies in cluster bean (Cyamopsis tetragonoloba* (L.) Taub.) with particular reference to seed yield and its quality. M.Sc. Thesis, Haryana Agricultural University, Hisar.
- Singh, J. 1981. *Inheritance studies in cluster bean (Cyamopsis tetragonoloba* (L.) Taub.) for seed yield and its quality. M.Sc. Thesis, Haryana Agricultural University, Hisar.