

Full Length Research Paper

Genetic studies in connection to yield and quality characteristics in rajmash (*Phaseolus vulgaris* L.)

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The experimental material comprised of 45 F₁s generated by crossing ten diverse genotypes of rajmash (*Phaseolus vulgaris* L.) in a diallel mating design. The set of 45 test cross progenies along with their ten parents were evaluated in a randomized block design with two replications at the Pulse Research Sub-station, SKUAST-K Habak, KVK Farm SKUAST- K Pombai, Anantnag and the Faculty of Agriculture, SKUAST-K Wadoora to study the gene action for yield and quality traits in rajmash (*P. vulgaris* L.). The component analysis indicated preponderance of non-additive gene effects in the inheritance of all the traits studied in the data pooled over environments. Net dominance effect over all loci in heterozygotes (h^2) was significant and positive for all the traits indicating unidirectional dominance, which was also confirmed from the value $2/4 \cdot \frac{1}{H}$ that indicated asymmetrical gene distribution. The value of KD/KR was

more than one (excepting 100 seed weight), indicating the presence of excess dominant genes in parents,

which was also verified by \hat{h}^2 / H_2 value in most of the cases. Heritability (n.s) was observed to be low for all the traits. The graphical analysis indicated dominance in the case of primary branches per plant, secondary branches per plant, number of pods per plant, pod length and seed yield per plant, whereas for rest of the traits, partial to complete dominance was observed. Intermating among the progenies within and between promising crosses in early segregating generations is suggested for further improvement.

Key words: Rajmash, diallel, genetic analysis, inheritance.

INTRODUCTION

Adoption of common bean breeding practices represents one of the most important strategies for evaluating grain yield. However, the success of common breeding programmes is intimately related to the appropriate choice of divergent parents, which when crossed, must provide wide genetic variability to be used for selection among segregating populations. Large differences in General Combining Ability (GCA) were found among dry bean cultivars, belonging to different races and gene pools. However, clear knowledge of parental performance and GCA among and within races and selection for yield per se are essential to breed for higher yield in common bean. One of the most commonly used

methodologies for choosing parents is diallel analysis. According to Santos (1981), Hayman's methodology (1954) has greatly contributed to breeding. It provides an efficient study of the genetic action involved in the control of traits and identifies the presence of epistatic interactions. However, the scope of such studies is limited if such studies are not conducted over environments and the inheritance of the quantitative traits vary with environments. Therefore, the present study was undertaken to study the nature and extent of gene action over the environments.

MATERIALS AND METHODS

The ten diverse lines of rajmash (*P. vulgaris* L.) namely SKUA-R-602, Shalimar Rajmash-1, SKUA-R-607, SKUA-R-608, SKUA-R-609, SKUA-R-612, SKUA-R-91, SKUA-R-106, SKUA-R-23 and

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Table 1. Estimation of genetic parameters and their proportions for yield, yield attributes and quality traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments.

Parameter	Primary branches per plant	Secondary branches per plant	No. of pods per plant	Pod length (cm)	No. of seeds per pod	100 seed wt. (g)	Seed yield per plant	Protein content (%)
\hat{D}	0.22** ± 0.02	0.22 ± 0.18	0.08 ± 0.16	0.13 ± 0.08	0.03 ± 0.04	1.13 ± 4.40 36.45**	0.45 ± 0.33	1.21 ± 1.51
\hat{H}_1	0.20** ± 0.04	2.10** ± 0.39	2.53** ± 0.35	0.97** ± 0.18	0.26** ± 0.09	±10.23	5.02** ± 0.70	13.64** ± 3.22
\hat{H}_2	0.15** ± 0.03	2.04** ± 0.33	2.40** ± 0.29	1.09** ± 0.15	0.24** ± 0.07	32.74** ± 8.69	3.97** ± 0.59	12.70** ± 2.74
\hat{h}	0.17** ± 0.02	7.20** ± 0.22	5.08** ± 0.19	4.48** ± 0.10	0.40** ± 0.05	64.62** ± 5.82	10.98** ± 0.40	7.49** ± 1.83
F	0.22** ± 0.04	0.11 ± 0.42	0.09 ± 0.37	0.23 ± 0.20	0.01 ± 0.10	8.09 ± 11.09	0.49 ± 0.76	1.27 ± 3.49
E	0.02** ± 0.006	0.36** ± 0.05	0.37 ± 0.20	0.40** ± 0.02	0.09** ± 0.01	6.01** ± 1.44	0.36** ± 0.09	0.05 ± 0.45
\hat{H}_1 / \hat{D}	0.97	3.08	5.59	2.67	2.95	2.96	3.34	3.35
\hat{H}_2 / \hat{H}_1	0.18	0.24	0.23	0.25	0.23	0.22	0.19	0.23
$\hat{K} / \hat{K}R$	3.17	1.17	1.22	0.51	1.12	0.51	1.40	1.37
\hat{h} / \hat{H}_2	1.16	3.53	2.11	4.10	1.66	1.97	2.76	0.60
b	0.72	0.31	0.60	0.76	-0.06	-0.19	0.21	0.16
b-0/S.E(b)	1.48	2.28*	3.18	3.38**	-0.20	-1.36	1.21	0.64
b-1/S.E(b)	-0.55	-4.87**	2.20**	-1.06	-3.58	-8.57**	-4.51**	-3.21
t	2.18	7.07**	1.02	0.002	0.24	8.51**	4.17**	0.71
Heritability (ns)	0.29	0.08	0.05	0.16	0.09	0.30	0.18	0.10

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

SKUA-R-153 were crossed in a diallel system without reciprocals during kharif 2007. The parents and hybrids in a total of 55 treatments were evaluated in a Randomized Block Design (RBD) with two replications at each location viz: Pulse Research Sub Station, SKUAST- K Habak, Krishi Vigan Kendra Farm, SKUAST-K Pumbai, Anantnag and Faculty of Agriculture SKUAST-K Wadoora during kharif 2008. Each cross/parent was represented by a 1 m double row with inter- and intra- spacings of 30 and 10 cm, respectively. The observations were recorded on 5 competent parents for different quantitative traits. The protein content (%) was also estimated by modified Kjeldhal's method of Piper (1966). Graphical analysis was

carried out by the diallel cross technique given by Jinks and Hayman (1954).

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among progenies indicating that the parents were diverse for the characters studied and this diversity was transmittable to the offspring. The component analysis is presented in

Table 1. Estimates of the components of genetic variation revealed that additive genetic variance

(D) was significant for primary branches per plant, whereas, both components of variance due to dominance deviations (H_1 and H_2) were significant for all the traits in the data pooled over environments. Contradictory results have been reported by Dahiya and Malhotra (2002) for the importance of both additive and dominance components for number of pods per plant, number

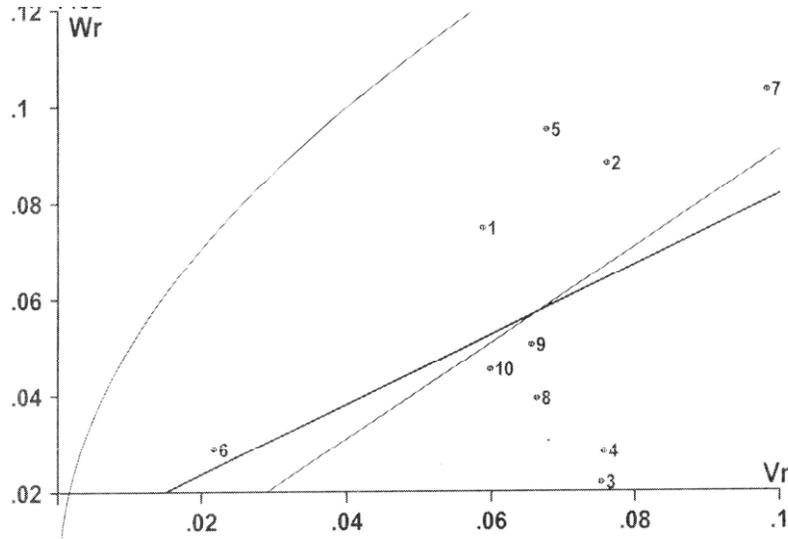


Figure 1. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Primary branches per plant.

of seeds per pod, test weight and seed yield per plant, whereas the predominant role of additive component for number of seeds per pod and mean seed weight were reported by Barelli et al. (1999). The net dominance effect over all loci in heterozygote measured in terms of h^2 was significant and positive for all the traits in the

data pooled over environments, showing unidirectional dominance which was also confirmed by the significant and positive value of F in primary branches per plant,

whereas for rest of the traits, positive and non significant estimates of F revealed the contribution of both

dominant and recessive alleles. Similar results have been reported by Sofi et al. (2006), whereas Singh and Jain (1971) reported the importance of recessive alleles for grain yield and number of pods per plant with the importance of dominant alleles for number of seeds per pod. The environmental component (E) was significant for all the characters except in the number of pods per plant and protein content.

The average degree of dominance (H_1 / D)^{0.5} was in the range over dominance for all the traits (except for primary branches per plant), indicating the importance of dominance components in the inheritance of these traits. The value of KD/KR was more than unity for all the traits except for pod length indicating the presence of excess dominant alleles in the parents, which was confirmed by h^2 / H_2 values in most of the cases. The proportion of

genes with positive and negative effects ($H_2 / 4 H_1$) was observed to be less than 0.25 thus revealing asymmetrical gene distribution in parents for all the traits studied, except for pod length which revealed

symmetrical gene distribution. Similar results have been reported by Dahiya and Malhotra (2002) and Singh et al. (2003) in French bean and garden pea. Narrow sense heritability reflecting the contribution of additive and additive type epistatic gene action is the most important selection parameter for the breeders involved in the improvement of self pollinated crops was observed to be low (less than 30%) for all traits. The significant deviation of the regression coefficient from unity for secondary branches per plant, number of pods per plant, 100 seed weight and seed yield per plant, indicated the presence of epistasis.

The graphical analyses (Figures 1 to 8) revealed that the regression line intersected the W_r axis below the point of origin indicating dominance in the case of primary branches per plant, secondary branches per plant, number of pods per plant, pod length and seed yield per plant. For number of seeds per pod and 100 seed weight, the average degree of dominance revealed by W_r - V_r graph indicated partial dominance, whereas a case of near complete dominance was observed in protein content in the data pooled over environments. The positions of parental arrays in the graph were scattered suggesting parental diversity for the various traits. Singh and Jain (1971) reported the gene action expressed by V_r - W_r and W_r - V_r graphs which indicated partial dominance for seeds per pod and pods per plant, whereas Kaul and Vaid (2003) reported a case of dominance for a number of pods per plant and pod length which is in conformity with the results achieved in this study.

The component analysis revealed the predominance of dominant alleles controlling the manifestation of various traits; therefore, using heterosis effects could give



Figure 2. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Secondary branches per plant.

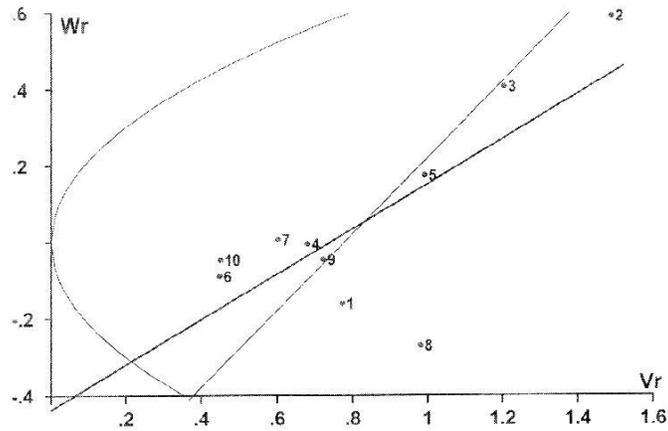


Figure 3. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Number of pods per plant.

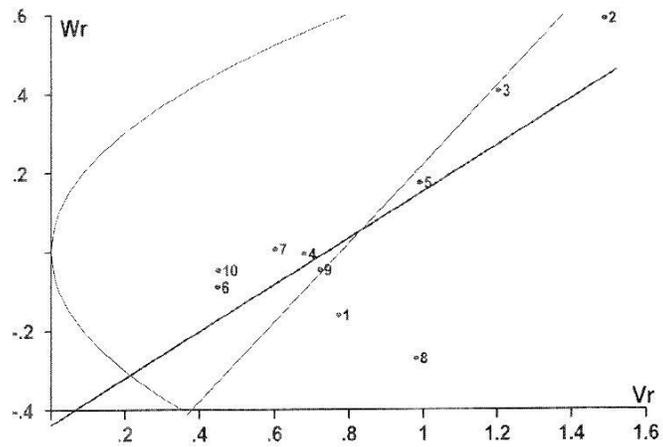


Figure 4. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Pod length.

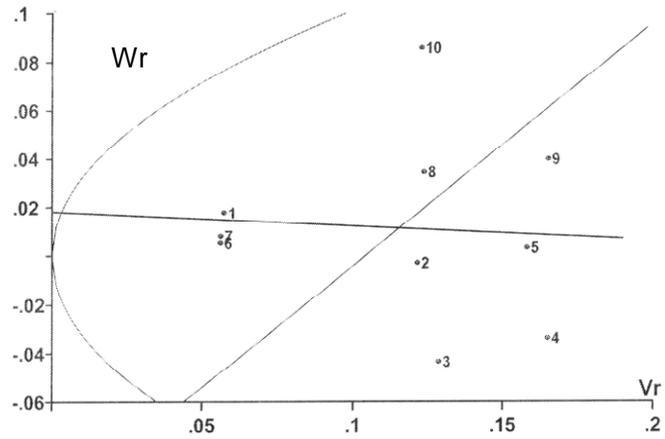


Figure 5. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Number of seeds per pod.

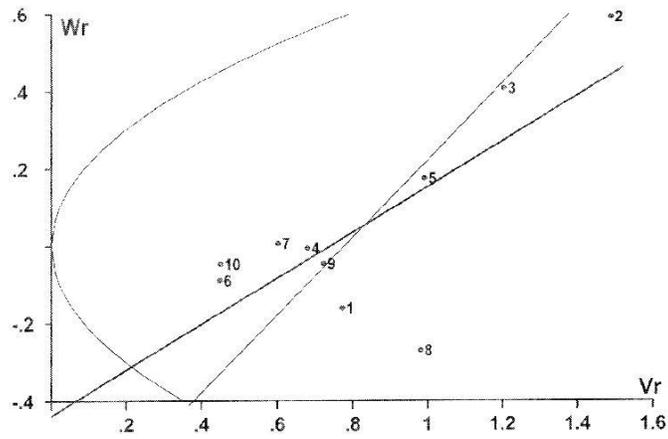


Figure 6. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; 100-seed weight.

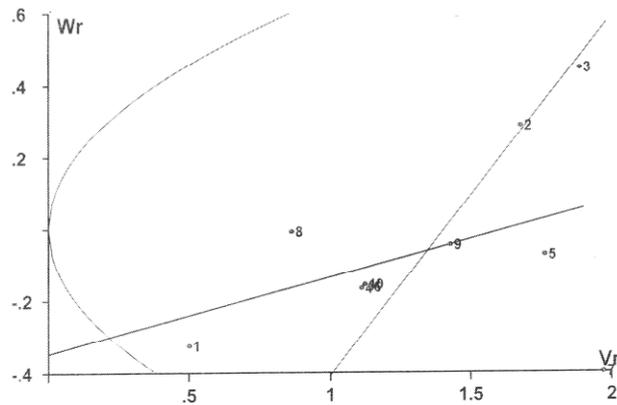


Figure 7. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Seed yield per plant.



Figure 8. W_r , V_r graphs for yield and quality traits for various traits in rajmash (*Phaseolus vulgaris* L.) pooled over environments; Protein content.

superior gains to these traits. The estimates of mean degree of dominance indicated that interactions were manifested in the form of over-dominance in most of the traits under study. However in an autogamous crop like rajmash, exploitation of non additive genetic variance as such would be impractical. Thus, the use of biparental or recurrent selection is likely to lead to substantial improvement of agriculturally important traits in rajmash.

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