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Full Length Research Paper

Combining ability studies over environments in Rajmash (*Phaseolus Vulgaris* L.) in Jammu and Kashmir, India

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The experimental material comprised 45 F1's generated by crossing ten diverse lines of common bean (*Phaseolus vulgaris* L.) in a half diallel fashion and their parents were evaluated in RBD in two replications at three locations during Kharif, 2008. The pooled analysis revealed that both *gca* and *sca* were influenced by environments, which suggested that studies are being conducted over the environments to get unbiased estimates. The sca x e interaction was greater than gca x e interaction for most of the traits. The compassion of relative magnitude of gca and sca variances indicated greater magnitude of sca variances for all the traits, indicating greater importance of non additive gene action for the inheritance of these traits. SKUA-R-607 and SKUA-R-608 showed high combining ability for seed yield and yield attributing traits. The most promising crosses, in order of merit for seed yield, were Shalimar rajmash 1 x SKUA-R-607, SKUA-R-608 x SKUA-R-106 and Shalimar rajmash -1 x SKUA- R-612.

Key words: Common bean, diallel, combining ability over environments, gene action.

INTRODUCTION

The common bean (*Phaseolus vulgaris* L.) is the world's most important grain legume for direct human consumption (Goncalves et al., 2008). It is grown in subtropical or temperate regions throughout the world and during the cool, dry season in tropical areas (Barelli et al., 2000). Like other legumes, they supply proteins, carbohydrates, vitamins and minerals and complement cereals, roots and tubers that compose of the bulk of diets in most developing countries. Brazil is the world's greatest common bean producer, producing more than 2.2 million tons, which represents 17.3% of the world's production (Goncalves et al., 2008). India, China, Myanmar, Mexico and the United States are the next highest producers and they produce XX of the world's production. In India, Rajmash (*P. vulgaris* L.) is a minor pulse crop confined to Himachal Pradesh, Uttar Pradesh, Jammu and Kashmir and North Eastern States, because it requires cool temperatures for growth. The genetic improvement of *P. vulgaris* L. in India has been accomplished primarily by targeting breeding strategies based on consumer preference for seed size, shape and colour. The North Western Himalayan regions, comprising parts of Himachal Pradesh and Jammu and Kashmir, are rich sources of rajmash diversity for seed, colour, shape and plant type.

The choice of parents in a breeding programme for hybridization is one of the most critical considerations, since the selection on the basis of performance does not provide clear information. Genetic parameters, such as combining ability, play a significant role in crop improvement, since they help in characterizing the nature and magnitude of genetic effects governing yield and component traits, besides pinpointing the promising parents to be used in the creation of genetic variability for eventual use in development of suitable varieties. Diallel analysis developed by Griffing (1956) offers an excellent means of obtaining information on differential parental combinations in terms of general and specific combination ability and nature and extent of gene action.

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Table 1. Analysis of variance for morphological, yield, yield attributing and quality traits in Rajmash (*P. vulgaris* L.) pooled-over environments.

Source of variation	d.f	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100-seed weight (g)	Seed yield plant^{-1}	Protein content (%)
Environments	2	0.14*	6.44**	10.49**	6.62**	0.39**	74.61	4.68	59.07
Replications	1	-	-	-	-	-	-	-	4.75**
Replications within the environments	3	0.20**	0.48	0.31	8.12**	0.27**	16.33	1.45**	4.75**
Genotypes	54	0.55**	5.14**	5.25**	4.02**	0.73**	88.6**	9.36**	23.41**
Parents	9	1.49**	2.00**	3.09**	2.70**	0.68**	42.92**	2.50**	13.64**
Crosses	44	0.31**	3.39**	4.09**	2.72**	0.61**	79.30**	7.19**	23.28**
Parents versus crosses	1	2.82**	110.34**	75.84**	72.88**	6.31**	885.26**	166.43**	117.34**
Genotypes x environments	108	0.16*	2.05**	2.11**	2.31**	0.55**	30.99**	2.14**	5.36**
Parents x environments	18	0.02	1.66**	0.39*	0.59	0.41**	11.16**	0.53	4.43**
Crosses x environments	88	0.19**	2.14**	2.47**	2.55**	0.58**	35.59**	2.50**	5.65**
Parents x crosses x environments	2	0.04	1.85**	1.44**	6.79**	0.64**	7.22	0.82	0.88
Pooled error	0.03	0.21	0.22	0.38	0.06	2.38	0.33	1.18	

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

However, the scope of such studies is limited if the environmental studies are not conducted in the different environments, as the combining ability and inheritance of quantitative traits vary with environments. Increasing the number of environments reduces the contribution of pooled error and additive wit environment variances (Eberhart et al., 1995). The use of diallel analysis procedures for choosing parents in *P. vulgaris* breeding programme has recently received higher emphasis from bean breeders (Barelli et al., 2000; Goncalves et al., 2008). Therefore, the present study was undertaken to study the combining ability estimates, combining ability x environment interaction and nature and magnitude of gene action in common bean.

MATERIALS AND METHODS

The present study was carried out at three locations, namely: Pulse Research Sub Station, SKUAST-K Habak Srinagar, Jammu and Kashmir, India; Krishi Vigyan Kendra Farm Pombai, SKUAST-K Anantnag, Jammu and Kashmir, India and Faculty of Agriculture, SKUAST-K Wadoora, Jammu and Kashmir, India. Ten diverse genotypes of rajmash 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 SKUA-R-153 were crossed in a diallel fashion of Griffing (1956) in all possible combinations without reciprocals. The 45 F1's and 10 parents were evaluated in RBD with two replications at each location during Kharif, 2008. Each progeny was grown with inter and intra spacing of 30 and 10 cm, respectively. The observations were recorded on five competent plants for different traits namely: primary branches plant^{-1}, secondary branches plant^{-1}, number of pods plant^{-1}, pod length (cm), number of seeds pod^{-1}, 100 seed weight (g), seed yield plant $^{-1}$ (g) and protein content (%). The protein was estimated according to the modified Kjeldhal's method of Piper (1966). The estimates of variance for both the general and specific combining abilities and their effects were computed according to Models I (fixed effect model) and II (parents and crosses, excluding reciprocals) as given by Griffing (1956).

RESULTS AND DISCUSSION

The pooled analysis over the environments (Table 1) revealed significant differences between genotypes, the parents and crosses interacted differentially for the traits under study in different environments. The crosses interacted more

Table 2. Analysis of variance for combining ability and estimates of components of variance for morphological, yield, yield attributing and quality traits in Rajmash (*P. vulgaris* L.) pooled-over environments.

Source of variation	d.f	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	No. of seeds pod^{-1}	100-seed weight (g)	Seed yield plant^{-1} (g)	Protein content (%)
Gca	9	0.72**	1.81**	1.42**	2.90**	0.31**	96.45**	4.13**	9.65**
Sca	45	0.19**	2.72**	2.86**	1.83**	0.37**	33.60**	4.78**	12.12**
gca x environments	18	0.04**	1.60**	0.65**	22.48**	0.32**	16.87**	0.77**	1.76**
sca x environments	90	0.09**	0.91**	1.13**	102.28**	0.26**	15.22**	1.13**	2.86**
$\hat{\sigma}^2 g$	-	0.02**	0.05	0.03	0.07	0.01	2.64	0.11	0.25
$\hat{\sigma}^2 s$	-	0.05**	0.87**	0.91**	0.54**	0.11**	10.80**	1.54**	3.84*
$\hat{\sigma}^2 g$ x environment	-	0.001	0.12	0.04	0.08	0.02	1.30	0.05	0.09
$\hat{\sigma}^2 s$ x environment	-	0.07	0.80	1.02	0.94	0.23	14.03	0.96	2.27
$[\hat{\sigma}^2 D/\hat{\sigma}^2 A]^{1/2}$	-	1.22	2.94	3.60	1.44	3.31	1.42	2.64	2.77

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

markedly with environments, thereby suggesting that hybrids did not have the same relative performance across locations. Dethe et al. (2008) reported significant difference among parents and crosses for numbers of pods plant^{-1}, 100 seed weight, primary branches plant^{-1} and seed yield plant^{-1}. The analysis of variance for the combining ability (Table 2) analysis revealed significant mean squares for both the general and specific combining abilities of all the traits under study in the data pooled over the environments. The significance of the interaction arising from *gca* and *sca* with the environments, revealed that the alleles controlling the *gca* and *sca* behaved differently in the different environments.

The presence of significant *gca* or *sca* x environment interaction have been reported by Matzinger et al. (1959) and Kunkaew et al. (2006) for seed yield plant^{-1}, with contradictory reports revealing non significant interaction of *gca* and *sca* x environment for number of pods plant^{-1} and 100 seed weight. Comparison of relative magnitude of *gca* and *sca* variances indicated greater magnitude of *sca* variance for all the traits studied in the data pooled over the environments, thereby indicating greater importance of non-additive gene action for the inheritance of these traits. Importance of non-additive gene action for number of seeds pod^{-1}, seed yield plant^{-1}, primary branches plant^{-1}, secondary branches plant^{-1} and seed weight have been reported by Barelli et al. (2000), Sofi et al. (2006) and Saleem (2009). However, the average degree of dominance was in the range of over-dominance for all the traits studied (Table 2), which was revealed by Sofi et al., 2008.

The perusal of *gca* effects of parents (Table 3) revealed that none of the parents was a good general combiner for all the traits studied. For bold seeds, high combining ability as indicated by SKUA-R-612 and SKUA-R-90 was associated with average or high combining ability for seed yield plant^{-1} and protein content (except SKUA-R-91). The high combining ability for seed yield plant^{-1} as indicated by SKUA-R-607 and SKUA-R-608 was accompanied with high combining ability for primary branches plants^{-1}, pod length and number of seeds pod^{-1} (SKUA-R-607); and for secondary branches plant^{-1}, number of pods plant^{-1}, 100 seed weight and protein content (SKUA-R-608) in pooled analysis. Further study revealed that there has been no correlation between seed yield and desirable *sca* effect for quality, as most of the cross combinations exhibiting desirable sca effect for quality revealed non-significant effect of *sca* for seed yield plant^{-1}. The best five cross (Table 4) combinations for yield and quality traits on the basis of *sca* and *per se* performance, revealed that SKUA-R-608 was involved in the maximum number of cross combination (16) revealing desirable *sca* effects, followed by Shalimar rajmash-1 (14) for yield and yield attributing traits in pooled environments. While

Table 3. Effects of general combining ability on morphological, yield and yield attributing quality traits in Rajmash (*P. vulgaris* L.) pooled-over environments.

Parents	**Primary branches plant^{-1}**	**Secondary branches plant^{-1}**	**No. of pods plant^{-1}**	**Pod length (cm)**	**No. of seeds pod^{-1}**	**100-seed weight (g)**	**Seed yield plant^{-1} (g)**	**Protein content (%)**
SKUA-R-602	-0.09** (2.86)	0.01 (6.53)	-0.20** (5.50)	-0.07 (7.76)	0.04* (4.31)	1.44** (34.15)	0.07 (7.06)	0.09 (19.89)
Shalimar rajmash 1	-0.02 (2.80)	0.07 (5.96)	-0.26** (5.26)	0.33** (8.66)	-0.03 (3.60)	1.16** (33.74)	-0.01 (5.03)	0.10 (20.45)
SKUA-R-607	0.24** (3.96)	-0.18** (4.96)	0.04 (5.10)	0.47** (9.60)	0.20** (4.00)	-3.47** (29.64)	0.61** (5.19)	-1.01** (17.99)
SKUA-R-608	0.27** (4.06)	0.45** (6.56)	0.13* (5.66)	0.25** (8.20)	0.03 (3.40)	2.08** (38.01)	0.43** (6.11)	0.34** (21.08)
SKUA-R-609	-0.06** (2.83)	-0.05 (5.76)	-0.01 (5.46)	0.06 (7.63)	-0.05** (3.36)	0.31 (37.77)	0.03 (6.26)	-0.21 (16.67)
SKUA-R-612	-0.05* (2.96)	-0.01 (5.63)	0.22** (6.00)	-0.24** (7.83)	-0.12** (3.56)	0.60* (36.36)	-0.10 (6.45)	0.45** (18.59)
SKUA-R-91	0.02 (2.80)	-0.04 (6.16)	-0.01 (6.16)	0.06 (8.26)	0.04** (3.70)	0.40 (36.53)	0.01 (6.62)	-0.70** (17.74)
SKUA-R-106	-0.14** (2.66)	-0.31** (5.63)	-0.07 (5.90)	-0.28** (7.26)	-0.07** (3.30)	-1.83** (31.93)	-0.57** (5.97)	0.34** (20.94)
SKUA-R-23	-0.04* (3.06)	0.26** (6.76)	0.36** (7.66)	-0.27** (7.56)	0.02 (3.66)	-0.39 (36.58)	-0.27** (5.63)	0.61** (20.97)
SKUA-R-153	-0.05* (2.90)	-0.18** (6.66)	-0.19* (5.73)	-0.31** (7.80)	-0.06** (3.20)	-0.301 (34.22)	-0.21* (5.53)	-0.02 (18.38)
SE(g)±	0.02	0.05	0.05	0.06	0.02	0.17	0.06	0.12
SE(g_i-g_j)±	0.03	0.07	0.07	0.10	0.04	0.25	0.09	0.18

* and ** Significant at 5 and 1% levels, respectively; Values in parentheses denote mean.

Table 4. Top ranking specific cross combinations on the basis of sca and *per se* performance in pooled-over environments.

Parameter	**Per se performance**	**Sca**	
Primary branches plant^{-1}	SKUA-R-607 x SKUA-R-609, SKUA-R-607 x SKUA-R-91, SKUA-R-608 x SKUA-R-153, Shalimar-Rajmash-1 x SKUA-R-608, SKUA-R-607 x SKUA-R-23	SKUA-R-602 x SKUA-R-106, Shalimar-Rajmash-1 x SKUA-R-91, SKUA-R-608 x SKUA-R-23, SKUA-R-612 x SKUA-R-106, SKUA-R-607 x SKUA-R-609	L x L A x A H x L L x L H x L
Secondary branches plant^{-1}	Shalimar-Rajmash-1 x SKUA-R-608, SKUA-R-608 x SKUA-R-106, SKUA-R-607 x SKUA-R-23, SKUA-R-608 x SKUA-R-609, Shalimar-Rajmash-1 x SKUA-R-23	Shalimar-Rajmash-1 x SKUA-R-608, SKUA-R-607 x SKUA-R-23, SKUA-R-608 x SKUA-R-106, SKUA-R-607 x SKUA-R-609, Shalimar-Rajmash-1 x SKUA-R-612	A x H L x H H x L L x A A x A
Number of pods plant^{-1}	Shalimar-Rajmash-1x SKUA-R-23, SKUA-R-612 x SKUA-R-106, SKUA-R-607 x SKUA-R-91, SKUA-R-602 x SKUA-R-106, SKUA-R-607 x SKUA-R-609	SKUA-R-602 x SKUA-R-106, Shalimar-Rajmash-1 x SKUA-R-23, Shalimar-Rajmash-1 x SKUA-R-608, SKUA-R-607 x SKUA-R-91, SKUA-R-608 x SKUA-R-153	L x A L x H L x H A x A H x L

Table 4. Contd.

Pod length (cm)	SKUA-R-608 x SKUA-R-609, SKUA-R-607 x SKUA-R-91, SKUA-R-602 x SKUA-R-607, Shalimar-Rajmash-1 x SKUA-R-608**,** SKUA-R-91 x SKUA-R-23	SKUA-R-608 x SKUA-R-609, SKUA-R-602 x SKUA-R-106, SKUA-R-91 xSKUA-R-23, SKUA-R-612 x SKUA-R-106, SKUA-R-608 x SKUA-R-153	H x A A x L A x L L x L H x L
Number of seeds pod^{-1}	SKUA-R-607 x SKUA-R-23, SKUA-R-608 x SKUA-R-609, SKUA-R-608 x SKUA-R-106, Shalimar-Rajmash-1 x SKUA-R-23, SKUA-R-607 x SKUA-R-153	SKUA-R-608 x SKUA-R-609, SKUA-R-608 x SKUA-R-106, SKUA-R-607 x SKUA-R-23, Shalimar-Rajmash-1 x SKUA-R-23, SKUA-R-607 x SKUA-R-153	A x L A x L H x A A x A H x L
100 seed weight (g)	Shalimar-Rajmash-1 x SKUA-R-612, SKUA-R-602 x SKUA-R-608, SKUA-R-608 x SKUA-R-106, SKUA-R-602 x SKUA-R-612, Shalimar-Rajmash-1 x SKUA-R-607	Shalimar-Rajmash-1 x SKUA-R-607, SKUA-R-608 x SKUA-R-106, Shalimar-Rajmash-1 x SKUA-R-612, SKUA-R-23 x SKUA-R-153, Shalimar-Rajmash-1 x SKUA-R-153	H x L H x L H x H A x A H x A
Seed yield plant^{-1} (g)	SKUA-R-607 x SKUA-R-609, SKUA-R-608 x SKUA-R-91, SKUA-R-607 x SKUA-R-612, SKUA-R-607 x SKUA-R-91, SKUA-R-609 x SKUA-R-612	SKUA-R-607 x SKUA-R-609, SKUA-R-608 x SKUA-R-91, SKUA-R-609 x SKUA-R-612, Shalimar-Rajmash-1 x SKUA-R-153, Shalimar-Rajmash-1 x SKUA-R-23	H x A H x A A x A A x L A x L
Protein content (%)	SKUA-R-612 x SKUA-R-23, SKUA-R-602 x SKUA-R-23, SKUA-R-608 x SKUA-R-612, SKUA-R-608 x SKUA-R-153, SKUA-R-612 x SKUA-R-153	Shalimar-Rajmash-1 x SKUA-R-91, SKUA-R-608 x SKUA-R-153, SKUA-R-602 x SKUA-R-23, SKUA-R-609 x SKUA-R-153, SKUA-R-612 x SKUA-R-153	A x L H x A A x H A x A H x A

assessing the performance of parents on the basis of general combining ability, it was observed that most of the desirable cross combinations involved high x low, average x low, high x average and average x average general combiners, which have also been reported by several workers in most of the crop species (Ram and Rajput, 1999; Ganesamurthy and Seshadri, 2002).

The overall ranking of genotypes studied revealed that genotypes like SKUA-R-602, Shalimar rajmash-1 SKUA-R-607, SKUA-R-608, SKUA-R-23 and SKUA-R-153 could be a useful source of elite allelic resources based on their general combining ability effects, specific combining ability effects and *per se* performance of both the parents and crosses. These parents are expected to give heterotic combinations resulting from the non-additive gene action and also results in the evolution of transgressive segregants for high yielding genotypes ensuing from complementary epitasis, additive type of gene action and recombination of latent genetic variability hidden in the heterogenetic blocks of such crosses. Normally, *sca* alone would not contribute tangibly in the improvement of self pollinated crops, except where commercial heterosis is feasible. However, *sca* resulting from the heterozygosity of polygenes governing yield and yield components may result in the evolution of recombinants possessing desirable gene aggregates in a homozygous line. The promising crosses, showing high yield (Shalimar rajmash 1 x SKUA-R -607, SKUA-R-608 x SKUA-R-106 and Shalimar rajmash -1 x SKUA- R-612) may be improved through conventional breeding methods such as bi-parental mating and diallel selective mating. Thereafter, it is followed by the pedigree method of selection, so that the tight linkage of any broken and transgressive segregants may be isolated.

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