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COMBINING ABILITY STUDY OVER ENVIRONMENTS IN DRY BEANS (*Phaseolus vulgaris L.*)

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ABSTRACT

Combining ability study was carried out in a 10 x 10 diallel set of dry beans (*Phaseolus vulgaris* L.) for seed yield and its component characters. The 45 F_1s generated by crossing ten diverse lines and their parents were evaluated in Randomized Block Design (RBD) in two replications at three locations during *Kharif*, 2008. Analysis of variance revealed that both gca and sca were influenced by environments, which suggested that studies be conducted over environments to get unbiased estimates. The sca x environment interaction was greater than gca x environment interaction for most of the traits. The relative magnitude of gca and sca variation indicated that 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. These promising crosses may be improved through conventional breeding methods such as biparental mating and diallel selective meeting, thereafter followed by pedigree method of selection, so as the tight linkage, if any, may be broken and transgressive segregants may be isolated.

Key Words: Dry beans, combining ability, gene action

INTRODUCTION

Grain legumes or pulses occupy an important place in human food and nutrition. They are important constituents in the diets of a very large number of people, particularly in the developing countries and are rich sources of protein, which help supplementation of cereal diets, improving their nutritive values. Among pulses dry beans contributed about 32% to global pulses production followed by dry peas

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(17%), (Faostat, 2010). Like other legumes, dry beans supply proteins, carbohydrates, vitamins and minerals and complement cereals, roots and tubers that compose of the bulk of diets in most developing countries. Genetic information on major yield attributing traits is a prerequisite of crop improvement. However, the choice of parents in a breeding programme for hybridization is one of the most critical consideration, as the selection on the basis of *per se* performance does not provide clear information. The genetic parameters such as combining ability plays a significant role in crop improvement, as it helps 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 combining ability (gca) and specific combining ability (sca) and nature and extent of gene action. The use of diallel analysis procedures for choosing parents in *Phaseolus vulgaris* breeding programme has recently received higher emphasis from bean breeders (Goncalves *et al.*, 2008). Therefore, the present investigation was carried out to understand the type of gene action governing yield and yield contributing traits and to identify the parents and crosses, which could be exploited for future breeding programme.

MATERIALS AND METHODS

The ten diverse lines of dry beans (*Phaseouas 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 SKUA-R-153 were crossed in a half diallel fashion during *kharif*, 2007. The parents and hybrids in a total of 55 treatments, were evaluated in 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, India, during *kharif*, 2008. Each cross/parent was represented by 1m double row with inter and intra spacing of 30 and 10 cm, respectively. The observations were recorded on five competent plants for different traits *viz*., primary branches plant^{-1}, secondary branches plant^{-1}, number of pods plant^{-1}, pod length (c.m), number of seeds pod^{-1}, 100 seed weight (g), seed yield plant $^{-1}$ (g) and protein content (%). The protein (%) was also estimated by modified Kjeldhal's method of Piper (1966).

RESULTS AND DISCUSSION

Analysis of variance pooled over environments (Table-1) revealed significant differences between the genotypes, parents and crosses interacted differentially for the traits under changed environments. Increasing the number of environments reduces the contribution of pooled error and additive x environment variances (Eberhart *et al.*, 1995). The crosses interacted more markedly with environments, suggesting the hybrids did not have the same relative performance across locations.

Similar results among parents and crosses for numbers of pods plant^{-1}, 100 seed weight, primary branches plant^{-1} and seed yield plant^{-1} were revealed by Dethe *et al*., (2008) in mungbean. The analysis of variance for combining ability (Table 2) revealed significant mean squares for gca and sca for all the traits pooled over environments .The significance of interaction arising from gca and sca with environments revealed that the alleles controlling the gca and sca behaved differently in the environments tested. 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 data pooled over 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) and Sofi *et al*., (2006) and Saleem (2009). The average degree of dominance was in the range of over dominance for all the traits. The gca effects of parents are presented in table-3. None of the parents was a good general combiner for the gca effects 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 (excepting 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); 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 protein content (quality), as most of the cross combinations exhibiting desirable sca effect for protein content (quality) revealed non significant sca effect for seed yield plant^{-1}.

Good combining ability for yield as indicated by SKUA-R-607 and SKUA-R-608 were also associated with good combining ability for primary branches plant^{-1}, secondary branches plant^{-1}, number of pods plant^{-1}, pod length, 100-seed weight (except for SKUA-R-607) and protein content, while, SKUA-R-153 was a poor combiner for yield and yield attributing traits (Table -4).

The best five cross 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) followed by Shalimar Rajmash-1 (14) for yield and yield attributing traits across the environments (Table 5). While 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 was also reported by several workers in most of the crop species (Ram and Rajput, 1999 and Ganesamurthy and Seshadri, 2002).

Table-1: Analysis of variance for yield and yield attributing traits in dry beans (*Phaseolus 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	-	-	-	-	-	-	-	-
Replications within Environments (Error a)	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 vs 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	165	0.21	0.22	0.38	0.06	2.38	0.33	1.18	0.34

*, ** Significant at 5 and 1 per cent levels, respectively

Table-2 : Analysis of variance for combining ability and estimates of components of variance for yield and yield attributing traits in dry beans (*Phaseolus vulgaris* L.)

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
$[\hat{\sigma}^2 D / \hat{\sigma}^2 A]^{½}$	-	1.22	2.94	3.60	1.44	3.31	1.42	2.64	2.77

*, ** Significant at 5 and 1 per cent levels, respectively.

Table-3: General combining ability effects for for yield and yield attributing traits in dry beans (*Phaseolus vulgaris* L.)

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

*, ** Significant at 5 and 1 per cent levels, respectively; Values in parentheses denote mean

Table : 4 Performance of parents on the basis of general combining ability 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	L	A	L	A	H	H	A	A
Shalimar Rajmash-1	A	A	L	H	A	H	A	A
SKUA-R-607	H	L	A	H	H	L	H	L
SKUA-R-608	H	H	H	H	A	H	H	H
SKUA-R-609	L	A	A	A	L	H	A	A
SKUA-R-612	L	A	H	L	L	H	A	H
SKUA-R-91	A	A	A	A	H	H	A	L
SKUA-R-106	L	L	A	L	L	L	L	H
SKUA-R-23	L	H	H	L	A	A	L	H
SKUA-R-153	L	L	L	L	L	A	L	A

H : High;   L : Low; A : Average

Table-5: Top ranking specific cross combinations on the basis of sca and *per se* performance over environments

Parameters	**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
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 x SKUA-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

CONCLUSION

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 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 the crosses. Promising crosses for seed yield plant $^{-1}$ (g) viz., 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 and SKUA-R-609 x SKUA-R-612 could be improved through conventional breeding methods such as biparental mating and diallel selective mating thereafter followed by pedigree method selection, so as the tight linkage if any may be broken and transgressive segregants may be isolated.

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