LR-5254
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RESEARCH ARTICLE Legume Research- An International Journal

Combining Ability Analysis and Association of Yield and Yield Components among Selected Rajmash (*Phaseolus vulgaris* L.) Lines

M.T. Gandhi[1], Manish Sharma[2], M.P. Patel[2], N.V. Soni[1], G.S. Dave[3]

10.18805/LR-5254

ABSTRACT

Background: Rajmash (*Phaseolus vulgaris* L.) is a significant leguminous crop known for its high protein content and dietary value. As global demand for nutritious food sources rises, enhancing the productivity and nutritional quality of Rajmash has become imperative. This research paper aims to investigate the combining ability and character associations in rajmash to facilitate the development of improved varieties with superior agronomic traits.

Methods: An experiment was carried out in Rajmash using line × tester mating design to estimate the gca effect of parents and sca effect of 21 hybrids for yield and its traits using 7 lines and 3 testers. Hybrids along with ten parents were studied for combining ability and phenotypic correlations for seed yield and nine yield related traits.

Result: The result indicated that the general combining ability (GCA) and specific combining ability (SCA) were significant for most characters indicating the importance of both additive and non-additive genetic components. This implies that a comprehensive understanding of both types of genetic effects is crucial for effective breeding programs. Among parent TRCR 3, SKAU-R-19, RR-21-01 and RKR 1033 were found to be good general combiners for seed yield per plant. This indicates their potential to consistently impart favorable traits to their progeny. The identification of such strong general combiners is valuable information for breeders aiming to enhance overall seed yield. The most promising specific combiners for seed yield were from crosses including SKAU-R-19 × RKR 1033, IPR-205-19 × HUR, RR-21-01 × RKR 1033, RR-21-12 × GR 1 and RR-21-01 × HUR. Significant desirable phenotypic correlations were observed between seed yield with days to flowering, days maturity, number of pods per plant, pod length and 100 seed weight these characters can act as indirect selection criteria in yield that could be used in rajmash breeding programs. The identification of strong general combiners, promising specific crosses and meaningful phenotypic correlations offers practical guidance for future breeding efforts, contributing to the development of improved varieties with enhanced yield potential and desirable agronomic traits.

Key words: Combining ability, Hybrids, Rajmash, Yield.

INTRODUCTION

Legumes are the important constituents of vegetarian Indian diet. They are important source of protein and calories. On average, pulses contain 22 to 24 per cent protein as against 8 to 10 per cent in cereals. Rajmash (*Phaseolus vulgaris* L.) is the third most important grain legume in the world and regarded as "Grain of hope" since it is an important component of subsistence agriculture and feeds about 300 million people in tropics and 100 million people in Africa alone (Kull *et al*., 2003). In India, Rajmash is mainly produced by resource-poor, small and marginal farmers in the traditional cropping system which includes rotation with vegetables and intercropping of climbing/ pole type beans with grain amaranth, potato and maize during the rainy season in the mountains/hills while as a sole crop of bushy types during winters (Rana *et al*., 2011). Rajamsh considered to be a very rich source of protein and vitamins. It also provides with carotenoids like beta-carotene, neoxanthin, lutein and violaxanthin. It also contains antioxidant capacity and hence helps to rid of harmful radicals which cause damage to cardiovascular system. It is rich source of dietary fiber which protects the mucosa in the colon by reducing exposure to toxins. It has rich source of zea-xanthin, a dietary carotenoid that gives protective UV filtering function. Its dry seed contains 21.1 per cent protein, 69.9 per cent carbohydrates, 1.7 per cent fat, 381 mg calcium, 425 mg phosphorus and 12.4 mg iron per 100 g of edible part (Ali and Kushwaha, 1987). The

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[1]Department of Genetics and Plant Breeding, C.P. College of Agriculture, S.D. Agricultural University, Sardarkrushinagar-385 506, Gujarat, India.
[2]Pulses Research Station, S.D. Agricultural University, Sardarkrushinagar-385 506, Gujarat, India.
[3]Bio Science Research Centre, S.D. Agricultural University, Sardarkrushinagar-385 506, Gujarat, India.

Corresponding Author: Manish Sharma, Pulses Research Station, S.D. Agricultural University, Sardarkrushinagar-385 506, Gujarat, India. Email: manisharmagpb@sdau.edu.in

How to cite this article: Gandhi, M.T., Sharma, M., Patel, M.P., Soni, N.V. and Dave, G.S. (2024). Combining Ability Analysis and Association of Yield and Yield Components among Selected Rajmash (*Phaseolus vulgaris* L.) Lines. Legume Research. doi: 10.18805/LR-5254.

Submitted: 25-09-2023 **Accepted:** 15-02-2024 **Online:** 04-04-2024

nutritional composition of tender Rajmash is moisture 12.0 g, protein 22.9 g, fat 1.3 g, minerals 3.2 g, crude fiber 4.8 g, carbohydrates 60.6g, energy 346 Kcal, calcium 260 mg, phosphorus 410 mg, iron 5.1 mg/100 g. of edible portion (Gopalan *et al*., 2012). It has both carminative and reparative properties against constipation and diarrhea, diuretic, dropsy, dysentery and kidney resolvent respectively. Targeted breeding programs are crucial for addressing the complex and evolving challenges in agriculture, food production and ecosystem conservation, with broad implications for global food security, economic development and environmental sustainability. Top of Form So, there is an urgent need to organize a strong and efficient breeding programme to develop high-yielding and good-quality varieties of Rajmash.

From a genetic standpoint, the most crucial step in the hybridization program is the selection of superior parents to produce new genotypes with desirable characteristics (Ahmad *et al.,* 2006). A high-performance genotype may not inevitably create better hybrids and transgressive segregants when employed in hybridization (Sharma *et al*., 2022). The yielding potential of the genotypes will be greatly affected if grown under different environmental conditions. The genotype which performs better in varied climatic situations will be an ideal one. (Patel *et al*., 2021a and Sharma *et al*., 2022b). Different types of breeding designs, like diallel, test crosses, bi-parental, line × tester and multiple crosses, are used to evaluate breeding material (Nduwumuremyi *et al.,* 2013). The primary goal of these designs is to assess the GCA and SCA impacts on parental lines, the SCA and heterosis of crossings and the heredity of the traits (Sharma and Shadakshari, 2021 and Singh *et al.,* 2022). Line × tester analysis is a modified version of the top cross design, is usually used for determining combining ability (GCA and SCA), identifying parental lines based on hybrid performance and estimating various sorts of gene activities (Kempthorne, 1957). Generally seed yield is a quantitative trait that is governed by polygenes in bean (Arunga *et al*., 2010). Selection based on seed yield alone is usually not effective, whereas selection along with yield components could be more efficient and reliable (Kwaye *et al*., 2008). Consequently, information on the association between seed yield and its components and among the yield characters themselves can improve the efficiency of selection in plant breeding programs (Muhammad *et al*., 1994; Shimelis, 2006; Kwaye *et al*., 2008). The objectives of this study are to determine the combining ability of yield and yield components (days to flowering, days to maturity, number of primary brancheses per plant, plant height, number of pods per plant, number of seed per pod, pod length, seed yield per plant and 100 seed weight,) among cross-combinations of ten selected parents.

MATERIALS AND METHODS

The experiment was conducted at Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during Rabi-2022-23. The experimental material consisting of 31 entries including 10 parents (seven females as lines and three males as testers) and resultant 21 crosses were raised in a Randomised Block Design with three replications. Procedure for hybridization is given in Fig 1. Each entry was grown in single row of 2m length with 15 cm spacing between plants, the rows were spaced 45 cm apart. Parents are grown along with F_1 and parents are utilized for calculating combining ability and heterosis analysis. Recommended agronomic practices and plant protection measures were adopted to raise healthy crops. The observations on days to flowering, days to maturity, number of primary branches per plant, plant height, number of pods per plant, number of seed per pod, pod length, seed yield per plant and 100 seed weight were recorded for five randomly selected plants in each entry and in each replication. The data were compiled for analysis of the variance of different traits using the method suggested by Panse and Sukhatme (1967). Combining ability was analyzed suggested by Kempthorne (1957) using TNAUSTAT software. Phenotypic correlation coefficients between all the traits were computed according to Know and Torrie (1964).

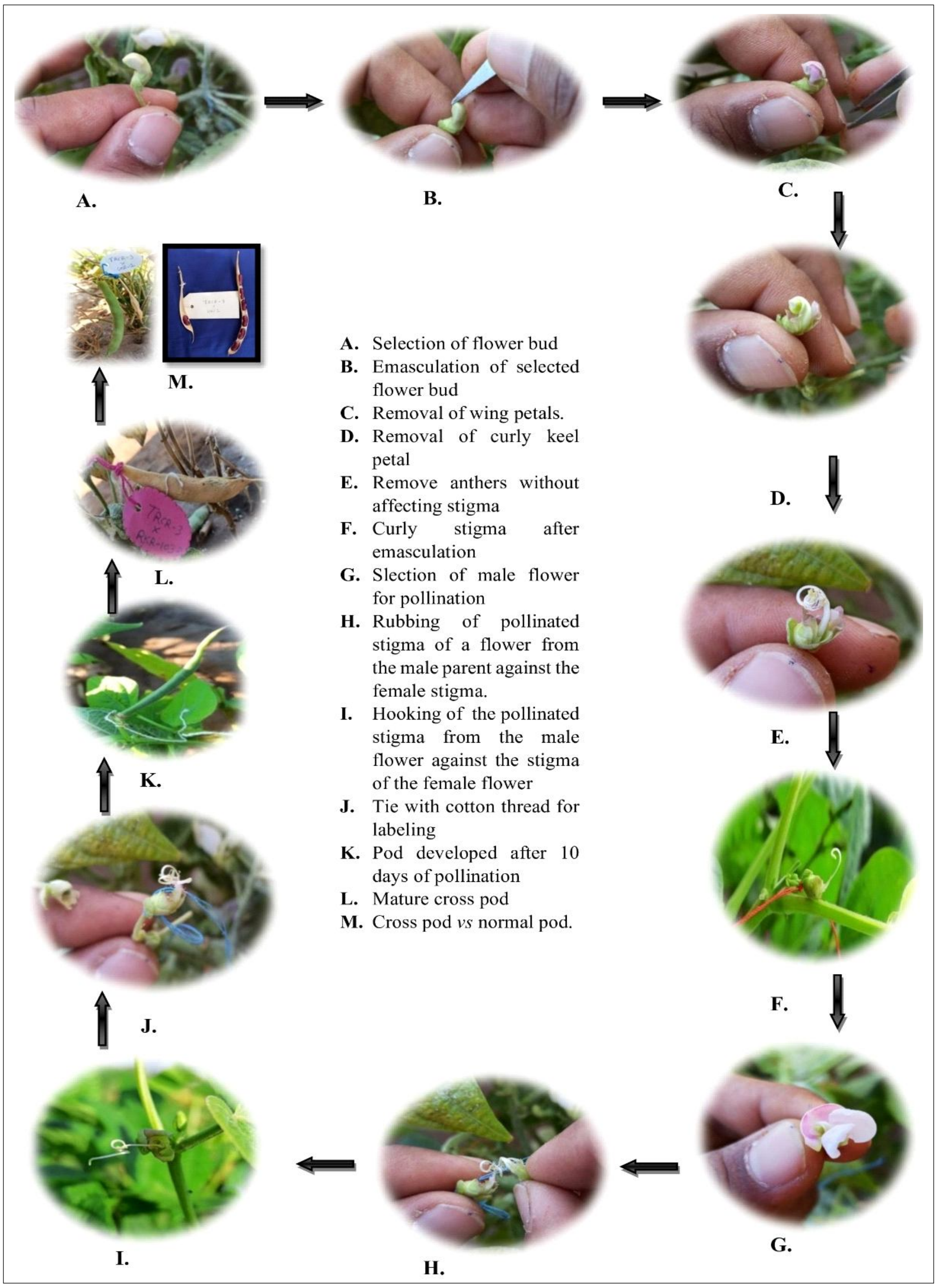
RESULTS AND DISCUSSION

The mean square due to genotype was found significant for all traits (Table 1). This indicates that experimental material possessed considerable variability and there were possibilities to improvement of various traits under study through heterosis breeding. In a breeding programme, once the appropriate parents and potential crosses are identified, the next important step is to adopt a suitable breeding strategy for the management of generated variability which largely depends upon type of gene action in the population for the traits under genetic improvement (Cockerham, 1961; Sprauge, 1966). The estimate of gca variance was greater than that of the sca for all characters except NPB, NPP, NSP and SYP. The ratio of gca variance to sca variance was greater than unity for DTF, DTM, PH, PL and HSW which indicates preponderance of additive gene action and found less than unity for NPB, NPP, NSP and SYP which indicate preponderance of non-additive gene action. In view of parallel role of both additive and non-additive genetic effects determining the inheritance of different characters, the population breeding approach in the form of biparental crosses followed by modified recurrent selection may likely result in greater genetic improvement by exploiting both additive and non-additive genetic variances. These results are similar to the results obtained by (Patil Atul *et al*., 2013; Selvakumar *et al*., 2014; Dias *et al.,* 2016).

Per se performance of parents and hybrids for different characters are detailed in Table 2. An estimate of GCA effects of the ten genotypes for nine characters showed that SKAU-R-19, RR-21-01, TRCR 3 and RKR 1033 were the best combiners for seed yield per plant (Table 3). Apart from seed yield SKAU-R-19 also reported best for days to earlier flowering, days to maturity, plant height, number of pods per plant, 100 seed weight.

The genotypes TRCR 3, TRCR 2, SKAU-R-19 and GR 1 were superior in early flowering, as indicated by their highly significant and negative general combining ability (GCA) effects. In addition, for days to maturity, similar effects of GCA were shown by parents *viz*, TRCR 3, TRCR 2, SKAU-R-19, RR-21-01 and RKR 1033. The minimum number of days to flowering and maturity is preferred to reduce the crop growth period. The kidney bean growers require short-duration hybrids, because such hybrids reduce the incidence of insect pest, disease attacks, adverse environmental effects and reduce the cost of cultivation. For days to flowering and days to maturity line TRCR 3, TRCR 2 and SKAU-R-19 exhibited significant negative gca effect for both these traits. Therefore, these lines could be used in the synthesis of early maturing hybrids.

For number of primary branches per plant TRCR 3, IPR-205-19 and RKR 1033 good general combiners. Lines TRCR 3, TRCR 2, SKAU-R-19, RR21-01, RR-21-12. and



- **A.** Selection of flower bud
- **B.** Emasculation of selected flower bud
- **C.** Removal of wing petals.
- **D.** Removal of curly keel petal
- **E.** Remove anthers without affecting stigma
- **F.** Curly stigma after emasculation
- **G.** Slection of male flower for pollination
- **H.** Rubbing of pollinated stigma of a flower from the male parent against the female stigma.
- **I.** Hooking of the pollinated stigma from the male flower against the stigma of the female flower
- **J.** Tie with cotton thread for labeling
- **K.** Pod developed after 10 days of pollination
- **L.** Mature cross pod
- **M.** Cross pod *vs* normal pod.

Fig 1: Procedure of hybridization in Rajmash.

tester RKR 1033 and HUR are good combiners for plant height. As reduced plant height promotes resistance to lodging, there is also a huge interest in the development of semi-dwarf hybrids. Therefore, these lines and testers can be used in breeding programme for development of dwarf type hybrids. Based on their highly significant and positive GCA effects lines IPR-205-19, SKAU-R-19, RR-21-01, RR-21-12 and tester RKR 1033 are found to be the best combiners for number of pods per plant. These identified lines and testers with positive GCA effect could be used in further breeding programme to synthesis hybrids with more number of pods per plant thus inturn contributing

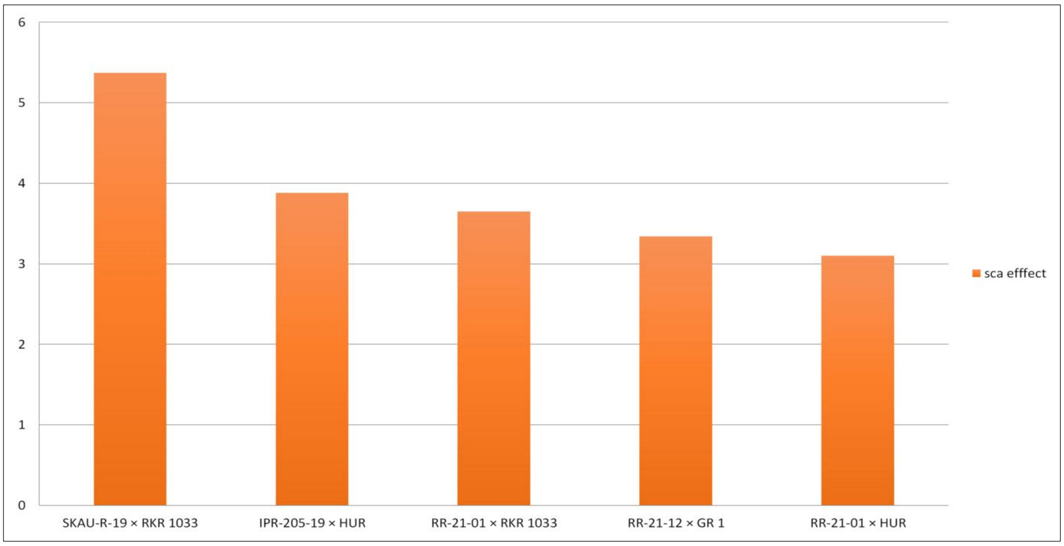


Fig 2: Best five crosses on basis of SCA effect for seed yield per plant.

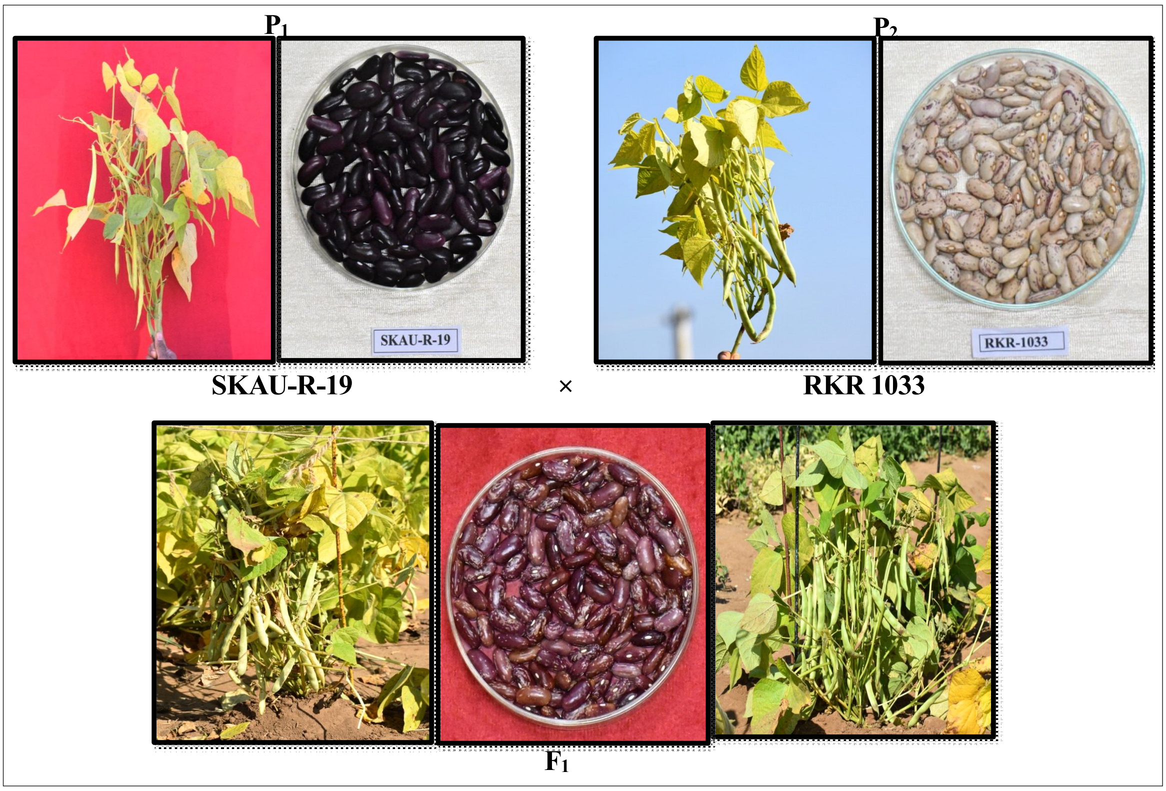


Fig 3 : Parents and their promising F$_1$.

to increased seed yield. IPR-205-19 is a good combiner for number of seeds per pod and TRCR 3, TRCR 2 for pod length. If pod length increases, the number of seeds per pod also increased thus contributing to increased seed yield. The seed weight of a genotype serves as an indicator to the expression of end product. Lines TRCR 3, TRCR 2, SKAU-R-19 and tester GR 1 are identified as good general combiner for 100 seed weight. These results are in conformity with previous reports by (Ceyhan *et al.,* 2014; Sen *et al*., 2019 and Sharma and Shadakshari, 2021).

SCA effects represent non-fixable components of variation, which are dominance, additive × dominance and dominance × dominance. Selecting crosses with positive and desirable SCA effects, indicating that the hybrid has better performance than expected from the average of the parents. Out of the 21 cross combinations, five crosses,

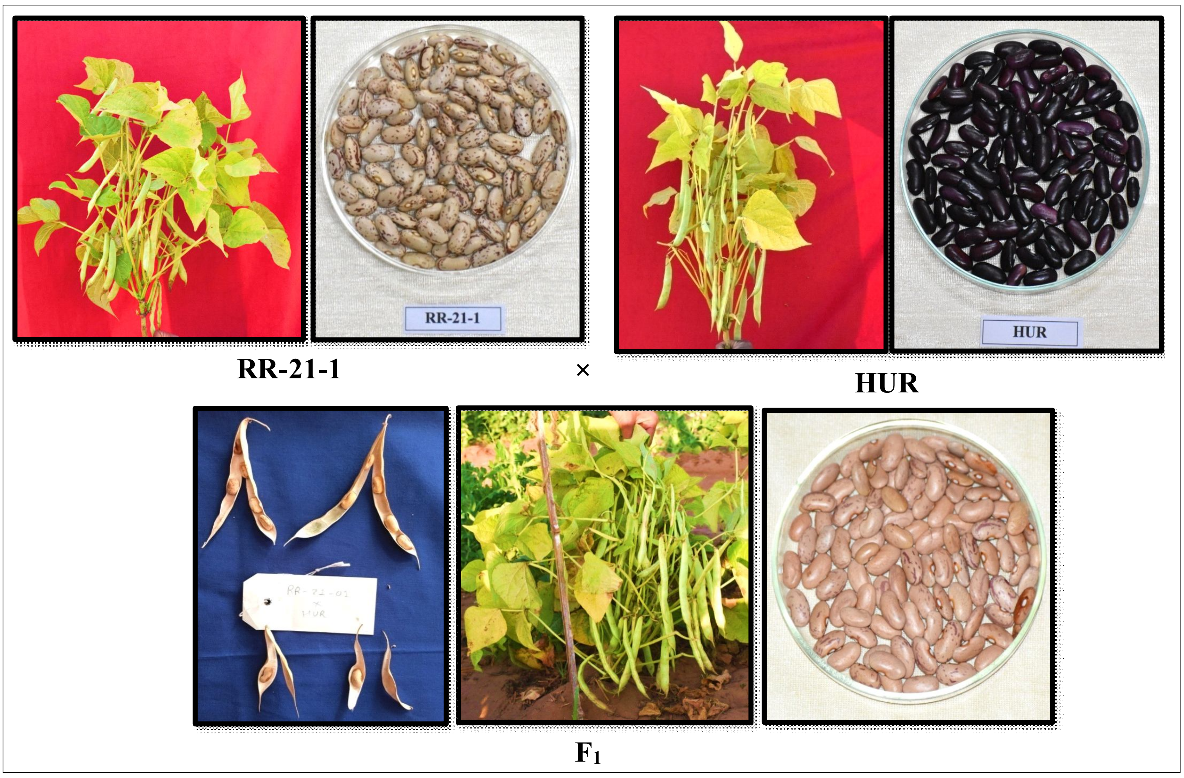


Fig 4: Parents and their promising F_1.

Table 1: Analysis of variance and combining abilities of nine traits in Rajmash.

Trait^a	Mean squares	Variance^b		Error	σ^2gca/σ^2sca
	genotypes	gca	sca		
DTF	45.48**	4.42**	1.56*	3.73	2.84
DTM	202.71**	20.92**	3.68*	2.93	5.68
NPB	0.12**	0.003	0.02*	0.03	0.10
PH	1859.92**	201.52**	22.45*	0.61	9.06
NPP	51.91**	0.71	14.06**	0.90	0.05
NSP	1.01**	0.04	0.12*	0.28	0.34
PL	4.57**	0.41**	0.15	0.49	2.65
SYP	98.01**	5.64	15.81**	4.92	0.36
HSW	76.95**	7.09**	2.71	17.99	2.61

^{a}DTF- Days to flowering, DTM- Days to maturity, NPB- Number of primary branches per plant, PH- Plant height, NPP- Number of pod per plant, NSP- Number of seed per plant, PL- Pod length, SYP- Seed yield per plant, HSW- 100 seed weight.

^{b}gca general combining ability variance, sca specific combining ability variance.

*, **Denote significant differences at 5 and 1% probability levels, respectively.

namely SKAU-R-19 × RKR 1033, IPR-205-19 × HUR, RR-21-01 × RKR 1033, RR-21-12 × GR 1 and RR-21-01 × HUR, were found to be positive and significant specific combiners for seed yield per plant (Table 4). Askander *et al*. (2018) and Sharma *et al*. (2023) also recorded good combiner for seed yield per plants.

For days to flowering none of the crosses showed significant SCA effects in the desirable direction. Two crosses SKAU-R-19 × RKR 1033 and SKAU-R-19 × GR 1 showed significant negative SCA effects for days to maturity. IPR-277-19 × RKR 1033 recorded significant positive SCA effect for number of primary branches per plant. For Plant height, high-negative SCA effects were displayed by the crosses TRCR 3 × GR 1, TRCR2 × HUR, IPR-205-19 × RKR1033, IPR-277-19 × HUR, SKAU-R-19 × GR 1, SKAU-R-19 × HUR, RR-21-01 × GR 1 and RR-21-12 × HUR. Six crosses SKAU-R-19 × RKR 1033, IPR-205-19 × GR 1, TRCR 3 × RKR 1033, RR-21-01 × HUR, RR-21-12 × GR 1 and TRCR 2 × GR1 recorded significant positive SCA effect for number of pods per plant. Similar results were observed by Bishnoi *et al*. (2018), Thangraj *et al*. (2018) for days to maturity, plant height and number of pod per plant. TRCR 2 × GR1 for number of seeds per pod. A positively significant SCA effects for pod length was recorded by PR-277-19 × GR 1. Where none of the

Table 2: *Per se* performance of parents and hybrids for different characters in Rajmash.

Cross -combination	Traits								
	DF	DM	NPB	PH	NPP	NSP	PL	HSW	SYP
Lines									
TRCR 3	44.00	109.67	5.47	52.16	14.80	4.23	15.59	45.39	22.46
TRCR 2	43.67	97.67	5.40	48.42	14.27	4.57	15.73	44.32	18.86
IPR-205-19	45.00	107.00	5.20	106.71	15.47	5.08	14.19	37.98	12.67
IPR-277-19	59.00	132.67	5.33	63.68	6.67	3.62	11.65	38.96	5.29
SKAU-R-19	44.00	97.33	5.20	47.41	14.93	4.33	14.25	43.48	13.09
RR-21-01	46.67	99.00	5.40	45.95	17.33	4.28	13.11	38.74	12.78
RR-21-12	48.00	102.33	5.27	40.87	18.27	3.72	13.09	30.41	12.66
Testers									
GR 1	41.67	95.00	5.53	48.31	16.87	4.15	13.79	38.49	14.98
RKR1033	50.00	102.00	5.53	45.27	18.87	4.52	13.67	29.47	12.78
HUR	44.33	99.00	5.20	56.93	13.07	4.45	14.20	37.73	11.54
Hybrids									
TRCR 3 × GR 1	43.67	98.00	5.67	50.55	22.40	4.38	15.31	43.99	24.13
TRCR 3 × RKR1033	44.67	96.67	5.53	49.69	27.73	4.27	16.04	39.63	26.21
TRCR 3 × HUR	44.00	99.67	5.53	51.21	20.67	4.50	17.15	47.48	22.02
TRCR 2 × GR1	44.00	103.33	5.27	48.72	21.80	4.98	16.17	44.78	23.12
TRCR 2 × RKR 1033	44.67	100.00	5.40	44.26	19.27	3.67	15.61	40.70	21.65
TRCR2 × HUR	44.00	99.67	5.47	43.42	20.07	4.73	16.01	43.04	16.05
IPR-205-19 × GR 1	50.33	105.00	5.67	126.67	29.93	4.20	13.99	40.14	22.56
IPR-205-19 × RKR1033	53.00	104.67	5.60	102.78	21.80	4.60	14.12	36.96	14.71
IPR-205-19 × HUR	53.33	102.33	5.27	117.60	22.87	5.15	14.72	35.86	21.23
IPR-277-19 × GR 1	48.67	121.33	4.90	63.60	19.00	2.98	14.75	39.18	14.42
IPR-277-19 × RKR 1033	51.33	121.33	5.47	57.53	19.07	3.57	13.62	37.56	13.10
IPR-277-19 × HUR	55.67	126.00	5.13	56.89	17.27	3.60	13.25	36.42	12.39
SKAU-R-19 × GR 1	45.67	103.00	5.40	50.32	20.20	4.02	14.23	49.79	26.78
SKAU-R-19 × RKR 1033	44.33	96.00	5.47	48.31	33.27	3.70	13.78	37.36	34.55
SKAU-R-19 × HUR	44.33	100.00	5.27	45.72	22.93	3.30	15.04	42.52	21.46
RR-21-01 × GR 1	47.67	99.67	5.13	45.27	23.33	3.73	13.62	38.36	18.38
RR-21-01 × RKR 1033	51.33	100.33	5.60	48.37	28.13	4.42	13.32	35.61	29.80
RR-21-01 × HUR	47.67	102.33	5.27	49.93	28.13	4.10	13.82	41.67	25.52
RR-21-12 × GR 1	49.33	102.33	5.47	45.81	27.13	3.67	13.25	33.34	23.14
RR-21-12 × RKR 1033	52.33	105.00	5.20	40.95	22.93	3.93	12.85	32.61	19.67
RR-21-12 × HUR	52.67	103.33	5.40	38.59	23.33	4.92	12.61	28.17	14.91
Range	41.67-59.00	95.00-132.67	4.90-5.67	38.59-126.67	6.67-33.27	2.98-5.15	11.65-17.15	28.17-49.79	5.29-34.55
S.E.m±	1.05	0.90	0.10	0.59	0.48	0.27	0.41	2.24	1.19

Table 3: GCA effects of lines and testers for different characters in Rajmash.

Characters	DF	DM	NPB	PH	NPP	NSP	PL	HSW	SYP
Lines									
TRCR 3	-4.11**	-6.17**	0.19**	-7.90**	0.21	0.27	1.72**	4.41**	2.89**
TRCR 2	-4.00**	-3.29**	-0.01	-12.92**	-3.02**	0.35	1.49**	3.55*	-0.95
IPR-205-19	4.00**	-0.29	0.13*	57.29**	1.47**	0.54**	-0.16	-1.64	-1.73*
IPR-277-19	3.67**	18.6**	-0.22**	0.95**	-4.95**	-0.73**	-0.57*	-1.57	-7.92**
SKAU-R-19	-3.44**	-4.62**	-0.01	-10.27**	2.07**	-0.44*	-0.09	3.93**	6.37**
RR-21-01	0.67	-3.51**	-0.05	-10.53**	3.14**	-0.03	-0.85**	-0.75	3.34**
RR-21-12	3.22**	-0.73	-0.03	-16.61**	1.07**	0.06	-1.54**	-7.92**	-1.99**
Testers									
GR 1	-1.17**	0.38	-0.03	3.17**	0.01	-0.12	0.03	2.07*	0.56
RKR 1033	0.59	-0.86*	0.08*	-2.41**	1.21**	-0.09	-0.25	-2.09*	1.58**
HUR	0.59	0.48	-0.05	-0.77**	-1.21**	0.21	0.22	0.01	-2.15**

*, **Significant at 5% and 1%, respectively, DF: Days to 50% flowering; DM: Days to maturity; NPB: Number of primary branchees per plant; PH: Plant height; NPP: Number of pod per plant; NSP; Number of seed per plant; PL: Pod length; SYP: Seed yield per plant; HSW: 100 seed weight.

Table 4: SCA effects of different crosses for different characters in Rajmash.

Cross-	Traits								
combination	DF	DM	NPB	PH	NPP	NSP	PL	HSW	SYP
TRCR 3 × GR 1	0.73	-0.49	0.12	-3.11**	-1.21*	0.12	-0.89*	-1.78	-0.55
TRCR 3 × RKR1033	-0.03	-0.59	-0.13	1.61**	2.93**	-0.02	0.12	-1.98	0.51
TRCR 3 × HUR	-0.70	1.08	0.01	1.49**	-1.72**	-0.10	0.77	3.76	0.04
TRCR 2 × GR1	0.95	1.95	-0.08	0.08	1.42*	0.64*	0.20	-0.14	2.28
TRCR 2 × RKR 1033	-0.14	-0.14	-0.06	1.20*	-2.32**	-0.70*	-0.07	-0.05	-0.21
TRCR2 × HUR	-0.81	-1.81	0.14	-1.28**	0.90	0.06	-0.14	0.19	-2.08
IPR-205-19 × GR 1	-0.71	0.62	0.18	7.81**	5.06**	-0.33	-0.32	0.42	2.50
IPR-205-19 × RKR1033	0.19	1.52	0.01	-10.50**	-4.27**	0.04	0.09	1.39	-6.37**
IPR-205-19 × HUR	0.52	-2.14*	-0.19	2.68**	-0.79	0.29	0.23	-1.81	3.88**
IPR-277-19 × GR 1	-2.05	-1.94	-0.24*	1.09*	0.55	-0.28	0.85*	-0.62	0.55
IPR-277-19 × RKR 1033	-1.14	-0.70	0.22*	0.59	-0.58	0.28	0	1.93	-1.79
IPR-277-19 × HUR	3.19**	2.63*	0.02	-1.68**	0.03	0.01	-0.84*	-1.31	1.23
SKAU-R-19 × GR 1	2.06	2.95**	0.05	-0.97*	-5.27**	0.46	-0.16	4.50	-1.38
SKAU-R-19 × RKR 1033	-1.03	-2.81**	0.01	2.60**	6.59**	0.12	-0.32	-3.78	5.37**
SKAU-R-19 × HUR	-1.03	-0.14	-0.06	-1.63**	-1.32*	-0.59	0.48	-0.72	-3.99**
RR-21-01 × GR 1	-0.05	-1.49	-0.17	-5.76**	-3.21**	-0.23	0	-2.26	-6.75**
RR-21-01 × RKR 1033	1.86	0.41	0.19	2.92**	0.39	0.43	-0.02	-0.85	3.65**
RR-21-01 × HUR	-1.81	1.08	-0.01	2.84**	2.81**	-0.20	0.02	3.11	3.10*
RR-21-12 × GR 1	-0.94	-1.60	0.14	0.85	2.66**	-0.39	0.31	-0.11	3.34*
RR-21-12 × RKR 1033	0.30	2.30*	-0.24*	1.57**	-2.74**	-0.15	0.20	3.33	-1.16
RR-21-12 × HUR	0.63	-0.70	0.10	-2.42**	0.08	0.53	-0.51	-3.22	-2.18

Table 5: Phenotypic correlation coefficients for pair wise comparison of eight agronomic traits in Rajmash.

	DM	NPB	PH	NPP	NSP	PL	HSW	SYP
DF	0.65**	-0.11	0.29**	-0.04	-0.11	-0.60**	-0.48**	-0.31**
DM		-0.27**	0.19	-0.41**	-0.33**	-0.36**	-0.09	-0.46**
NPB			0.06	0.24*	0.18	0.12	0.10	0.27**
PH				0.07	0.25*	-0.01	-0.01	-0.09
NPP					-0.01	0.07	-0.12	0.76**
NSP						0.21*	-0.02	0.02
PL							0.52**	0.34**
HSW								0.24 *

*, **Denote significant differences at 5 and 1% probability levels, respectively.

crosses are for 100 seed weight. Best five crosses on basis of SCA effect for seed yield per plant are shown in Fig 2 and Fig 3 and 4 are depicting morphology of parents and their promising $F_{1s.}$

The performance of different crosses based on SCA is used to construct the gene action. High SCA effects resulting from crosses involving both parents with good general combiners (*e.g.*, SKAU-R-19 × RKR 1033 and RR-21-01 × RKR 1033 for seed yield per plant) may be attributed to additive × additive gene action whereas high SCA effects derived from crosses including good × poor general combiners (*e.g.*, RR-21-01 × HUR for seed yield per plant) may be due to favorable additive effects of the good general combiner parent and epistatic effects of the poor general combiner. In crosse IPR-205-19 × HUR involving poor × poor general combiners, dominance × dominance interaction might be playing major role in the inheritance of these characters.

The various quantitative characters were studied and their relations with yield as well as among themselves were examined by using correlation analysis. Correlation coefficients between yield and its components are presented in Table 5. Significant desirable correlations were observed for DF, DM, NBP, NPP, PL and HSW with seed yield per plant. The very strong significant positive correlations was recorded between days to flowering with days to matrity (0.65) and number of pod per plant with seed yield and moderataly strong significant positive correlation was recorded between pod length with 100 seed weight. Number of pods per plant, pod length, 100-seed weight showed significant positive correlation with seed yield per plant and among themselves indicating that simultaneous selection for this character would result in improvement of high yielding Rajmash bean genotypes. Similar, findings were reported by Asati and Singh (2008), Karasu and Oza (2010), Pandey *et al.* (2013), Sharma and Sridevi (2016) and Patel *et al.* (2021b). Positive correlation between pod length and number of seeds per pod indicates that with longer pods more space is provided for seeds increases yield. However, there are generally negatively significant correlations between seed yield and days to flowering and days to maturity.

CONCLUSION

The general assessment of the results from these studies indicates that yield and its contributing traits are under the control of additive and non-additive genes. To utilize both types of gene actions, a breeding program involving some inter-mating in segregating generations to infuse genes in a population, like the diallel selective mating system or multiple crossings or mass selections followed by inter-mating might be helpful in breaking yield barriers in this crop. Five crosses, namely SKAU-R-19 × RKR 1033, IPR-205-19 × HUR, RR-21-01 × RKR 1033, RR-21-12 × GR 1 and RR-21-01 × HUR, were found to be positive and significant specific combiners for seed yield per plant. Hence, these crosses were identified as potential for getting good transgressive segregants for seed yield per plant and its component traits and suggested for further evaluation in future breeding programme.

Conflict of interest

Authors declare there is no conflict of interest to disclose.

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