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Research Note

Combining ability of yield and yield attributing traits in fieldpea (*Pisum sativum* L.)

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Abstract

Combining ability analysis of six diverse genotypes of fieldpea *viz*., SKUA-P-8, SKUA-P-16, SKUA-P-17, SKUA-P-19, SKUA-P-42 and SKUA-P-60 crossed in all possible combinations without reciprocals for yield and yield related traits revealed significant differences among the parents and their crosses for most of the traits. The traits studied were days to 50% flowering, days to maturity, plant height, number of branches/plant, number of pods/plant, number of seeds/pod, 100-seed weight and seed yield/plant. The variances due to general combining ability (gca) and specific combining ability (sca) effects and their relationship revealed predominantly non-additive effects for the traits. None of the parents/crosses was found to be good general/specific combiner for all the traits. The parents SKUA-P-8 and SKUA-P-19 were the best general combiners for most of the traits including seed yield/ plant. Among the hybrids SKUA-P-19 x SKUA-P-17, SKUA-P-19 x SKUA-P-60 and SKUA-P-19 x SKUA-P-16 exhibited highest significant sca effects for yield and yield attributing traits.

Key words
Field pea, combining ability, crosses, yield attributes

Fieldpea (*Pisum sativum* L.) belonging to the family Paplionaceae and having chromosome number 2n=14 is the second most important food legume of the world (Smykal *et al*., 2012). As many as 84 countries grow field pea; Canada, France, China, Russia, India, Ukraine and Australia contribute 75 per cent of the global output (Singh *et al*. 2013).In India with less than 6% of the total global production there has been a positive growth in area under its cultivation, production and productivity during last two to three decades and currently fieldpea in the country is grown over an area of 0.76 million hectares with an annual production of 0.84 million tones and average productivity of 1100 kgs per hectare (Anonymous, 2013).Because of its high protein content (20-30 %) and thus increasing demand for protein-rich raw materials for animal feed or intermediate products for human nutrition, there is a rising interest in this crop as a protein source (Ceyhan *et al*. 2008).The demand for this crop is therefore increasing day by day necessitating breeding of varieties with enhanced yield potential. Relatively narrow gene pool and use of a small number of varieties as parents by competing breeding programmes have led to a low genetic diversity among pea cultivars (Esposito *et al*. 2007).

Genetic information on major yield attributing traits is a prerequisite in crop improvement programmes. However, the choice of parents in a breeding programme for hybridization is one of the most critical considerations, as the selection on the basis of *per se* performance does not provide clear information and the results can sometimes be misleading. Combining ability plays a significant role in crop improvement, as it helps in characterizing the nature and magnitude of genetic effects governing yield and component traits, besides identifying promising parents to be used in the creation of genetic variability for eventual use in development of suitable varieties (Basbag *et al*. 2007).Combining ability analysis improves the selection and assessment of parental inbred lines, thus increasing the opportunity of selecting excellent crosses. Therefore, knowledge of combining ability is essential for the selection of suitable parents with different genes to produce transgressive segregation lines with high combining ability and produce hybrids with higher yield than lines with low combining ability (Turbin *et al*. 1974).The estimation of additive and non-additive gene action through combining ability analysis could be useful for isolating pure lines among the progenies of the good hybrids (Stuber, 1994).Some information on additive and non-additive effects associated with yield and yield attributing traits in pea is available (Narayan *et al*. 1998, Ceyhan 2003, Zaman and Hazarika 2005, Dhillon *et al*. 2006, Singh *et al*. 2007, Sharma *et al*. 2007, Ceyhan *et al*., 2008, Singh *et al*. 2013, Kumari *et al*. 2015) but that is relevant to a specific region, genetic material involved and particular environmental conditions in the country. Therefore, the present work was undertaken to generate information on general and specific combining ability to understand the type of gene action governing yield and yield contributing traits and to identify desirable parents for utilization in future fieldpea breeding programmes in the region.

The experimental material comprised of six diverse genotypes of fieldpea viz. SKUA-P-8, SKUA-P-16, SKUA-P-17, SKUA-P-19, SKUA-P-42 and SKUA-P-60 crossed in all possible combinations without reciprocals. The set of 15 crosses (Table 4) along with their 6 parents were evaluated in randomized block design with three replications at Dry land Agriculture Research Station SKUAST-K, Srinagar during *rabi* 2014-15.Each experimental unit comprised of two rows of 3 meter length with inter and intra row spacing of 30 cms and 10 cms, respectively. Recommended agronomical practices were followed to raise an ideal crop Data were recorded on eight individual plants taken at random from each genotype for days to 50% flowering, days to maturity, plant height (cm), number of branches/plant, number of pods/plant, number of seeds/pod, 100-seed weight (g) and seed yield/plant (g). The estimates of variance for *gca* and *sca* and their effects were computed according to Model I (fixed effect model) and Model II (parents and crosses excluding reciprocals) as given by Griffing (1956).

The analysis of variance revealed highly significant differences in all the traits investigated viz, days to 50% flowering, days to maturity, plant height, primary branches plant/plant, number of pods/plant, number of seeds/pod, 100-seed weight and seed yield/plant indicating the existence of considerable variability among the parents for these traits (Table 1). The hybrids however, showed significant differences for all traits excepting number of seeds/pod. Analysis of variance for combining ability (Table 2) revealed that general combining ability (*gca*) and specific combining ability (*sca*) effects were highly significant for all the traits excepting number of pods/plan and number of seeds/pod in former case indicating the importance of both additive and non-additive genetic components of variation in the expression of inheritance of these traits. The variance due to gca ($\sigma^2 g$) was lower than variance due to sca ($\sigma^2{}_S$) for all the traits excepting plant height. This indicates the predominant role of non-additive gene action in the inheritance of all these traits. So for the improvement of these traits, heterosis breeding followed by pedigree breeding can be resorted to. Higher estimate of specific combining ability variances than general combining ability for yield related trades in field pea grown under recommended agronomic practices with suitable plant protection measures adopted have been reported earlier also (Singh and Singh 2003, Singh *et al*. 2013). When translated into genetic components of variance ($\sigma^2{}_A$ and $\sigma^2{}_D$) the inference with regard to nature of gene action did not change. The average degree of dominance was greater than unity for all characters excepting plant height and primary branches/plant indicating over-dominance. An important influence of non-additive gene action on seed yield and yield attributing traits in pea has been reported earlier (Kalia and Sharma 1998, Singh *et al*. 1999, Srivastava *et al*. 2000, Ceyhan 2003, Singh and Singh 2003).

The estimates of general combining ability effects for parental lines revealed that no parents had significant *gca* effects for all the traits simultaneously (Table 3). Hence none of the parents was a good general combiner for all traits. However the parent SKUA-P-19 had significant gca effects and was the best general combiner for seed yield plant/plant. The parent SKUA-P-8 was a good general combiner for most of the traits including seed yield/plant which implies that it contains favorable alleles for these traits.SKUA-P-42 was a poor combiner for most of the traits evident from the negative value of its gca effects.SKUA-P-17 was good general combiner for days to flowering, days to maturity, plant height and primary branches/plant but did not combine well for yield traits as shown by negative gca effects for 100-seed weight and seed yield/plant. The comparison of mean performance *per se* and gca effects of parents revealed that parents with high mean performance were also good and desirable general combiners particularly for number of pods/plant, 100-seed weight and seed yield/plant although such a correspondence could not be generalized for all the traits. Non correspondence of mean performance and *gca* effects for traits such as days to flowering and days to maturity have also been reported by Katiyar *et al*. (1987).

Specific combining ability effects for fifteen crosses are presented in the table 4. None of the crosses exhibited significant *sca* effects for all the characters. For yield the cross SKUA-P-19 x SKUA-P-16 had highest *sca* effects closely followed by SKUA-P-19 x SKUA-P-17 and SKUA-P-42 x SKUA-P-60.The cross SKUA-P-19 x SKUA-P-60 even though a good specific combiner for yield attributing traits particularly number of pods/plant, number of seed/pod and 100-seed weight was strikingly a poor combiner for seed yield. In contrast the cross SKUA-P-19 x SKUA-P-17 exhibited high *sca* effects for yield component traits. The crosses SKUA-P-42 x SKUA-P-16, SKUA-P-42 x SKUA-P-16 and SKUA-P-8 x SKUA-P-16 exhibited significant desirable sca effects for both days to 50% flowering and days to maturity. A comparison of gca and sca effects revealed that parent SKUA-P-42 even though a poor general combiner for most of the traits was involved in a sizeable number of superior combinations. Such an observation indicated that yield and other traits are complex in inheritance and that specific performances of crosses were more important for these traits than *gca* effects possibly due to preponderance of non-additive gene effects for most of the quantitative traits as was already demonstrated by estimated combining ability variances. The significant sca effect observed in different crosses for different characters have the combination of either high x high, high x poor, high x average, average x average, poor x high or poor x poor combining parents. For seed yield/plant plant the promising cross combinations involved either high x high or high x poor general combiners, while as for other traits even poor x poor combinations were superior. The superiority of crosses due to good x good general combiners can be attributed to concentration of favorable alleles whereas the superiority of the crosses as a result of good x poor or poor x poor general combiners could be due to favorable interaction between alleles with positive and negative effects (over-dominance or complementary epistasis). Since only a small number of crosses exhibited significant sca effects for yield, heterosis breeding within the current level of feasibility of large scale seed production cannot be a viable option. However, since both additive and non-additive gene effects were observed to be predominant, breeding strategies that generate transgressive segregants would be advantageous for effecting fruitful improvement in the present set of materials. 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 has also been reported in other crops (Ram and Rajput 1999, Ganesamurthy and Seshadri 2002).

On the basis of our present study we therefore conclude that SKUA-P-19, SKUA-P-8 and SKUA-P-17 were found to be promising parents as these showed significant gca effects in most of the traits. Among the crosses SKUA-P-19 x SKUA-P-16, SKUA-P-19 x SKUA-P-17 and SKUA-P-19 x SKUA-P-60 were the most promising hybrids as they exhibited high sca effects for seed yield /plant as well as for other yield contributing characters. The promising genotypes exhibiting significant desirable *gca* and *sca* effects could be useful source of elite allelic resources and can be easily exploited in segregating generations to develop high-yielding varieties. Best crosses for economic traits could be improved through conventional breeding methods such as biparental mating and diallel selective mating thereafter followed by pedigree selection so as the tight linkage if any may be broken and isolating desirable transgressive segregants and good recombinants.

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Table 1. Analysis of variance for different yield and yield contributing traits in Fieldpea (*Pisum sativum* var. arvense)

Source of Variation	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)
Replicates	2	1.20	0.09	3.62	0.81	0.26	0.28	0.48	0.56
Treatments	20	3.32**	6.30**	525.90**	7.66**	2.23**	6.17**	4.40**	3.67**
Parents	5	1.20	3.35	878.90	17.10	1.82	0.22	4.12	1.60
Hybrids	14	4.17**	7.54**	440.59**	3.93**	2.46**	0.17	4.27**	4.15**
Parents x Hybrids	1	2.07	3.42	64.40	11.96	0.91	0.010	7.82	6.62**
Error	40	0.74	1.44	1.32	0.16	0.29	0.04	0.29	0.15

*Significant at 0.05% probability, ** Significant at 0.01% probability

Table 2. Analysis of variance for combining ability for different characters of fieldpea (*Pisum sativum* var. arvense)

Source of Variation	d.f	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)
GCA	5	1.02**	2.01**	535.29**	5.80**	0.18	0.02	1.47**	0.72**
SCA	15	1.12**	2.10**	54.80**	1.47**	0.93**	0.06**	1.47**	1.36**
Error	40	0.22	0.48	0.43	0.05	0.09	0.01	0.09	0.04
σ^2g	--	0.08	0.18	66.85	0.71	0.01	0.01	0.17	0.07
σ^2s	--	0.87	1.64	54.43	1.40	0.83	0.06	1.39	1.30
σ^2_A	--	0.19	0.37	133.71	1.43	0.02	0.00	0.34	0.18
σ^2_D	--	0.87	1.64	54.43	1.40	0.83	0.06	1.39	1.31
2 σ^2g /2 σ^2g + σ^2s	--	0.09	0.09	0.55	0.33	0.01	0.01	0.11	0.07
$\begin{pmatrix}\sigma^2_D \\ \sigma^2_A\end{pmatrix}^{0.5}$	--	2.16	2.10	0.63	0.99	6.28	4.08	2.00	2.80

Table 3. General combining ability effects of parents for yield and yield contributing traits in Fieldpea (*Pisum sativum* var. arvense)

Source of Variation	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)
SKUA-P-19	0.62**	0.39	-15.06**	-1.24**	0.07	0.003	0.52**	0.31**
SKUA-P-42	-0.44**	-0.66**	-1.60**	-0.64**	-0.29**	-0.110**	-0.04	-0.51**
SKUA-P-60	-0.07	0.64**	1.76**	0.08	0.04	6.030	-0.18	0.07
SKUA-P-8	-0.005	0.02	7.05**	1.17**	0.06	-0.001	0.36**	0.27**
SKUA-P-16	-0.05	0.08	0.64**	0.14**	0.03	0.040	0.02	0.02
SKUA-P-17	-0.03	-0.49*	7.16**	0.48**	0.10	0.030	-0.68**	-0.16*
S.E (g) ±	0.15	0.22	0.21	0.07	0.10	0.030	0.10	0.07
C.D (50%)	0.30	0.45	0.43	0.15	0.20	0.080	0.20	0.14

*Significant at 0.05% probability, ** Significant at 0.01% probability

Table 4. Specific combining ability effects of crosses for yield and yield contributing traits in Fieldpea (*Pisum sativum* var. arvense)

Crosses	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	100 seed weight (g)	Seed yield plant^{-1} (g)
SKUA-P-19 x SKUA-P-42	0.57	1.40**	-3.63	-0.03	-0.51	-0.05	-0.33	0.35
SKUA-P-19 x SKUA-P-60	-0.15	0.56	4.92**	0.80**	0.62**	0.31*	-0.23	-0.43**
SKUA-P-19 x SKUA-P-8	0.95**	-0.38	10.69**	1.00**	0.15	0.45*	0.46	0.35
SKUA-P-19 x SKUA-P-16	0.70	1.82**	-14.84	-1.24**	-0.56*	-0.04	0.92**	1.10*
SKUA-P-19 x SKUA-P-17	0.62	0.33	10.54**	0.10	2.13**	0.01	1.25**	0.89**
SKUA-P-42 x SKUA-P-60	1.05**	0.00	0.81	1.12**	0.54	-0.08	0.10	0.59**
SKUA-P-42 x SKUA-P-17	0.40	1.15**	3.12**	-1.77**	0.44	-0.08	-2.35**	0.04
SKUA-P-42 x SKUA-P-16	-1.41**	-2.85**	1.12	-0.47**	-0.026	-0.34**	-0.62**	-2.13**
SKUA-P-42 x SKUA-P-8	-1.47**	-0.83	-9.50**	-0.74**	-0.59**	0.28**	-0.45	-1.44**
SKUA-P-60 x SKUA-P-8	-0.55	0.23	2.73**	0.14	0.27	-0.05	0.35	0.31
SKUA-P-60 x SKUA-P-16	-0.04	0.13	4.21**	0.00	0.31	0.05	-1.44**	0.39
SKUA-P-60 x SKUA-P-17	1.82**	0.02	1.70**	-1.113**	-1.28**	-0.29*	-1.39**	-0.85**
SKUA-P-8 x SKUA-P-16	-1.06**	-1.39**	-6.28**	-1.57**	-0.78**	-0.25*	-0.52	-2.03**
SKUA-P-8 x SKUA-P-17	-0.33	-2.11**	-0.85	-0.49**	-0.58**	0.19	1.12**	-0.02
SKUA-P-16 x SKUA-P-17	0.60	-0.30	4.83**	-0.740	-0.29	-0.13	-0.19	-0.21
SE (S_{ij}) ±	0.42	0.52	0.58	0.20	0.27	0.10	0.27	0.20
SE (S_{ij} x S_{jk}) ±	0.52	0.70	0.66	0.23	0.31	0.12	0.31	0.22
SE (S_{ij} x S_{ik}) ±	0.64	0.92	0.87	0.31	0.41	0.16	0.41	0.30
SE (S_{ij} x S_{kj}) ±	0.60	0.85	0.80	0.28	0.38	0.15	0.38	0.28
CD at 5%	0.92	1.25	1.17	0.42	0.55	0.18	0.58	0.41
(S_{ij} –S_{ik})	1.32	1.93	1.63	0.58	0.77	0.30	0.77	0.56

*Significant at 0.05% probability, ** Significant at 0.01% probability