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Genetics of grain yield and its components in field pea (*Pisum sativum* L.)

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Abstract

An experiment consisting 8 parents diallel crosses excluding reciprocals were evaluated at Oilseeds Research Farm of C. S. Azad University of agriculture and technology, Kanpur during Rabi season of 2020-21 to evaluate the combining ability and gene action for grain yield and its components in field pea. The result indicated that non- additive type of gene action was more than that of additive type of gene action for most of the characters. Average degree of dominance also indicated presence of over dominance for most of the characters. The general combining ability with negative value for characters were observed in *viz.*, the parent KPMR 400, KPMR 522, KPMR 940 for days to flowering, RACHNA, KPMR 522 for days to maturity, KPMR 400, SAPNA, KPMR 913 for short height of plant. GCA with positive value were observed in the parents *viz.*, SHIKHA, KPMR 522 for branches per plant, RACHNA, KPMR 940 for pods per plant, KPMR 940 for grains per pod, KPMR 400, KPMR 522, KPMR 940 for 100 seed weight, KPMR 940, KPMR 522 for grain yield per plant, KPMR 940 for biological yield per plant, KPMR 522 for harvest index. The significant and desirable SCA effect for grain yield per plant were observed in crosses SWATI x KPMR 400, SHIKHA x KPMR 913, SWATI x KPMR 940, RACHA X KPMR 940.

Keywords: Pea, *Pisum sativum*, grain yield, combining ability, gene action, dominance, over dominance

Introduction

Field pea (*Pisum sativum* L.), also known as dry pea is a leguminous plant in the Papilionoideae subfamily that belongs to the general class of dicotyledonous. The chromosome number of field pea is 2n=14. It is a South Western Asian native that is commonly cultivated in temperate climates. It is mostly a cold-weather crop that can tolerate mild frost. Uttar Pradesh is the largest producer of pea, occupying 3.60 lakh ha area under cultivation with the production of 5.6 lakh tonnes and productivity of 15q./ha.

The field pea is commonly used as a pulse crop, whereas, the garden pea is commonly used as a vegetable. The nitrogen-fixing properties of pulses improve soil fertility, increasing and extending the productivity of the farmland. In many regions, farmers plant legumes along with other crops, a practice known as intercropping, to improve yield and promote soil biodiversity. Pulse crops are also known to fight off plant disease-causing pests, thereby reducing dependency on chemical fertilizers and pesticides. Pulses also produce a smaller carbon footprint, indirectly reducing greenhouse gas emissions, and contributing to climate action. Peas like many legumes, contain symbiotic bacteria called Rhizobia within root nodules of their root systems. These bacteria have the special ability to fix nitrogen from atmospheric, molecular nitrogen (N_2) into ammonia (NH_3). Ammonia is then converted to another form, ammonium (NH_4+), usable by (some) plants. The root nodules of peas and other legumes are sources of nitrogen that they can use to make amino acids, constituents of proteins. Hence, legumes are good source of plant proteins. In general, field pea had the most consistent biological nitrogen fixation ability, suggesting that field pea is more suitable for cultivation in the semi-arid region than other pulses evaluated. When a pea plant dies in the field, for example following the harvest, all of its remaining nitrogen, incorporated into amino acids inside the remaining plant parts, is released back into the soil. In the soil, the amino acids are converted to nitrate (NO_3-) that is available to other plants, thereby serving as fertilizer for future crops. Field pea had the most stable BNF ability, fixing 55 kg N ha^{-1} with an average seed yield of 2418 kg ha^{-1} (Hossain *et al*., 2017) [9].

Material and Methods

The experiment was conducted at Oilseeds Research Farm, Kalyanpur of Chandra Shekhar Azad University of Agriculture & Technology, Kanpur during the *Rabi* season of 2020-2021. The experimental material consists 8 germplasm lines of field pea (*Pisum sativum* L.) namely; SWATI, RACHNA, KPMR 400, KPMR 522, SAPNA, SHIKHA, KPMR 940 and KPMR 913 along with 28 F1s derived from all possible combinations between the above parents excluding reciprocals during 2019-20. The experiment was laid out in a randomized block design with three replications. Two rows of each parent and single row of F1s were planted in each replication in five-meter row length spaced at 45 cm x 15 cm between rows and plants respectively. All the recommended agronomical package of practices was adopted to raise a good crop. Five plants were taken randomly from each treatment for the purpose of collecting the data. The data was collected on growth and yield attributes *viz.* days to flowering, days to maturity, plant height (cm), branches per plant, pods per plant, grains per pod, 100 seed weight(g), grain yield per plant(g), biological yield per plant(g) and harvest index (%). The collected data were subjected to various statistical analyses as usual procedures while the combining ability analysis was done as per the methods suggested by Hayman (1954) and Griffings (1956) [8] method 2 model I.

Result and Discussion

Combining ability refers to the ability of a genotype to transmit superior performance to its progenies. The general combining ability has been equated with additive gene action and specific combining ability with non-additive gene action (Griffings, 1956) [8]. The analysis of variance for combining ability reflected significant value for both GCA and SCA variances for all the characters except for 100 seed weight. It indicated that both parents and crosses had sufficient variability for the characters under study (Table 1). The significant values of these two also indicated that both additive and non-additive gene effects were involved for the expression of these characters. If both additive and non-additive genetic components are significant in diallel analysis, it is too difficult to identify which one is more effective, and it can be easily identify only on the basis of the ratio of the estimates of both the variances. Lower the value of the ratio for days to maturity, branches per plant, pods per pod, grain yield per plant 100 seed weight, biological yield, harvest index indicated the presence of non-additive gene action while higher the ratio indicates the presence of additive gene action for remaining traits. Borah (2009) [3], Jyothula and Guttala (2009) [10] and Tampha *et al.* (2018) [17] were in accordance with these results.

Table 1: ANOVA for Combining Ability for 10 Characters based on 8 Parent Diallel Cross in field pea

Sources of variations	DF	Days to Flowering	Days to Maturity	Plant height	Branches /Plant	Pods /Plant	Grains /pod	100 seed wt.	Grain yield/plant	Biological yield/plant	Harvest index
GCA	7	32.88**	35.25**	3411.74**	0.10**	3.89**	0.22**	1.86	13.15**	47.62**	59.02**
SCA	28	2.79**	7.44**	9.23**	0.01**	0.52**	0.02**	0.23	1.43**	5.35**	9.03**
ERROR	70	0.54	0.57	0.73	0.0006	0.07	0.0002	0.0001	0.02	0.02	0.94
σGCA		5.39	3.47	341.00	0.010	0.38	0.03	0.19	1.31	4.76	5.80
σSCA		2.2	6.87	8.50	0.018	0.45	0.02	0.23	1.40	5.33	8.09
σ GCA/σSCA		2.45	0.50	40.11	0.55	0.84	1.5	0.82	0.93	0.89	0.71
$(\sigma\ SCA/\ \sigma\ GCA)^{0.5}$		0.83	1.40	0.15	1.27	1.08	1.05	1.10	1.03	1.05	1.17

*Significant at p = 0.05, ** Significant at p =0.01

General combining ability effects

General combining ability is a measure of additive gene action. GCA is primarily a function of additive genetic variance and additive x additive type of epistasis and successfully leads towards the choice of suitable parents.

GCA effects include both additive and additive x additive type of gene action (Griffing, 1956a, b) [6-7] and Sprague (1966) [15], which represents fixable genetic variance. Gilbert (1967) [11] reported that additive parental effect as measured by GCA effect is of practical importance and cannot be manipulated. Based on comparison of GCA effect with mean performance the genotypes for all characters are presented in Table 2. None of the parent was common as good general combiner for all the characters; however, the good general combiners with significant negative GCA effect and lower mean values are considered desirable for the characters - days to flowering, days to maturity, plant height. For the remaining characters positive and significant GCA value with high per se performance is desirable. Comparing the GCA effects and mean performance for desirable parents good general combiners for days to flowering are KPMR 522, KPMR 940, KPMR 400 and RACHNA for developing early flowering/maturing genotypes. The parents KPMR 400, SAPNA, KPMR 522, KPMR 940, KPMR 913 was good general combiner for short statured plants. SAPNA, SHIKHA, KPMR 940 for branches per plant, parents showed positive and significant GCA effect and higher mean value. Parents KPMR 913, RACHNA, KPMR 522 were desirable for pods per plant; RACHNA, KPMR 522, KPMR 940 for grains per pod. KPMR 940, KPMR 522, SWATI, KPMR 400 for 100 seed weight, KPMR 940, KPMR 522, KPMR 400, RACHNA for grain yield / plant, KPMR 940, RACHNA for biological yield per plant while KPMR 522, KPMR 400, SWATI were desirable for harvest index.

Consistent general combining ability effects may prove advantageous while evaluating varieties for combining ability. Further, the varieties showing good general combining ability for particular component may be used in crop improvement for particular component thereby affecting improvement in yield. Parents KPMR 940, KPMR 522, KPMR 400, RACHNA showed good general combining ability for yield appear to be worthy of exploitation in practical plant breeding. It is suggested that segregating population involving these lines may be useful for development of suitable varieties through multiple crossing programme.

Table 2: GCA effects of parents and mean values for 10 Characters in 8 parent diallel cross in field pea

Parent	Days to flowering		Days to maturity		Plant height		Branches per plant		Pods per plants	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
SWATI	62.33	0.22	115.33	-0.07	136.33	34.65**	2.10	-0.16**	12.33	-0.96**
RACHNA	61.33	-0.25	108.66	-0.90*	118.00	24.17**	1.95	-0.12**	15.80	0.86**
KPMR 400	58.33	-1.35**	109.66	-0.34	46.66	-13.88**	2.36	-0.02**	14.66	0.16*
KPMA 522	56.33	-2.45**	107.00	-2.10**	54.33	-9.20**	2.35	0.02**	15.33	0.49**
SAPNA	63.67	0.92**	113.66	-0.27	50.33	-11.38**	2.71	0.15**	14.00	-0.39**
SHIKHA	68.67	2.45**	120.33	2.02**	57.00	-7.37**	2.55	0.08**	14.00	-0.15**
KPMR 940	58.67	-1.78**	109.00	-1.77**	53.33	-8.80**	2.31	0.05**	15.66	0.53**
KPMR 913	66.33	2.25**	116.00	3.45**	54.00	-8.12**	2.45	-0.01	13.66	-0.55**
SE (gi)		0.21		0.22		0.25		0.01		0.08
SE (gi-gj)		0.33		0.34		0.38		0.01		0.12

*Significant at p = 0.05, ** Significant at p =0.01

Table 2: Contd……

Parents	Grains per pod		100 seed weight		Grain yield / plant		Biological yield/plant		Harvest index	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
SWATI	4.48	-0.07	21.14	0.19**	16.91	0.07	32.58	-0.15	51.88	0.24
RACHNA	4.96	0.07	20.65	0.21**	11.88	0.11**	24.01	0.3**	49.99	-0.21
KPMR 400	4.68	-0.02	20.75	0.13**	14.62	0.41	29.23	-0.18*	49.99	1.87**
KPMR 522	4.73	0.05	20.91	0.39**	16.05	1.20**	28.19	-0.26**	56.91	4.34**
SAPNA	4.61	-0.12**	19.97	-0.38**	12.95	-1.32**	28.98	-0.36**	42.50	-3.94**
SHIKHA	4.55	-0.21**	19.88	-0.46**	12.63	-1.43**	24.5	-2.63**	51.47	-0.37
KPMR 940	5.22	0.29**	21.37	0.54**	17.83	1.77**	35.04	4.86**	50.82	-1.78**
KPMR 913	4.87	0.01	19.96	-0.62**	13.67	-0.81	27.01	-1.56**	50.59	-0.15
S.E. (gi)		0.08		0.01		0.05		0.05		0.28
S.E. (gi-gj)		0.12		0.01		0.07		0.07		0.43

*Significant at p = 0.05, ** Significant at p =0.01

Specific combining ability (SCA) effect

Specific combining ability effect is an important parameter for judging the specific combination for exploiting it through heterotic breeding programme. Its effects represent non additive component of genetic variance which would contribute much for improvement of crops. SCA is function of dominance variance, additive x dominance variance and dominance x dominance type epistasis. Among 28 cross combinations, none of the hybrid exhibited high significant SCA effect for all the characters. However, the good cross combination with high per se performance is presented in Table 3.

On the basis of significant SCA effect, negative significant SCA with lower mean value is desirable for days to flowering, days to maturity, plant height. The best cross combination for days to flowering showing highly significant and negative SCA effect was found to be SHIKHA x KPMR 940, KPMR 522 x SAPNA, KPMR 400 x KPMR 913 and SWATI x KPMR 913 desirables for early blooming. The desirable cross for days to maturity with negative SCA effect was shown by SWATI x KPMR913, KPMR 522 x SAPNA, KPMR522 x SHIKH, SHIKHA x KPMR 940 for earliness. The best combination of cross for plant height was shown by SWATI x RACHNA, KPMR 400 x KPMR 913, KPMR 522 x SHIKHA, KPMR 522 x SAPNA, KPMR 400 x SAPNA were marked as superior cross for decreasing plant height. The SCA with positive value was observed for branches per plant in cross RACHNA x SHIKHA followed by KPMR 522 x KPMR 940, KPMR 400 x KPMR 940, RACHNA x KPMR 940, SWATI x KPMR 913. SWATI x KPMR 913 followed by KPMR 400 x KPMR 522, SWATI x KPMR 400, KPMR400 x SAPNA were found desirable cross for pods per plant. These results are in the way of Dagla *et al*. (2013) [5], Sharma *et al*. (2013) [12] and Chauhan *et al*. (2016) [4].

Desirable cross combination for grains per pod was shown by KPMR400 x KPMR 940, followed by RACHNA x KPMR 940, SWATI x KPMR 940, KPMR522 x KPMR940, KPMR522 x KPMR913 with positive SCA and high per se performance. KPMR 400 x KPMR 940 followed by RACHNA x KPMR 940, SWATI x KPMR 940, KPMR 522 x KPMR 940 was observed for 100 seed weight. Best cross combination for grain yield/ plant was shown by RACHNA x KPMR940 followed by SWATI x KPMR 940, KPMR 522 X SHIKHA, RACHNA X KPMR522, SWATI X KPMR 522 which showed positive SCA effect and significant value. Best cross combination for biological yield/ plant was shown by the cross RACHNA x KPMR 522 followed by RACHNA x KPMR 400 SWATI x RACHNA, RACHNA x KPMR 940, RACHNA x SWATI while best cross combination for harvest index was shown by SAPNA x KPMR 913 followed by SWATI x KPMR 522, RACHNA x KPMR 940, KPMR 400 x KPMR 913, SWATI x KPMR 400. Singh *et al.* (1989) [14] and Shinde (2000) [13] were also reported similar results.

The *per se* performance and SCA effect along with GCA status of five top ranked combinations for all the characters are presented in Table 3 which revealed that majority of the crosses which showed desirable SCA effect with high per se performance falls in the category of high x low *i.e.* one parent with positive and other with negative GCA status which indicates that these cross combinations were produced due to complementary gene action and may produce transgressive segregates in advanced generations if additive effect of one parent and non-additive effect of another works in same direction. (Baker, 1978) [2].

Table 3: Ranking of desirable crosses their SCA and GCA status for 10 Characters in field pea

Characters	Cross Combination	SCA Effect	Mean	GCA Effect	
				P1	P2
Days to Flowering	KPMR522 X SAPNA	-2.78	56.00	-2.45	0.92
	KPMR400 X KPMR913	-1.88	56.33	-1.35	2.25
	SWATI X KPMR913	-1.78	57.33	0.22	2.25
	RACHNA X SHIKHA	-1.51	57.67	-0.25	2.45
	RACHNA X SWATI	-1.31	57.67	-0.25	0.22
Days to Maturity	SWATI X KPMR913	-4.17	106.33	-0.07	3.45
	KPMR522 X SHIKHA	-3.07	108.00	-2.10	2.02
	KPMR522 X SAPNA	-3.07	108.33	-2.10	-0.27
	RACHNA X SHIKHA	-2.90	108.66	-0.90	2.02
	SWATI X KPMR400	-2.71	108.66	-0.07	-0.34
Plant height	SWATI X RACHNA	-6.67	48.23	34.65	24.17
	KPMR940 X KPMR913	-2.35	48.43	-8.80	-8.12
	KPMR400 X KPMR913	-2.11	48.66	13.88	-8.12
	KPMR522 X SHIKHA	-1.74	50.39	-9.20	-7.37
	KPMR522 X SHIKHA	-1.57	50.50	-9.20	7.37
Branches / plant	RACHNA X SHIKHA	0.21	2.75	-0.12	2.55
	KPMR522 X KPMR940	0.21	2.75	0.02	0.05
	RACHNA X KPMR940	0.17	2.70	-0.12	0.05
	KPMR400 X KPMR940	0.17	2.67	-0.02	0.05
	SWATI X KPMR522	0.16	2.67	-0.16	0.02
Pods / Plant	SWATI X KPMR913	1.33	16.60	-0.39	-0.55
	RACHNA X SHIKHA	1.25	16.46	0.49	0.49
	KPMR400 X KPMR522	1.13	16.40	0.86	0.53
	SWATI X KPMR400	0.95	16.30	-0.96	-0.55
	KPMR400 X SAPNA	0.76	15.90	0.16	-0.55

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