# **IJPSINTERNATIONAL JOURNAL OF PLANT SCIENCES** © e ISSN-0976-593X Volume 13 | Issue 1 | January, 2018 | 196-200

**DOI: 10.15740/HAS/IJPS/13.1/196-200** Visit us - www.researchjournal.co.in

## **R**ESEARCH ARTICLE

# Genetics of green pod yield in table pea (*Pisum sativum* L. Hort.)

Pallavi Pathak and S.S. Gahalain

### **SUMMARY**

An experiment consisting 45  $F_1$ s derived from ten pea varieties/strains *i.e.* AP-2, AP-4, AP-5, AP-1, KS-185, KS-218, KS-601, KS-701, KS-801 and AP-3, during the rabi season of 2014-15 were raised in crossing block and all possible combination excluding reciprocals were made to obtained 45 crosses. The crosses were evaluated at Vegetable Research Farm, Kalyanpur, Kanpur during *Rabi* of 2015-16. The analysis of variance for combining ability showed significant differences both for GCA and SCA variances. The estimated values of  $\sigma^2$  GCA were higher than  $\sigma^2$  SCA for number of fertile branches per plant, pod width, number of pods per plant, seed-shell ratio and protein content indicated the more contribution of additive genetic variances for controlling these characters. Higher estimates of  $\sigma^2$  SCA than  $\sigma^2$  GCA for green pod yield, pod length and number of seeds per pod indicated the role of non additive genes for controlling these traits. Parents AP-1, AP-3, AP-4, KS-601 and KS-701 were found good general combiners for majority of the characters under study including green pod yield per plant. Cross combinations namely; AP2 x AP3, AP2 x KS801, KS218 x KS601, AP4 x AP1, KS801 x AP3, AP4 x KS701, KS185 x KS218, KS185 x KS601, KS701 x KS801 and AP4 x KS601 were the top ten crosses which showed higher mean values and significant SCA effects for green pod yield and some other characters under study. Significant contribution of non additive genes were observed for controlling the expression of pod width, number of seeds per pod while additive genes were found effective for controlling the series and number of pod per plant, seed-shell ratio and protein controlling the green pod yield, pod length and number of pod per plant, seed-shell ratio and protein controlling the expression of pod width, number of pod per plant, seed-shell ratio and protein controlling the expression of pod width, number of pod per plant, seed-shell ratio and protein content.

Key Words : Gene action, Green pod yield, Combining ability, GCA effect, SCA effect, Table pea Pisum sativum

How to cite this article : Pathak, Pallavi and Gahalain, S.S. (2018). Genetics of green pod yield in table pea (*Pisum sativum* L. Hort.). *Internat. J. Plant Sci.*, **13** (1): 196-200, **DOI: 10.15740/HAS/IJPS/13.1/196-200**.

Article chronicle : Received : 10.11.2017; Revised : 12.12.2017; Accepted : 27.12.2017

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Address of the Co-authors: S.S. Gahalain, S.S.J. Campus, Kumaun University, Almora (Uttarakhand) India The peak is one of the most important vegetable crop among Indian diets as majority of the people of India are vegetarian in nature and the main source of minerals and vitamins in vegetarian diets mainly comes from vegetables. Among various green vegetables grown in India. The table pea plays an important role not only in protein malnutrition but also in mineral

supplements. It is used as green vegetable mixed with potato, paneer, mushroom, carrot and other green vegetables except cucurbits.

The information regarding genetics of other vegetables of economic values has got more reliance but the genetic information on genetic behaviour in table pea is extremely limited. Hence the present article is an attempt to collect the genetic information in respect to green pod yield and its component through combining ability analysis.

#### MATERIAL AND METHODS

The material comprises of ten pea varieties/strains of table pea namely; AP-2, AP-4, AP-5, AP-1, KS-185, KS-218, KS-601, KS-701, KS-801 and AP-3, during the Rabi season of 2014-15 were raised in crossing block and all possible combination excluding reciprocals were made to obtained 45 crosses. The crosses along with parents were evaluated at Vegetable Research Farm, Kalyanpur, Kanpur during Rabi of 2015-16. Each of the parents and F<sub>1</sub>s were sown in single row of 5.0 m long spaced at 45×15 cm apart between rows and plant, respectively replicated thrice. All the recommended package of practices was adopted to raise a good crop. The observations were recorded on ten randomly selected plants from both parents and F<sub>1</sub>s from each replication and each treatment for number of fertile branches per plant, pod length (cm), pod width (cm), number of seeds per pod, number of pods per plant, seed shell ratio, Protein content (%) and green pod yield per plant (g). The protein content in dried seeds was estimated by the method as suggested by Williams (1961) The mean data were subjected for various statistical analysis as usual procedure while combining ability analysis of diallel cross were carried out following Griffing (1956) method 2 model I.

#### **RESULTS AND DISCUSSION**

The combining ability variances and their effect are most convergent technique to assess the genetic material for inheritance of the characters. The numerical approach of diallel analysis provides the information about GCA and SCA variances and their effects Sharma et al. (2003). The combining ability analysis also exploited the best combiners and their appropriate use in hybridization programme to assess the various genetic effects for commercial utilization of heterotic crosses as also suggested by Kumar et al. (2002) and Gillbert (1967). In present study the analysis of variance for combining ability revealed highly significant differences both for variances due to GCA and SCA based on all the characters. The ratio of variance  $\sigma^2 GCA/\sigma^2 SCA$  also in the view of preponderance role of additive gene action for number of fertile branches per plant, pod width, number of pods per plant, seed shell ratio and protein content (Table 1). Additive gene action for most of the above characters is also reported by Kumar et al. (2006) and Katiyar et al. (2014)

The remaining characters advocated the role of non additive genes including green pod yield per plant as also in conformity with earlier reports of Sharma *et al.* (2003) and Kumar and Tewatia (2003).

GCA effects consists both additive and/or additive  $\times$  additive components of gene action (Griffing, 1956a and b; Sprage, 1966 and Gillbert, 1967) which is fixable in nature. The additive effects of parents due to GCA are of practical utility, whereas, non-additive interactions are non-predictable and cannot be easily manipulated. An examination of the best combiners has revealed that majority of them are derived from Indian origin. Hence, the derivatives from these parents in vegetable pea varieties/strains did not lower the yield and its attributes. The parents namely; AP-1 for yield attributing characters; namely pod length, pod width, seeds per pod, pods per

Table 1 : Analysis of variance for combining ability, their ratios and average degree of dominance in 10x10 diallel cross for various traits in table pea

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Source of variation	D. F.	No. of fertile branches per plant	Pod length	Pod width	Number of seed per pod	Number of pods per plant	Seed shell ratio	Protein content	Green pod yield
GCA	9	0.313*	2.569**	0.003**	4.614**	70.471**	46.002**	4.183**	375.038**
SCA	45	0.108	0.474**	0.0003	0.713**	3.016**	2.442**	0.315**	41.694**
Error	108	0.108	0.061	0.0003	0.119	0.289	0.209	0.034	0.902
<sup>2</sup> GCA		0.017	0.209	0.0002	0.375	5.849	3.816	0.346	31.178
<sup>2</sup> SCA		0.000	0.413	0.000	0.612	2.727	2.233	0.281	40.792
$\frac{^2g}{^2s}$		0.000	0.506	0.000	0.612	2.145	1.709	1.230	0.764

\* and \*\* indicate significance of values at P=0.05 and 0.01, respectively

plant, seed shell ratio protein content. KS-601 for number of fertile branches per plant, pod length, pod width, seeds per pod, pods per plant, seed shell ratio, protein content. AP-3 for, pod length, pod width, seeds per pod, pods per plant, seed shell ratio, protein content. AP-4 for pod length, seeds per pod, pods per plant; KS-701 for pod length, pod width, seeds per pod, pods per plant. Therefore, the use of these varieties/strain in further breeding programme, the importance will be effective for yield attributes for majority of characters.

How ever; none of the parent in present study was common for all the characters (Table 2). However, parents namely AP-1, AP-3, AP-4, KS-601, KS-701 exhibited their desirability for yield traits. The best general combiner is one which has at least desirable significant GCA effects and high *per se* performance for the character in question.

The good general combiners may be used in developing population involving all possible combinations among themselves and may be subjected to bi-parental mating in early generations which helps in releasing inherent genetic variability due to faster rate of recombination. Jensen (1970) suggested the idea of using developing population. There is provision in the method to make all possible bi-parental crosses among selected parents depending upon the number of  $F_1s$ . A diallel or partial diallel set or cross among  $F_1s$  would be the material for initiating the breeding population. This was suggested by Frey (1975) in self pollinated crops.

The parents of diverse origin having high additive  $\times$  additive interactions effects are likely to produce better recombinants in their progenies with high yield in

Table 2 : General combining ability effects and corresponding mean performance of 10 parents in table pea

	Parents	No. of fertile branches per plant		Pod length		Pod width		Seeds/pod		Number of		Seed-shell		Protein content		Green pod yield	
Sr. No.											pods/plant		ratio				
		Mean	G.C.A	Mean	G.C.A	Mean	G.C.A	Mean	G.C.A	Mean	G.C.A	Mean	G.C.A	Mean	G.C.A	Mean	G.C.A
1.	AP-2	1.67	-0.21*	8.15	0.00	1.24	-0.01**	5.00	-0.68**	24.00	-3.72**	45.37	-2.19**	19.39	0.11*	95.13	-6.50**
2.	AP-4	2.00	-0.04	9.07	0.20**	1.28	-0.01**	8.00	0.29**	32.33	0.64**	50.22	0.19	17.55	-1.15**	105.33	-3.12**
3.	AP-5	2.67	0.07	8.83	-0.05	1.26	-0.01**	6.33	-0.52**	23.33	-4.72**	55.09	4.04**	20.23	0.30**	122.83	1.00**
4.	AP-1	1.67	-0.18*	9.39	0.38**	1.32	0.01**	8.33	0.51**	36.33	2.86**	48.02	0.43**	19.38	0.17**	125.33	5.39**
5.	KS-185	2.67	0.21*	6.10	-0.77**	1.28	-0.01**	5.33	-0.52**	33.00	1.50**	44.33	-1.62**	19.01	0.06	105.67	-4.48**
6.	KS-218	2.67	0.15	5.97	-0.79**	1.28	-0.01**	5.33	-0.96**	34.67	1.64**	45.00	-2.65**	19.34	0.12*	108.00	-5.01**
7.	KS-601	3.00	0.21*	9.00	0.42**	1.32	0.02**	8.00	0.71**	31.67	1.00**	52.00	1.18**	20.00	0.55**	128.47	7.26**
8.	KS-701	1.67	-0.18*	9.00	0.32**	1.32	0.01**	7.33	0.48**	29.67	0.69**	47.33	-0.74**	19.03	-0.05	122.33	2.56**
9.	KS-801	1.67	-0.07	7.00	-0.16*	1.25	-0.02**	5.33	0.01	25.33	-0.86**	50.33	0.15	17.10	-0.88**	98.67	-3.99**
10.	AP-3	2.67	0.07	9.03	0.46**	1.33	0.03**	8.67	0.68**	30.00	0.97**	51.67	1.22**	20.42	0.77**	131.80	8.89**
	S.E.±		0.09		0.07		0.00		0.09		0.14		0.12		0.05		0.26

\* and \*\* indicates significance of values at P=0.05 and 0.01, respectively

Table 3 : Ranking of top 10 desirable crosses based on SCA effect and per se performance for green pod yield in table pea

Sr. Cross		SCA effect	Per se value	GCA	status	SCA effect in other characters @		
No.	· · ·			<b>P</b> <sub>1</sub>	P <sub>2</sub>			
1.	AP2 x AP3	18.81**	140.18	-6.50**	8.89**	No. of pods per plant		
2.	AP2 x KS801	11.81**	120.33	-6.50**	-3.99**	No. of fertile branches per plant, pod length, no. of sees per		
						pod, no. of pods per plant, protein content		
3.	KS218 x KS601	11.10**	132.33	-5.01**	7.26**	-		
4.	AP4 x AP1	9.42**	130.67	-3.12**	5.39**	-		
5.	KS801 x AP3	8.45**	132.33	-3.99**	8.89**	Pod length, no. of seeds per pod, no. of pods per plant,		
						seed-shell ratio		
6.	AP4 x KS701	8.25**	126.67	-3.12**	2.56**			
7.	KS185 x KS218	8.17**	117.67	-4.48**	-5.01**	Pod length, no. of seeds per pod, no. of pods per plant.		
8.	KS185 x KS601	6.90**	128.67	-4.48**	7.26**	No. of pods per plant, protein content.		
9.	KS701 x KS801	6.78**	124.33	2.56**	-3.99**	Pod length, seed-shell ratio, protein content		
10.	AP4 x KS601	6.55**	129.67	-3.12**	7.26**	Pod width, seed-shell ratio, protein content		

@ Desirable and significant only \*\* indicates significance of values at P= 0.01, respectively

Internat. J. Plant Sci., 13 (1) Jan., 2018 : 196-200 198 Hind Agricultural Research and Training Institute

advanced generations. The inherent variability in the genetic material may be a good compromise between the demand for uniformity and advantage of diversity as suggested by Allard and Bradshaw (1964).

SCA effects on the other hand, representing dominance and epistatic component and will not contribute much more improvement in self pollinated crops except in cases where commercial exploitation of heterosis or composite breeding programme is convenient. However, crosses involving high general combiners and showing high sca effects may be utilized for further breeding programme. Desirable trasngressive segregates are expected to be produced by making large number of crosses. Khrostovaka and Ske (1975). Jinks and Jones (1958) were in view that the superiority of mean of hybrids did not indicate their ability to produce transgressive segregates due to non-fixable genetic effects. However, in peas, the study of SCA in segregating generations may be helpful for upgrading the breeding material.

For green pod yield cross combination AP2 x AP3, KS218 x KS601, AP4 x AP1, KS801 x AP3, AP4 x KS 701, KS185 x KS 601, KS701 x KS 801 and AP4 x KS601 (Table 3) showed high per se performance and positively significant sca effects. The GCA status of these crosses showed one parent as desirable and other with undesirable gca effects means, high × low. These crosses showed dominance and epistatic nature of gene action. Such specific combiners could produce desirable transgressive segregates in advance generations as reported by Jensen (1970), Redden and Jensen (1974) in case of self pollinated crops. Cross combinations namely, AP2x KS801 and KS185 x KS218 showed high per se performance and positively significant SCA effects when both the parents showed negative and undesirable GCA effects means low x low gca status. Such type of crosses was produced due to involvement of non additive genetic effects and could not be easily exploited in self pollinated crops. Although the finding of Pederson (1974) and Sneep (1977) were not in agreements with those of Hanson (1959), Jensen (1970) and Redden and Jensen (1974) that inter-mating in advance generation might results in remarkable improvement in raising the productivity or increase in the number of plants with the desirable genotypes. Handling of desirable crosses can be taken further by Pedigree/recurrent selections as advocated by Frey (1975) and Rachie and Gardner (1975).

Further the desirable diverse parents can put into central gene pool for utilization in further breeding programme aimed for improving the green pod yield and its components.

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