



## Research Article

# EFFECT OF CLIMATE ON THE GENETIC ANALYSIS AND SELECTION PARAMETER IN TABLE PEA (*Pisum sativum* L.)

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**Abstract:** An experiment consisting ten parents and their all possible combinations (excluding reciprocals) was conducted at Research Farm of BNV College Rath (Hamirpur) during the *rabi* 2007-08. The results showed high level of variability both among parents and F<sub>1</sub> for all the characters. The parent's vs F<sub>1</sub>s were also highly variable for all the characters. Genetic components of variance analysis showed that both additive (D) and dominance (H<sub>1</sub> and H<sub>2</sub>) were significant for all the traits under study. The degree of dominance (H<sub>1</sub>/D) 0.5 showed the presence of over dominance for all the characters except green pod yield which was under control of partial to complete dominance. All the characters showed high heritability coupled with high Genetic Advance except pod width, pod length and number of seeds per pod. An advancement of 26.93% was observed for green pod yield per plant at K = 2.06. Simple selection procedure may be recommended for improving the green pod yield.

**Keywords:** Genetic analysis, Gene action, Combining ability

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## Introduction

The role of vegetables in vegetarian diet is well known as majority of the people of India are vegetarian in nature and vegetables are main source of minerals and vitamins in vegetarian diets. Among various purpose 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 etc.

The information's regarding genetics of other vegetables have got more reliance but the genetic information in Table pea is extremely limited hence the present article is an attempt to collect the genetic information in respect of green pod yield and its component through the genetic component of variance and the transmission of characters through heritability and genetic advance.

## Materials and Methods

The material comprises of ten pea varieties/strains i.e. Azad Pea-1, Arkel, Azad Pea-3, Azad Pea-4, KS-156, KS-175, KS-150, E-6, PMR-20 and PSM-3 were raised in crossing block and all possible combination were made to obtain 45 crosses. The final experiment comprised of 45 each of F<sub>1</sub>s and parents were sown in a Randomized Block Design in three replications at Experimental farm of Department of Genetics and Plant Breeding of Brahmanand Mahavidyalaya, Rath, Hamirpur during *rabi* 2007-08 their performance in a single row-length of 3.50 cm maintaining row to row 50cm and plant to plant spacing of 10 cm. Observations were recorded on ten randomly selected plants from both parents and F<sub>1</sub>s from each replication. The compounds analyses of diallel cross were carried out following [1]

## Result and Discussion

The analysis of variance indicated appreciable genetic variability among the parents and their all possible hybrids for all the traits studied [Table-1].

Over dominance of consistent nature was observed by component analysis (H<sub>1</sub>/D)<sup>1/2</sup> for all the characters except green pod yield only which was partial dominance in nature [Table-2]. The expression of over dominance might be due to linkage which caused an upward estimation of dominance from parents to their progenies. [2,3] suggested that over dominance might be attributed due to epistatic gene interaction. Complete to over dominance was also reported for yield and its components by [4-7].

The additive component (D) was highly significant for all the characters studied except pod width. The dominance component (H<sub>1</sub> and H<sub>2</sub>) also revealed highly significant values for all the characters. The positive and non significant values of F<sub>1</sub> component they're by showing the equal distribution of dominance and recessive genes in the parents. The values of the ratio H<sub>2</sub>/4H<sub>1</sub> was less than its theoretical values for all the characters showing asymmetrical distribution of positive and negative alleles in parents. The fraction (h<sup>2</sup>/H<sub>2</sub>) indicated that at least one major gene group was involved for expression of the traits under study except pod yield per plant where more than two gene group were observed. These findings are in accordance to [8]. Liang and walter suggested that complementation also seems to lower down the ratio of h<sup>2</sup>/H<sub>2</sub>.

Considering the additive and dominance model (D, H<sub>1</sub> and H<sub>2</sub>) both of the models showed highly significant values for all the characters indicating that both additive and non-additive genes are prevailing for controlling the traits. Higher values of dominance component than additive ones indicated that non-additive genes are more frequent than additive. The proportion of recessive and dominance alleles in parents showed that dominant genes are more frequent than recessive one for pod width, number of seed per pod, length of first fruiting internode, number of first fruiting node and green pod yield while number of pods per plant and pod length expressed equal proportion of dominant and recessive genes. Similar reports have also been observed reported [9].

Table-1 Analysis of variance for 7 yield characters in Vegetable Pea (*Pisum sativum* L.)

Source of variation	d.f.	Number of pods per plant	Pod length (cm)	Pod width (mm)	Number of seeds per pod	Length to first fruiting inter node(cm)	Number of first fruiting node	Green pod yield per plant (g)
Replication	2	1.655	0.013	0.059	0.077	1.190	0.081	9.181
Treatment	54	32.794**	2.831**	0.776**	2.562**	108.120**	7.116**	395.71**
Parents	9	37.294**	2.277**	0.267**	3.260**	168.432**	16.430**	618.314**
F <sub>1s</sub>	44	31.286**	2.662**	0.791**	2.359**	99.695**	5.305**	299.075**
P vs F <sub>1</sub>	1	58.622**	15.231**	4.691**	5.240**	24.148**	2.917**	2645.27**
Error	108	1.321	0.024	0.088	0.684	1.319	1.004	8.943

\*Significant at 5% level, \*\* Significant at 1% level

Table-2 Estimates of genetic components & related statistics for 7 yield characters in Vegetable Pea (*Pisum sativum* L.)

Characters	D	H <sub>1</sub>	H <sub>2</sub>	F	h <sup>2</sup>	E	(H <sub>1</sub> /D) <sup>0.5</sup>	(H <sub>2</sub> /4H <sub>1</sub> ) <sup>0.5</sup>	(4DH <sub>1</sub> ) <sup>0.5</sup> + F / (4DH <sub>1</sub> ) <sup>0.5</sup> - F	h <sup>2</sup> /H <sub>2</sub>
Number of pods per plant	11.99**	18.87**	16.58**	0.26	7.58*	0.44	1.25	0.22	0.98	0.46
SE	2.52	5.37	4.56	5.82	3.05	0.76				
Pod length (cm)	0.75**	2.36**	2.23**	0.01	2.01**	0.01	1.77	0.24	1.00	0.90
SE	0.24	0.5	0.43	0.54	0.28	0.07				
Pod width (mm)	0.06	0.97**	0.87**	0.06	0.61**	0.03	4.02	0.22	1.26	0.70
SE	0.12	0.26	0.22	0.28	0.15	0.04				
Number of seeds per pod	0.86**	1.61**	1.53**	0.18	0.61	0.23*	1.37	0.24	1.17	0.40
SE	0.28	0.6	0.51	0.65	0.34	0.09				
Length to first fruiting inter node	55.70**	62.69**	58.18**	14.73	3.03	0.44	1.06	0.23	1.28	0.05
SE	4.3	9.15	7.78	9.92	5.21	1.3				
Number of first fruiting node	5.14**	9.60**	6.76**	7.19**	0.26	0.33	1.37	0.18	3.09	0.04
SE	0.59	1.25	1.06	1.36	0.71	0.18				
Green pod yield per plant (g)	203.12**	191.18**	171.64**	54.33	348.10**	2.98	0.97	0.22	1.32	2.03
SE	13.55	29.06	24.7	31.5	16.53	4.12				

\* Significant at 5% level, \*\* Significant at 1% level

Table-3 Heritability, genetic advance and genetic advance in percent over mean for 7 characters in vegetable pea (*Pisum sativum* L.)

SN	Characters	Population mean	Heritability	G. A.	G. A. in % over mean
1	Number of pods/plant	15.41	36.46	4.31	27.97
2	Pod length (cm)	9.17	23.85	0.82	8.94
3	Pod width (mm)	13.45	5.50	0.10	0.74
4	Number of seed/pod	8.38	26.84	0.88	10.50
5	Length to first fruiting inter node (cm)	31.19	52.84	11.31	36.26
6	Number of first fruiting node	11.92	57.83	3.18	26.68
7	Green pod yield/plant (g)	87.77	57.72	23.64	26.93

Heritability of character provide statistical concept and is used for estimated progress determining the extent to which the character is transmitted from parents to the offspring's. It also provides the comparative value of heredity and environment on character. The effective improvement in a particular trait/character for which the selection is made would be based on the quantum of genetic advance. [10] reported that the estimates of heritability could not be of practical utility without genetic advance for selection based on phenotypic appearance. As per [11] heritability was influenced by methods of estimation, generation to study, environment, samples employed. [12] reported that genetic gain would be overestimated in either of the following condition (i) low selection pressure with high heritability and (ii) high selection pressure with low heritability.

Study of one or more characters results in correlated response [13, 14] and the pattern of variation will also be changed [15]. Hence, the component of selection parameter from a selected group of material will probably be different from those involving diverse material. Such changes would be quite substantial with the useful genes and intensive selection for an ideal plant type, which includes developmental, componential and qualitative characters pertaining to productivity. High heritability estimates in narrow sense for all the characters were observed except number of seeds per pod and pod width which showed moderate to low heritability. The high heritability for the traits was mainly due to more contribution of additive component for inheritance of the characters. It is obvious to indicate that these traits are subjected to mass selection and/or any other selection scheme aimed to exploit the fixable component (additive). Widely adapted genotypes could be developed which might process good quality and productivity. High heritability for various characters were also reported earlier by [16-22]. Genetic advance confirms the heritability estimates, an advancement of 23.64 g/cycle of selection was realized for green pod yield per plant at K-2.06. Very low genetic advance was realized for pod width and number of seed per pod. High heritability coupled with high genetic advance was associated with additive genetic

component which can easily be improved through simple selection scheme while the characters showing high heritability with low genetic advance were mainly due to involvement of both additive and non-additive gene effect and for these type of characters a modified pedigree method can be practiced for improving the characters and the characters which showed low heritability with low genetic advance are under the control of purely non additive genes which can be improved only through recurrent selection and/or bi parental mating with growing large size of population in case of self-pollinated crops.

**Application of research:** The estimated value of heterosis over economic parent revealed that that none of the crosses showed useful significant heterosis for all the characters. Estimated value of heterosis showed that the degree and direction of heterosis varied not only from character to character but also in cross to cross.

**Research Category:** Plant Breeding

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**Study area / Sample Collection:** Experimental farm, Department of Genetics and Plant Breeding, Brahmanand Degree College, Rath, 210431

**Cultivar / Variety / Breed name:** Azad Pea-1, Arkel, Azad Pea-3, Azad Pea-4, KS-156, KS-175, KS-150, E-6, PMR-20 and PSM-3

**Conflict of Interest:** None declared

**Ethical approval:** This article does not contain any studies with human participants or animals performed by any of the authors.  
Ethical Committee Approval Number: Nil

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