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## Studies on phenotypic and genotypic coefficient of variation (PCV and GCV) between different characters in Pea (*Pisum sativum* L.) genotypes in sodic condition

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#### Abstract

Pea (*Pisum sativum* L.)  $2n = 2x = 14$ , belongs to the family *Fabaceae*. It originated in central Asia, the Near East, Abyssinia and Mediterranean. In India huge range of variability is available in the land races or cultivars, in terms of qualitative as well as quantitative characters of pea. Analysis of Variance in the present investigation indicated that the genotypes evaluated differed significantly among all the treatment for all the twelve traits. The genotypes NDVP-10, NDVP-250, NDVP-8, VRPMR-9 and CHPMR-2 produced highest green pod yield per plant (g). These genotypes also exhibited average mean performance for pods per plant, pod length, number of seeds per pod and shelling percentage. Phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) for all characters. Both PCV and GCV were high for branches per plant followed by pods per plant and days to 50% flowering. While Shelling percentage exhibited low value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) and likely to show less response under selection.

**Keywords:** Pea (*Pisum Sativum* L.), Variance, Phenotype, Genotypes, Phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV)

#### Introduction

The pea (*Pisum Sativum* L.) is one of the earliest human foods crops belong to the family *Fabaceae*. The exact origin and progenitor of pea is unknown, but it is one of the oldest cultivated plants. Vavilove (1959) listed central Asia, the Near East, Abyssinia and Mediterranean as the centre of origin based on the genetic diversity. Archaeological evidences have showed that smooth seed form was cultivated in Near East and Europe as early as 700 BC. *Pisum* is considered to have originated in Ethiopia, from where it had spread in pre – historic times to Mediterranean region. Central Europe and Near East, and subsequently to the rest of the world. Near Eastern Centre is considered to be its secondary centre of diversity.

The inflorescence is raceme arising from the axil of a leaf. The lowest node at which flower initiation occurs is normally constant under a given set of condition and is used in classifying the varieties into early and late types. Early cultivars are often single flowered or bear some single- double flowers. Late cultivars are usually double / triple flowered. The flowers are typical papilionaceous with green calyx comprising of five united sepals, five petals (one slandered, two wings and two keels). The stamens are in diadelphous (9+1) condition. Nine filaments are fused to form a staminal tube while the tenth is free throughout its length. The gynoecium is monocarpellary, with ovules (upto 13) alternately attached to the two placentas. Style normally bends at right angle to the ovary. Stigma is sticky. Pea ( $2n= 2x=14$ ) is strictly self-pollinated in nature. Stigma is receptive to pollen from several days prior to anthesis until one day or more after the flower wilts. Pollen is viable from the time of anther dehiscence until several days thereafter. Anonymous (1998) [1]. This area can be utilized by pea cultivation which is semi tolerance against this condition.

The possibility of improvement in any crop is measured by available variability in the crop. In past a number of pea varieties has been recommended by the central and state government for cultivation in eastern Uttar Pradesh. But no systematic work on evaluation of existing cultivars has been done so far. Genetic variability is essential for crop improvement programme for obtaining high yielding varieties. The screening of genetic variability is prerequisite to know the nature and magnitude of genetic variation and also the influence of environmental in the expression of yield and other traits. Greater the variability in the initial genetic material better would be the chance of selecting desirable type (Vavilove, 1959). On other hand, yield is a

complex character and is associated with some yield contributing characters. Yield is not only a polygenically controlled trait, but it is also directly or indirectly constituted by the associated yield characters.

### Methods and Materials

The experimental material consisting of thirty five pea genotypes was sown during Rabi season of 2009-10 to study the phenotypic and genotypic coefficient of variation (PCV and GCV) between different characters in Pea (*Pisum sativum* L.) genotypes in sodic condition. The experimental field had sandy loam soil, low in organic carbon, nitrogen, medium in phosphorous, potash, and slightly sodic in nature with pH 8.5,

Electronic Conductivity (EC) 04 and exchangeable sodium percentage (ESP) 29.9.

The experimental material for the present investigation comprised 35 genotypes of Pea collected from different places in India and being maintained at main experiment station in the Department of Vegetable Science, N.D. University of Agriculture & Technology, Narendra Nagar (Kumarganj), Faizabad (U.P.) Table 1. The experiment was conducted in Randomized Block Design with three replications to assess the performance of 35 genotypes. Seed of each genotype were sown in a plot measuring 3.0 X 0.90 meter at spacing of 30 cm and 10 cm were maintained between row to row and plant to plant, respectively.

**Table 1:** List of genotypes

S. No.		Source of origin
1.	DDP-9414	H.P.K.V.V., Palampur
2.	PHPMR- 1	H.A.U. Hisar
3.	CHP-1	Ranchi- (CHES)
4.	NDVP-250	N.D.U.A.&T., Faizabad
5.	NDVP-24	N.D.U.A.&T., Faizabad
6.	KS-216	C.S.A.U.A.T., KANPUR.
7.	NDVP-12	N.D.U.A.&T., Faizabad
8.	CHPMR-2	Ranchi- (CHES)
9.	VRPMR-9	I.I.V.R., Varansi.
10.	DPP-68	H.P.K.V.V., Palampur
11.	NDVP-10	N.D.U.A.&T., Faizabad
12.	PMR-19	G.B.P.U.A.T., Pantnagar
13.	NDVP-92	N.D.U.A.&T., Faizabad
14.	JP-19	J.N.K.V.V. Jabalpur
15.	AP-1	C.S.A.U.A.&T., Kanpur
16.	NDVP-8	N.D.U.A.&T., Faizabad
17.	VP-5	V.P.K.A.S., Almora
18.	JP-501	JNKVV Jabalpur
19.	IP-3	G.B.P.U.A.&T., Pantnagar
20.	VL-3	V.P.K.A.S., Almora
21.	PH-1	I.A.R.I. New Delhi
22.	DDP-4	H.P.K.V.V., Palampur
23.	DPP-62	H.P.K.V.V., Palampur
24.	VP-7906	V.P.K.A.S., Almora
25.	P-88-7	G.B.P.U.A.&T., Pantnagar
26.	Bonneville	I.A.R.I., New Delhi
27.	KS-221	C.S.A.U.A.&T., Kanpur
28.	CHPMR-1	Ranchi- (CHES)
29.	VRP-7	I.I.V.R., Varanasi
30.	NDVP-7	N.D.U.A.&T., Faizabad
31.	NDVP-19	N.D.U.A.&T., Faizabad
32.	VP-9003	V.P.K.A.S., Almora
33.	NDVP-117	N.D.U.A.&T., Faizabad
34.	JP-83	J.N.K.V.V., Jabalpur
35.	Arkel(c)	I.A.R.I., New Delhi

### Results and Discussion

The prime objective of most of the plant breeding programme is to make an improvement in yield, but yield is a complex character and a combined result of a number of component traits. Since yield is controlled polygenically and influenced greatly by the environmental fluctuations. Therefore, the selection of superior genotype based on yield alone would not be effective; one has to put attention on the component characters, which contribute yield in positive direction. In such a situation the available variability in the gene pool provides opportunity for selecting superior genotypes, which can be obtained through screening and evaluation. The knowledge of association between the characters helps to plant breeders in deciding the selection criteria.

### Phenotypic and genotypic coefficients of variability

Variability is a very important and essential pre-requisite in any breeding programme and such variability will be driving force for improving the crop plants (Harlan, 1956 and Simond, 1962) [3, 7]. In general, the phenotypic coefficient of variability was higher than genotypic coefficient of variability for all the 12 characters under study which indicates that environment played a considerable role in the expression of their traits. The range of variability of different traits alone does not allow a decision as to which character was showing the highest degree of variability. Therefore, accurate relative comparison can be made with the help of phenotypic and genotypic coefficient of variation. Phenotypic variation was partitioned into genotypic and environmental components.

The maximum phenotypic and genotypic coefficient of variation was observed for branches per plant followed by pods per plant, days to 50% flowering, node at 1<sup>st</sup> pod appears, plant height and green pod yield per plant. Singh (1995) [8] Chaudhary and Sharma (2003) [2], Kumar *et al.* (2003) [4] and Singh *et al.* (2003) [9] have also reported similar result in their studies. The genotypic and phenotypic coefficients of variations were lower for shelling percentage has also observed for poor genotypic variance for all character was lower than phenotypic variance. It may be due to the fact

that the environment influenced the observed variance. Such influences were also evident for genotypic coefficient of variation. Genotypic coefficient of variation for different characters ranged from 2.79 (shelling percentage) to 31.16 (branches per plant) Table 2. In similar study of Kumara *et al.* (2008) [5] low level of phenotypic and genotypic coefficient of variation were observed. While Singh and Sharma (2007) [10] and Rathi and Dhaka (2007) [6] found high PCV and GCV for branches per plant.

**Table 2:** Estimates of phenotypic (P) & genotypic (G) correlation coefficient between different characters in Pea genotypes.

S. No.	Character		Days to 50% flowering	Plant height (cm)	Nodes/ plant	Internodal length (cm)	Node At first pod appears	Branches/ plant	Pods/ plant	Pod length (cm)	Shelling (%)	Seeds/ pod	100 Seed weight (g)	Green pod yield/ plant (g)
1	Days to 50% flowering	P	1.000	0.533**	0.732**	0.516**	0.871**	0.541**	0.389**	0.052	0.272*	0.132	0.293*	0.559**
		G	1.000	0.551	0.877	0.692	0.976	0.940	0.496	0.036	0.397	0.180	0.335	0.716
2	Plant height (cm)	P		1.000	0.672**	0.655**	0.492**	0.270*	0.239*	-0.112	0.099	-0.004	-0.015	0.249*
		G		1.000	0.795	0.882	0.542	0.480	0.306	0.229	0.143	0.107	0.020	0.318
3	Nodes/plant	P			1.000	0.505**	0.699**	0.448**	0.420**	0.065	0.364**	0.142	0.242*	0.513**
		G			1.000	0.821	0.890	1.005	0.621	0.071	0.424	0.312	0.263	0.746
4	Internodal length (cm)	P				1.000	0.456**	0.424**	0.235*	-0.043	0.159	0.016	-0.003	0.262*
		G				1.000	0.690	0.809	0.329	0.056	0.238	0.008	0.001	0.397
5	Node at first pod appears	P					1.000	0.571**	0.423**	0.006	0.332**	0.100	0.265*	0.578**
		G					1.000	0.939	0.487	0.007	0.416	0.181	0.352	0.695
6	Branches/ plant	P						1.000	0.550**	0.145	0.249*	0.137	0.219*	0.582**
		G						1.000	0.655	0.411	0.777	0.560	0.406	0.718
7	Pods/ plant	P							1.000	0.416**	0.550**	0.487**	0.474**	0.800**
		G							1.000	0.726	0.869	1.164	0.622	0.851
8	Pod length (cm.)	P								1.000	0.251*	0.752**	0.405**	0.413**
		G								1.000	0.595	0.753	0.581	0.675
9	Shelling %	P									1.000	0.261*	0.539**	0.499**
		G									1.000	0.978	0.693	0.866
10	Seeds/ pod	P										1.000	0.346**	0.372**
		G										1.000	0.831	0.844
11	100 seed weight (g)	P											1.000	0.475**
		G											1.000	0.654
12.	Green pod yield per plant (g)	P												1.000
		G												1.000

## Conclusion

All the 35 genotypes of pea showed significant genetic diversity. Based on *per se* performance for green pod yield per plant and other characters taken into consideration, genotype NDVP-10 was considered as the best genotype for green pod yield per plant followed by NDVP-250 and NDVP-8. The estimates of phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all characters. Both PCV and GCV were high for branches per plant followed by pods per plant and days to 50% flowering the occurrence of moderate value for these parameters reveals reasonable scope of improvement through selection. Shelling percentage exhibited low value of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) and likely to show less response under selection.

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