



## **Exploration of Genetic Parameters of Pea Genotypes Using Different Environmental Conditions**

**R. P. Jaiswal<sup>a</sup>, B. R. Pandey<sup>a</sup>, V. Kumar<sup>b\*</sup> and S. K. Pandey<sup>a</sup>**

<sup>a</sup> *Department of Horticulture, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.), 482004, India.*

<sup>b</sup> *Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur (M.P.), 482004, India.*

### **Authors' contributions**

*This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.*

### **Article Information**

DOI: 10.9734/IJECC/2021/v11i1230565

#### Editor(s):

(1) Dr. Wen-Cheng Liu, National United University, Taiwan.

#### Reviewers:

(1) Talbi Fatima Zahra, Hassan First University, Morocco.

(2) Md. Zonayet, Khulna Agricultural University, Bangladesh.

Complete Peer review History, details of the editor(s), Reviewers and additional Reviewers are available here:

<https://www.sdiarticle5.com/review-history/80388>

**Original Research Article**

**Received 06 October 2021**

**Accepted 12 December 2021**

**Published 15 December 2021**

### **ABSTRACT**

The estimate of genetic variability was observed for fifteen traits on fifty two genotypes. The ANOVA indicated that the mean sum of squares due to genotypes were highly significant for all the traits, respectively in all the environmental conditions. High magnitude of phenotypic coefficient of variation was observed than the genotypic coefficient of variation for all the characters under study. High genotypic and phenotypic coefficient of variations were exhibited for number of secondary branches/plant, Pod bearing length, number of primary branches/plant, number of pods/plants, number of seeds/plant, seed yield/plant (gm), biological yield/plant (gm), First flowering node and harvest index (%) in all six and pooled over environments. The above finding revealed the presence of substantial amount of genetic variability for the traits, which exhibited high magnitudes as well as less influence of environment on the expression of concerned traits. Day to first flowering node, number of seed/pods, hundred seed weight (gm), harvest index and days to flower initiation exhibited moderate genotypic and phenotypic coefficient variation in all the environments. Low genotypic and phenotypic coefficient of variation was observed for pod bearing length in all the environments, this revealed high influence of environment.

**Keywords:** Pea; genetic variability; environment; GCV and PCV.

## 1. INTRODUCTION

Pea belongs to family fabaceae (earlier leguminaceae sub family papilionaceae). The pea belongs to the genus *Pisum* and consist of two species. *Pisum sativum* (garden pea) and *Pisum hortense* (field pea). Pea (*Pisum sativum* L.) had been used as a good source of nutritious food since Neolithic times [1]. It is cultivated in about more than 50 countries in the arid, semi-arid and temperate regions, whereas; about 90% of world field pea is grown under rainfed conditions [2]. Pea has various uses in consumption aspects and fulfils the dietary nutrition. Accordingly, garden pea used for table purpose, hence harvest at green pod condition. Field pea is used as dry, whole or split as dal or used as flour (Besan) for various food preparations [3]. Dry pea seed has high protein (22.5%) with all the essential amino acids. It also contains 56.5% carbohydrate, 1.1% fat, 2.2% minerals, 4.5% fiber and important vitamins like vit B<sub>1</sub> and B<sub>5</sub> [4,5]. Now a days, protein markets are shifting away from dairy, egg, soy, and wheat ingredients toward alternative sources (e.g., pea) due to consumers' perceived fears about consuming animal-derived products, dietary choices based on religious or moral preferences, allergenicity and genetic modification [6]. Being third most important pulse crop in India, the pea has quite low productivity in comparison to other growing countries. In India it is cultivated in an area of 311.87 (000, in ha.) which production of 321.87 (000, in MT.) and productivity of 1032 Kg/ha. (Source: www.eands.dacnet.nic.in). In Madhya Pradesh the area production and productivity Kg/ha are 540, 542.2 and 1004, respectively. (Sources: Department of Agriculture, Cooperation and Farmer Welfare). This may be due to lack of improved high yielding varieties, narrow genetic base of released varieties, use of poor quality seeds and non-availability of irrigation [7]. Genotypes also respond to changes in environmental conditions such as temperature, rainfall, soil type, moisture and so on [8]. A critical analysis of genetic variability is a pre-requisite for initiating any crop improvement programme and for adopting the appropriate selection techniques [9]. The essential feature is the partitioning of total variation into genotypic and environmental components and determines the magnitude of these components for various traits assessment of the type of genetic variation and thus helps in deciding a breeding procedure for the genetic

improvement of a trait [10]. Considering the importance of pea as an economic value in the agriculture throughout the world and also the genetic components contributing their role in the high yield and quality. The present investigation was conducted to study the variation under the genotypes over different environmental conditions in this crop.

## 2. METHODS AND MATERIALS

Experimental material consists of fifty two genotypes of field pea included two check variety KN-5 and JP-885 were grown in a Randomized Complete Block Design (RCBD) with two replications at three different dates of sowing at an interval of 21 days during both Rabi Season i.e. 2018-19 and 2019-20 respectively at Seed Production Farm of BSP (Vegetable) JNKVV, Jabalpur (M.P.). All the agronomic practices were made to raise the healthy crop. Each plot consisted of two rows of 3.0 meter length. Data were recorded on five randomly and competitive plants of each genotype from each replication for fifteen quantitative traits viz. days to flower initiation, first flowering node, day to maturity, number of primary branches/plant, number of secondary branches/plant, number of nodes/plant, pod bearing length (cm), number of pods/plants, pod length (cm), number of seed/pods, number of seeds/plant, hundred seed weight (gm), biological yield/plant (gm), harvest index (%) and seed yield/plant (gm). Averages of the data from the sampled plants in respect of different quantitative characters were used for various statistical analyses. The analysis of variance was carried out as per methods suggested by [11]. The genotypic and phenotypic coefficients of variation were computed by formula suggested by [12].

## 3. RESULTS AND DISCUSSION

### 3.1 Genetic Variability

The breeding programme of any crop mainly depends upon the magnitude of genetic variability. Fifty two genotypes were evaluated for fifteen quantitative characters related to grain yield. Analysis of variance refers to the observable differences in individuals for a particular trait. To know the extent of variation for observed traits among the genotypes of pea, analysis of variance under six environments and pooled over environmental (POE) conditions was performed. The mean sums of square were

significant in almost all the genotypes for different characters, which revealed that there was considerable genetic variability present amongst the material under study (Table 1). Result of analysis of variance indicated that the mean sum of square due to genotypes were significant for all the characters, indicating the presence of genetic variability in the material under study, mean sum of square was maximum and highly significant for pod bearing length (cm) and minimum for pod length (cm) in E1, mean sum of square was maximum and highly significant for pod bearing length (cm) and minimum for number of secondary branches/plant in E2, mean sum of square was maximum and highly significant for pod bearing length (cm) and minimum for number of secondary branches/plant in E3, mean sum of square was maximum and highly significant for Number of seeds/plants and minimum for Number of seeds/pod in E4, mean sum of square was maximum and highly significant for Pod bearing length (cm) and minimum for number of secondary branches/plant in E5, mean sum of square was maximum and highly significant for Pod bearing length (cm) and minimum for number of secondary branches/plant in E6, mean sum of square was maximum and highly significant for Pod bearing length (cm) and minimum for number of secondary branches/plant in pooled over environments (POE).

These findings are supported by Sahoo [5], Jaiswal et al. [13], Katoch et al. [14], Kumar et al. [15] and Toppo [16], whereas, Patel [17] also supported all the characters except, days to 50% flowering, number of primary branches per plant, number of seeds per pod and pod length for which non-significant differences were observed. However, on contrary to the present result, non-significant difference for plant height among 50 Ethiopian grasspea accessions was also reported by [16]. This difference may be due to differences in accessions and environmental conditions of the research sites used by the researchers.

### 3.2 Genotypic and Phenotypic Coefficient of Variation (GCV and PCV %)

Genotypic variation is the heritable portion of phenotypic or total variation. It gives the variation between genotypes. Environmental variation is the non-heritable portion of observable variation. Phenotypic variance refers to the total variation in a population. It is sum of genotypic and

environment variance. Genotypic and phenotypic coefficients of variation (GCV and PCV) were classified as low (< 10 per cent), moderate (10-20 per cent) and high (> 20 per cent) according to [18]. The estimation of genotypic and phenotypic coefficient of variation (GCV and PCV) for yield and yield attributing traits over different environments and pooled over environments were computed and results are presented in Table 2.

Result indicated that the value of phenotypic coefficient of variation were higher than the genotypic coefficient of variation [19] for all the characters in all six environments as well as pooled over environment.

#### 3.2.1 Environment-I

High genotypic and phenotypic coefficient of variation was observed for number of secondary branches/plant (47.08 and 47.78), Pod bearing length (44.74 and 46.84), number of primary branches/plant (38.06 and 39.31), number of pods/plants (35.31 and 35.52), number of seeds/plant (33.34 and 34.50), seed yield/plant (gm) (31.68 and 32.28), biological yield/plant (gm) (26.22 and 27.12), First flowering node (24.43 and 27.93) and harvest index (%) (24.43 and 27.93). However, moderate GVC and PCV were recorded for number of nodes/plant (19.96 and 21.21), number of seed/pods (19.94 and 24.34), pod length (cm) (15.49 and 15.68), hundred seed weight (gm) (14.80 and 14.89) and days to flower initiation (12.00 and 12.33); whereas, low GVC and PCV were recorded for day to maturity (8.54 and 8.94).

#### 3.2.2 Environment-II

High genotypic and phenotypic coefficient of variation was exhibited by seed yield/plant (gm) (50.34 and 50.54), number of primary branches/plant (38.72 and 39.68), biological yield/plant (gm) (37.74 and 37.97), number of pods/plants (32.1 and 35.61), number of nodes/plant (31.27 and 31.43), pod length (cm) (26.24 and 29.6), day to maturity (24.83 and 27.2), hundred seed weight (gm) (24.61 and 29.46), number of seeds/plant (22.8 and 23.39) and number of secondary branches/plant (20.22 and 21.1). However, harvest index (%) (19.82 and 20.12), number of seed/pods (15.79 and 15.88), first flowering node (15.62 and 15.79) and days to flower initiation (12.36 and 14.18) showed medium genotypic and phenotypic coefficient of variation. The low GCV and PCV % were observed for Pod bearing length (7.87 and 7.88).

**Table 1. Analysis of variances for yield and yield attributing traits of pea genotypes over environments**

Env.	Source of Variation	DF	Mean sums of square														
			DFI	FFN	DM	NPB	NSB	NNP	PBL	NPP	PL	NSPI	NSPII	HSW	BYP	HI	SYP
E1	Replication	1	0.58	0.01	7.98	0.02	0.02	1.86	66.06	8.89	0.01	0.28	6.45	0.01	0.14	0.87	0.09
	Genotypes	51	68.72	2.58	118.49	1.98	1.48	25.60	1227.06	73.44	1.33	1.98	876.72	12.72	116.55	368.48	33.75
	Error	51	1.87	0.09	5.43	0.06	0.02	1.57	56.20	0.45	0.02	0.39	29.78	0.08	1.94	49.10	0.64
E2	Replication	1	16.48	0.05	0.56	0.00	0.00	0.09	0.63	0.21	0.01	0.06	1.29	0.87	25.05	552.00	0.00
	Genotypes	51	66.39	1.04	87.82	1.75	0.31	20.35	1066.10	52.69	1.10	1.32	446.50	9.42	22.09	460.67	5.41
	Error	51	9.06	0.04	0.11	0.04	0.03	0.51	4.26	0.33	0.01	0.02	2.19	0.06	2.65	82.07	0.49
E3	Replication	1	2.11	0.00	1.00	0.17	0.00	0.35	17.04	0.14	0.08	0.08	20.70	1.25	1.80	13.80	0.76
	Genotypes	51	56.37	1.37	73.01	1.27	0.17	7.89	798.79	23.23	0.78	1.03	280.41	7.11	2.97	314.45	1.07
	Error	51	2.67	0.04	3.71	0.03	0.03	0.15	24.57	1.73	0.02	0.02	5.65	0.40	0.34	106.00	0.19
E4	Replication	1	2.16	0.42	4.08	1.58	0.08	2.65	171.11	6.50	0.19	0.01	9.60	0.06	2.91	58.43	0.43
	Genotypes	51	86.03	4.39	112.49	4.91	1.97	41.96	1303.68	57.29	1.70	1.26	1595.63	10.00	89.94	271.71	24.06
	Error	51	2.29	0.13	28.35	0.06	0.03	0.95	55.46	1.96	0.20	0.03	3.42	0.07	1.14	10.46	0.23
E5	Replication	1	0.15	0.20	1.75	2.71	0.06	18.79	181.53	0.26	0.05	0.00	3.19	0.38	0.21	19.84	0.15
	Genotypes	51	70.27	1.57	100.70	2.28	0.51	21.06	1081.39	39.10	1.68	1.08	748.44	12.76	24.70	496.26	2.91
	Error	51	0.47	0.03	0.96	0.11	0.06	1.81	38.55	0.52	0.12	0.02	6.34	0.11	0.61	17.92	0.07
E6	Replication	1	2.11	2.11	1.00	0.17	0.00	0.35	17.04	0.14	0.08	0.08	20.70	1.25	1.80	13.80	0.76
	Genotypes	51	56.37	56.37	73.01	1.27	0.17	7.89	798.79	23.23	0.78	1.03	280.41	7.11	2.97	314.45	1.07
	Error	51	2.67	2.67	3.71	0.03	0.03	0.15	24.57	1.73	0.02	0.02	5.65	0.40	0.34	106.00	0.19
POE	Replication	1	6.98	0.26	0.00	1.87	0.11	12.69	223.31	10.70	0.06	0.14	12.21	0.26	13.11	266.45	0.01
	Genotypes	51	358.83	9.63	514.55	11.30	3.06	72.97	5425.53	194.58	5.65	5.53	3026.36	44.33	116.62	1041.86	31.18
	Error	51	6.83	0.33	10.18	0.26	0.18	5.60	76.15	6.36	0.27	0.23	123.52	1.46	13.51	136.91	3.52

*DFI=Days to first flowering, FFN=First flowering node, DM=Days to maturity, NPB=Number of primary branches/plant, NSB=Number to secondary branches/ plant, NNP=Number of nodes/plants (main branch) PBL=Pod bearing length, NPP = Number of pods/plants, PL= Pod length cm, NSPI= Number of seeds/pod NSPII =Number of seeds/plants, HSW=Hundred seed weight (gm), BYP =Biological yield/plant (gm), HI= Harvest index (%), SYP= Seed/yard/plant (gm), POE=Pooled over environment*

**Table 2. GCV% and PCV% for yield and yield attributing traits of pea genotypes over environments**

Traits	GCV %							PCV %						
	E1	E2	E3	E4	E5	E6	POE	E1	E2	E3	E4	E5	E6	POE
DFI	12	12.36	12.88	13.38	13.48	13.97	12.24	12.33	14.18	13.51	13.74	13.57	14.24	13.6
SYP	31.68	50.34	49.11	43.87	47.17	45.62	44.75	32.28	50.54	50.65	45.78	48.89	46.03	48.42
NPB	38.06	38.72	40.98	56.09	49.56	38.5	42.06	39.31	39.68	42.02	56.76	52.08	47.9	47.72
NPP	35.31	32.1	33.79	53.6	45.67	45.85	39.2	35.52	35.61	39.98	54.42	51.41	50.66	51.62
NNP	19.96	31.27	30.61	45.69	41.11	36.36	31.71	21.21	31.43	31.24	45.79	41.46	36.72	38.97
BYP	29.88	37.74	29.94	33.94	34.44	25.89	29.85	30.38	37.97	32.26	35.13	34.9	26.93	35.38
NSB	47.08	20.22	24.35	34.4	25.79	30.39	24.04	47.78	21.1	25.03	35.45	26.28	31.24	28.76
PL	15.49	26.24	23.02	26.08	29.6	17.56	20.73	15.68	29.6	25.79	26.41	30.33	20.12	33.25
DM	8.54	24.83	24.9	26.39	18.11	22.53	20.41	8.94	27.2	29.86	26.65	18.53	23.35	32.45
NSPII	33.34	22.8	19.64	24.78	23.3	23.63	17.13	34.5	23.39	20.02	25.35	25.4	24.66	24.21
HI	24.43	19.82	18.39	18.45	18.59	17.3	16.44	27.93	20.12	18.71	18.89	18.97	17.78	20.21
HSW	14.8	24.61	18.66	21.76	25.87	21.11	15.57	14.89	29.46	26.5	22.61	26.82	22.72	26.13
FFN	26.22	15.62	14.38	16.92	18.44	19.51	13.99	27.12	15.79	14.82	19.05	19.87	20.12	17.76
NSPI	19.94	15.79	15.84	13.27	18.32	16.84	13.48	24.34	15.88	16.75	13.36	18.49	17.22	16
PBL	44.74	7.87	7.32	7.53	8.66	8.72	7.81	46.84	7.88	7.71	9.74	8.75	8.9	8.71

*DFI=Days to first flowering, FFM=First flowering node, DM=Days to maturity, NPB=Number of primary branches/plant, NSB=Number to secondary branches/ plant, NNP=Number of nodes/plants (main branch) PBL=Pod bearing length, NPP = Number of pods/plants, PL= Pod length cm, NSPI= Number of seeds/pod NSPII =Number of seeds/plants, HSW=Hundred seed weight (gm), BYP =Biological yield/plant (gm), HI= Harvest index (%), SYP= Seed/yard/plant (gm), POE=Pooled over environment*

### 3.2.3 Environment-III

High genotypic and phenotypic coefficient of variation was observed for seed yield/plant (gm) (49.11 and 50.65), number of primary branches/plant (40.98 and 42.02), number of pods/plants (33.79 and 39.98), number of nodes/plant (30.61 and 31.24), biological yield/plant (gm) (29.94 and 32.26), Day to maturity (24.9 and 29.86), number of secondary branches/plant (24.35 and 25.03) and pod length (cm) (23.02 and 25.79). However, moderate GVC and PCV were recorded for number of seeds/plant (19.64 and 20.02), hundred seed weight (gm) (18.66 and 26.5), harvest index (%) (18.39 and 18.71), number of seed/pods (15.84 and 16.75), first flowering node (14.38 and 14.82) and days to flower initiation (12.88 and 14.82); whereas, low GVC and PCV were recorded for pod bearing length (7.32 and 7.71).

### 3.2.4 Environment-IV

High genotypic and phenotypic coefficient of variation was exhibited by number of primary branches/plant (56.09 and 56.76), number of pods/plants (53.6 and 54.42), number of nodes/plant (45.69 and 45.79), seed yield/plant (gm) (43.87 and 45.78), number of secondary branches/plant (34.4 and 35.45), biological yield/plant (gm) (33.94 and 35.13), day to maturity (26.39 and 26.65), pod length (cm) (26.08 and 26.41), number of seeds/plant (24.78 and 25.35) and hundred seed weight (gm) (21.76 and 22.61). However, harvest index (%) (18.45 and 18.89), first flowering node (16.92 and 19.05), number of seed/pods (13.27 and 13.36), days to flower initiation (13.38 and 13.74) showed medium genotypic and phenotypic coefficient of variation. The low GCV and PCV % were observed for pod bearing length (7.53 and 7.94).

### 3.2.5 Environment-V

High genotypic and phenotypic coefficient of variation was observed for number of primary branches/plant (49.56 and 52.08), seed yield/plant (gm) (47.17 and 48.89), number of pods/plants (45.67 and 51.41), number of nodes/plant (41.11 and 41.46), biological yield/plant (gm) (34.44 and 34.9), pod length (cm) (29.6 and 30.33), hundred seed weight (gm) (25.87 and 26.82), number of secondary branches/plant (25.79 and 26.28), number of seeds/plant (23.3 and 25.4). However, moderate GVC and PCV were recorded for harvest index (%) (18.59 and 18.97), first flowering node (18.44 and 19.87), number of seed/pods (18.32 and

18.49), day to maturity (18.11 and 18.53), days to flower initiation (13.48 and 13.57); whereas, low GVC and PCV were recorded for pod bearing length (8.66 and 8.75).

### 3.2.6 Environment-VI

High genotypic and phenotypic coefficient of variation was exhibited by number of pods/plants (45.85 and 50.66), seed yield/plant (gm) (45.62 and 46.03), number of primary branches/plant (38.5 and 47.9), number of nodes/plant (36.36 and 36.72), number of secondary branches/plant (30.39 and 31.24), biological yield/plant (gm) (25.89 and 26.93), number of seeds/plant (23.63 and 24.66), day to maturity (22.53 and 23.35) and hundred seed weight (gm) (21.11 and 22.72). However, First flowering node (19.51 and 20.12), pod length (cm) (17.56 and 20.12), harvest index (%) (17.3 and 17.78), number of seed/pods (16.84 and 17.22) and days to flower initiation (13.97 and 14.24) showed medium genotypic and phenotypic coefficient of variation. The low GCV and PCV % were observed for Pod bearing length (8.72 and 8.9).

### 3.2.7 Pooled over environment

High genotypic and phenotypic coefficient of variation was observed for seed yield/plant (gm) (44.75 and 48.42), number of primary branches/plant (42.06 and 47.72), number of pods/plants (39.2 and 51.62), number of nodes/plant (31.71 and 38.97), biological yield/plant (gm) (29.85 and 35.38), number of secondary branches/plant (24.04 and 28.76), pod length (cm) (20.73 and 33.25), day to maturity (20.41 and 32.45). However, moderate GVC and PCV were recorded for number of seeds/plant (17.13 and 24.21), harvest index (%) (16.44 and 20.21), hundred seed weight (gm) (15.57 and 26.13), first flowering node (13.99 and 17.76), number of seed/pods (13.48 and 16.0), days to flower initiation (12.24 and 13.6); whereas, low GVC and PCV were recorded for pod bearing length (7.81 and 8.71).

The above finding for high GCV and PCV revealed the presence of substantial amount of genetic variability for the traits, which exhibited high magnitudes as well as less influence of environment on the expression of concerned traits. Similar results for different characters have also been reported by Saxena et al. [20]; Katiyar et al. [21]; Ahmad et al. [22]; Kosev [23]; Patel [17] and Sahoo [5]. Day to first flowering node, number of seed/pods, hundred seed weight

(gm), harvest index and days to flower initiation exhibited moderate genotypic and phenotypic coefficient variation in all of the environments except. Mishra [24], Jeberson et al. [25] and Sahoo [5] also reported similar result. Low genotypic and phenotypic coefficient of variation was observed for pod bearing length in all of the environments (Table 2). Yadav [26], Saxena et al. [20] and Sahoo [5] supported similar result for these traits. In last it were revealed in this study that the presence of substantial amount of genetic variability like, high variability, GCV and PCV for various traits, which exhibited high magnitudes as well as less influence of environment on the expression of concerned traits. So selection of such traits for heterotic group development will be useful.

#### 4. CONCLUSION

High genotypic and phenotypic coefficient of variations were exhibited for number of secondary branches/plant, Pod bearing length, number of primary branches/plant, number of pods/plants, number of seeds/plant, seed yield/plant (gm), biological yield/plant (gm), First flowering node and harvest index (%) in all six and pooled over environments. The above finding revealed the presence of substantial amount of genetic variability for the traits, which exhibited high magnitudes as well as less influence of environment on the expression of concerned traits.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

#### REFERENCES

- Majid A, Dar SA, Wani SH, Bhat MA, Ambardar VK and Lone AA. Genotype x environment interaction for seed yield and protein content in fieldpea genotypes under Kashmir conditions. *International Journal of Current Microbiology and Applied Sciences*. 2017;(6)7: 3880-3884.
- FAO. *FAO Statistical division*; 2011. Available:<http://www.faostat.fao.org>
- Datta SK, Singh BB. *Production and productivity of pulses: Indian perspectives. Pulses handbook*. 2015;34.
- AICRP MULLaRP- Available:<http://www.aicrpmullarp.res.in>.
- Sahoo. Genetic analysis for yield, yield components and quality traits in Pea. M.Sc. thesis, JNKVV, Jabalpur; 2018
- Toews R and Wang N. Physicochemical and functional properties of protein concentrates. *Food Research International*. 2013;52:445-451.
- Singh BD. *Plant Breeding: Principles and Methods*. Kalyani Publishers, New Delhi-Ludhiana, India;2002.
- Acikgoz E, Sincik M, Karasu A, Tongel O, Wietgreffe G, Bilgili U, Albayrak S, Turan ZM, Goksoy AT. Forage soybean production for seed in Mediterranean environments. *Field Crop. Res.*, 2009;110:213-218.
- Patel. Genetic Analysis of F1 Crosses of bread wheat raised under different environments. Ph.D. thesis, JNKVV, Jabalpur; 2016.
- Wuletaw T and Endashaw B. Variation and association of morphological and biochemical characters in grass pea (*Lathyrus sativus* L.). *Euphytica*. 2003; 130:315-324.
- Panse VG. Shukhatme PV. *Statistical methods for agriculture workers* (2nd eds.). Indian Council of Agriculture Research, New Delhi; 1967.
- Burton GW. Quantitative inheritance in grasses *Proceedings 6th International, grassland congress*. 1952;1:227-283.
- Jaiswal NK, Gupta AK, Dewangan H, Lavanya GR. Genetic variability analysis in field pea (*Pisum sativum* L.). *Int. J. Sci. Res*. 2015;4(1).
- Katoch V, Singh P, Mayanglambam BD, Sharma A, Sharma GD, Sharma JK. Study of genetic variability, character association, path analysis and selection parameters for heterotic recombinant inbred lines of garden peas (*Pisum sativum* var. *Hortense* L.) under mid- hill conditions of Himachal Pradesh, India. *Legume Research*. 2016;39(2):163-169.
- Kumar M, Jeberson MS, Singh NB, Sharma R. Genetic analysis of seed yield and its contributing traits and pattern their inheritance in field pea (*Pisum sativum* L.). *International Journal of Current Microbiology and Applied Sciences*. 2017;6 (6):172-181.
- Toppo. Genetic variability and character association analysis for seed quality and yield traits in field pea (*Pisum sativum* L.). M.Sc. (Ag.) Thesis. IGKVV, (Chhattisgarh); 2015.
- Patel. Combining ability and heterosis studies for yield and its components in field

- pea (*Pisum sativum* L.). M.Sc. (Ag.) Thesis Indira Gandhi Krishi Vishwavidyalaya, Raipur (Chhattisgarh); 2017.
18. Sivasubramanian J and Madhavamenon P. Genotypic and phenotypic variability in rice. Madras Agricultural Journal. 1973; 12:15-16.
  19. Kumar Vinod and Bisen Rajani. Genetic study for yield and yield attributing traits in Niger Germplasm. International Journal of Agriculture Sciences. 2016;8(56):3044-3046.
  20. Saxena RR, Vidyakar V, Vishwakarma MK, Yadav PS, Meena ML and Lal GM. Genetic variability and heritability analysis for some quantitative traits in field pea (*Pisum sativum* L.). The Bioscan. 2014;9(2): 895-898.
  21. Katiyar S, Singh HC, Verma MC, Katiyar M and Singh RK. Genetic analysis for of heterotic crosses in table pea (*Pisum sativum* L.). Trends in Biosciences. 2014;7(9):733-735.
  22. Ahmad HB, Rauf Rafiq MS, Mohsin AU and Iqbal A. Estimation of Genetic Variability In pea (*Pisum sativum* L.). Journal of global innovation in agricultural and social sciences. 2014;2(2): 62-64.
  23. Kosev VI. Multivariate analysis of spring field pea genotypes. Banats Journal of Biotechnology. 2015;6(11):23-29.
  24. Mishra R. Genetic variability and diversity analysis for improvement of yield and its related characters in field pea (*Pisum sativum* L.). Journal of Food Legumes. 2014;27(3):255-257.
  25. Jeberson MS, Shashidhar KS and Iyanar K. Estimation of genetic variability, expected genetic advance, correlation and path analysis in field pea (*Pisum sativum* L.). Electronic Journal of Plant Breeding. 2016;7(4):1074-1078.
  26. Yadav SK. Diallel cross analysis for yield and quality attributes in field pea (*Pisum sativum* L.). M. Sc. Thesis, IGKV, Raipur. 2013;88-90.

© 2021 Jaiswal et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

*Peer-review history:*

The peer review history for this paper can be accessed here:  
<https://www.sdiarticle5.com/review-history/80388>