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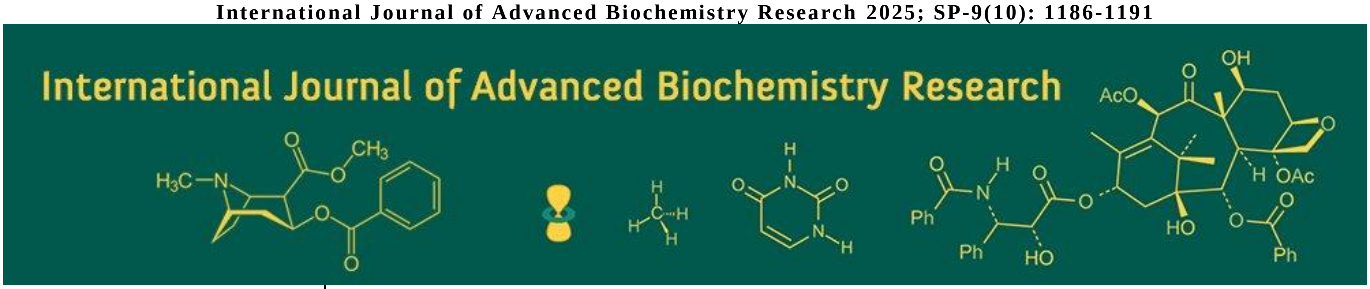

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Studies on Genetic Variability, Heritability for Yield and its Attribute in Pea (*Pisum sativum* L.)

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Abstract

The present investigation entitled "Variability studies in pea (*Pisum sativum* L.)" was carried out during *Rabi* season of 2024-25 at Instructional Cum-Research Farm, Department of Horticulture, College of Agriculture, Latur. The statistical design adapted was Randomized Block Design (RBD) with twenty two treatments replicated twice. Pea sowing was done on 25th November 2024 at the spacing of 30 cm x 15 cm. In each treatment there were 111 plants of each genotype in a replication. Five plants were randomly selected from each treatment to record observations on twenty two characters. A wide range of variation observed among the genotypes for all the characters. The high genotypic coefficient of variation as well as phenotypic coefficient of variation were observed for number of primary branches per plant, number of tendril per plant, green pod yield per plot, green pod yield per hectare, green pod yield per plant, pod width, pod length, number of seed per pod, number of pod per cluster.The high heritability were found for protein content, number of primary branches per plant, total soluble solid, pod width, shelling percentage, pod length, number of seed per pod, number of cluster per plant, crop duration, number of picking, number of tendril per plant, plant height, number of pod in cluster, number of picking, green pod yield per plot, green pod yield per hectare, green pod yield per plant, days to 1st picking and days to 50% flowering. Highest value of genetic advance were recorded for number of primary branches per plant, number of tendril per plant, pod width, green pod yield per plot, pod length, green pod yield per hectare, green pod yield per plant, number of seed per pod, protein content, number of pod per cluster, plant height, number of picking, number of cluster per plant, shelling percentage and days to 1st picking. There was wide range of variation in pea genotypes for all the character, from the present investigation, it can be concluded that genotype Arka Uttam, Green Arrow and Arka Priya was found superior performance than rest of genotype. The genotype Arka Priya was found early observed for character days to initiation of first flowering, days to 50% flowering, days to first picking and highest number of primary branches per plant was found in Kashi Uday. Therefore, based on the current investigation, it can be said that the genotypes Arka Uttam, Green Arrow and Arka Priya were superior for yield and yield contributing characters. The genotypes Arka Uttam, Green Arrow and Arka Priya were found to be superior for yield and quality contributing characters in the Marathwada region for commercial cultivation and to further enhance pea through breeding programs.

Keywords: Pea, variability, heritability, genetic advance

1. Introduction

One of India's most significant annual herbaceous legume crops, peas (*Pisum sativum* L.) have chromosomal number 2n=14. They are also a popular and significant winter vegetable crop from an economic standpoint. It most likely originated in south-western Asia, most likely in Pakistan, Northwestern India, or the neighboring regions of Afghanistan and the former Soviet Union. The pea is a member of the Leguminosae family's genus Pisum. *Pisum abyssinicum, pisum sativum spp. arvense* (Field pea), *pisum sativum spp. hortense* (Garden pea), *Pisum aucheri, Pisum elatius* (Ancestor of pea), *pisum formosum, Pisum fulvum,* and *pisum syriacum* are among the eight species that make up the genus Pisum (Choudhary *et al.* 2010) [5]. After the common bean (*Phaseolus vulgaris* L.), peas are the second-highest-yielding legume in the world and one of the six main pulse crops grown worldwide (FAO, 2010). Peas have been there in the Near East and Central Asia since 10,000 B.C., according to archeological data (Zohary and Hopf, 1973) [26]. An essential vegetable crop, peas are often eaten fresh and juicy, canned, frozen, dehydrated, or infrequently as a dry pulse.

Vegetarians consider peas, which are high in vitamins and minerals, to be a useful part of their diet. Bose *et al.* (1993) [3] state that the nutritional value of one hundred grams of edible peas is as follows: 72% moisture content, 15.8% carbohydrates,7.2 grams of protein, 0.1 grams of fat, 139 I. U. of vitamin A, 0.25 mg of thiamine, 0.01 mg of riboflavin, 9 mg of vitamin C, 20 mg of calcium, and 1.5 mg of iron. In addition to having a wealth of health-promoting compounds, peas are a significant source of lysine, which is the limiting amino acid in cereals and enhances soil fertility due to their symbiotic relationship with the nitrogen-fixing bacterium *Rhizobium leguminosarium*. Additionally, it works well with cover crops and green manuring, which reduce soil erosion.

2. Materials and Methods

2.1 Experimental site and layout of experiment

The current study, "Variability studies in pea (*Pisum sativum* L.)," was conducted during the *Rabi* season of 2024-2025 at the Instructional-Cum-Research Farm, Department of Horticulture, College of Agriculture Latur, Vasantrao Naik Marathwada Krishi Vidyapeeth. Parbhani. The statistical design adapted was Randomized Block Design (RBD) with twenty two treatments replicated twice. Pea sowing was done on 25th November 2024 at the spacing of 30 cm x 15 cm.

2.2 Character studied

The observation were recorded on plant height (cm), number of primary branches per plant, number of tendril per plant, Days to Initiation of First Flowering, Days to 50 Per Cent Flowering, Crop Duration (Days), Colour of Flower, Days to First Picking, No. of Pickings, Number of Cluster Per Plant, No of Pod in clusters, Pod Length (cm), Pod Width (cm), No. of Seed Per Green Pod, Green pod yield per plant (g), Green pod yield per plot (kg), Green pod yield per hectare (q), Shelling Percentage, Total Soluble Solid (%), Pod Stringiness, Protein Content (%).

2.3 Experimental material

The material under study was constituted of 22 genotypes of pea (*Pisum sativum* L.) which were collected from various places. The details are given in Table 1.

Table 1: Name of the genotype and their Sources

Sr. No	Treatments	Name of genotype	Source of Seed
1	T_1	GS-10	Shastri Nagar, Meerut
2	T_2	Arka Priya	IIHR, Banglore
3	T_3	Arka Ajit	IIHR, Banglore
4	T_4	AP_3	Mahabeej
5	T_5	AP_1	Safal Seed, Jalna
6	T_6	Arka Chaitra	IIHR, Banglore
7	T_7	Pusa Pragati	Dayal bagh, Ambala
8	T_8	Kashi Nandini	IIVR, Varanasi
9	T_9	Green Arrow	Shastri Nagar, Meerut
10	T_{10}	Little Marvel	Shastri Nagar, Meerut
11	T_{11}	Sonali-10	Rajgurunagar
12	T_{12}	Green -10	Mahabeej Bhavan,Akola
13	T_{13}	Lincoln	Krishidhan Seed Limited
14	T_{14}	Harbhajan	Safal Seed, Jalna
15	T_{15}	Wonder- 10	Ajinkya Seed, Pune
16	T_{16}	Rachana	Ajinkya Seed, Pune
17	T_{17}	Kanchan-33	Dayal bagh, Ambala
18	T_{18}	VLR- 498	Shastri Nagar, Meerut
19	T_{19}	KSP-110	Nanded district
20	T_{20}	Kashi Uday	IIVR, Varanasi
21	T_{21}	Arka Uttam	Arka uttam
22	T_{22}	Alaska	Shastri Nagar, Meerut

2.4 Statistical Analysis

The overall mean values of different characters were subjected to statistical analysis. Analysis of variance was done by subjecting the data to the statistical method on randomized block design (RBD) as described by Panse and Sukhatme (1985) [18]. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was computed according to the method suggested by Burton and de Vane. The expected genetic advance (GA) expressed in percentage of mean were calculated by using the method suggested by Johnson *et.al.* (1955) [9].

3. Results and Discussion

3.1 Analysis of variance

An analysis of variance for twenty two characterstics was conducted, and the sum of squares are summarized in (Table In this study significant genotypic differences were identified for all nineteen trait. The presence of variability suggest that there is considerable apportunity to select superior genotype that can either be used directly as new variety or as parent sources in upcoming breeding programme. This study indicated that the variability observed in these twenty two genotype is due to the presence of diverse genotype with different genetic backgrounds as well as environmental influences. Similar finding reported by Kaur *et al.*, (2007) [10], Nawab *et al.*, (2008) [16], Pal and Singh (2013) [17], Selvi *et al.*, (2014) [20], Tambolkar *et al.*, (2016) [24], Gudadinni *et al.*, (2017) [7], Sharma *et al.*, (2017) [21], Srinivas *et al.*, (2017) [23] and Thouseem *et al.*, (2018) [25].

Table 2: Analysis of variance for different characters studied in the genotypes of pea

Sr. No.	Character	Mean Sum of square		
		Treatment	Replication	Error
1.	Plant height(cm)	291.9**	0.004	0.786
2.	No.of Primary Branches per plant	10.004**	0.001	0.003
3.	No. of Tendril per plant	957.73**	0.018	0.166
4.	Days to initiation of 1st flowering	56.67**	93.178	15.53
5.	Days to 50% flowering	65.435**	0.552	1.222
6.	Days to 1st Picking	205.71**	0.002	1.506
7.	No of picking	2.006**	0.014	0.003
8.	No of cluster per plant	1.969**	0.001	0.009
9.	No.of Pod in cluster	0.369**	0.001	0.001
10.	Pod Length	8.117**	0.003	0.013
11.	Pod Width	0.185**	0.075	0.003
12.	No. of Seed per Pod	4.433**	0.027	0.005
13.	Crop duration	224.6**	0.423	2.463
14.	Shelling percentage	97.454**	3.386	1.721
15.	Total Soluble Solid(TSS)	3.68**	0.26	0.05
16.	Protein content	37.96**	0.13	0.12
17.	Pod Yield Per Plant	136.76**	0.001	0.16
18.	Pod Yield per plot	0.495**	0.001	0.001
19.	Pod Yield per hectare	0.466**	0.003	0.004

3.2 Mean performance

The average performance of 22 genotypes along with mean, CV (%) and CD (5%) are presented in (Table 3). Based on mean performance, genotype Arka Uttam followed by Green Arrow, Arka Priya, Alaska and GS-10 exhibited higher green pod yield per hectare. While minimum green pod yield per hectare was noticed in genotype Harbhajan followed by Kashi Nandini and Kashi Uday Therefore, high variability for twenty one traits of twenty two pea genotypes indicated that there was reasonably sufficient variability to allow plant breeders to pick superior and desired genotypes for further improvement. In general, all of the traits studied had a wide range of variation.

3.3 Genotypic and Phenotypic coefficient of Variation

The estimates of mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for nineteen characters studied are presented in (Table 4). The PCV values were higher than GCV values for all the characters. However, differences among them were small indicating that the influence of environment on the expression of traits was low. The genotypic coefficient of variation varied from 8.01% for days to 50% flowering to 78.76% for number of primary branches per plant. The genotypic coefficient of variations was highest for characters viz. number of primary branches per plant (78.76%), number of tendril per plant (47.72%), green pod yield per plot (29.11%), green pod yield per hectare (28.24%), pod width (27.57%), pod length (26.56%), green pod yield per plant (25.05%) and number of seed per pod (20.86%). similar result were reported by Basaiwala *et al.* (2013) [2], Ahmad *et al.* (2014) [1], Choudhary *et al.* (2010) [5].

The rest of the characters such as number of pod per cluster (19.89%), protein content (19.11%), plant height (16.64%), number of picking (16.54%), number of cluster per plant (15.38%), shelling percentage (12.88%), and days to 1st picking (12.01%) exhibited moderate genotypic coefficient of variation. Similar results were reported by Singh and Singh (2006) [22], Singh and Lavanya (2014) [14].

The low variability noted in days to initiation of 1st flowering (9.66%), crop duration (9.3%), total soluble solid (8.76%) and days to 50% flowering which indicated the major influence of environment. Similar results were reported by Tambolkar *et al.*, (2016) [24], Meena *et al.* (2006) [15], Kumar *et al.* (2010) [13], Korla and Singh (1988) [12].

Table 3: Mean performance of twenty two genotype

Sr. No	Character	Plant Height (cm)	No. of primary branches / plant	No. of tendril per plant	Days to initiation of 1st flowering	Days to 50% flowering	Days to 1st picking	No. of Picking	No. of cluster/ plant	No. of pod in cluster	Crop duration
1	GS-10	53.35	0.9	14.3	51.04	56.23	75.45	6.43	6.33	1.99	120.86
2	Arka Priya	47.20	0.9	10.7	38.08	53.68	48.03	7.08	6.92	1.48	103.55
3	Arka Ajit	53.09	1.0	12.6	41.43	54.32	59.40	6.90	7.11	1.70	98.81
4	Azad-P_3	55.37	0.9	11.4	40.16	53.86	62.69	6.48	6.53	1.82	106.82
5	Azad-P_1	53.50	0.9	9.8	46.51	59.20	64.27	5.59	5.63	1.69	107.37
6	Arka Chaitra	72.49	2.3	22.10	50.93	59.27	77.8	6.14	6.01	2.22	121.04
7	Pusa Pragati	65.86	2.8	32.85	51.30	59.51	85.42	5.94	5.96	2.19	120.12
8	Kashi Nandini	70.01	2.3	37.30	56.21	52.82	83.35	4.99	5.04	1.90	118.3
9	Green Arrow	58.94	1.9	22.13	47.88	58.47	56.96	6.93	6.98	1.76	98.27
10	Little	75.27	2.7	50.39	46.53	55.70	75.54	4.86	4.99	1.80	89.71

	Marvel										
11	Sonali-10	66.91	4.0	63.02	49.75	51.96	71.54	3.93	4.03	2.38	96.45
12	Green -10	51.46	3.2	30.59	44.01	57.26	62.30	6.50	6.37	1.68	95.27
13	Lincoln	71.02	4.8	74.07	56.79	52.54	83.33	6.46	6.67	2.29	90.43
14	Harbhajan	94.70	2.3	93.23	46.20	54.58	68.70	7.90	7.80	1.21	98.49
15	Wonder 10	75.75	3.7	41.95	54.51	54.38	82.58	5.88	6.01	2.70	117.11
16	Rachana	77.45	3.0	46.08	53.55	52.21	79.43	5.99	5.98	2.41	123.34
17	Kanchan -33	83.53	1.7	33.20	47.18	52.66	75.72	3.92	3.93	2.32	117.84
18	VLR- 498	73.62	3.2	43.91	52.03	48.17	74.07	6.0	6.09	1.85	111.57
19	KSP-110	63.77	0.9	15.57	40.86	50.37	60.65	6.45	6.52	2.04	100.46
20	Kashi Uday	76.45	4.0	35.24	46.18	47.38	80.07	7.48	7.63	1.07	98.84
21	Arka Uttam	75.21	2.1	19.22	46.11	48.60	66.80	6.5	6.49	2.44	108.21
22	Alaska	66.87	2.0	20.08	54.77	45.89	63.06	6.62	6.79	2.63	107.59
	Mean	66.95	2.80	33.64	48.27	53.32	70.78	6.14	6.17	1.98	106.84
	S.E ±	0.62	0.04	0.28	2.7	0.78	0.86	0.04	0.06	0.02	1.11
C.D.5%	1.84	0.12	0.84	8.20	2.29	2.55	0.11	0.19	0.06	3.26	C.D.5%

Sr. No	Character	Pod Length	Pod width	No. of seed/ green Pod	Shelling percentage	TSS (%)	Protein content	Green pod yield/plant (g)	Green Pod Yield/plot (q)	Green pod Yield / ha(g)
1	GS-10	8.78	1.02	6.54	69.62	17.12	20.50	37.38	2.05	75.99
2	Arka Priya	8.74	1.55	9.54	66.86	16.47	23.50	41.13	2.4	91.04
3	Arka Ajit	9.98	1.5	7.20	60.72	17.70	21.00	31.08	1.7	65.18
4	Azad-P_3	10.03	1.4	7.56	59.99	15.09	20.00	33.54	1.8	69.41
5	Azad-P_1	10.20	1.4	7.86	58.26	15.30	23.50	29.25	1.5	58.00
6	Arka Chaitra	4.97	1.3	7.75	56.37	16.82	18.50	21.32	1.1	41.87
7	Pusa Pragati	5.88	1.2	6.86	54.41	14.05	27.00	22.03	1.1	43.35
8	Kashi Nandini	5.75	1.3	9.65	54.24	15.19	14.50	21.02	0.9	35.42
9	Green Arrow	8.77	1.4	8.46	52.71	12.35	19.50	45.26	2.5	91.39
10	Little Marvel	6.23	1.22	8.50	52.03	15.61	14.00	21.76	1.1	43.84
11	Sonali-10	5.49	1.55	7.70	51.62	13.24	19.50	23.44	1.2	48.32
12	Green -10	9.64	1.00	7.42	50.84	15.31	24.50	30.93	1.7	63.68
13	Lincoln	5.62	1.25	9.6	50.59	13.98	23.50	28.69	1.5	55.97
14	Harbhajan	4.13	0.93	6.5	49.58	16.06	24.50	17.35	0.8	32.00
15	Wonder 10	5.63	0.9	7.63	49.39	15.21	29.00	29.33	1.5	59.37
16	Rachana	6.61	0.87	7.82	48.79	16.98	27.00	23.10	1.1	43.87
17	Kanchan -33	6.71	1.09	7.96	48.45	15.22	29.00	25.91	1.1	41.29
18	VLR- 498	6.75	1.03	6.72	47.01	15.61	25.00	22.63	1.0	40.74
19	KSP-110	9.77	1.0	7.25	46.83	14.50	28.50	28.22	1.5	57.40
20	Kashi Uday	3.74	1.00	8.48	45.41	16.12	26.50	18.41	1.0	40.23
21	Arka Uttam	8.05	1.54	5.87	44.90	13.59	19.00	47.48	2.4	94.69
22	Alaska	7.20	1.03	6.81	41.53	15.91	21.00	28.39	1.5	80.63
	Mean	7.21	1.10	6.78	52.73	15.33	22.68	28.53	1.5	57.89
	S.E ±	0.08	0.03	0.05	0.92	0.50	1.05	0.28	0.01	0.01
	C.D.5%	0.24	0.11	0.15	2.72	1.47	3.10	0.83	0.04	0.04

Table 4: Mean, range and different genetic parameters in pea

Sr. No	Genetic Parameters	Mean	Range	GV	PV	GCV	PCV	Heritability (h^2) %	GA% as Mean
1.	Plant Height(cm)	66.95	47.20 - 94.70	124.01	146.58	16.64	18.09	84.6	31.53
2.	No.of Primary branches per plant	2.80	0.98 - 4.85	4.88	5.00	78.76	79.66	97.8	160.42
3.	No. of tendril per plant	33.64	9.89 - 93.23	222.22	251.87	47.72	50.80	88.2	92.33
4.	Days to initiation of 1st flowering	48.27	38.08 - 56.79	21.75	36.54	9.66	12.52	59.5	15.35
5.	Days to 50% flowering	53.32	45.89 - 59.20	20.10	33.32	8.01	10.31	60.3	12.81
6.	Days to 1st picking	70.78	48.03 - 85.42	70.95	96.48	12.01	14.00	73.5	21.22
7.	No of picking	6.14	3.92 - 7.90	1.05	1.26	16.54	18.11	83.4	31.13
8.	No of cluster per plant	6.17	3.93 - 7.80	0.91	1.02	15.38	16.27	89.4	29.95
9.	No.of Pod per cluster	1.98	1.07 - 2.70	0.15	0.18	19.89	21.66	84.3	37.63
10.	Pod Length	7.21	3.74 - 10.20	3.67	4.06	26.56	27.93	90.4	52.03
11.	Pod Width	1.10	0.87 - 1.55	0.09	0.09	27.57	28.02	96.8	55.88
12.	No. of Seed per Pod	6.78	4.47 - 9.49	2.00	2.21	20.86	21.96	90.3	40.83
13.	Crop duration	106.84	89.71 - 123.3	100.52	113.09	9.384	9.95	88.9	18.22
14.	Shelling percentage	52.73	41.53 - 69.62	46.15	49.58	12.88	13.35	93.1	25.60
15.	Total Soluble Solid(TSS)	15.33	12.35 - 17.70	1.81	1.86	8.76	8.88	97.3	17.80
16.	Protein Content	22.68	14 - 29	18.92	19.04	19.11	19.17	99.3	39.24
17.	Green Pod Yield per plant	28.53	17.35 - 47.48	51.10	68.25	25.05	28.95	74.9	44.65
18.	Green Pod Yield per plot	1.52	0.85 - 2.57	0.19	0.24	29.11	32.51	80.2	53.69
19.	GreenPod Yield per hectare	57.89	32 - 94.6	0.18	0.23	28.24	31.87	78.5	51.56

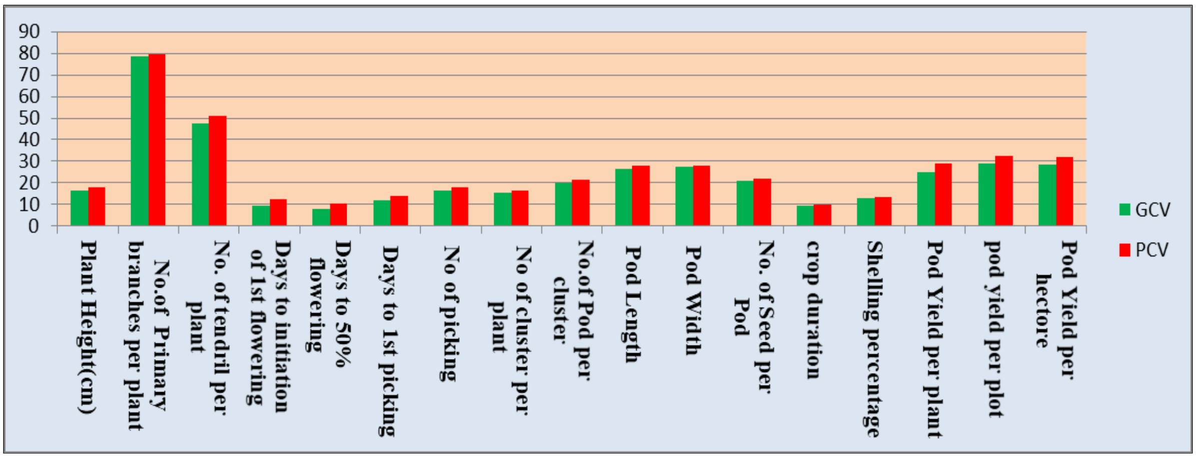

Fig 1: Genotypic and Phenotypic Coefficient of Variation for 17 Characters in Pea

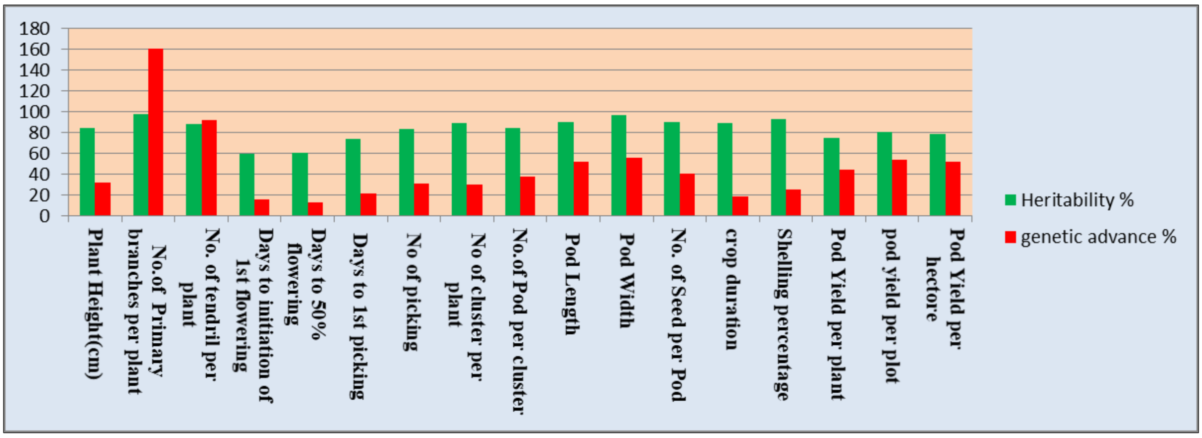

Fig 2: Heritability and Genetic Advance as per cent of Mean for 17 Characters in Pea

3.4 Heritability and Genetic Advance as percent of mean

Heritability in broad sense estimates were highest for protein content (99.3 %), number of primary branches per plant (97.8%), total soluble solid (97.3%), pod width (96.8%), shelling percentage (93.1 %), pod length (90.4%), number of seed per pod (90.3%), number of cluster per plant (89.4%) crop duration (88.9%), number of picking (89.9 %), number of tendril per plant (88.2%), plant height (84.6%), number of pod in cluster (84.3%), number of picking (83.4 %), green pod yield per plot (80.2%), green pod yield per hectare (78.5%), green pod yield per plant (74.9%), days to 1st picking (73.5%) and days to 50% flowering (60.3%). Similar finding was reported by Gupta *et al.* (2018) [8], Kaur *et al.* (2018) [11], Thouseem *et al.*, (2018) [25], Gudadinni *et al.*, (2017) [7], Santosha *et al.*, (2017) [19], Sharma *et al.*, (2017) [21], Srinivas *et al.*, (2017) [23], Tambolkar *et al.*, (2016) [24], Ahmad *et al.*, (2014) [1], Selvi *et al.*, (2014) [20] and Pal and Singh (2013) [17].

Heritability estimate were moderate for days to initiation of 1st flowering (59.5%).

The range of genetic advancement as a percentage of mean was 12.81 % for days to 50% flowering and (160.42%) for the number of primary branches per plant. The highest estimate of genetic advance as percent of mean was recorded for number of primary branches per plant (160.42%), number of tendril per plant (92.33%), pod width (55.88%), green pod yield per plot (53.69%), pod length (52.03%), green pod yield per hectare (51.56%), green pod yield per plant (44.65%), number of seed per pod (40.83%), protein content (39.24%), number of pod per cluster (37.63%), plant height (31.53%), number of picking (31.13%), number of cluster per plant (29.95%), shelling percentage (25.60%) and days to 1st picking (21.22%). Similar finding reported by Gupta *et al.* (2018) [8], Kaur *et al.*, (2018) [11], Thouseem *et al.*, (2018) [25], Gudadinni *et al.*, (2017) [7], Santosha *et al.*, (2017) [19], Sharma *et al.*, (2017) [21], Srinivas *et al.*, (2017) [23], Tambolkar *et al.*, (2016) [24], Ahmad *et al.* (2014) [1], Selvi *et al.*, (2014) [20] and Pal and Singh (2013) [17].

Whereas, moderate genetic advance estimates was observed for crop duration (18.22%), total soluble solid (17.80%), days to initiation of 1st flowering (15.35%), days to 50% flowering (12.81%). Similar finding was reported by Thouseem *et al.*, (2018) [25] and Tambolkar *et al.*, (2016) [24].

4. Conclusion

The analysis of variance indicated highly significant differences among the genotypes for all nineteen trait. It states that all genotypes under investigation were genetically differed. On the basis of mean performances, the genotypes Arka Uttam, Green Arrow, Arka Priya, Alaska and GS-10 can be exploited for developing as high yielding genotypes. Genetic variability study demonstrated that the material used in the current research had significant variability which provided a suitable basis for selection. Higher values of phenotypic coefficient of variation than genotypic coefficient of variation for a trait indicate that the traits are influenced by their environment. While there was a close correspondence between GCV and PCV for the majority of the characters, environmental factors had less influence on the appearance of these characters. Selection is expected to be more successful when traits exhibit moderate to high heritability combined with moderate to high genetic advance. Also, the phenotypic coefficient of variation (PCV) exceeded the genotypic coefficient of variation (GCV) for all traits indicates that influence of environmental factors on expression of traits. The small difference between PCV and GCV for certain traits further suggests strong genetic control, enhancing the potential for effective selection.

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