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Estimation of genetic variability, heritability and genetic advance for yield and its component traits of garden pea (*Pisum sativum* L.) in North East India

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Abstract

30 genotypes of garden pea were evaluated at Vegetable Research Farm, CHF, CAU, Pasighat, East Siang, Arunachal Pradesh, for twenty two parameters through genetic variability, heritability and genetic advance for yield and yield attributing. Results revealed that, heritability exerts at high degree for all the plant characters studied viz. plant height, days to first flowering, days to first pod harvesting, ascorbic acid, protein content, pod weight, shelling percentage, internodal length, number of primary branches per plant, pod yield per plant, pod yield per hectare as well for other yield attributing characters. Plant height, internodal length and number of primary branches per plant showed highest genetic advance and lowest for days to first pod harvest. High heritability coupled with high genetic advance was observed for plant height, internodal length and number of primary branches per plant. Therefore, from the above obtained results it can be concluded that the characters studied are governed by additive gene effect. Hence, adoption for selection of elite genotype on the basis of these characters will result in effective crop improvement for higher yield and yield attributing characters.

Keywords: Genetic variability, heritability, genetic advance, gene effects and pod yield

Introduction

Legumes are important crops worldwide and they have major contribution on agriculture, environment, animal and human nutrition (Graham and Vance, 2003) [10]. Legumes can interact symbiotically with specific soil-borne bacteria called Rhizobia, allowing them to fix atmospheric nitrogen thereby improve the physical condition of the soil and possibly protect them against certain fungal pathogens (Chakraborty *et al.*, 2003) [4]. Among legumes, pea (*Pisum sativum* L.) belonging to family Leguminosae (Fabaceae), is an important crop with a rich history in genetic research dating back to the classical work by the father of genetics Gregor J. Mendel.

Pea is one of the six major pulse crops cultivated globally and it is the second highest yielding legume in the world after common bean (*Phaseolus vulgaris* L.) (FAO, 2010). Pea (*Pisum sativum* L.) is one of the world's oldest domesticated crops. Archaeological evidence dates the existence of pea back to 10,000 B.C. in Near East and Central Asia (Zohary and Hopf, 1973) [35].

Large proportion of peas are processed (canned, frozen or dehydrated) for consumption in off season. The crop is grown for its green pods and dried seeds and is known for its superior quality protein like lysine content, the limiting amino acid in cereals. Pea has great nutrient value and contains vitamin A, B and C, along with minerals, dietary fiber and antioxidant compounds (Urbano *et al.*, 2003) [34]. In addition, it is also important vegetable crop due to its high nutritive value, particularly proteins 7.2g/100g (Singh *et al.*, 2007) [30]. In major part of the world and also consumed as green vegetables (whole pods or immature Seed) in Asian countries as well as dry seed in Europe, Australia, America and Mediterranean regions (Ghafoor *et al.*, 2008) [9].

Estimating the parameters of variability, especially heritability and genetic gain are important indicators for improvement of characters through selection whereas the selection for highly heritable characters is more effective. Therefore, heritability along with other parameters of variability can be used in predicting the gain for a given selection intensity and expected genetic gain further gives the idea of the extent of improvement in a character through simple selection. However, selection for yield and quality traits can be better achieved if the information with respect to correlation between such traits is also available followed by a better understanding of the association between the relevant characters provided through path coefficient analysis. Similarly, for improvement of those characters which didn't respond to

selection, there is a need for partitioning of non additive component of genetic variance further by hybridization which is achieved through genetic divergence studies.

Materials and Methods

This experiment was conducted at Vegetable Research Farm, College of Horticulture and Forestry, Central Agricultural University, Pasighat, East Siang, Arunachal Pradesh, India during 2017-2018. The research farm is situated in the foot hills of Eastern Himalayan Range at an altitude of 153 m above mean sea level, 28°04'N latitude and 95°22'E longitude. The climate of this area is humid, sub-tropical and maximum rainfall occurs between April-September. The experimental material for the present study consisted of 30 diverse genotypes of pea (Table 1). The experiment was laid out in Randomized complete block design (RCBD) with three replications. The standard cultural practices as mentioned in Package of Practices for Vegetable Crops (Rana, 2014). The seeds were sown in beds of 2.5 m length and 2.5 m width were prepared. Seeds were sowed at a spacing of 30 cm between the lines and 10 cm within the lines. After sowing the seed, the rows were covered with a thin layer of soil and FYM mixture. The observations were recorded from five randomly selected plants *viz.*, plant height (cm), Inter-nodal length (cm), number of primary branches, days to first flowering, days to first pod harvest, pod weight (g), pod length (cm), pod diameter (cm), no. of pod per plant, no. of seed per pod, 100 seed weight (green) (g), 100 seed weight (dry) (g), pod yield per plant (g), pod yield per hectare (q), shelling % total sugar (mg/100g), reducing sugar (mg/100g), non-reducing sugar (mg/100g), total free amino acids (mg/100g), ascorbic acid (mg/100g), total protein content (g/100g) and vitamin A (mg/100g).

Statistical Analysis of parameters

The phenotypic and genotypic coefficient of variability was calculated as per formula given by Burton and de Vane (1953) [3]. PCV and GCV were classified as suggested by Shivasubramanian and Menon (1973) [27] as follows: 0-10% = low, 10-20% = Moderat, > 20% = High. Heritability (h^2 bs) was calculated as per formula given by Burton and de Vane (1953) [3]. The expected genetic advance resulted from selection of 5 percent superior individuals were worked out as suggested by Johnson *et al.* (1955) [14]. The genetic advance as percentage of mean was categorised into low, moderate and high as suggested by Johnson *et al.* (1955) [14]. < 20 = Low, 20 – 30 = Moderate, >30 = High.

Results and Discussion

From the experiment conducted, it was observed that magnitude of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters under study which is an indicator of additive gene effect influenced by environment on the expression of the traits. Similar finding were also reported by Katoch *et al.* (2016) [15], Siddika *et al.* (2013) [28], Kumar *et al.*, (2013) [16] and Ahmad *et al.* (2014) [2]. In other words, it is likely that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The finding of Mahanta *et al.* (2001) [19] and Sanjay *et al.* (2008) [24] were similar to the present findings.

The phenotypic coefficient of variation ranged from 10.78 % for days to first pod harvest to 44.04% for plant height. The

phenotypic coefficient of variation was highest for plant height (44.04%), followed by characters *viz.*, number of primary branches (37.7%), internodal length (35.57%), vitamin A (28.98%), non-reducing sugars (28.97%), number of seeds per pod (27.24%), number of pods per plant (21.27%), indicating that, these characters would respond to selection. Similar findings were also reported by Afreen *et al.* (2017) [1], Katoch *et al.* (2016) [15], Jaiswal *et al.* (2013) [12] and Kumar *et al.*, (2015) [18]. These results are also in conformity with the findings of the result of Singh *et al.*, (2012) [31] and Kumar *et al.*, (2013) [16] for number of pods per plant, Singh *et al.*, (2012) [31], Sharma and Bora (2013) [26] and Tambolkar *et al.* (2017) [33] for plant height, Sharma and Bora (2013) [26] and Singh *et al.* (2013) [6, 16, 20, 32] for pod yield per plant, Jaberson *et al.* (2016) for number of pods per plant. Gudadinni *et al.* (2017) [11] recorded higher magnitude of PCV for number of pods per plant, days to first flowering and pod yield per plant. Kumar *et al.* (2015) [18] reported the similar results with the present finding for the characters like number of pods per plant, pod length, number of seeds per pod in pea (Table 2 and Figure 1).

The rest of the characters showed moderate PCV such as days to first flowering (17.72%), number of seeds per pod (15.55%), 100 green seed weight (16.55%) pod length (16.06%), pod diameter (16.88%), pod yield per hectares (14.82), shelling % (14.25), days to first pod harvest (10.78%), ascorbic acid (11.93%) and total protein content (11.66%) were recorded to be moderate PCV. The results were conformity with Georgieva *et al.*, (2016) [8]. Gudadinni *et al.* (2017) [11] also recorded the moderate amount of PCV for days to first pod harvest, pod diameter, pod length and protein content. This result was also quite supported by Katoch *et al.* (2016) [15] for ascorbic acid and shelling %. Kumar *et al.* (2015) [18] found the similar results with the present finding for the characters like shelling % and total sugars content (Table 2, Figure 1).

Genotypic coefficient of variation varied from 10.47% for days to first pod harvest to 43.92% for plant height. High genotypic coefficient of variation was noted for number of plant height (43.92%), number of primary branches per plant (37.59%), internodal length (35.45%), vitamin A (28.85%), non-reducing sugars (28.76%) and number of pods per plant (21.13%), pods yield per plant (20.91%). The high values of GCV suggested greater genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. Similar findings were also reported by Afreen *et al.* (2017) [1], Katoch *et al.* (2016) [15], Jaiswal *et al.* (2015) and Kumar *et al.*, (2015) [18]. The findings are agreement with the result of Singh *et al.* (2012) [31] and Kumar *et al.* (2013) [16] for number of pods per plant, Singh *et al.*, (2012) [31], Sharma and Bora (2013) [26] and Tambolkar *et al.* (2017) [33] for plant height, Sharma and Bora (2013) [26] and Singh *et al.*, (2013) [6, 16, 20, 32] for pod yield per plant, Jaberson *et al.* (2017) for number of pods per plant. Gudadinni *et al.* (2017) [11] recorded higher magnitude of GCV for number of pods per plant, days to first flowering and pod yield per plant. Kumar *et al.* (2015) [18] found the similar results with the present finding for the characters like number of pods per plant, pod length, number of seeds per pod in pea (Table 2, Figure 1).

While it was moderate for rest of the characters such as days to first flowering (17.56%), number of seeds per pod (16.07%), 100 green seed weight (16.31%) pod length (16.06%), pod diameter (16.70%), pod yield per hectares

(14.61), shelling % (14.02%), days to first pod harvest (10.47%), ascorbic acid (11.68%) and total protein content (11.38%). The results were conformity with Georgieva *et al.* (2016) [8]. Gudadinni *et al.* (2017) [11] also recorded the moderate amount of GCV for days to first pod harvest, pod diameter, pod length and protein content. This result was quite supported by Katoch *et al.* (2016) [15] for ascorbic acid and shelling %. Kumar *et al.* (2015) [18] found the similar results with the present finding for the characters like shelling % and total sugars content in pea.

Heritability is a measure of genetic relationship between parent and progeny and has been widely used in determining the degree to which a character may be transmitted from parents to off springs. Estimation of heritability in broad sense gives the extent of heritable component of variation. Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character which is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. Result of present investigation indicated that the heritability estimates were observed very high for the entire traits. High heritability (broad sense) was recorded for all the characters. Similar results were noticed by Afreen *et al.*, (2017) [1], Georgieva *et al.*, (2016) [8], Kumar *et al.*, (2015) [18] and Ahmad *et al.*, (2014) [2]. The heritability was found as plant height (99.47%) followed by number of primary branches per plant (99.39%), inter-nodal length (99.32%), vitamin A (99.12%), number of pods per plant (99.00%), protein content (95.12%), total free amino acids (98.70%), non-reducing sugar (98.59%), total sugar (98.57), pod weight (95.94%), pod length (97.68%), shelling percentage (96.75%), days to first pod harvest (88.57%), days to first pod harvest (88.57%), pod yield per hectare (86.33%), days to first flowering (85.24%) and pod yield per plant (83.84). These results are in conformity with Gudadinni *et al.* (2017) [11] for most of the characters like plant height, number of primary branches per plant, days to first flowering, number of pods per plant, pod length, pod diameter, pod weight, pod yield per plant, number of seeds per pod and shelling percentage. Tambolkar *et al.* (2017) [33] found high heritability for the characters like number of primary branches per plant, plant height, days to first flowering, number of seeds per pod, pod yield per hectare in pea. Kumar *et al.*, (2015) [18] found that the similar results of high heritability for days to first flowering, number of pods per plant, pod length, plant height, pod yield per plant and total sugar in pea. Pal and Singh (2013) [6, 16, 20, 32] found similar result of high heritability with the present finding for most of the characters like plant height, days to first flowering, number of primary branches per plant, pod length, number of pods per plant, number of seeds per pod, 100 seeds weight, shelling percentage, pod yield per plant in pea. Rana and Jamawal (2007) also found for the character like days to first pod harvesting, pod weight, pod length in pea. Choudhary *et al.* (2010) [5] also found high heritability for internodal length, pod yield per plant, plant height in pea. Katoch *et al.* (2016) [15] found the high heritability for protein content and ascorbic acid content in pea. Very high values of broad sense heritability for the above characters expressed that they were

less influenced by environmental conditions. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable (Table 2, Figure 1).

The estimated values of genetic advance as percent of mean were classified as high (more than 30%), moderate (20-30%) and low (less than 20%). In the present study, genetic advance as percentage of mean ranged between 20.95% for days to first pod harvest to 90.24% for plant height. The highest estimate of genetic advance as percentage of mean was recorded for number in plant height (90.24%), followed by number of primary branches per plant (77.19%), internodal length (72.77%), vitamin A (59.17%), non-reducing sugars (58.83%), number of pods per plant (55.54%), number of seeds pr pod (43.23%), pod yield per plant (42.76%), total sugars (40.00%), days to first flowering (35.85%), reducing sugar (35.65%) pod diameter (34.055) and 100 green seed weight (33.13%). Moderate value of genetic advance as percentage of mean was observed in pod yield per hectare (29.66%), 100 seed weight (dry) (29.16%), shelling % (28.40%), ascorbic acid (23.58%), total protein (22.86%), pod weight (24.64%) and days to first pod harvest (20.95%). These results was as per the guidelines agreement with Choudhary *et al.* (2010) [5] for the characters like plant height, number of primary branches per plant, pod yield per plant, internodal length and number of pods per plant. Kumar *et al.* (2014) also found the similar findings for the characters like pod length, number of pods per plant, 100 seed weight, shelling percentage, number of primary and branches per plant. Pal and Singh (2013) [6, 16, 20, 32] found the similar finding for the characters like plant height, days to first flowering, number of primary branches per plant, pod yield per plant. Kumar *et al.* (2007) [17, 21, 30] also found high heritability for protein content in pea (Table 2, Figure 1).

High heritability coupled with high genetic advance were noticed for traits like plant height, followed by number of primary branches per plant, internodal length, vitamin A, non-reducing sugars, number of pods per plant, number of seeds per pod, pod yield per plant, total sugars, days to first flowering, reducing sugar, pod diameter and 100 green seed weight. High heritability in these traits were observed mainly due to favorable environment rather than their genotype and the selection for these characters may not be rewarding as suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions. These findings were agreement with Pal and Singh (2013) [6, 16, 20, 32] in pea for plant height, days to first flowering, number of primary branches per plant, number of pods per plant, pod yield per plant. Kumar *et al.* (2015) [18] also observed the similar findings in pea for the characters like numer of pods per plant, total sugars and pod yield per hectare. Siddika *et al.* (2013) [28] also found the similar results in pea for the characters like 100 green seed weight, plant height etc. (Table 2, Figure 1).

High heritability supplemented with moderate genetic advances as percentage of mean were exhibited by mean pod yield per hectare (29.66%), 100 seed weight (dry), shelling %, ascorbic acid, total protein, pod weight, and days to first pod harvest which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability can be brought about. Kumar *et al.* (2007) [17, 21, 30] also found high heritability coupled with moderate genetic advance as percentage of mean for protein content,

Singh *et al.* (2011), Kumar *et al.* (2013) ^[16] and Dagla *et al.* (2013) for 100 seed weight, Sanjay *et al.* (2008) and Kumar *et al.* (2013) ^[16] for number of seeds per pod in pea. The findings were in agreement to the findings of Sardana *et al.*

(2007) ^[25], Rakesh Kumar *et al.* (2007) ^[17, 21, 30], Singh *et al.* (2011), Kumar *et al.* (2013) ^[16] and Dagla *et al.* (2013) for 100 seed weight, Sanjay *et al.* (2008) and Kumar *et al.* (2013) ^[16] for number of seeds per pod.

Table 1: List of pea genotypes with their sources.

Sl. No.	Genotypes	Sources
1	CHFP-1	IIVR, Varanasi
2	CHFP-2	IIVR, Varanasi
3	CHFP-3	IIVR, Varanasi
4	CHFP-4	IIVR, Varanasi
5	CHFP-5	IIVR, Varanasi
6	CHFP-6	IIVR, Varanasi
7	CHFP-7	IIVR, Varanasi
8	CHFP-8	IIVR, Varanasi
9	CHFP-9	IIVR, Varanasi
10	CHFP-10	IIVR, Varanasi
11	CHFP-11	IIVR, Varanasi
12	CHFP-12	IIVR, Varanasi
13	CHFP-13	IIVR, Varanasi
14	CHFP-14	IIVR, Varanasi
15	CHFP-15	IIVR, Varanasi
16	CHFP-16	IIVR, Varanasi
17	CHFP-17	IIVR, Varanasi
18	CHFP-18	IIVR, Varanasi
19	CHFP-19	Khergao, Manipur
20	CHFP-20	Thoubal, Manipur
21	CHFP-21	Lamphel, Manipur
22	CHFP-22	Noney, Manipur
23	CHFP-23	A landrace of Aizawl, Mizoram
24	CHFP-24	A Landrace of Barapani, Meghalaya
25	CHFP-25	A landrace of Sikkim
26	CHFP-26	A landrace of Tripura
27	CHFP-27	Arkel variety
28	CHFP-28	A landrace of Dimapur, Nagaland
29	CHFP-29	A landrace of Arunachal Pradesh
30	CHFP-30	A landrace from Assam

Table 2: Genetic parameters for yield and yield attributing characters in Garden pea genotypes

Character	Range Lowest	Range Highest	General Mean	Phonotypic variance	Genotypic variance	PCV	GCV	h ² (Broad Sense)	Genetic Advance	Genetic Advance as % of Mean
1	2.02	118.16	64.55	807.94	803.65	44.04	43.92	99.47	58.24	90.24
2	1.10	3.90	2.09	0.55	0.55	35.57	35.45	99.32	1.52	72.77
3	1.00	4.20	2.23	0.71	0.70	37.70	37.59	99.39	1.72	77.19
4	31.84	64.81	47.80	96.73	70.46	20.57	17.56	85.24	17.14	35.85
5	56.07	84.22	71.26	70.97	55.65	11.82	10.47	88.57	14.93	20.95
6	4.40	7.40	6.10	0.58	0.55	12.47	12.21	95.94	1.50	24.64
7	5.16	10.45	8.02	1.66	1.62	16.06	15.87	97.68	2.59	32.31
8	0.94	1.93	1.44	0.06	0.06	16.88	16.70	97.96	0.49	34.05
9	6.08	18.32	11.73	10.20	10.10	27.24	27.10	99.00	6.51	55.54
10	3.39	8.25	6.26	1.77	1.75	21.27	21.13	98.68	2.71	43.23
11	31.05	54.77	39.65	43.05	41.84	16.55	16.31	97.17	13.13	33.13
12	11.62	21.21	16.26	5.68	5.48	14.66	14.40	96.59	4.74	29.16
13	31.26	71.19	46.11	132.27	92.92	24.94	20.91	83.84	19.71	42.76
14	62.76	116.68	83.00	181.24	146.98	16.24	14.61	86.33	24.62	29.66
15	33.29	72.53	52.63	56.26	54.43	14.25	14.02	96.75	14.95	28.40
16	10.14	20.88	15.30	9.08	8.95	19.70	19.56	98.57	6.12	40.00
17	4.76	8.92	6.52	1.38	1.32	18.01	17.66	96.10	2.32	35.65
18	5.11	12.88	8.78	6.47	6.38	28.97	28.76	98.59	5.17	58.83
19	2.04	4.64	2.86	0.44	0.43	23.15	23.00	98.70	1.35	47.07
20	24.61	36.67	31.15	13.8	13.24	11.93	11.68	95.95	7.34	23.58
21	6.24	9.47	8.20	0.92	0.87	11.66	11.38	95.12	1.88	22.86
22	0.48	1.26	0.84	0.06	0.06	28.98	28.85	99.12	0.50	59.17

Where, 1. Plant height (cm), 2. Inter-nodal length (cm), 3. Number of primary branches 4. Days to first flowering 5. Days to first pod harvest 6. Pod weight (g), 7. Pod length (cm), 8. Pod diameter (cm), 9.No. of pod per plant, 10.No. of seed per pod, 11.100 seed weight (green) (g), 12. 100 seed weight (dry) (g), 13.Pod yield per plant (g) 14. Pod yield per hectare (q). 15. Shelling % 16. Total sugar (mg/100g) 17. Reducing sugar (mg/100g) 18. Non-reducing sugar (mg/100g) 19. Total free amino acids (mg/100g) 20.Ascorbic acid (mg/100g) 21. Total protein content (g/100g) 22. Vitamin A (mg/100g).

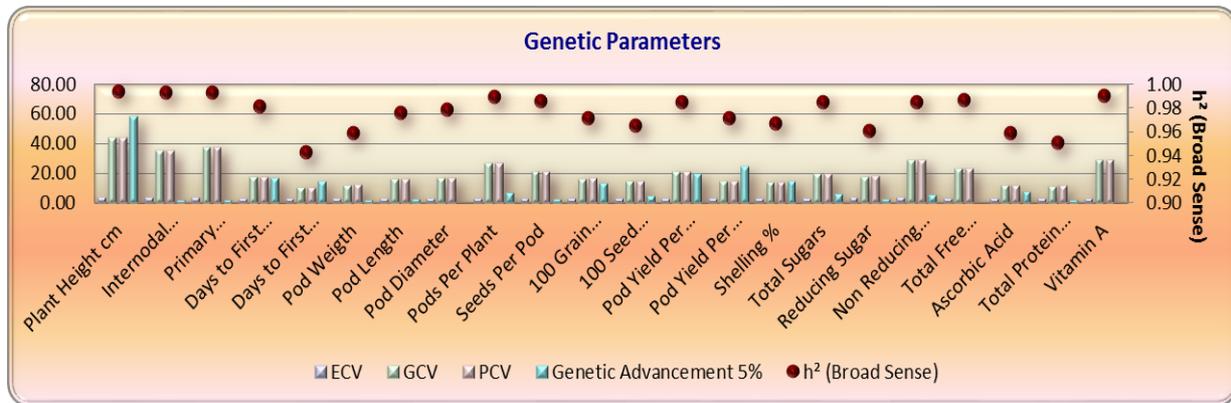


Fig 1: Genetic parameters for yield and yield attributing characters in garden pea

Conclusion

High heritability coupled with high genetic advance was observed for plant height, internodal length and number of primary branches per plant. These characters are therefore, governed by additive gene effects. It may also be concluded that selection on the basis of these characters will be more useful for the improvement of this crop towards attaining higher pod yield per plant.

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