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## Identification of elite genotypes for certain quantitative traits in field pea (*Pisum sativum* L. var. *arvense*)

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**Abstract**

Ninety genotypes were assessed with four check varieties of field pea to identify elite genotypes for certain quantitative traits. For the fulfillment of this, data on various quantitative characters were recorded on the basis of mean values of recorded data such as genetic variability, character association, path coefficient, mean performance of the genotypes and genetic divergence analysis were done in Augmented Block Design. Through the analysis of genetic variance it was found that moderate to high level of genetic variability were exhibited by all the genotypes for almost all the characters except pod length. Higher GCV were recorded for pod length (22.84), number of pods per plant (20.96), for these characters PCV were 25.30 and 21.02, respectively, indicated that the effects of environment on the expression of the characters was quite meager. Correlation analysis indicated that the pods per plant had highly significant and positive correlation with seed yield per plant followed by number of branches per plant. Path analysis indicated that biological yield per plant, harvest index and number of pods per plant has higher direct as well as indirect effects on seed yield per plant. On the basis of non-hierarchical Euclidean cluster analysis, all the genotypes were grouped into ten distinct non-overlapping clusters in which cluster number IV and X were found largest having twelve genotypes while cluster IX had lowest (2) number of genotypes e.g., Pant Pea 223 and NDP 14-11. The highest intra cluster distance was observed within cluster IV (12.79) followed by cluster III (12.00). The maximum (84.87) inter cluster distance was recorded between cluster II and VIII and between cluster II and cluster V (75.30), indicated that promising segregants could be obtained through mating between the genotypes of these clusters.

**Keywords:** *Pisum sativum* L. var. *arvense*, correlation coefficient, path coefficient and divergence

**Introduction**

Pulses are the second most important group of food crops after cereals. Globally, more than two dozen pulse crops are grown. Endowed with the unique ability to trap atmospheric N<sub>2</sub> in their root nodules in association with *Rhizobium* bacteria and thrive well under harsh and fragile eco-system, pulses remained an integral component of subsistence farming system of the dry land regions since the start of agriculture. Being a rich source of protein, minerals, vitamins and crude fiber, pulses are considered as "health food" and important in nutritional security to millions of population suffering with protein malnutrition, especially in South Asia and Africa. India is the largest producer and consumer of pulses in the world and also a key player with 25 per cent share in the global pulse basket from an area about 33 per cent. Pulses are grown in a semi arid region of India since time immemorial. Total pulses were grown on an area of 25.26 mha with production of 16.47 mt and productivity 652kg/ha in 2015-16 (Anonymous, 2016) <sup>[1]</sup>.

The area under pulses remained almost stagnant. Dry beans (*Phaseolus* beans, urd bean, mung bean etc. contribute 31.7 per cent share in total pulse production followed by dry peas 17.7 per cent, chickpea 13.9 per cent, cowpea 7.7 per cent, broad beans 7.6 per cent, lentil 6.0 per cent and pigeon pea 5.6 per cent (Gowda *et al.*, 2009) <sup>[9]</sup>. Even though India has largest cultivated area of pulses in the world, but average productivity is very low, and the production is not sufficient to meet the per capita requirement. Pulses shortfall may increase to 6.8 mt by 2020-21 and the anticipated increase in per capita consumption of pulses from 9 kg/year in 2007-08 to 10.9 kg by 2020-21 (Joshi, 2009) <sup>[10]</sup>. The recommendation of per capita availability of pulse is 65 g/day/capita by Indian Council of Medical Research in 2008 (Reddy, 2009) <sup>[16]</sup>, whereas FAO/WHO recommendation of minimum requirement of 80 g/day/person.

The decreasing per capita availability of pulses from 69 g in 1961 to 41.6 g in 2012 ([www.dacnet.nic.in](http://www.dacnet.nic.in)) in the country has been a serious concern. With assured supply of cereals at an affordable price, the main focus of policy makers and researchers is now on nutritional

security in the country, which houses more than one-fourth of the undernourished living in the world. Therefore emphasis should be made to evolve high yielding varieties having a high protein content and resistance to biotic and abiotic stresses coupled with suitability for different agro-climatic conditions and cropping systems. Taking these facts under consideration the present investigation was carried out to identify the most divergent genotypes that could be hybridized with each to get desirable segregants.

### Materials and Methods

The experiment was conducted to evaluate 90 genotype lines along with 4 check varieties *viz.*, Rachana, HFP-4, HFP-8909 and HUDP-15 under irrigated, a normal soil condition in Augmented Block Design during *Rabi* 2016-17 at Genetics and Plant Breeding Research Farm of Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya (U.P.). These genotypes exhibit a wide spectrum of variation for agronomical and morphological characters which were available at the Pulse Section of the University. The experimental plot was divided into six blocks of equal size. Each block had 19 plots in which four plots were randomly allotted to the four check varieties, while remaining 15 plots of a block were used for accommodating the un-replicated test genotypes. Each plot was consist of a single row of 4 m length, following inter and intra row spacing of 30 cm and 10 cm respectively. Five competitive plants from each plot were randomly selected for recording observations on nine quantitative characters *viz.*, plant height (cm), number of primary branches per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight, biological yield per plant, harvest index and seed yield per plant (g). Two characters *viz.*, days to 50 per cent flowering and days to maturity, were recorded on the plot basis. The mean value of recorded data were used for the mean performance of selected genotypes for various quantitative characters, analysis of variance for augmented block design (Federer, 1956) <sup>[7]</sup>, Phenotypic and Genotypic coefficient of variation (Burton and de Vane, 1953) <sup>[5]</sup>, correlation coefficient (Searle, 1961) <sup>[17]</sup>, path coefficient (Dewey and Lu, 1959) <sup>[6]</sup> and genetic divergence (Beale, 1969 and Spark, 1973) <sup>[4, 20]</sup> were estimated.

### Results and Discussion

The highest seed yield per plant was obtained in Pant P-266 and constituted the top significant group for high seed yield along with five entries. Among the high yielding genotypes, six most promising genotypes were PANT P 266 (6.773), EC 507770 (6.573), PANT P 195 (6.436), IPFD 13-4 (6.376), EC 281864 (6.196), VL 58 (6.186). These genotypes also exhibited average to high mean performance for biological yield, days to 50% flowering, number of primary branches per plant, harvest index, days to maturity and for other trait. Genotypes PANT P 247, HFP 1010, KPMR 853, PANT P 195, LFP 431, PANT P 223, PANT P-101 were earlier for days to 50 percent flowering and days to maturity (Table 1). Population mean for plant height was 87.37 cm, which ranged from 39.55 (NDP 14-11) to 137.683 (Rachna). Out of 94 genotypes fifty nine entries were significantly shorter in plant stature than the general mean. However, best four genotypes showing tallest plant stature in order of merit were Rachna (137.683), VL 58(118.35), PANT P 247(117.550) and IPF 11-15(113.250). Genotype NDP 14-11 had shortest plant stature followed by IPFD 2014-2, PRAKASH, PANT P 223, LFP 431, HFP 8909 ©, JPP 3, while genotype KPF 1023 had

tallest plant stature followed by RACHNA © (137.683 cm), VL 58 (118.350 cm), PANT P 247 (117.550 cm), IPF 11-15(113.250) as compare to general mean.

The entries EC 507770(12.889) had maximum number of pods per plant. The genotype KPMR 936(4.886) had highest pod length as compare to the general mean. The entries KPMR 4(3.119) had maximum number of primary branches per plant and the maximum number of seeds per pod was recorded in IPF 13-14 (5.168). PANT P 195 emerged with boldest seed size (28.504 g/100 seeds), whereas, IPF 2014-16 as smallest seed size (16.62 g/100 seed).

The genotypes EC 507770, IPF 11-13 and EC 281864 have maximum biological yield per plant. The genotype IPFD 13-4 (46.632%) showed highest harvest index.

Thus, the genotypes PANT P 266 (6.773), EC 507770(6.573), PANT P 195 (6.436), IPFD 13-4(6.376), EC 281864(6.196) and VL 58(6.186) exhibiting higher mean performance for seed yield per plant as well as average mean performance for 100-seed weight, harvest index, biological yield per plant, plant height, number of primary branches per plant, pods per plant, seeds per pod, pod length, days to 50% flowering and days to maturity, identified on the basis of mean performance may be mentioned as elite genotypes.

Analysis of variance for Augmented Block Design accommodating ninety germplasm lines and four checks in fifteen blocks was carried out for each of the eleven characters in field pea. It was revealed that the variation due to checks was highly significant for majority of the traits except pod length (Table 2). Mehta *et al.* (2005) <sup>[13]</sup> and Georgieva *et al.* (2016) <sup>[8]</sup> also noted that the genotypes differed significantly for all the traits except the Pod length (cm).

The success of any breeding programme depends upon the genetic variability present in the population. Knowledge of variability does not only give clear understanding for the improvement in selection but it is also the most distinctive feature of living being and forms the base of plant improvement.

The estimates of genotypic and phenotypic coefficient of variation for the 11 characters are presented in Table 3. The magnitude of phenotypic coefficient of variation (PCV) was slightly higher than their genotypic coefficient of variation (GCV) for all the characters indicating very less environmental influence on the expression of the characters. Higher estimates (25.30 %) of PCV was recorded for pod length followed by pods/plant (21.02 %), while higher estimates of GCV was recorded for pod length (22.84 %) followed by number of pods per plant (20.96 %). The characters which exhibited moderate estimates (between 4.99 to 21.02 %) of PCV and GCV were 100-seed weight, number of pods per plant, biological yield per plant, harvest index, pod length. Bashir *et al.* (2017) <sup>[3]</sup> and Meena *et al.* (2017) <sup>[12]</sup> also reported that relative magnitude of phenotypic coefficients of variation was higher than their genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits.

The grain yield or seed yield, in almost all the crops, is referred as super character, which results from multiplicative interactions of several other component characters that are termed as yield components. Thus, identification of important yield components and information about their inter-relationship with each other will be very useful for developing efficient breeding strategy in developing high yielding varieties. In this respect, the correlation coefficient, which provides symmetrical measurement of degree of association

between variables or characters, help us in understanding the nature and magnitude of association among yield and yield components.

In the present investigation it was found that the genotypic correlation coefficients between different characters were generally similar in sign and nature to the corresponding phenotypic correlation coefficients. However, in general the values of genotypic correlations were higher in magnitude from the corresponding phenotypic values. Similar, results have also been reported by Singh *et al.* (2014) <sup>[19]</sup>.

Seed yield per plant exhibited highly significant and positive correlation with plant height, primary branches per plant, seeds per pod, pod length, biological yield per plant and harvest index; positive association with 100-seed weight (Table 4). Harvest index per plant exhibited highly significant and positive correlation with seed yield per plant followed by number of pods per plant, number of primary branches per plant. However, seed yield per plant had negative and non-significant correlation with days to 50% flowering and days to maturity. Biological yield per plant showed highly significant and positive association with seed yield per plant followed by plant height and pod per plant; positive association with number of primary branches per plant, pod length, 100-seed weight (0.1735). However, biological yield per plant showed negative and highly significant association with day to maturity followed by day to 50 % flowering. 100-seed weight had positive association with seeds per pod, pod length. Singh *et al.* (2014) <sup>[19]</sup> also reported that biological yield per plant was highly significant with grain yield per plant. Earlier reports in field pea have also indicated existence of positive and highly significant association of weight of seeds per plant with the weight of pods per plant, biological weight per plant and harvest index recording (0.839, 0.694 and 0.505) respectively, Tofiq *et al.* (2015) <sup>[22]</sup>. In addition Basaiwala *et al.* (2013) <sup>[2]</sup> also found that seed yield per plant was positively and significantly correlated with seeds per pod and harvest index. One another report in field pea also indicated that length and width of pod and 100- seed weight were associated positively and significantly with grain yield per plant, Singh *et al.* (2008) <sup>[18]</sup>.

Path-coefficient analysis is a tool to partition the observed correlation into direct and indirect effects of yield components on seed yield, which provide very clear picture of character association for formulating efficient selection strategy. In the present study path coefficient analysis was estimated using simple correlation coefficients (Table 5).

High positive and direct effect on seed yield per plant was exerted by biological yield per plant followed by harvest index, pods per plant whereas very low positive and direct effect on seed yield per plant was exerted by primary branches per plant and pod length. However, negative and direct effect on seed yield per plant was exerted by plant height and number of seeds per pod Tofiq *et al.* (2015) <sup>[22]</sup> also reported that biological weight per plant and harvest index exhibited maximum positive direct effect in weight of seeds per plant recording (0.630 and 0.456) respectively. Singh *et al.* (2014) <sup>[19]</sup> also reported that biological yield per plant, harvest index and plant height had positive and direct effect on grain yield per plant. Similarly days to 50% flowering and pod length had positive and direct effect on grain yield per plant. Bashir *et al.* (2017) <sup>[3]</sup> also reported that 100-seed weight and number of seeds per pod had maximum direct effect on grain yield per plant. The occurrence of negative as well as positive indirect effects on yield by one or another character presents a complex situation where a

compromise balance is required to attain proper balance of different yield components, for determining the ideotype of seed yield in field pea.

The selection of suitable diverse parents for hybridization is an important feature of any crop improvement programme for getting desired recombinants. The importance of genetic divergence in plant breeding has been emphasized by several researchers.

All genotypes were grouped into ten distinct non-overlapping clusters using Non-hierarchical Euclidian cluster analysis (Table 6) in which Cluster IV and X had highest number of genotypes (12) followed by cluster II, cluster VI & VII (10), cluster III (9), cluster I& VIII (8), cluster V (6) and cluster V had lowest number of genotypes (2) and the highest intra cluster distance was observed in cluster IV followed by cluster III, cluster I, cluster V, cluster VI, cluster VII While, the lowest values recorded in case of cluster X, cluster VIII and cluster IX. The maximum inter cluster distance was recorded between cluster II and VIII followed by cluster II and V, cluster II and VI, cluster II and X (Table 7), which suggested that members of these two clusters are genetically very diverse to each other. This indicated the presence of considerable genetic diversity in the germplasm collections under study. Yadav *et al.* (2009) <sup>[23]</sup> also assessed 62 genotypes of field pea to estimate the genetic divergence for various agronomic traits and stated that all the accessions were significantly different for the traits and a wide range of variability exists for most of the traits. The genotypes of Cluster I had average mean values for all characters. The genotypes of Cluster II had highest mean values for 100-seed weight, harvest index, seeds yield per plant and lowest mean value for days to 50% flowering. The genotypes of cluster III had highest mean value for plant height (106.036 cm). The genotypes of cluster IV had highest mean value for number of primary branches/plant (2.844) as well as number of pods per plant (11.4) and biological yield per plant (14.611). The genotypes of cluster V had highest value for days to 50% flowering (85.617) as well as days to maturity (138.858) and lowest mean value for pod length (3.141 cm). The genotypes of cluster VI had lowest mean value for number of seeds per pod (3.106). The genotypes of cluster VII had highest value for number of seed/pod (4.668). The genotypes of cluster VIII had highest mean value for number of seeds per pod (4.196) as well as pod length (4.34 cm). The genotypes of cluster VII had lowest mean value for 100-seed weight. The genotypes of cluster IX had lowest mean value for harvest index (33.938%). The genotypes of Cluster X had lowest mean values for number of days to maturity (127.633) as well as number of primary branches per plant (1.486), plant height (66.675cm), pods per plant (4.73), biological yield per plant (10.083 g) and seed yield per plant (Table 8).

The analysis of character contribution towards genetic divergence between ninety four genotypes of field pea is given in Table 9. The maximum contribution in manifestation of total genetic divergence were made by plant height (75.15%) followed by day to 50% flowering (6.91%) pods per plant (0.39%), biological yield per plant (0.27%), 100 seed weight (0.37%). The minimum contributions in manifestation of total genetic divergence were made by number of primary branches per plant, seeds per pod, pod length, seed yield per plant (0.01%).

The minimum contributions in manifestation of total genetic divergence were made by branches per plant, seeds per pod, pod length and seed yield per plant (0.01). Similar results were reported by Srivastava *et al.* (2012) <sup>[21]</sup>.

**Table 1:** Most desirable Field pea genotypes identified for 11 characters

| S. N. | Charecter                            | Genotype  |
|-------|--------------------------------------|---|
| 1.    | Days to 50% flowering                | PANT P 101(70.292), PANT P223(70.29), LFP 431 (71.02), PANT P195(71.29), KPMR 853(71.79), HFP 1010(72.04), PANT P 247(72.29).   |
| 2.    | Days to maturity                     | KFP 2009-2 (142.583), KPF 12-04 (141.583), VL 202 (141.583), AMAN (140.583), KPMR 916 (140.583), RFP 2009-2-1 (140.583), IDM (139.833), RFG 79 (139.833), RFPG 79(139.083).                   |
| 3.    | Plant height (cm)                    | Rachna (137.68), VL 58 (118.35), PANT P 247 (117.55), IPF 11-15 (113.25), SKUA P-8 (112.75) Tallness<br>PANT P 223 (58.55), PRAKASH (57.45), IPFD 2014-2 (48.85), NDP 14-11 (39.55) Dwarfness |
| 4.    | Number of primary branches per plant | KPMR-4(3.119), EC 507770 (3.092), EC 548810 (3.017), EC 386742 (2.992), VL 61(2.889), NDP 12-102 (2.889) and PANT P138 (2.819).   |
| 5.    | Number of pods per plant             | EC 507770(12.889), EC 281864(11.748), EC 386742(11.089), KPMR 4(11.021), EC548810 (10.759), PANT P 266 (10.589), PLK 108 (10.205).  |
| 6.    | Pod length (cm)                      | KPMR 936 (4.886), VL 82 (4.591), IPF 11-13 (4.446), IPF 2014-13 (4.391), RFPG 81 (4.384), IPLK 85 (4.344).  |
| 7.    | Number of seeds per pod              | IPF 13-14 (5.168), KPMR 502 (5.168), LFP 431 (4.668), IPLK 109 (4.416), VL 82 (4.391), KPMR 936 (4.358).  |
| 8.    | Biological yield per plant (g)       | EC 507770 (15.439), IPF 11-13 (15.355), EC 281864 (15.315), KPMR 931 (15.30), KPMR 853 (15.15.28), VL 82 (15.24), VL 61 (15.15.24).   |
| 9.    | Seed yield per plant (g)             | PANT P 266 (6.773), EC 507770(6.573), PANT P 195 (6.436), IPFD 13-4(6.376), EC 281864(6.196), VL 58(6.186).   |
| 10.   | Harvest index (%)                    | IPFD 13-4 (46.63), VL 58 (44.565), PANT P 266 (44.447), PANT P 195 (44.345), IPFD 2014-2 (44.232), IPF 13-14 (44.065), RFP 61 (44.065).   |
| 11.   | 100-seed weight (g)                  | PANT P-195 (28.504), IPLK 112 (22.314), RFPG 79(21.80), RFG 61 (21.734), AMAN (21.654), VL 58(21.404).  |

**Table 2:** Analysis of variance of augmented block design for 11 characters in field pea genotypes

| S. V.                       | d.f. | Days of 50% flowering | Days to maturity | Plant height (c) | Number of Pods/plant | Pod length (cm) | Number of Primary branches/ plant | Number of Seeds/ Pod | 100- Seed weight (g) | Biological yield/ plant (g) | Seed yield (g) | Harvest index (%) |
|-----------------------------|------|-----------------------|------------------|------------------|----------------------|-----------------|-----------------------------------|----------------------|----------------------|-----------------------------|----------------|-------------------|
| Block (ignoring Treatments) | 5    | 42.58**               | 15.02            | 481.78**         | 3.189**              | 18.207**        | 0.224**                           | 0.962**              | 7.637**              | 4.343**                     | 2.238**        | 37.89**           |
| Checks                      | 3    | 41.38**               | 24.78*           | 7631.9**         | 4.463**              | 0.051           | 0.230**                           | 0.128**              | 2.113**              | 2.0553**                    | 0.441**        | 35.10**           |
| ERROR                       | 15   | 4.48                  | 4.78             | 4.83             | 0.0167               | 0.158           | 0.001                             | 0.0045               | 0.118                | 0.0820                      | 0.009          | 0.848             |

\*,\*\* Significant at 5% and 1% probability level respectively

**Table 3:** Range, mean, coefficient of variation and least significant differences for 11 character of field pea

| Characters                                     | Range (Min-Max) | Mean Value | Coefficient of variation (%) |         |                              | Range of parameters |                     |                     |                     |
|--|-----------------|------------|------------------------------|---------|------------------------------|---------------------|---------------------|---------------------|---------------------|
|  |                 |            | GCV (%)                      | PCV (%) | Coefficient of variation (%) | LSD <sub>1</sub> 5% | LSD <sub>2</sub> 5% | LSD <sub>3</sub> 5% | LSD <sub>4</sub> 5% |
| Days to 50% flowering                          | 70.292-88.792   | 79.746     | 4.99                         | 5.66    | 5.892                        | 2.604               | 6.378               | 7.130               | 5.446               |
| Days to maturity                               | 122.583-142.583 | 133.067    | 2.99                         | 3.41    | 3.715                        | 2.691               | 6.591               | 7.369               | 5.628               |
| Plant height (cm)                              | 39.550-137.68   | 87.370     | 17.40                        | 17.58   | 20.219                       | 2.70                | 6.62                | 7.40                | 5.65                |
| Number of primary branches plant <sup>-1</sup> | 1.292-3.11      | 2.091      | 20.78                        | 20.83   | 22.511                       | 0.039               | 0.096               | 0.108               | 0.082               |
| Number of pods plant <sup>-1</sup>             | 4.181-12.88     | 7.688      | 20.96                        | 21.02   | 22.835                       | 0.159               | 0.389               | 0.435               | 0.333               |
| Number of seeds pod <sup>-1</sup>              | 2.049-5.16      | 3.527      | 13.37                        | 13.51   | 14.439                       | 0.083               | 0.203               | 0.227               | 0.174               |
| Pod length (cm)                                | 2.626-4.88      | 3.650      | 22.84                        | 25.30   | 11.796                       | 0.489               | 1.198               | 1.339               | 1.023               |
| 100-seed weight (g)                            | 16.620-28.50    | 19.230     | 7.62                         | 7.83    | 8.445                        | 0.423               | 1.037               | 1.159               | 0.886               |
| Biological yield plant <sup>-1</sup> (g)       | 3.405-6.77      | 4.923      | 11.434                       | 11.646  | 17.154                       | 0.352               | 0.863               | 0.965               | 0.737               |
| Harvest index (%)                              | 8.494-15.43     | 12.953     | 9.53                         | 9.83    | 12.609                       | 1.134               | 2.777               | 3.104               | 2.371               |
| Seed yield/plant(g)                            | 28.702-46.63    | 37.960     | 15.96                        | 16.08   | 10.445                       | 0.118               | 0.288               | 0.322               | 0.246               |

- LSD<sub>1</sub> = difference between two check means.
- LSD<sub>2</sub> = difference between adjusted yield of two genotype in the same block.
- LSD<sub>3</sub> = difference between adjusted mean of two genotypes in the different block.
- LSD<sub>4</sub> = difference between adjusted yield of genotype and check mean

GCV = genotypic coefficient of variance  
PCV = phenotypic coefficient of variance.

**Table 4:** Simple correlation coefficients between different characters in field pea germplasm

| Characters                 | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of primary Branches /plant | Number of Pods / Plant | Number of Seeds / pod | Pod length (cm) | 100-seed Weight | Seed yield/ plant (g) | Biological yield/ plant | Harvest Index (%) |
|----------------------------|-----------------------|------------------|-------------------|-----------------------------------|------------------------|-----------------------|-----------------|-----------------|-----------------------|-------------------------|-------------------|
| Days to 50% flowering      | 1.0000                | 0.868**          | 0.0687            | -0.0397                           | -0.0313                | -0.0834               | 0.0494          | -0.1613         | -0.1272               | -0.0936                 | -0.0956           |
| Days to maturity           |                       | 1.0000           | 0.0196            | -0.0854                           | -0.0889                | -0.0088               | -0.0004         | -0.1210         | -0.1853               | -0.1885                 | -0.0753           |
| Plant height(cm)           |                       |                  | 1.0000            | 0.1692                            | 0.3471**               | 0.1215                | 0.1099          | 0.0547          | 0.3641                | 0.3697**                | 0.1561            |
| Branches / plant           |                       |                  |                   | 1.0000                            | 0.7535**               | -0.2163               | -0.2794         | -0.1437         | 0.4189**              | 0.2922*                 | 0.3225**          |
| Pods / plant               |                       |                  |                   |                                   | 1.0000                 | -0.1158               | 0.0326          | -0.1018         | 0.6828**              | 0.5225*                 | 0.4744**          |
| Seeds / pod                |                       |                  |                   |                                   |                        | 1.0000                | 0.3977**        | 0.2124          | 0.3034**              | 0.1655                  | 0.3115**          |
| Pod length(cm)             |                       |                  |                   |                                   |                        |                       | 1.0000          | 0.1961          | 0.3270**              | 0.2486*                 | 0.2333*           |
| 100-Seed weight (g)        |                       |                  |                   |                                   |                        |                       |                 | 1.0000          | 0.1897                | 0.1735                  | 0.0895            |
| Seed Yield/plant (g)       |                       |                  |                   |                                   |                        |                       |                 |                 | 1.0000                | 0.7881**                | 0.6807**          |
| Biological yield/ plant(g) |                       |                  |                   |                                   |                        |                       |                 |                 |                       | 1.0000                  | 0.0906            |
| Harvest index (%)          |                       |                  |                   |                                   |                        |                       |                 |                 |                       |                         | 1.0000            |

\*,\*\*Significant at 5% & 1% probability level Respectively.

**Table 5:** Direct and indirect effects of different characters on seed yield per plant in Field pea germplasm

| Characters                        | Days to 50% flowering | Days to maturity | Plant height (cm) | Number of primary branches / Plant | Number of Pods / plant | Number of Seeds / pod | Pod length(cm) | 100-seed weight (g) | Biological yield / plant(g) | Harvest index (%) | Seed yield / plant(g) |
|-----------------------------------|-----------------------|------------------|-------------------|------------------------------------|------------------------|-----------------------|----------------|---------------------|-----------------------------|-------------------|-----------------------|
| Days to 50% flowering             | 0.0088                | -0.0076          | -0.0006           | 0.0000                             | -0.0006                | 0.0005                | -0.0002        | -0.0019             | -0.0748                     | -0.0483           | -0.1248               |
| Days to maturity                  | 0.0076                | -0.0088          | -0.0003           | -0.0001                            | -0.0019                | 0.0000                | -0.0004        | -0.0012             | -0.1565                     | -0.0325           | -0.1941               |
| Plant height (cm)                 | 0.0009                | -0.0004          | -0.0060           | 0.0002                             | 0.0074                 | -0.0007               | 0.0006         | 0.0008              | 0.2751                      | 0.0918            | 0.3699                |
| Number of primary Branches /plant | -0.0003               | 0.0008           | -0.0010           | 0.0012                             | 0.0159                 | 0.0013                | -0.0020        | -0.0021             | 0.2134                      | 0.1986            | 0.4258                |
| Number of Pods/plant              | -0.0002               | 0.0008           | -0.0021           | 0.0009                             | 0.0210                 | 0.0007                | 0.0003         | -0.0014             | 0.3761                      | 0.2905            | 0.6866                |
| Number of Seeds/pod               | -0.0007               | 0.0000           | -0.0007           | -0.0003                            | -0.0025                | -0.0057               | 0.0027         | 0.0032              | 0.1226                      | 0.1837            | 0.3022                |
| Pod length(cm)                    | -0.0003               | 0.0006           | -0.0005           | -0.0004                            | 0.0010                 | -0.0024               | 0.0065         | 0.0036              | 0.1898                      | 0.1670            | 0.3649                |
| 100 seed weight (g)               | -0.0012               | 0.0007           | -0.0004           | -0.0002                            | -0.0021                | -0.0013               | 0.0017         | 0.0139              | 0.1293                      | 0.0562            | 0.1966                |
| Biological yield/ plant (g)       | -0.0009               | 0.0019           | -0.0023           | 0.0004                             | 0.0111                 | -0.0010               | 0.0017         | 0.0025              | 0.7133                      | 0.0755            | 0.8021                |
| Harvest Index (%)                 | -0.0007               | 0.0005           | -0.0009           | 0.0004                             | 0.0104                 | -0.0018               | 0.0018         | 0.0013              | 0.0914                      | 0.5888            | 0.6912                |

R SQUARE = 0.9958, Residual factor = 0.0647, Bold figures indicate the direct effects

**Table 6:** Clustering pattern of 94 field pea genotypes on the basis of non-hierarchical Euclidean cluster analysis

| Cluster No. | Number of genotypes | Genotypes   |
|-------------|---------------------|---|
| I           | 8                   | FP 13-97, PANT P-101, HUP 2, PANT 269, LFP 431, ADARSH, Pant P-137, FP 2009-4   |
| II          | 10                  | KPMR 936, IPLK 112, EC 384275, HFP 1125, IPF 2014-13, KPF 1024, HUDP 11, IPF 12-17, HFP 529, EC 5117                    |
| III         | 9                   | IPF 13-13, PANT P-217, PANT P 247, PANT P 266, VL 58, IPF 13-14, EC 548810, HFP 1010, IPFD 13-4                         |
| IV          | 12                  | IPLK 85, NDP 11-101, EC 281864, FP 868, PANT P-138, IPF 11-15, VL 82, KPMR 4, HUP 2, HUDP 11, KPMR 902, KPF 1024        |
| V           | 6                   | PANT P 222, PANT P 195, VL 61, IPF 2014-16, KPMR 970, KPMR 853  |
| VI          | 10                  | IPFD 2014-2, VL-42, DMR 63, VL 56, KPF 1023, IPFD 1-10, JPP 3, EC 392177, HFP 4, HFP 8909                               |
| VII         | 10                  | EC 386742, HFP 554, IPLK 85, SKUA P-8, IPLK 109, RFP 61, P 1089, KPMR 931, NDP 12-102, RACHNA                           |
| VIII        | 8                   | PRAKASH, KPF 1036, AMAN, FP 34, EC 588004, VL 55, RFP 79, KPF 1023  |
| IX          | 2                   | PANT P 223, NDP 14-11   |
| X           | 12                  | PANT P 244, RFG 79, KPMR 916, VL 37, HUDP-17, PLK 108, IPFD 12-2, RFP 2009-2-1, KPF 12-04, KFP 2009-2, VL 202, HUDP 15, |

**Table 7:** Estimates of average intra-and inter-cluster distances for 10 clusters in field pea germplasm

|              | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII | Cluster VIII | Cluster IX | Cluster X |
|--------------|-----------|------------|-------------|------------|-----------|------------|-------------|--------------|------------|-----------|
| Cluster I    | 11.529    | 43.316     | 20.182      | 22.041     | 29.645    | 19.470     | 24.387      | 37.840       | 25.045     | 35.081    |
| Cluster II   |           | 9.67       | 49.754      | 49.841     | 75.302    | 61.321     | 52.176      | 84.873       | 58.821     | 67.276    |
| Cluster III  |           |            | 12.002      | 19.286     | 18.23     | 19.509     | 17.820      | 27.991       | 19.618     | 39.156    |
| Cluster IV   |           |            |             | 12.787     | 27.632    | 21.655     | 30.226      | 42.472       | 33.488     | 54.888    |
| Cluster V    |           |            |             |            | 10.9      | 16.942     | 29.049      | 18.553       | 16.553     | 39.710    |
| Cluster VI   |           |            |             |            |           | 10.555     | 22.590      | 17.649       | 15.481     | 25.061    |
| Cluster VII  |           |            |             |            |           |            | 9.486       | 24.109       | 16.223     | 24.813    |
| Cluster VIII |           |            |             |            |           |            |             | 8.365        | 13.053     | 18.522    |
| Cluster IX   |           |            |             |            |           |            |             |              | 7.536      | 20.266    |
| Cluster X    |           |            |             |            |           |            |             |              |            | 8.865     |

Bold figures indicate the intra-cluster distance

**Table 8:** Cluster means for different characters in field pea germplasm

| Characters   | Days to 50% flowering | Days to maturity | Plant height (c) | Number of primary branches/ plant | Number of Pods/ plant | Number of seeds/Pod | Pod length (cm) | 100-Seed weight | Biological yield/plant | Harvest index (%) | Seed yield/plant(g) |
|--------------|-----------------------|------------------|------------------|-----------------------------------|-----------------------|---------------------|-----------------|-----------------|------------------------|-------------------|---------------------|
| Cluster I    | 73.337                | 125.356          | 94.509           | 2.316                             | 8.565                 | 3.728               | 3.297           | 19.526          | 14.494                 | 39.676            | 5.744               |
| Cluster II   | 71.292*               | 127.333          | 84.150           | 2.500                             | 10.145                | 3.708               | 4.136           | 28.504**        | 14.515                 | 44.345**          | 6.436**             |
| Cluster III  | 82.461                | 135.006          | 106.036**        | 2.245                             | 8.658                 | 3.837               | 3.687           | 19.560          | 13.585                 | 41.018            | 5.562               |
| Cluster IV   | 79.492                | 132.633          | 84.755           | 2.844**                           | 11.40**               | 3.425               | 3.929           | 18.421          | 14.611**               | 42.180            | 6.170               |
| Cluster V    | 85.617**              | 138.858**        | 94.715           | 2.243                             | 8.336                 | 3.090               | 3.141*          | 18.351          | 12.591                 | 37.831            | 4.753               |
| Cluster VI   | 77.708                | 131.483          | 80.475           | 2.403                             | 8.197                 | 3.106*              | 3.621           | 18.130          | 12.506                 | 37.460            | 4.674               |
| Cluster VII  | 79.117                | 133.008          | 92.450           | 1.610                             | 6.687                 | 4.196**             | 4.340**         | 19.620          | 13.751                 | 37.851            | 5.191               |
| Cluster VIII | 83.181                | 136.417          | 70.767           | 1.746                             | 6.104                 | 3.340               | 3.652           | 18.135*         | 10.519                 | 36.022            | 3.766               |
| Cluster IX   | 81.461                | 135.143          | 80.837           | 1.802                             | 6.310                 | 3.438               | 3.572           | 20.205          | 13.165                 | 33.938*           | 4.464               |
| Cluster X    | 72.842                | 127.633*         | 66.675*          | 1.486*                            | 4.730*                | 3.655               | 3.885           | 20.120          | 10.083*                | 36.851            | 3.693*              |

**Table 9:** Contribution of characters towards genetic divergence

| Source                              | Times Ranked 1 <sup>st</sup> | Contribution % |
|-------------------------------------|------------------------------|----------------|
| 1. Days to 50% flowering            | 302.000                      | 6.91           |
| 2. Days to maturity                 | 430.000                      | 9.84           |
| 3. Plant height (cm)                | 3285.000                     | 75.15          |
| 4. Number of primary branches/plant | 0.000                        | 0.01           |
| 5. Number of pods/ plant            | 17.000                       | 0.39           |
| 6. Number of seeds/ pod             | 0.000                        | 0.01           |
| 7. Pod length (cm)                  | 0.000                        | 0.01           |
| 8. 100-seed Weight (gm)             | 16.000                       | 0.37           |
| 9. Biological Yield/ Plant (gm)     | 0.000                        | 0.01           |
| 10. Harvest index (%)               | 12.000                       | 0.27           |
| 11. Seed yield/ plant (gm)          | 309.000                      | 7.07           |

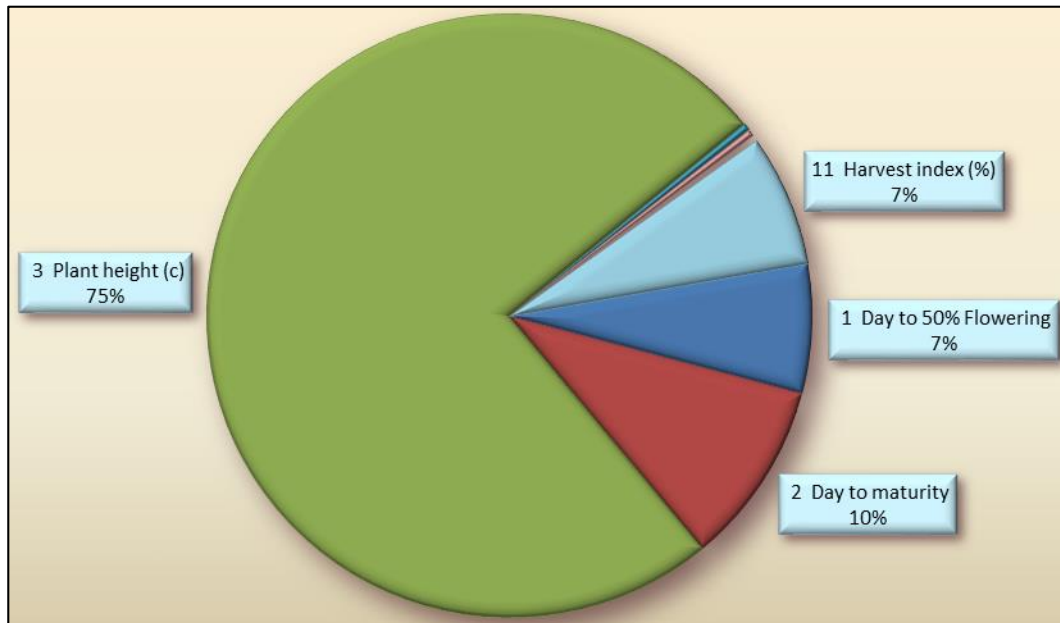


Fig 1: Contribution% towards Divergence

The overall review of the result obtained by genetic diversity study in present investigation revealed that the crosses between the entries separated by the large inter-cluster distances and having high cluster mean values for one or other character to be improved is likely to be more useful. The results of Non-hierarchical Euclidian cluster analysis obtained under present study are also in agreement with the result of Khan *et al.* (2016) <sup>[11]</sup>, Parihar *et al.* (2014) <sup>[14]</sup>, Ramjan *et al.* (2014) and Srivastava *et al.* (2012) <sup>[21]</sup>.

### Concluding Remarks

From all over the investigation the genotypes PANT P 266 (6.773), EC 507770(6.573), PANT P 195 (6.436), IPFD 13-4(6.376), EC 281864(6.196) and VL 58(6.186) exhibiting higher mean performance for seed yield per plant as well as average mean performance for 100-seed weight, harvest index, biological yield per plant, plant height, number of primary branches per plant, pods per plant, seeds per pod, pod length, days to 50% flowering and days to maturity, identified on the basis of their mean performance may be mentioned as elite genotypes.

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