

## Selection criteria for genetic improvement of sugar snaps (*Pisum sativum* var. *saccharatum*) based on components of genetic variability

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### Abstract

The present investigation was conducted on newly generated material of sugar snaps comprising of 29 advanced breeding lines (F<sub>7</sub>) developed from 4 interspecific crosses at HP Agricultural University, Palampur along with 7 lines collected from different institutes in randomized complete block design over three replications during winter 2016-17. The phenotypic (PCV) and genotypic (GCV) coefficients of variation were high for straw yield/plant while branches/plant, internodal length, pods/plant, dry pod weight and seed yield/plant showed high PCV with moderate GCV. High heritability and genetic advance was recorded for internodal length, plant height, straw yield/plant, dry pod weight and seed yield/plant, indicating additive gene effect for their inheritance. Seed yield/plant was positively associated with pod length, seeds/pod, protein content of seed, straw yield/plant and 100-seed weight both at phenotypic and genotypic levels. Harvest index and straw yield contributed maximum via their direct and indirect contributions towards total association of these traits with seed yield while, nodes/plant, internodal length, 100-seed weight and seeds/pod also contributed to some extent. Therefore, these traits would be of great significance for achieving enhanced performance of genotypes for seed yield.

**Key words:** Edible pod pea, variability, heritability, correlation, direct effects, selection.

### Introduction

Edible pod pea is an oriental vegetable which shares the cultivation pattern with the garden pea. It is grown for its tender fresh pods lacking parchment layer inside the pod (Sneddon 1970). Edible-pod peas consist of snow pea (*Pisum sativum* var. *macrocarpon*) and sugar snaps/

snap peas (*Pisum sativum* var. *saccharatum*) which are eaten as whole tender pods without shelling although the tough strings along the edges are usually removed before eating. Snap pea is also known as sugar snap pea and is a cross between snow pea and garden pea. Pods of sugar snaps are like a green bean with thick walls and are sweet, crisp, mildly flavoured and have less fibre in pods than snow pea with flat pods and very small peas. The combinations of two recessive genes 'p' and 'v' ('p' is responsible for reducing the sclerenchymatous membrane on the inner pod wall, while 'v' reduces pod wall thickness) contribute to make the whole pod suitable for consumption in the fresh stage.

Most of the horticultural research on peas has dealt with the green-shell crop. Sugar snap is newly introduced crop in India and the most important task involves the development of high yielding varieties with stable productivity carrying resistance to diseases and unfavorable environmental conditions. High yield is the basic objective of all crop breeding programmes, and it is essential to develop genotypes with potential to surpass commercially adopted/adapted cultivar(s) otherwise the genotype will be of no significance even if it has excellent performance for other traits (Sharma et al. 2019). One major approach in any crop improvement programme is to maximize the genetic diversity which serves as a reservoir for identifying superior alleles controlling key agronomic and quality traits. An improvement in yield of self-pollinated crops like pea is affected mainly through selection of genotypes with desirable characters from the variation through recombination followed by selection (Singh and Dhali 2018). The response of selection depends upon the relative proportion of the heritable component which can be predicted with the help of genetic parameters namely, coefficient of variation, heritability and genetic advance.

Since yield is a complex trait, indirect selection through correlated, less complex and easier measurable traits would be an advisable strategy to increase the yield.

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Correlation coefficients are very useful in quantifying the size and direction of trait associations. Correlation index predict yield response in relation to changes associated with a particular character (Malek et al. 2014). However, it may provide ambiguous measure if the high magnitude of correlation between two traits is the result of indirect effect via other traits (Bizeti et al. 2004). The aim of indirect selection is to find yield components with strong direct effect and little negative influence from other yield component traits (Cramer and Wehner 2000). In this context, path coefficient analysis is an effective tool to partition correlation coefficients into unidirectional and alternative pathways (Salahuddin et al. 2010). These pathways precisely assess the specific factors that contribute towards association among traits of interest which can be effectively utilized in formulating an effective selection programme to improve crop yield (Ali et al. 2009). Keeping these aspects in consideration, the present investigation was planned to assess the genetic parameters of variability, associations among component traits, and their direct and indirect contributions towards seed yield of edible pod pea. The literature pertaining to variability studies in edible pod pea is not available and therefore, literature pertaining to garden pea was used for supporting the results of present study.

## Materials and Methods

**Experimental site:** The present investigation was carried out at the Research Farm, Department of Vegetable Science and Floriculture, C. S. K. Himachal Pradesh Krishi Vishvavidyalaya, Palampur (Himachal Pradesh) located at height of 1,290.8 m above mean sea level with 32° 6' N latitude and 76° 32' E longitude. The location is characterized by humid and temperate climate with annual rainfall of 2,500 mm and the soil is classified as Alfisols Typic Hapludalf clay having with pH of 5.7.

**Experimental material and design:** The experimental material comprised of 36 genotypes of sugar snap pea of which 29 advanced breeding lines ( $F_7$ ) isolated from four interspecific crosses between snow pea × garden pea varieties and seven varieties collected from different institutes (Table 1). The  $F_7$  progenies were derived from hybridization between 'Pb-89 × DPEPP-1', 'Pb-89 × DPEPP-2', 'Palam Priya × DPEPP-1', 'Palam Priya × DPEPP-2' followed by pedigree method of selection on the basis of desirable plant and pod characters. The lines 'DPEPP-1' and 'DPEPP-2 (afilla growth habit)' belong to snow pea while other ones are garden pea varieties with high yield potential. The experiment was laid out in Randomized Complete Block Design with three replications during winter 2016-17 by raising each

genotype in two rows of 1.8 m length with inter and intra-row spacing of 45 cm and 10 cm, respectively. These genotypes were sown on November 07, 2016. The cultural practices recommended for garden pea were followed for raising the crop. The recommended farmyard manure @ 20 tonnes per hectare was mixed in the soil and NPK fertilizers @ 50:60:60 kg of N,  $P_2O_5$  and  $K_2O$  were applied in the rows at the time of sowing through urea, single super phosphate and murate of potash, respectively. Seed treatment with 'Bavistin' at the rate of 3 g/kg of seed was done. Irrigation was provided prior to sowing and as per requirement thereafter at least 15 days intervals. Weeds were controlled with pendimethalin @ 1.5 kg a.i./ha as pre-emergence application followed by two manual weeding at 40 days and 60 days after sowing.

**Parameters recorded:** The observations were recorded on randomly selected 10 plants of each genotype in each replication followed by computing their means for days to flowering, number of branches/plant, internodal length (cm), nodes/plant, plant height (cm), pod length (cm), pod breadth (cm), seeds/pod, pods/plant, dry pod weight (g), straw yield/plant (g), seed yield/plant (g), harvest index, 100-seed weight (g), protein content (%) and total sugars (%).

**Statistical Analysis:** The means of each observation over the replications were subjected to analysis of variance as per Gomez and Gomez (1983) for randomized block design. Different parameters of variability (Burton and De Vane 1953; Johnson et al. 1955), coefficients of correlation (Al-Jibouri et al. 1958) and path coefficients (Dewey and Lu 1959) were estimated by following standard procedures.

## Results and Discussion

The main aim of plant breeders is to generate breeding materials through evaluation of germplasm. The success depends upon the magnitude of genetic variability present in the breeding materials which provides proper strategy and selection criteria for the improvement of target traits (Akram 2016). The increase in yield would be made easier by selecting yield components as yield is some total of these traits which are more often easily inherited than total yield itself (Ukaoma et al. 2013). The analysis of variance revealed that mean squares due to genotypes were significant for all the traits, highlighting the presence of sufficient genetic variability among the genotypes. The knowledge of phenotypic (PCV) and genotypic coefficients of variation (GCV) predict the amount of variation present in the genetic stock and provides an insight to formulate efficient breeding programme. The estimates of PCV were higher

Table 1: Details of genotypes and their plant characteristics

| S. No. | Genotypes | Plant type              | S. No. | Genotypes      | Plant type              |
|--------|-----------|-------------------------|--------|----------------|-------------------------|
| 1      | EPP-10-1  | Afilla, medium tall     | 19     | EPP-P-4-1      | Afilla, medium tall     |
| 2      | EPP-10-2  | Afilla, medium tall     | 20     | EPP-P-4-2      | Afilla, medium tall     |
| 3      | EPP-11-1  | Afilla, medium tall     | 21     | EPP-P-4-3      | Afilla, medium tall     |
| 4      | EPP-11-2  | Afilla, medium tall     | 22     | EPP-P-5        | Afilla, medium tall     |
| 5      | EPP-12-1  | Afilla, medium tall     | 23     | EPP-P-7-1      | Non-afilla, medium tall |
| 6      | EPP-12-2  | Afilla, medium tall     | 24     | EPP-P-7-2-1    | Non-afilla, medium tall |
| 7      | EPP-13-1  | Afilla, medium tall     | 25     | EPP-P-8-1      | Non-afilla, medium tall |
| 8      | EPP-13-2  | Afilla, medium tall     | 26     | EPP-P-9        | Non-afilla, medium tall |
| 9      | EPP-14-1  | Afilla, medium tall     | 27     | EPP-P-9-1      | Non-afilla, medium tall |
| 10     | EPP-14-2  | Afilla, medium tall     | 28     | DPEPP-1        | Non-afilla, medium tall |
| 11     | EPP-15-1  | Non-afilla, medium tall | 29     | DPEPP-2        | Afilla, medium tall     |
| 12     | EPP-15-2  | Non-afilla, medium tall | 30     | Sugar Snap     | Non-afilla, tall        |
| 13     | EPP-15-3  | Non-afilla, medium tall | 31     | VRPO-1         | Non-afilla, tall        |
| 14     | EPP-P-2   | Afilla, medium tall     | 32     | VRPO-2         | Non-afilla, medium tall |
| 15     | EPP-P-2-1 | Afilla, medium tall     | 33     | VRPO-3         | Non-afilla, tall        |
| 16     | EPP-P-2-2 | Afilla, medium tall     | 34     | Arka Sampoorna | Non-afilla, semi tall   |
| 17     | EPP-P-3   | Afilla, medium tall     | 35     | Arka Apoorva   | Non-afilla, semi tall   |
| 18     | EPP-P-3-1 | Afilla, medium tall     | 36     | Mithi Phali    | Non-afilla, medium tall |

Source: S. No. 1-29 are advance breeding lines ( $F_7$ ) isolated through interspecific crosses at HP Agricultural University Palampur; Genotypes 30-33 from Indian Institute of Vegetable Research, Varanasi; 34-35 from Indian Institute of Horticultural Research, Hesaraghatta (Bengaluru) and 36 from Punjab Agricultural University, Ludhiana (Punjab)

than corresponding GCV for all the characters (Table 2) with relatively low differences indicating heritable and comparatively stable nature of the characters and thus, selection based on phenotypic performance would be quite effective in the improvement of these traits. The magnitude of PCV and GCV was high for straw yield/plant. In addition, number of primary branches/plants, internodal length, pods/plant, dry pod weight and seed yield/plant also showed high PCV but moderate GCV, ensuring ample scope for improvement of these traits through selection (Iqbal *et al.*, 2015; Katoch *et al.*, 2016). The moderate estimates of PCV and GCV were recorded for plant height, pod breadth, total sugars and harvest index suggesting cautious approach while following direct selection for these traits.

The magnitude of heritability indicates the reliability with which a genotype can be recognized by its phenotypic expression. However, high heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by substantial amount of genetic advance (Sharma and Kalia, 2002). Hence, high genetic advance coupled with high heritability offers the most effective selection criteria for selection (Karimizadeh *et al.*, 2011) which was recorded for internodal length, plant height, straw yield/plant, dry pod weight and seed yield, suggesting the importance of additive gene action and possibility of selection in the early generations. High heritability along with moderate genetic advance was observed for days to flowering, pod length, pod breadth, pods/plant, total

Table 2: Components of genetic variability for various yield component traits in sugar snaps

| Traits                 | Range        | Population Mean<br>(mean $\pm$ S.E.) | PCV (%) | GCV (%) | $h^2_{bs}$ (%) | Genetic Advance<br>(% of mean) |
|------------------------|--------------|--------------------------------------|---------|---------|----------------|--------------------------------|
| Days to flowering      | 90.33-112.66 | 100.25 $\pm$ 2.71                    | 6.55    | 5.65    | 74.49          | 10.05                          |
| Primary branches/plant | 1.13-2.60    | 1.71 $\pm$ 0.22                      | 23.09   | 16.61   | 51.74          | 24.61                          |
| Internodal length (cm) | 4.65-10.06   | 6.51 $\pm$ 0.39                      | 21.28   | 19.94   | 87.81          | 38.50                          |
| Nodes per plant        | 16.53-22.47  | 20.10 $\pm$ 1.17                     | 9.09    | 5.65    | 38.65          | 7.24                           |
| Plant height (cm)      | 60.27-135.53 | 82.95 $\pm$ 3.90                     | 18.45   | 17.54   | 90.40          | 34.36                          |
| Pod length (cm)        | 6.27-11.28   | 9.23 $\pm$ 0.45                      | 10.67   | 8.89    | 69.39          | 15.26                          |
| Pod breadth (cm)       | 1.40-2.19    | 1.87 $\pm$ 0.09                      | 11.77   | 10.05   | 72.96          | 17.69                          |
| Seeds/pod              | 4.60-7.37    | 6.06 $\pm$ 0.39                      | 11.99   | 9.03    | 56.76          | 14.02                          |
| Pods/plant             | 8.58-23.83   | 17.02 $\pm$ 1.74                     | 20.91   | 16.77   | 64.35          | 27.72                          |
| Dry pod weight (g)     | 14.64-36.68  | 22.32 $\pm$ 1.77                     | 21.22   | 18.86   | 78.97          | 34.53                          |
| Straw yield/plant (g)  | 16.17-43.62  | 28.83 $\pm$ 1.97                     | 26.47   | 25.11   | 90.00          | 49.07                          |
| Seed yield/plant (g)   | 11.74-34.47  | 23.82 $\pm$ 2.74                     | 23.95   | 19.37   | 65.44          | 32.28                          |
| Harvest index (%)      | 35.28-55.87  | 45.48 $\pm$ 2.99                     | 13.19   | 10.45   | 62.76          | 17.05                          |
| 100 seed weight (g)    | 19.33-29.33  | 23.42 $\pm$ 2.07                     | 14.53   | 9.71    | 44.60          | 13.35                          |
| Protein content (%)    | 20.13-28.23  | 23.83 $\pm$ 1.77                     | 11.12   | 6.39    | 33.09          | 7.58                           |
| Total sugars (%)       | 4.27-9.87    | 6.91 $\pm$ 0.37                      | 16.15   | 14.76   | 83.49          | 27.79                          |

Where, PCV and GCV represent phenotypic and genotypic coefficients of variations, respectively;  $h^2_{bs}$ : Heritability in Broad sense

Table 3: Phenotypic (P) and genotypic (G) coefficient of correlation among different horticultural traits in sugar snaps

| traits                        |   | Primary<br>branches/<br>plant | Internodal<br>length | Nodes/<br>plant | Plant<br>height | Pod<br>length | Pod<br>breadth | Seeds/<br>pod | Pods/<br>plant | Protein<br>content | Total<br>sugars | Straw<br>yield/<br>plant | 100<br>Seed<br>weight | Dry pod<br>weight | Harvest<br>index | Seed<br>yield/<br>plant |
|-------------------------------|---|-------------------------------|----------------------|-----------------|-----------------|---------------|----------------|---------------|----------------|--------------------|-----------------|--------------------------|-----------------------|-------------------|------------------|-------------------------|
| Days to<br>flowering          | P | 0.039                         | -0.153               | 0.255*          | -0.121          | 0.152         | 0.343*         | 0.060         | 0.145          | 0.015              | 0.044           | -0.074                   | 0.004                 | 0.004             | 0.038            | -0.056                  |
|                               | G | 0.092                         | -0.253*              | 0.348*          | -0.174          | 0.108         | 0.410*         | -0.018        | 0.219*         | 0.094              | 0.081           | -0.098                   | 0.053                 | 0.002             | 0.082            | -0.064                  |
| Primary<br>branches/<br>plant | P |                               | -0.125               | -0.010          | -0.180          | -0.057        | 0.270*         | -0.220*       | -0.041         | -0.150             | 0.015           | -0.088                   | -0.216*               | 0.192*            | -0.099           | -0.236*                 |
|                               | G |                               | -0.234*              | 0.178           | -0.234*         | 0.011         | 0.395*         | -0.107        | 0.063          | -0.261*            | 0.069           | -0.146                   | -0.248*               | 0.290*            | -0.085           | -0.320*                 |
| Internodal<br>length          | P |                               |                      | 0.177           | 0.795*          | -0.246*       | -0.219*        | -0.098        | 0.197*         | 0.146              | 0.219*          | -0.193*                  | 0.060                 | -0.173            | 0.180            | -0.059                  |
|                               | G |                               |                      | 0.344*          | 0.898*          | -0.340*       | -0.329*        | -0.134        | 0.278*         | 0.277*             | 0.293*          | -0.242*                  | 0.096                 | -0.242*           | 0.311*           | -0.043                  |
| Nodes/<br>plant               | P |                               |                      |                 | 0.504*          | -0.131        | 0.119          | 0.000         | 0.486*         | -0.027             | 0.088           | -0.116                   | -0.106                | -0.072            | -0.001           | -0.249*                 |
|                               | G |                               |                      |                 | 0.601*          | -0.466*       | 0.316*         | -0.195*       | 0.571*         | -0.234*            | 0.242*          | -0.192*                  | -0.376*               | -0.078            | 0.086            | -0.419*                 |
| Plant height                  | P |                               |                      |                 |                 | -0.252*       | -0.212*        | -0.017        | 0.339*         | 0.140              | 0.122           | -0.166                   | 0.055                 | -0.234*           | 0.156            | -0.087                  |
|                               | G |                               |                      |                 |                 | -0.376*       | -0.265*        | -0.064        | 0.353*         | 0.201*             | 0.162           | -0.174                   | 0.093                 | -0.283*           | 0.252*           | -0.054                  |
| Pod length                    | P |                               |                      |                 |                 |               | 0.338*         | 0.515*        | 0.017          | 0.068              | 0.042           | 0.141                    | 0.163                 | -0.101            | 0.058            | 0.304*                  |
|                               | G |                               |                      |                 |                 |               | 0.288*         | 0.557*        | -0.104         | 0.085              | 0.103           | 0.162                    | 0.211*                | -0.093            | 0.154            | 0.481*                  |
| Pod breadth                   | P |                               |                      |                 |                 |               |                | -0.008        | 0.044          | 0.064              | 0.066           | -0.265*                  | -0.196*               | 0.402*            | 0.236*           | -0.097                  |
|                               | G |                               |                      |                 |                 |               |                | -0.098        | 0.028          | 0.097              | 0.127           | -0.339*                  | -0.323*               | 0.448*            | 0.375*           | -0.133                  |
| Seeds/pod                     | P |                               |                      |                 |                 |               |                |               | -0.046         | 0.114              | -0.035          | 0.248*                   | 0.184                 | -0.290*           | -0.130           | 0.268*                  |
|                               | G |                               |                      |                 |                 |               |                |               | -0.221*        | -0.016             | -0.123          | 0.335*                   | 0.299*                | -0.375*           | -0.205*          | 0.411*                  |
| Pods/plant                    | P |                               |                      |                 |                 |               |                |               | -0.010         | 0.176              | -0.011          | 0.134                    | -0.298*               | 0.068             | -0.090           |                         |
|                               | G |                               |                      |                 |                 |               |                |               |                | -0.279*            | 0.295*          | 0.036                    | -0.007                | -0.339*           | 0.039            | -0.129                  |
| Protein content               | P |                               |                      |                 |                 |               |                |               |                |                    | 0.117           | -0.024                   | 0.238*                | -0.209*           | 0.169            | 0.201*                  |
|                               | G |                               |                      |                 |                 |               |                |               |                |                    | 0.213*          | -0.022                   | 0.299*                | -0.200*           | 0.281*           | 0.380*                  |
| Total sugars                  | P |                               |                      |                 |                 |               |                |               |                |                    |                 | -0.311*                  | 0.065                 | -0.191*           | 0.252*           | -0.033                  |
|                               | G |                               |                      |                 |                 |               |                |               |                |                    |                 | -0.348*                  | 0.061                 | -0.213*           | 0.308*           | -0.113                  |
| Straw<br>yield/plant          | P |                               |                      |                 |                 |               |                |               |                |                    |                 |                          | 0.040                 | -0.194*           | -0.657*          | 0.351*                  |
|                               | G |                               |                      |                 |                 |               |                |               |                |                    |                 |                          | 0.030                 | -0.222*           | -0.781*          | 0.420*                  |
| 100 seed<br>weight            | P |                               |                      |                 |                 |               |                |               |                |                    |                 |                          |                       | -0.246*           | 0.356*           | 0.548*                  |
|                               | G |                               |                      |                 |                 |               |                |               |                |                    |                 |                          |                       | -0.257*           | 0.240*           | 0.552*                  |
| Dry pod<br>weight             | P |                               |                      |                 |                 |               |                |               |                |                    |                 |                          |                       |                   | 0.098            | -0.184                  |
|                               | G |                               |                      |                 |                 |               |                |               |                |                    |                 |                          |                       |                   | 0.179            | -0.204*                 |
| Harvest index                 | P |                               |                      |                 |                 |               |                |               |                |                    |                 |                          |                       |                   |                  | 0.400*                  |
|                               | G |                               |                      |                 |                 |               |                |               |                |                    |                 |                          |                       |                   |                  | 0.164                   |

\*Significant at  $Pd \leq 0.05$

sugars and harvest index, indicating the preponderance of additive and non-additive gene effects for their inheritance (Kumar et al. 2015) and hybridization followed by selection in the later generations would be applicable for their improvement.

Yield is a complex polygenic trait that results from multiple interactions between component traits. Selection for yield may not be effective unless other yield components influencing it directly or indirectly are taken into consideration. The correlation studies help in simultaneous selection of traits of interest influencing yield (Semahegn and Tesfaye 2016). Therefore, identification of key traits is important which contribute effectively for enhancing yield (Jain et al. 2015) and defining an ideal plant type. In general, the genotypic correlation coefficients were higher in magnitude than the corresponding phenotypic ones (Table 3) which revealed that though there is a strong inherent association between various characters, the phenotypic expression of the correlation gets reduced under the influence of environment (Kumar et al. 2015).

Seed yield/plant had positive and significant correlation with pod length, seeds/pod, protein content, straw yield/plant and 100-seed weight at both phenotypic and genotypic level. This reflects that selection on the basis of these traits might lead to higher yield and need to be

given special focus. However, it showed negative correlation with number of branches/plant and nodes/plant. Seed yield also showed positive association with harvest index at phenotypic level while it was negatively associated with dry pod weight at genotypic level. Sharma and Kalia (1998) and Awasthi et al. (2011) also recorded positive association of yield with majority of these traits in garden pea. Pod characteristics determine the overall performance of the genotypes. Plant growth habit is also important selection criteria and needs special consideration. Plant height revealed positive association with pods/plant and internodal length while it was conversely associated with pod length, pod breadth and dry pod weight at both the levels. This clearly indicates that more plant height contributed to more pod bearing but resulted in decreased pod size. Also, internodal length also resulted in more plant height. Therefore, it would be imperative to maintain a balance among these traits to achieve maximum gain with respect to desirable pod size and seed yield.

Correlation coefficients alone are insufficient to recognize cause and effect relationships among traits associated with yield. Path coefficient analysis permits a better understanding of associations between different characters by dividing the magnitude of association with the dependent character into direct and indirect effects

Table 4: Estimates of direct and indirect effects of different traits on seed yield per plant at phenotypic (P) and genotypic (G) levels in sugar snaps

| traits                 |   | Primary branches/plant | Internodal length | Nodes/plant | Plant height | Pod length | Pod breadth | Seeds/pod | Pods/plant | Protein content | Total sugars | Straw yield/plant | 100 Seed weight | Dry pod weight | Harvest index | Primary branches/plant | r       |
|------------------------|---|------------------------|-------------------|-------------|--------------|------------|-------------|-----------|------------|-----------------|--------------|-------------------|-----------------|----------------|---------------|------------------------|---------|
| Days to flowering      | P | 0.004                  | 0.001             | 0.000       | -0.004       | 0.006      | 0.005       | -0.019    | 0.006      | -0.023          | 0.000        | 0.001             | -0.072          | 0.000          | 0.000         | 0.039                  | -0.056  |
|                        | G | -0.068                 | 0.009             | -0.060      | 0.116        | 0.106      | -0.004      | -0.091    | -0.002     | -0.060          | 0.004        | -0.004            | -0.138          | 0.011          | 0.000         | 0.117                  | -0.064  |
| Primary branches/plant | P | 0.000                  | 0.013             | 0.000       | 0.000        | 0.009      | -0.002      | -0.015    | -0.021     | 0.007           | 0.000        | 0.000             | -0.086          | -0.023         | -0.015        | -0.104                 | -0.236* |
|                        | G | -0.006                 | 0.098             | -0.055      | 0.059        | 0.144      | 0.000       | -0.088    | -0.012     | -0.017          | -0.011       | -0.003            | -0.206          | -0.049         | -0.050        | -0.123                 | -0.320* |
| Internodal length      | P | -0.001                 | -0.002            | 0.000       | -0.003       | -0.040     | -0.009      | 0.012     | -0.010     | -0.032          | 0.000        | 0.006             | -0.188          | 0.006          | 0.013         | 0.188                  | -0.059  |
|                        | G | 0.017                  | -0.023            | 0.237       | 0.115        | -0.550     | 0.012       | 0.073     | -0.015     | -0.076          | 0.011        | -0.015            | -0.341          | 0.019          | 0.042         | 0.448                  | -0.043  |
| Nodes/plant            | P | 0.001                  | 0.000             | 0.000       | -0.017       | -0.026     | -0.005      | -0.007    | 0.000      | -0.078          | 0.000        | 0.002             | -0.112          | -0.011         | 0.006         | -0.002                 | -0.249* |
|                        | G | -0.024                 | 0.017             | 0.082       | 0.335        | -0.368     | 0.017       | -0.070    | -0.021     | -0.156          | -0.010       | -0.012            | -0.271          | -0.075         | 0.014         | 0.124                  | -0.419* |
| Plant height           | P | 0.000                  | -0.002            | 0.000       | -0.009       | -0.051     | -0.009      | 0.012     | -0.002     | -0.054          | 0.000        | 0.003             | -0.161          | 0.006          | 0.018         | 0.163                  | -0.087  |
|                        | G | 0.012                  | -0.023            | 0.213       | 0.201        | -0.612     | 0.014       | 0.059     | -0.007     | -0.096          | 0.008        | -0.008            | -0.246          | 0.018          | 0.049         | 0.363                  | -0.054  |
| Pod length             | P | 0.001                  | -0.001            | 0.000       | 0.002        | 0.013      | 0.036       | -0.019    | 0.050      | -0.003          | 0.000        | 0.001             | 0.137           | 0.017          | 0.008         | 0.061                  | 0.304*  |
|                        | G | -0.007                 | 0.001             | -0.081      | -0.156       | 0.230      | -0.037      | -0.064    | 0.061      | 0.028           | 0.003        | -0.005            | 0.228           | 0.042          | 0.016         | 0.221                  | 0.481*  |
| Pod breadth            | P | 0.001                  | 0.004             | 0.000       | -0.002       | 0.011      | 0.012       | -0.055    | -0.001     | -0.007          | 0.000        | 0.002             | -0.257          | -0.021         | -0.031        | 0.247                  | -0.097  |
|                        | G | -0.028                 | 0.039             | -0.078      | 0.106        | 0.162      | -0.011      | -0.223    | -0.011     | -0.008          | 0.004        | -0.006            | -0.478          | -0.064         | -0.078        | 0.540                  | -0.133  |
| Seeds/pod              | P | 0.000                  | -0.003            | 0.000       | 0.000        | 0.001      | 0.018       | 0.000     | 0.097      | 0.007           | 0.000        | -0.001            | 0.241           | 0.020          | 0.022         | -0.136                 | 0.268*  |
|                        | G | 0.001                  | -0.010            | -0.032      | -0.065       | 0.039      | -0.020      | 0.022     | 0.109      | 0.060           | -0.001       | 0.006             | 0.473           | 0.059          | 0.065         | -0.296                 | 0.411*  |
| Pods/plant             | P | 0.001                  | -0.001            | 0.000       | -0.008       | -0.017     | 0.001       | -0.002    | -0.005     | -0.161          | 0.000        | 0.005             | -0.010          | 0.014          | 0.023         | 0.071                  | -0.090  |
|                        | G | -0.015                 | 0.006             | 0.066       | 0.191        | -0.216     | 0.004       | -0.006    | -0.024     | -0.273          | -0.011       | -0.015            | 0.051           | -0.001         | 0.059         | 0.056                  | -0.129  |
| Protein content        | P | 0.000                  | -0.002            | 0.000       | 0.000        | -0.007     | 0.002       | -0.004    | 0.011      | 0.002           | 0.000        | 0.003             | -0.023          | 0.025          | 0.016         | 0.177                  | 0.201*  |
|                        | G | -0.006                 | -0.026            | 0.066       | -0.078       | -0.123     | -0.003      | -0.022    | -0.002     | 0.076           | 0.041        | -0.011            | -0.031          | 0.059          | 0.035         | 0.405                  | 0.380*  |
| Total sugars           | P | 0.000                  | 0.000             | 0.000       | -0.002       | -0.006     | 0.002       | -0.004    | -0.003     | -0.028          | 0.000        | 0.026             | -0.303          | 0.007          | 0.015         | 0.264                  | -0.033  |
|                        | G | -0.005                 | 0.007             | 0.070       | 0.081        | -0.099     | -0.004      | -0.028    | -0.013     | -0.080          | 0.009        | -0.051            | -0.490          | 0.012          | 0.037         | 0.443                  | -0.113  |
| Straw yield/plant      | P | 0.000                  | -0.001            | 0.000       | 0.002        | 0.008      | 0.005       | 0.015     | 0.024      | 0.002           | 0.000        | -0.008            | 0.972           | 0.004          | 0.015         | -0.687                 | 0.351*  |
|                        | G | 0.007                  | -0.014            | -0.057      | -0.064       | 0.107      | -0.006      | 0.075     | 0.037      | -0.010          | -0.001       | 0.018             | 1.410           | 0.006          | 0.039         | -1.125                 | 0.420*  |
| 100 seed weight        | P | 0.000                  | -0.003            | 0.000       | 0.002        | -0.003     | 0.006       | 0.011     | 0.018      | -0.021          | 0.000        | 0.002             | 0.039           | 0.107          | 0.019         | 0.372                  | 0.548*  |
|                        | G | -0.004                 | -0.024            | 0.023       | -0.126       | -0.057     | -0.008      | 0.072     | 0.033      | 0.002           | 0.012        | -0.003            | 0.042           | 0.199          | 0.045         | 0.346                  | 0.552*  |
| Dry pod weight         | P | 0.000                  | 0.003             | 0.000       | 0.001        | 0.012      | -0.004      | -0.022    | -0.028     | 0.048           | 0.000        | -0.005            | -0.188          | -0.026         | -0.076        | 0.102                  | -0.184  |
|                        | G | 0.000                  | 0.028             | -0.057      | -0.026       | 0.173      | 0.003       | -0.100    | -0.041     | 0.093           | -0.008       | 0.011             | -0.313          | -0.051         | -0.174        | 0.258                  | -0.204* |
| Harvest index          | P | 0.000                  | -0.001            | 0.000       | 0.000        | -0.008     | 0.002       | -0.013    | -0.013     | -0.011          | 0.000        | 0.006             | -0.639          | 0.038          | -0.007        | 1.045                  | 0.400*  |
|                        | G | -0.006                 | -0.008            | 0.074       | 0.029        | -0.154     | -0.006      | -0.083    | -0.022     | -0.011          | 0.011        | -0.016            | -1.101          | 0.048          | -0.031        | 1.440                  | 0.164   |

Unexplained variation (P): 0.107; (G): 0.059; \*Significant at  $P_d \leq 0.05$ ; r-correlation coefficient with seed yield per plant; bold values indicate direct effect

(Ukaoma *et al.* 2013) thus, helps in formulating an effective selection programme. Harvest index and straw yield/plant at both genotypic and phenotypic levels revealed maximum positive direct effects suggested the importance of these traits towards seed yield (Table 4). Besides, nodes/plant followed by inter-nodal length, 100 seed weight and seeds/pod had also substantial positive contribution as direct effects towards seed yield at genotypic level. A critical scrutiny of path coefficients revealed that straw yield/plant and harvest index, in general, contributed maximum via their indirect effect to the total association of majority of traits with seed yield while plant height, pod breadth, pods/plant, 100 seed weight and dry pod weight also contributed to some extent. Therefore, these traits would be of great significance for achieving enhanced performance of genotypes for seed yield/plant.

Based on parameters of variability, it can be concluded that selection for internodal length, plant height, straw yield/plant, dry pod weight and seed yield/plant in early generations would be effective. Significant correlation of seed yield/plant was recorded with pod length, seeds/pod, protein content, straw yield/plant and 100-seed weight which was mainly due to direct and indirect

effects via harvest index and straw yield/plant. Therefore, these traits provide an important criterion of selection procedures for achieving enhanced performance of genotypes for higher seed yield.

## I k j k k

मीठी मटर के 4 अन्तः प्रजाति संकरणों के एफ<sub>7</sub> पीढ़ी से प्राप्त 29 उच्चिकृत प्रजनन वंशक्रमों का मूल्यांकन 7 एकत्रित जननद्रव्यों के साथ मूल्यांकन रैण्डोमाइज्ड ब्लॉक डिजाइन में 3 बार प्रतिकृति वर्ष 2016–17 के शीतकाल में हिमाचल प्रदेश कृषि विश्वविद्यालय, पालमपुर (हिमाचल प्रदेश) के प्रक्षेत्र में किया गया। बाह्यदृश्य गुणांक विविधता एवं आनुवांशिक गुणांक विविधता पुआल उपज प्रति पौध में सबसे ज्यादा था, जबकि शाखायें प्रति पौध, पार्श्व गांठ लम्बाई, फलियाँ प्रति पौध, शुष्क फली भार एवं बीज उपज प्रति पौध में उच्च बाह्यदृश्य गुणांक विविधता के साथ मध्यम आनुवांशिक गुणांक विविधता पाया गया। उच्च वंशागतत्व एवं आनुवांशिक उन्नयन पार्श्व गांठ लम्बाई, पौध ऊँचाई, पुआल उपज प्रति पौध, शुष्क फली भार एवं बीज उपज प्रति पौध की उच्चता यह संकेत देता है कि योग्य जीन प्रभाव इनके वंशागतत्व स्थान्तरण में प्रभावी है। बीज उपज प्रति पौध सकारात्मक रूप से फली लम्बाई, बीज की संख्या प्रति फली, बीज में प्रोटीन की मात्रा, पुआल उपज प्रति पौध एवं 100 बीज भार, बाह्यदृश्य एवं आनुवांशिक प्रारूप दोनों स्तरों पर सम्बन्धित पाया गया। तुड़ाई गुणांक एवं पुआल उपज ने सबसे ज्यादा योगदान प्रत्यक्ष एवं परोक्ष रूप से अन्य सम्बन्धित गुणों के

साथ बीज उपज के साथ पाया गया जबकि पार्श्व गांठों की संख्या प्रति पौध, पार्श्वपर्वों की लम्बाई, 100 बीजों का भार एवं बीज प्रति फली का योगदान कुछ स्तर तक देखा गया। इसलिए बीज उपज हेतु प्रभेदों के बेहतर निष्पादन को प्राप्त करने के लिए इन लक्ष्यों का महत्वपूर्ण योगदान होगा।

## References

- Akram S, Hussain BMN, Bari MAA, Burritt DJ and Hossain MA (2016) Genetic variability and association analysis of soybean (*Glycine max* (L.) Merrill) for yield and yield attributing traits. *Plant Gene and Trait* 7(13):1-11.
- Al-Jibouri HA, Miller PA and Robinson HF (1958) Genotypic and environmental variance and co-variance in upland cotton crops of inter-specific origin. *Agronomy Journal* 50:633-636.
- Awasthi S, Lavanya GR and Babu GS (2011) Character association and component analysis in garden pea (*Pisum Sativum* L. *hortense*). *Environment and Ecology* 29:133-135.
- Bizeti HS, De Carvalho CGP, De Souza JRP and Destro D (2004) Path Analysis under Multicollinearity in Soybean. *Brazilian Archives of Biology and Technology: An International Journal* 47(5):669-676.
- Burton GW and De Vane EH (1953) Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal* 54:478-81.
- Cramer CS and Wehner TC (2000) Path analysis of the correlation between fruit number and plant traits of cucumber populations. *Hort science* 35(4):708-771.
- Dewey DR and Lu KH (1959) A correlation and path analysis of components of crested wheat-grass seed production. *Agronomy Journal* 51:515-518.
- Gomez KA and Gomez AA (1983) *Statistical procedures for agricultural research*. 2nd Edn. John Wiley and Sons, New York, pp 357-427.
- Iqbal M, Bashir I, Nadeem K, Lateef A, Chishti SAS and Niaz S (2015) Association pattern among yield and its related attributes in pea (*Pisum sativum* L.). *Journal of Agricultural Research* 53:173-177.
- Jain S, Srivastava SC, Singh KS, Indapurkar YM and Singh BK (2015) Studies on genetic variability, character association and path analysis for yield and its contributing traits in soybean [*Glycine max* (L.) Merrill]. *Legume Research* 38(2):182-184.
- Johnson HW, Robinson HF and Comstock RE (1955) Estimates of genetic and environmental variability in soybeans. *Agronomy Journal* 47:314-318.
- Karimizadeh R, Mohammadi M, Mamo MS, Bavi V, Hoseinpour T, Khanzadeh H, Ghoghogh H and Armion M (2011). Application of multivariate methods in determining grain yield stability of durum wheat genotypes in semi-warm dryland areas of Iran. *Modern Genetics Journal* 16:33-48.
- Katoch V, Singh P, Devi MB, Sharma A, Sharma GD and Sharma JK (2016) 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* 39:163-169.
- Kumar R, Kumar M, Dogra RK and Bharat NK (2015) Variability and character association studies in garden pea (*Pisum sativum* var. *hortense* L.) during winter season at mid hills of Himachal Pradesh. *Legume Research* 38:164-168.
- Malek MA, Raffi MY, Afroj MSS, Nath UK and Mondol MMA (2014) Morphological characterization and assessment of genetic variability, character association and divergence in soybean mutants. *The Scientific World Journal* 1-12. <https://doi.org/10.1155/2014/968796> PMID:25197722 PMID:PMC4146355.
- Salahuddin S, Abro M, Kandhro M, Salahuddin L and Laghari S (2010) Correlation and path coefficient analysis of yield components of upland cotton [*Gossypium hirsutum* (L.)] symodial. *World Applied Science Journal* 8:71-75.
- Semahegn Y and Tesfaye M (2016) Characters associations and path analysis in safflower (*Carthamus tinctorious*) accessions. *Molecular Plant Breeding* 7(31):1-5.
- Sharma A and Kalia P (1998) Correlation and path analysis of biparental progenies in garden pea (*Pisum sativum* L.). *Vegetable Science* 25(1):26-31.
- Sharma A and Kalia P (2002) Genetic analysis of pod yield and its contributing traits in garden pea (*Pisum sativum* L.). *Vegetable Science* 29(2):106-109.
- Sharma A, Sekhon BS, Sharma S and Kumar R (2019) Newly isolated intervarietal garden pea (*Pisum sativum* L.) progenies ( $F_7$ ) under north western Himalayan conditions of India. *Experimental Agriculture* <https://doi.org/10.1017/S00144797190001151>.
- Singh G and Dhall RK (2018) Heterotic potential and combining ability of yield and quality traits in garden pea (*Pisum sativum* L.). *Vegetable Science* 45(1):7-13.
- Sneddon JL (1970) Identification of garden pea varieties. Grouping, arrangement and use of continuous characters. *Journal of the National Institute of Agricultural Botany* 12:1-16.
- Ukaoma AA, Okocha PI and Okechukwu RI (2013) Heritability and character correlation among some rice genotypes. *Journal of Plant Breeding and Genetics* 1(2):73-78.