

## Estimates on Characters Association and Path Coefficient Analysis in Garden Pea (*Pisum sativum* L.) Varieties in Satna District of Madhya Pradesh

Ayodhya Prasad Pandey<sup>1</sup>, Abhshek Sahu<sup>2</sup>, Rajbeer Singh Gaur<sup>3</sup>, Brindaban Singh<sup>4</sup>,  
Neeraj Verma<sup>5</sup>

Department of Genetics and Plant Breeding, Faculty of Agriculture Science and Technology  
AKS University, Satna- 485001 (M.P.)

### Abstract:

Twenty distinct pea cultivars were planted in a Completely Randomized Block Design (CRBD) at AKS University, Satna, in the Rabi season of November 2022. Data was collected for ten quantitative traits and analyzed for variance, correlation and path coefficient analysis. The experimental setup showed significant differences in all traits due to the treatments. The analysis of variance revealed a notable amount of variability among genotypes for all the traits under study. Genotypic correlation was higher than phenotypic ones in magnitude for all the characters except correlation between plant height and days to maturity, plant height and number of pods per plant, plant height and seed yield per plant, number of pod per cluster and number of seed per pod, number of seed per pod and 100 seed weight (g). Path coefficient analysis revealed that number of pods per plant, number of pod per cluster and days to maturity had exerted maximum direct effect on seed yield at both genotypic and phenotypic levels. Plant height (cm) and 100 seed weight (g) had exhibited negative direct effect on seed yield at both genotypic and phenotypic levels. So these important characters that could be taken into consideration for selection and improvement of seed yield in pea. The residual effect was 0.3766 at genotypic level was moderate indicating that most of the characters affecting seed yield has to be include in the future study. The residual effect was 0.3026 at phenotypic level was moderate and indicating that less influence of environment on the expression of some characters affecting seed yield has to be also include in the future study.

**Keyword:** Pea, Variance, Correlation and Path coefficient.

### Introduction

Pea is one of the most important legume vegetables grown all over the world during the cool season. It belongs to the circle of relatives of the Fabeaceae subfamily. Pea is a self-pollinated crop. It has diploid chromosomes number  $2n = 14$  and  $n = 7$ , which are found in the reproductive gamete. It is most commonly grown in temperate areas around the world. In tropical and subtropical areas, it is grown at cooler altitudes and during the winter season.

Pea is a winter annual herbaceous plant native to the Mediterranean region. It is also found in the Near East, and is considered to have a secondary centre of origin Ethiopia, (Blixt 1974). This plant has an angular stem with glaucous alternate leaves. The leaves are distichous. According to the study of Brahmappa and Pal (1981) The variety Bonneville exhibited five distinct stages of floral bud development. The release of pollen from the anthers and the

blooming of the flower took place during stages III and V, respectively, between the hours of 05.45 and 07.30.

The stigmas were able to receive pollen 48 hours prior to anthesis and up to 24 hours after anthesis. The viability of the pollen was measured at 98% during dehiscence, 88.7% at anthesis, and 52.9% 24 hours after anthesis. On average, 83% of pods were successfully formed through natural pollination, while artificial pollination with pollen from 10 other varieties resulted in pod set percentages ranging from 33% to 66%. Self pollination occurred during stage III, before the flower had fully opened.

Androecium has 10 stamens arranged in a 9+1 pattern. The filaments of 9 stamens become fused together for most of their length, forming a tube known as filamental tube (Tucker, 1989). The 10th stamen is free. It has 5 petals in (2+2+1) condition. The 5 petals have 2 wings and 1 standard, fused except at the base. The keel petal covers the pistil. It is proposed that differences in the roles and relationships of these regulators may lead to the diverse range of floral symmetries observed in legume species and other flowering plants (Wang *et al.* 2008)

According to Khan *et al.* (2021), yields of this crop are now uncertain and low due to farmers' continuous reliance on native landraces rather than established high-yielding cultivars. However, studies by Khan *et al.* (2020), Khan *et al.* (2021) and Obidiebube *et al.* (2020) have found this crop can potentially produce much higher yields of 1049-5267 kg/ha. Examining genetic diversity is important for developing disease/insect resistance and increasing breeding success of high-yield traits (Molosiwa, 2012). Plants with favorable traits survive better under climate fluctuations, so sufficient genetic variation promotes sustainability. Breeders have utilized morphological features to develop stable, high-yielding lines across environments, including chickpea (Yaghotipoor & Farshadfar, 2007), groundnut (Puttha *et al.*, 2007; Painawadee *et al.*, 2009), and bean landraces (Duran *et al.*, 2005).

The results of this study, which are presented in Table 6, demonstrate the correlation coefficients (both genotypic and phenotypic) for various vegetative characteristics, pod yield, and yield contributing factors. These coefficients indicate the potential positive or negative relationship between these variables. While the r-value for Pearson's correlation coefficient helps identify a relationship between two independent variables, it does not quantify the strength of the association. Ratner (2009) outlines a commonly used method for analyzing correlation coefficients, while Wright (1921) distinguishes between direct and indirect effects by assigning correlations to better evaluate cause-and-effect relationships. The findings of this study reveal significant correlations among several vegetative, yield, and yield contributing components. Due to their interconnectedness, these variables have both direct and indirect effects on pod yield and its contributing traits. As a result, Misangu *et al.* (2007), Oyiga and Uguru (2011), Ofori (1996) in Bambara groundnut, Usman *et al.* (2017) in chili, and Oladosu *et al.* (2018) in rice effectively employ path coefficient analysis to investigate the direct and indirect correlations between component characteristics through the partitioning of correlation coefficients.

## Materials and Methods

The present investigation was carried out, and the techniques applied and materials used there in have been described under the following heads. The field experiment under present investigation was conducted during *Rabi*, 2022-23 at Research Farm, Genetics and Plant Breeding, AKS University, Sherganj, Satna, Madhya Pradesh. Geographically, Sherganj is situated at 24°58' N latitude, 80°83' E longitude and at about 4 km away from the district head quarter of Satna and on 322 meters above mean sea level.

The collection of 20 varieties/strains of Pea (*Pisum sativum* L.) germplasm comprising indigenous genotypes constituted the experimental materials for this study. These genotypes, exhibiting a wide spectrum of variability for various agronomic and morphological characters, were obtained from the KVK Surgi, Rajnandgaon (C.G), KVK, Balod (C.G), KVK, Bemetara (C.G), Horticulture Department, Balod (C.G), KVK, Ambikapur (C.G), and some varieties/strains are also provided by AKS University, Satna, M.P

An evaluation of 20 pea germplasm under irrigated conditions was carried out through a Completely Randomized Block Design experiment. The experimental field was divided into 3 blocks of equal size, each containing 20 plots. Each plot consisted of 3 rows, each 2 meters in length, with a row-to-row spacing of 40 cm and a plant-to-plant spacing of 10 cm. Recommended cultural practices were implemented to ensure a successful crop yield.

The characters studied were days to 50 % flowering, plant height (cm), days to maturity, no. of pods per plant, pod length, no. of cluster per plant, no. of pods per cluster, number of seeds per pod, 100-seed weight (g) and seed yield per plant. The experiment's design underwent analysis of variance following the procedure outlined by Panse and Sukhatme (1967). The correlation between various characters at both genotypic and phenotypic levels was calculated using the method proposed by Searle (1961). Path coefficient analysis was conducted using the formula recommended by Dewey & Lu (1959).

## Result and Discussion

### Analysis of variance (ANOVA) for the design of experiment.

The analysis of variance for the design of the experiment involving 20 pea strains/varieties was evaluated in Randomized Block Design with three replications for the ten quantitative characters. The design of the experiment indicated highly significant differences for all the characters. Non-significant differences due to replications were observed for all the characters. **Table 1**

A broad spectrum of intergenotypic variability of phenotypic traits indicates a wide scope of selection and chances of further improvement of these traits singly or in combinations. All the ten characters selected for study showed highly significant inter-varietal variation and hence these characters can be used for selection in formulating breeding programmes. The analysis of variance exhibited that mean sum squares due to genotypes were significant for all the growth parameters, yield contributing traits, and quality characters, indicating thereby the presence of sufficient genetic variability in the genotypes. Earlier researchers namely Kumar *et al.* (2015), Iqbal *et al.* (2015), Thakur *et al.* (2016), Gudadinni *et al.* (2017), Khan *et al.*

(2017), Barcchiya *et al.* (2018) and Kumawat (2018) Ali *et al.* (2018) Bishnoi *et al.* (2021), Ertiro (2022), Kumar *et al.* (2022) have also reported significant amount of variability in the genetic material for all the characters studied in field pea.

### **Correlation coefficient:**

The grain yield of a crop is determined by the interplay of various interconnected traits. As such, it is crucial to choose based on these individual traits after evaluating their correlation with grain yield. Understanding the association between characters sheds light on their mutual relationship, serving as a key factor in determining the selection strategy for enhancing the crop being studied. The correlation coefficient was calculated for all twelve traits at genotypic and phenotypic levels in the current study, and the results are shown in Table 2. It was observed that while there was a significant inherent relationship among the traits examined, the phenotypic correlation was weakened by environmental factors. These results align with the conclusions drawn by Saxena and Asthana (1962).

The direction of genotypic and phenotypic correlation was similar for almost all the characters. In general, genotypic correlation was higher than phenotypic correlation in magnitude for all the characters except correlation between plant height and days to maturity, plant height and number of pods per plant, plant height and seed yield per plant, number of pods per cluster and number of seeds per pod, number of seeds per pod and 100 seed weight (g).

### **Days to 50 % flowering:**

Days to 50 % flowering positive but non-significant correlation with days to maturity (0.405, 0.391) and pod length (0.215, 0.213) at both genotypic and phenotypic levels, respectively and a negative but non-significant correlation with plant height (cm) (-0.308, -0.303) and number of pods per cluster (-0.272, -0.269) at both genotypic and phenotypic levels, respectively.

### **Plant height (cm):**

Plant height showed a positive significant correlation with shelling (%) (0.545\*, 0.524\*) at both genotypic and phenotypic levels, respectively. It also showed a negative but significant correlation with Number of seeds per pod (-0.500\*, -0.483\*) and 100 seed weight (g) (-0.594\*\*, -0.584\*\*) at both genotypic and phenotypic levels, respectively.

### **Days to maturity:**

Days to maturity exhibited significant positive correlation with Pod length (0.478\*, 0.472\*) and Number of seeds per pod (0.460\*, 0.441\*) at both genotypic and phenotypic levels, respectively. It also exhibited a non-significant but negative correlation with No. of pod per cluster (-0.266, -0.245) and 100 seed weight (g) (-0.207, -0.204) at both genotypic and phenotypic level, respectively.

**Number of pods per plant:**

Number of pods per plant showed high positive significant correlation with seed yield per plant (0.985\*\*, 0.915\*\*) at both genotypic and phenotypic levels, respectively. It is also exhibited a negative but non-significant correlation with shelling (%) (-0.236, -0.201) and 100 seed weight (g) (-0.197, -0.174) at both genotypic and phenotypic levels, respectively.

**Pod length:**

Pod length exhibited the high significant positive correlation with Number of seed per pod (0.755\*\*, 0.690\*\*) at both genotypic and phenotypic levels, respectively. It is also showed negative but non-significant correlation with 100 seed weight (g) (-0.173, -0.172), shelling (%) (-0.085, -0.074) and number of pod per cluster (-0.056, -0.060) at both genotypic and phenotypic levels, respectively.

**Shelling (%):**

Shelling (%) showed high negative but significant correlation with 100 seed weight (g) (-0.587\*\*, -0.565\*\*) at both genotypic and phenotypic levels, respectively. It is also showed negative but non-significant correlation with number of seed per pod (-0.386, -0.368) seed yield per plant (-0.182, -0.179) at both genotypic and phenotypic levels, respectively.

**Number of pod per cluster:**

No. of pod per cluster showed positive but non-significant correlation with seed yield per plant (0.299, 0.280) and negative but non-significant correlation with 100 seed weight (g) (-0.189, -0.169) and number of seed per pod (-0.047, -0.055) at both genotypic and phenotypic levels, respectively.

**Number of seed per pod:**

Number of seeds per pod showed positive but non-significant correlation with seed yield per plant (0.415, 0.394) 100 seed weight (g) (0.066, 0.067) at both genotypic and phenotypic levels, respectively.

**100 seed weight (g):**

100 seed weight (g) showed negative but non-significant correlation with seed yield per plant (-0.288, -0.284) at both genotypic and phenotypic levels, respectively.

Genotypic correlation coefficients were higher in magnitude than the related phenotypic correlation coefficients which revealed that although there is a strong inherent association among various traits, the phenotypic expression of the correlation gets lesser under the influence of environment. **Pal and Singh (2013), Kumar et al. (2015), Iqbal et al. (2015), Gautam et al. (2017), Kumawat et al. (2018), Kalapchieva et al. (2021) and Meena et al. (2022)** also observed high genotypic correlation coefficients in magnitude than their respective phenotypic correlation coefficients for most of the characters studied in their investigation.

Earlier reports of many workers have also shown significant and positive association of pod yield per plant with days to 50% flowering (**Verma et. al. 2021**) pods per plant (**Pal and Singh 2013; Kumar et al. 2015; Katoch et al. 2016; Thakur et al. 2016; Gautam et al. 2017;**

Kalapchieva *et al.* 2021; Verma *et al.* 2021; Tasnim *et al.* 2022; Meena *et al.* 2022 and Uhlarik *et al.* 2022), seeds per pod (Azmat *et al.* 2011; Kumar *et al.* 2015; Pal and Singh 2013; Kumawat *et al.* 2018; Thakur *et al.* 2016; Verma *et al.* 2021; Tasnim *et al.* 2022; Meena *et al.* 2022; and Uhlarik *et al.* 2022), pod length (Azmat *et al.* 2011, Kumar *et al.* 2015; Katoch *et al.* 2016; Thakur *et al.* 2016; Verma *et al.* 2021; Meena *et al.* 2022 and Uhlarik *et al.* 2022), plant height (Pal and Singh 2013; Verma *et al.* 2021 and Tasnim *et al.* 2022), shelling percent (Kumar *et al.* 2015), days to maturity (Tasnim *et al.* 2022), 100 seed weight (Meena *et al.* 2022 and Uhlarik *et al.* 2022), number of cluster per plant (Meena *et al.* 2022)

### Path coefficient analysis:

It is a standardized partial regression coefficient, which splits the correlation coefficients into the measures of direct and indirect effects. Yield is the sum total of the several component characters which directly or indirectly contributed to it. The information derived from the correlation studies indicated only mutual association among the characters. Whereas, Path coefficient analysis helps in understanding the magnitude of direct and indirect contribution of each character on the dependent character like grain yield. Partitioning of correlation coefficient into direct and indirect effects provides the information about the nature and magnitude of effects of other characters on grain yield.

The genotypic and phenotypic correlation coefficient of seed yield with the remaining characters under study were further partitioned into direct and indirect effects using path coefficient analysis and are presented in **Table 3**, **Table 4** And Figure 1 and Figure 2, respectively.

### Direct and indirect effects on seed yield at genotypic level:

Path coefficient analysis revealed that number of pods per plant (1.0586) followed by pod length (0.1567), number of pods per cluster (0.0925), shelling (%) (0.0911), days to maturity (0.0371) and days to 50 % flowering (0.069) had exerted maximum direct effect on seed yield at the genotypic level. Plant height (cm) (-0.1231) followed by Number of seeds per pod (-0.1128) and 100 seed weight (g) (-0.0448) had exhibited negative direct effect on seed yield at genotypic level.

Plant height (cm) (0.0379), pod length (0.0337) and days to maturity (0.015) via days to 50 % flowering, number of seed per pod (0.0564), shelling (%) (0.0497), number of pod per cluster (0.0398) and 100 seed weight (g) (0.0266) via plant height (cm), number of pods per plant (0.2745), pod length (0.075) and days to 50 % flowering (0.0279) via days to maturity, number of pod per cluster (0.0236) via number of pods per plant, plant height (cm) (0.0452), no. of pods per plant (0.033), days to maturity (0.0178) and days to 50 % flowering (0.0148) via pod length, number of seed per pod (0.0436), 100 seed weight (g) (0.0263) and number of pod per cluster (0.0132) via shelling (%), number of pods per plant (0.2697) and shelling (%) (0.013) via number of pod per cluster, number of pods per plant (0.3699), pod length (0.1184) plant height (cm) (0.0616) and days to maturity (0.0171) via number of seed per pod, plant height (cm) (0.0732) via 100 seed weight (g) exerted substantial positive indirect effect on seed



yield per plant at genotypic level. Number of pods per plant (-0.2501) via shelling (%), number of pods per plant (-0.2082) via 100 seed weight (g) exerted a substantial negative indirect effect on seed yield per plant at genotypic level. The R square and residual effect was (1.1419 and 0.3766) at genotypic level, respectively.

### **Direct and Indirect effect on seed yield at phenotypic level:**

At phenotypic level, path coefficient analysis revealed that no. of pods per plant (0.7594) followed by no. of pod per cluster (0.2106), days to maturity (0.1371), number of seed per pod (0.0715) and days to 50 % flowering (0.0656) had exerted maximum direct effect on seed yield. 100 seed weight (g) (-0.2708) followed by plant height (cm) (-0.2609), pod length (-0.11), and shelling (%) (-0.0021) had exhibited negative direct effect on seed yield at phenotypic level.

Plant height (cm) (0.079), days to maturity (0.0536) via days to 50 % flowering, 100 seed weight (g) (0.1584), number of pod per cluster (0.0851) and pod length (0.0391) via plant height (cm), number of pods per plant (0.1706), 100 seed weight (g) (0.0552), number of seed per pod (0.0315) and days to 50 % flowering (0.0257) via days to maturity, no. of pod per cluster (0.0492), 100 seed weight (g) (0.0471), days to maturity (0.0308) and number of seed per pod (0.0225) via number of pods per plant, plant height (cm) (0.0928), days to maturity (0.0648), number of seed per pod (0.0493), 100 seed weight (g) (0.0467) and number of pods per plant (0.0227) via pod length, 100 seed weight (g) (0.1504) and number of pod per cluster (0.0254) via shelling (%), number of pods per plant (0.1774), 100 seed weight (g) (0.0457) via number of pod per cluster, number of pods per plant (0.2387), plant height (cm) (0.1261) and days to maturity (0.0605) via number of seed per pod, plant height (cm) (0.1526) and pod length (0.019) via 100 seed weight (g) had exerted substantial positive indirect effect on seed yield per plant at phenotypic level. The R-square and residual effect were 0.9084 and 0.3026, moderate effect, indicating that some of the characters affecting seed yield have to be included in future studies.

Path coefficient analysis revealed that number of pods per plant, number of pods per cluster and days to maturity had exerted maximum direct effect on seed yield at both genotypic and phenotypic levels. Plant height (cm) and 100 seed weight (g) had exhibited negative direct effect on seed yield at both genotypic and phenotypic levels. On the basis of path coefficient analysis showed that number of pods per plant, pod length, number of pods per cluster, shelling (%), and days to maturity were important characters that could be taken into consideration for selection and improvement of seed yield in pea.

The results of path analysis obtained under present study are also in agreement with the results of (Narsinghani *et al.* 1979), and (Prasad *et al.* 2019), (Verma *et al.* 2021) and (Tasnim *et al.* 2022) Biological yield per plant, harvest index, seed number per pod, days to maturity, and 100-seed weight all played a significant role in determining seed output per plant. These traits have also been identified in the literature as crucial direct factors influencing pea seed yield per plant by Rajangam *et al.* (2014), Vartika *et al.* (2012), Manggoel *et al.* (2012), Parihar *et al.* (2014), and Sanwal *et al.* (2021).

Table 1 Analysis of variance for 10 quantitative characters in Pea.

| S.No. | Traits                 | Replications (df = 2) | Treatments (df = 19) | Error (df = 38) |
|-------|------------------------|-----------------------|----------------------|-----------------|
| 1     | Days to 50 % flowering | 1.50                  | 208.76**             | 6.56            |
| 2     | Plant height (cm)      | 3.73                  | 242.31**             | 3.04            |
| 3     | Days to maturity       | 5.73                  | 167.89**             | 2.88            |
| 4     | No. of Pods per plant  | 285.25                | 127.29**             | 30.02           |
| 5     | Pod length             | 0.01                  | 1.94**               | 0.06            |
| 6     | Shelling (%)           | 1.42                  | 60.49**              | 5.01            |
| 7     | No. of pod per cluster | 3.14                  | 4.66**               | 0.56            |
| 8     | Number of seed per pod | 1.03                  | 8.62**               | 0.83            |
| 9     | 100 seed weight (g)    | 11.17                 | 141.82**             | 1.69            |
| 10    | Seed yield per plant   | 16.07                 | 701.19**             | 7.94            |

\*Significant at 5% probability level.

\*\*Significant at 1% probability level.

Table 2. Genotypic and Phenotypic correlation coefficient for 10 quantitative traits in pea.

| Traits |     | DFF   | PH     | DM     | NPP    | PL     | SP     | NPC    | NSP     | HSW      | SYP     |
|--------|-----|-------|--------|--------|--------|--------|--------|--------|---------|----------|---------|
| DFF    | Gen | 1.000 | -0.308 | 0.405  | 0.004  | 0.215  | -0.248 | -0.272 | 0.041   | 0.078    | 0.104   |
|        | Phe | 1.000 | -0.303 | 0.391  | 0.002  | 0.213  | -0.229 | -0.269 | 0.025   | 0.076    | 0.102   |
| PH     | Gen |       | 1.000  | -0.025 | -0.030 | -0.367 | 0.545* | 0.430  | -0.500* | -0.594** | -0.062  |
|        | Phe |       | 1.000  | -0.026 | -0.034 | -0.356 | 0.524* | 0.404  | -0.483* | -0.584** | -0.063  |
| DM     | Gen |       |        | 1.000  | 0.259  | 0.478* | -0.232 | -0.266 | 0.460*  | -0.207   | 0.329   |
|        | Phe |       |        | 1.000  | 0.225  | 0.472* | -0.219 | -0.245 | 0.441*  | -0.204   | 0.324   |
| NPP    | Gen |       |        |        | 1.000  | 0.031  | -0.236 | 0.255  | 0.349   | -0.197   | 0.985** |
|        | Phe |       |        |        | 1.000  | 0.030  | -0.201 | 0.234  | 0.314   | -0.174   | 0.915** |
| PL     | Gen |       |        |        |        | 1.000  | -0.085 | -0.056 | 0.755** | -0.173   | 0.177   |
|        | Phe |       |        |        |        | 1.000  | -0.074 | -0.060 | 0.690** | -0.172   | 0.168   |



|     |     |  |  |  |  |  |       |       |        |          |        |
|-----|-----|--|--|--|--|--|-------|-------|--------|----------|--------|
| SP  | Gen |  |  |  |  |  | 1.000 | 0.143 | -0.386 | -0.587** | -0.182 |
|     | Phe |  |  |  |  |  | 1.000 | 0.121 | -0.368 | -0.565** | -0.179 |
| NPC | Gen |  |  |  |  |  |       | 1.000 | -0.047 | -0.189   | 0.299  |
|     | Phe |  |  |  |  |  |       | 1.000 | -0.055 | -0.169   | 0.280  |
| NSP | Gen |  |  |  |  |  |       |       | 1.000  | 0.066    | 0.415  |
|     | Phe |  |  |  |  |  |       |       | 1.000  | 0.067    | 0.394  |
| HSW | Gen |  |  |  |  |  |       |       |        | 1.000    | -0.288 |
|     | Phe |  |  |  |  |  |       |       |        | 1.000    | -0.284 |
| SYP | Gen |  |  |  |  |  |       |       |        |          | 1.000  |
|     | Phe |  |  |  |  |  |       |       |        |          | 1.000  |

\*Significant at 5% probability level. \*\*Significant at 1% probability level.

DFF= Days to 50 % flowering, PH= Plant height (cm), DM= Days to maturity,

NPP= No. of Pods per plant,

PL= Pod length,

SP= Shelling (%),

NPC= No. of pod per

cluster, NSP= Number of seed per pod,

HSW= 100 seed weight (g),

SYP= Seed yield per plant

**Table 3 Direct and indirect effect for different characters on seed yield per plant at genotypic level in pea.**

| S.N. | Traits | DFF     | PH      | DM      | NPP     | PL      | SP      | NPC     | NSP     | HSW     | SYP     |
|------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| 1    | DFF    | 0.069   | -0.0213 | 0.0279  | 0.0003  | 0.0148  | -0.0171 | -0.0188 | 0.0028  | 0.0054  | 0.104   |
| 2    | PH     | 0.0379  | 0.1231  | 0.0031  | 0.0037  | 0.0452  | -0.0671 | -0.0529 | 0.0616  | 0.0732  | -0.062  |
| 3    | DM     | 0.015   | -0.0009 | 0.0371  | 0.0096  | 0.0178  | -0.0086 | -0.0099 | 0.0171  | -0.0077 | 0.329   |
| 4    | NPP    | 0.0044  | -0.0317 | 0.2745  | 1.0586  | 0.033   | -0.2501 | 0.2697  | 0.3699  | -0.2082 | 0.985** |
| 5    | PL     | 0.0337  | -0.0575 | 0.075   | 0.0049  | 0.1567  | -0.0133 | -0.0088 | 0.1184  | -0.0271 | 0.177   |
| 6    | SP     | -0.0226 | 0.0497  | -0.0211 | -0.0215 | -0.0077 | 0.0911  | 0.013   | -0.0352 | -0.0535 | -0.182  |

|   |     |             |        |             |             |             |        |               |                    |                    |               |
|---|-----|-------------|--------|-------------|-------------|-------------|--------|---------------|--------------------|--------------------|---------------|
| 7 | NPC | -<br>0.0252 | 0.0398 | -<br>0.0246 | 0.0236      | -<br>0.0052 | 0.0132 | <b>0.0925</b> | -<br>0.0043        | -<br>0.0174        | <b>0.299</b>  |
| 8 | NSP | -<br>0.0046 | 0.0564 | -<br>0.0519 | -<br>0.0394 | -<br>0.0852 | 0.0436 | 0.0053        | -<br><b>0.1128</b> | -<br>0.0074        | <b>0.415</b>  |
| 9 | HSW | -<br>0.0035 | 0.0266 | 0.0093      | 0.0088      | 0.0077      | 0.0263 | 0.0085        | -<br>0.0029        | -<br><b>0.0448</b> | <b>-0.288</b> |

R Square = 1.1419

Residual effect = 0.3766

Note: Diagonal Bold =Direct path &amp; Red color = Correlation value

DDF= Days to 50 % flowering, PH= Plant height (cm), DM= Days to maturity,  
NPP= No. of Pods per plant,

PL= Pod length, SP= Shelling (%), NPC= No. of pod per  
cluster, NSP= Number of seed per pod,

HSW= 100 seed weight (g), SYP= Seed yield per plant

Table 4. Direct and indirect effect for different characters on seed yield per plant at phenotypic level in pea.

| S.N. | Traits | DDF           | PH                 | DM            | NPP           | PL           | SP                 | NPC         | NSP         | HSW         | SYP            |
|------|--------|---------------|--------------------|---------------|---------------|--------------|--------------------|-------------|-------------|-------------|----------------|
| 1    | DDF    | <b>0.0656</b> | -<br>0.0199        | 0.0257        | 0.0001        | 0.014        | -0.015             | -<br>0.0176 | 0.0017      | 0.005       | <b>0.102</b>   |
| 2    | PH     | 0.079         | -<br><b>0.2609</b> | 0.0069        | 0.0089        | 0.0928       | -<br>0.1367        | -<br>0.1054 | 0.1261      | 0.1526      | <b>-0.063</b>  |
| 3    | DM     | 0.0536        | -<br>0.0036        | <b>0.1371</b> | 0.0308        | 0.0648       | -0.03              | -<br>0.0336 | 0.0605      | -<br>0.0279 | <b>0.324</b>   |
| 4    | NPP    | 0.0017        | -<br>0.0258        | 0.1706        | <b>0.7594</b> | 0.0227       | -<br>0.1524        | 0.1774      | 0.2387      | -<br>0.1322 | <b>0.915**</b> |
| 5    | PL     | -<br>0.0234   | 0.0391             | -0.052        | -<br>0.0033   | <b>-0.11</b> | 0.0081             | 0.0066      | -<br>0.0759 | 0.019       | <b>0.168</b>   |
| 6    | SP     | 0.0005        | -<br>0.0011        | 0.0005        | 0.0004        | 0.0002       | -<br><b>0.0021</b> | -<br>0.0003 | 0.0008      | 0.0012      | <b>-0.179</b>  |

|   |     |             |             |             |        |             |             |               |               |                    |               |
|---|-----|-------------|-------------|-------------|--------|-------------|-------------|---------------|---------------|--------------------|---------------|
| 7 | NPC | -<br>0.0566 | 0.0851      | -<br>0.0516 | 0.0492 | -<br>0.0127 | 0.0254      | <b>0.2106</b> | -<br>0.0116   | -<br>0.0355        | <b>0.280</b>  |
| 8 | NSP | 0.0018      | -<br>0.0345 | 0.0315      | 0.0225 | 0.0493      | -<br>0.0263 | -<br>0.0039   | <b>0.0715</b> | 0.0048             | <b>0.394</b>  |
| 9 | HSW | -<br>0.0205 | 0.1584      | 0.0552      | 0.0471 | 0.0467      | 0.1504      | 0.0457        | -0.018        | -<br><b>0.2708</b> | <b>-0.284</b> |

R Square = 0.9084

Residual effect = 0.3026

Note: Diagonal Bold =Direct path & Red color = Correlation value

DFF= Days to 50 % flowering, PH= Plant height (cm), DM= Days to maturity,  
NPP= No. of Pods per plant,

PL= Pod length, SP= Shelling (%), NPC= No. of pod per  
cluster, NSP= Number of seed per pod,

HSW= 100 seed weight (g), SYP= Seed yield per plant

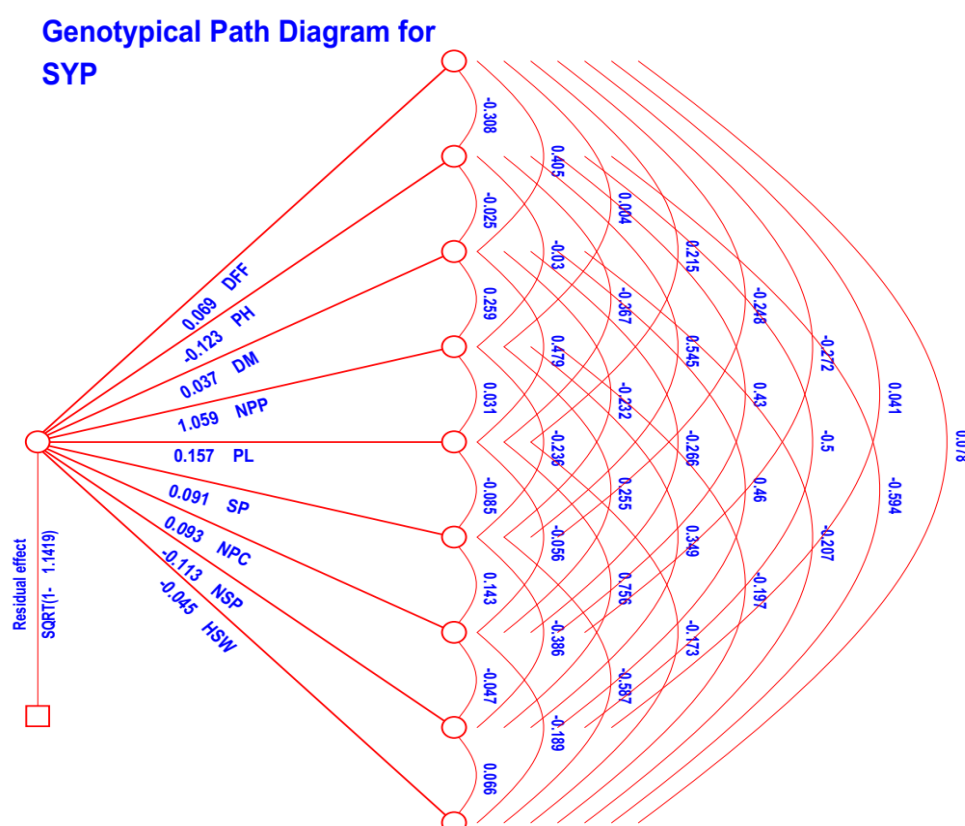


Fig. 1. Genotypical path diagram

## Phenotypal Path Diagram for SYP

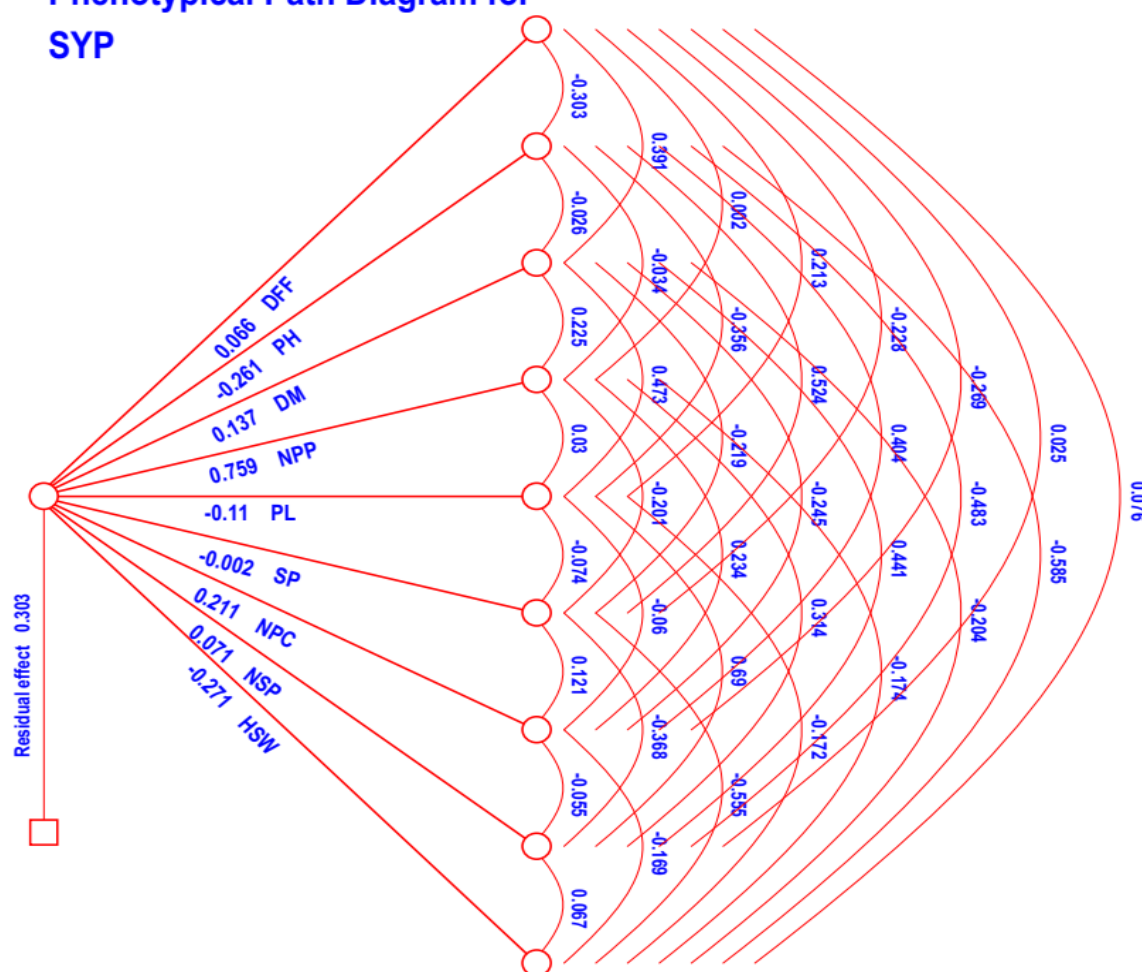


Fig. 2. Phenotypic path diagram

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