

RESEARCH PROGRAMME

Genetic Variability and Correlation Studies in Pea (*Pisum sativum* L.)

DISSERTATION-1

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IN
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BY

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CERTIFICATE

Certified that this synopsis of Amanpreet Singh, registration no. 11719042, entitled “Genetic Variability and Correlation Studies in Pea (*Pisum sativum* L.)” has been formulated and finalized by the student himself on the subject.

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1.INTRODUCTION

Pea (*Pisum sativum* L.) is one of the most important nutritional legume crop of family Fabaceae (Leguminosae), is native of region between Mediterranean and Near East. Pea is one of the 6 major pulse crops cultivated globally and is the second highest yielding legume in the world after common bean (*Phaseolus vulgaris* L.) (FAO, 2010). It is one of the world's oldest crops, as it was first cultivated with cereals like barley and wheat, 7000 years ago. According to FAO statistics, India is one of the largest producers of pea in the world and stands at the 5th place in the list of major pea producers next to France. The Indian production contributes to around 7% in the world's total produce with the production figures of 7.8 lakh tonnes. Uttar Pradesh is a major pea producing state in India producing about 60% of the country's produce. Punjab contributes 3.2% to India's total production of pea with Jalandhar, Amritsar and Hoshiarpur districts as major garden pea producing belt, having total production of 112 thousand metric tons from area of 18,480 hectares. Pea is an important leading off-season legume vegetable in Himachal Pradesh as produce from hilly areas is available at the time when it cannot be grown in nearby areas of Punjab, Haryana, Delhi and UP. The consumers also have a special preference for pea from hilly regions due to its characteristic flavor, good quality and sweetness. In India it is grown on an area of 498 thousand hectare with an annual production of 4811 thousand metric tonnes (NHB, 2017).

Pea is a cool season, self-pollinated crop which is harvested at succulent immature stage and consumed fresh or preserved through canning or freezing. The crop is cultivated for its tender and immature pods for use as vegetable and mature dry pods for use as a pulse. It is highly nutritive crop containing digestible proteins (6.2g/100g of fresh peas), carbohydrates (16.9g/100g), fats (0.4g/100g) along with minerals (Ca, P and Mg) and vitamins A, B and C (Choudhary, 1967). Tender seeds are also used in soups. Canned, frozen and dehydrated peas are very common for use during off-season. Like any legume crop, pea is an integral component of sustainable agriculture due to its soil enriching and conditioning properties. Crop improvement depends largely on availability of genetic variability in breeding material, their effective evaluation and utilization. Moreover, genetic variation is valuable for understanding gene function. Conventionally, varietal identification and genetic diversity in plants is based on phenotypic evaluation of morphological characteristics. Morphological descriptors are widely used in defining genotype groups and remain the only legitimate marker type accepted by the International Union for the Protection of New Varieties of Plants (Smykal *et al.*, 2008), but they demand collection of extensive data at different locations. In fact, many of the traits having polygenic control are influenced by environment.

Furthermore, the level of polymorphism for morphological characteristics in elite genotype is sometimes too limited and inadequate to allow for variety discrimination. So, cultivar identification and estimates of genetic diversity using phenotypic markers only, have several limitations. The pea is a significant contributor in agricultural sustainability due to its specificity to fix atmospheric nitrogen in soil by root nodules. In order to maximize such

benefits, there is a need to restructure the genetic resource of garden pea. Genetic variability is pre requisite for effective improvement programme of any crop (**Azmat *et al.*, 2011**). A good understanding of genetic variability in different characters is a useful tool for identification of suitable genes and their nature of adherence to improve the genetic behaviour of crop (**Nwangburuka *et al.*, 2011**).

The knowledge about the magnitude and nature of genetic variability available in the genotype and the extent to which the desirable traits are heritable is a pre-requisite for the effective breeding programme. In order to formulate breeding strategy for developing elite genotype through selection in advance generation, the knowledge of genotypic and phenotypic correlation of yield component and path analysis is the prerequisite. Therefore, present investigation is proposed to find out the nature and magnitude of genetic variability in various morphological and biochemical parameters and association among various traits of pea genotypes with the following objectives:

- 1) To evaluate pea genotypes for morphological traits.
- 2) To evaluate pea genotypes for biochemical traits.
- 3) To study the correlation between various traits of pea genotypes.

2. REVIEW OF LITERATURE

Ramesh *et al.* (2002) observed considerable amount of phenotypic coefficient of variation and genotypic coefficient of variation for most of the characters in pea such as number of pods per plant, plant height and weight of grains per pod, while the variation was low for the other characters tested.

Tyagi and Srivastava (2002) reported wide range of variability in pea was for plant height, pods per plant, and biological yield per plant. The phenotypic and genotypic coefficients of variability were higher for pods per plant, biological yield per plant, and seed yield per plant in parents.

Sharma *et al.* (2003) reported that all the characters in pea (seed yield per plant, biological yield per plant, harvest index, plant height, 100-seed weight, seeds per pod, pods per plant, days to 50% flowering, pod length and days to maturity) exhibited significant variability. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in pea were highest for seed yield per plant, followed by pods per plant and biological yield per plant.

Mehta *et al.* (2005) observed wide range of variability for plant height along with high estimates of phenotypic and genotypic coefficients of variation in pea indicated that these characters would respond to selection. However, low PCV and GCV were recorded for pod length. A small difference between PCV and GCV was observed for node at which the first flower appear followed by the number of grains per pod.

Singh and Singh (2005) reported that the out of the 18 pea genotypes, VL-7 recorded highest seed yield (17.59 q/ha) followed by Arkel (16.33 q/ha), Azad-P3 (16.33 q/ha) and Azad-P-1 (15.72 q/ha). High genotypic coefficient of variation and phenotypic coefficient of variation were observed for the number of branches per plant, number of pods per plant and seed yield (q/ha).

Sardana *et al.* (2007) observed high variability for qualitative as well as quantitative traits in pea. Analysis of variance revealed that the differences among 33 accessions were significant for all the characters except seeds per pod. Moderate to high levels of genotypic coefficient of variability were observed for plant height, 100-seed weight, pod length, seed yield per plant, and pods per plant which suggested that these traits would respond to selection owing to their high genetic variability and transmissibility.

Nawab *et al.* (2008) reported highly significant differences among genotypes of pea for days to 50 per cent flowering, number of pods per plant, weight of pods per plant (g), pod length (cm), number of seeds per pod and 100-seed weight (g). 100-seed weight, number of pods per plant and weight of pods per plant showed high genetic coefficient of variation (GCV) indicating good scope for selection.

Sanjay *et al.* (2008) observed sufficient genetic variation in pea for number of pods per plant and grains per pod. The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation in pea for all the traits.

Choudhary *et al.* (2010) found considerable amount of genetic variability in pea for all the characters studied except pod breadth. Number of pods per plant and plant height exhibited higher values of genotypic and phenotypic coefficient of variation in pea.

Lal *et al.* (2011) reported significant differences among 30 genotypes of pea for growth and yield characters. Moderate to high levels of genotypic coefficient of variability (GCV) were observed for plant height, number of primary branches per plant, pods per plant, seeds per pod, 100 seed weight, harvest index, biological yield per plant and grain yield per plant. Among all traits plant height exhibited high estimates of GCV and PCV (38.8 and 38.82) followed by biological yield (36.88 and 37.1) and harvest index (32.13 and 33.78).

Kumar *et al.* (2015) estimated the parameters of variability and association of important characters with yield in 54 garden pea genotypes and observed significant differences among the genotypes for all the morphological characters. The genotypic and phenotypic coefficients of variation were high for total soluble solids, total sugars, pod yield per hectare and total phenols. High heritability estimates coupled with high to moderate genetic gain observed for pod yield (kg/plot), node at which the first flower appear (number), number of pods per plant and total Phenols (g/100g). Pod yield was positively correlated with number of pods per plant, pod length (cm), number of seeds per pod and shelling percentage thereby indicating that the selection based on these traits could be effective for improvement of green shelled peas yield.

Singh *et al.* (2016) evaluated 32 genotypes of pea to determine the genetic variability and reported greater among diversity different traits of horticultural importance. The Principal component analysis showed more than 84 % of total multivariate variation for important traits in different genotypes. Pod yield, pod length, 10 pods weight and pods per plant were found to be major traits contributing towards principal component-I. Similarly, seeds per pod, secondary branches/plant, pod length were main positive contributing traits towards second component. Ten pod weight, pod width were positively contributing component towards principal component third.

Thakur *et al.* (2016) concluded that highest pod yield per plant was recorded in Punjab-89 which can replace the existing Azad P-1 variety. Phenotypic and genotypic coefficients of variation were moderate in magnitude for most of the traits. High heritability coupled with high genetic gain were observed for plant height, pod length, number of grains per pod, shelling percentage and number of pods per plant which indicated the presence of additive gene action and thus offers more scope for reliable and effective selection. A significant positive association of pod yield was observed with number of pods per plant, pod length, pod width and number of grains

per pod. Therefore, these traits may be considered as the most reliable selection indices for effective improvement in green pod yield in garden pea.

Jeberson *et al.* (2016) estimated the genetic parameters for nine characters with 12 genotypes of field pea and observed significant variability among all genotypes. The correlation coefficients revealed positive and highly significant association of yield with plant height, cluster/plant, pods/plant, pod length, seeds/pod and 100 seed weight. The pods/plant exhibited highly positive and direct effect on grain yield followed by pod length and days to maturity. Therefore these characters can be considered for selecting genotypes to improve the grain yield in the field pea.

Georgieva *et al.* (2016) evaluated five genotypes of pea and reported significant differences among genotypes for the traits pod width, seeds per plant, seed weight per plant and 1000 seed weight. The estimates of genetic parameters of five varieties of *Pisum sativum L.* indicated a good amount of genetic variation in the experimental materials under investigation. Moderate phenotypic and genotypic coefficients of variation were observed for most of traits except pod length and pod width. For the traits studied seeds per plant, seed weight per plant and plant height were found high heritability along with high genetic gain indicating preponderance of additive effects. The seed yield was positively and significantly correlated with 1000 seed weight and pod stem, which suggested the possibilities of improving seed yield by simultaneous improvement of these traits.

Gautam *et al.* (2017) observed wide range of phenotypic variation, along with high heritability in pea. Highest pod yield per plant was recorded in VRP-229 followed by VRP-372 and VRP-305. The characters namely, plant height and weight of seeds per pod showed high magnitude, while number of pods per plant, number of branches per plant and pod yield per plant showed moderate magnitude for phenotypic and genotypic coefficient of variation. The heritability and genetic advance were high for days to first pod initiation, plant height and pod yield per plant indicating its additive gene action for their expression. Pod yield per plant exhibit positive and highly significant correlation with number of pods per plant, number of branches per plant and days to fifty percent flowering.

Singh *et al.* (2017) observed that phenotypic correlation coefficient (PCV) values were marginally bigger than genotypic correlation coefficient (GCV), revealing tiny sway of environment in character expression of 12 pea genotypes. High heritability coupled with high genetic advance and high GCV were observed for length of branch from main axis, number of seeds/plant and weight of 100 seeds indicating the multitude of additive gene action. Results of genotypic and phenotypic correlation coefficients showed significant positive correlation of stem circumference, number of seeds/ plant, number of pods/plant, weight of 100 seeds, number of seeds/pod with each other and other yield attributes.

Khan *et al.* (2017) observed that phenotypic variance was higher than the corresponding genotypic variance for all morphological characters. Genotypic coefficient of variation was the

highest for hundred seed weight (37.24) followed by number of branches plant (15.96) 1 and seeds plant (15.27). Hundred seed weight had the highest heritability (95.97). Pod length, hundred seed 1 weight, pods plant and seeds plant showed significant positive genotypic and phenotypic correlation with 11 seed yield. In path analysis, plant height, internode length, hundred seed weight, number of seeds pod and 1 seeds plant showed positive direct effect on yield.

Srivastava *et al.* (2018) evaluated 113 genotypes of pea and observed wide range of variability for different characters. Seed yield per plant exhibited highly significant and positive correlation with 100 seed weight (0.3775), number of pods/plant (0.3524), harvest index (0.3270), number of seeds/pod (0.3262) and biological yield (g) (0.2828). The highest positive direct effect on seed yield per plant was exerted by harvest index (0.7902) followed by biological yield (g) (0.7820), 100 seed weight (0.3406), number of seeds per pod (0.2788) and number of pods per plant (0.2622).

3. MATERIALS AND METHOD

1. Experiment Details:

1.1 Experimental Site: Lovely Professional University Farm.

1.2 Total Area : 192 meter square.

1.3 Design of the Experiment: Randomized Block Design(For field experiment)
Complete Randomized Block Design(For lab experiment)

1.4 Treatments: Seven pea genotypes.

1.5 Replications : 4

1.6 Spacing : 30*10cm.

1.7 Common fertilizer Dose:

1.7.1 Vermi-compost : 50 kg

1.7.2 D.A.P : 20 kg

1.7.3 Year of Study : 2017-2018

1.8 Date of sowing : 23 November 2017

2. Observation to be recorded

2.1 Morphological Parameters

2.1.1 Number of days to sprouting

2.1.2 Plant height(cm)

2.1.3 Number of branches per plant

2.1.4 Number of leafs per plant

2.1.5 Leaf size

2.1.6 Days to first flowering

2.1.7 Days to 50% flowering

2.1.8 Number of days to pod formation

2.1.9 Number of pods per plant

2.1.10 Pod colour

2.1.11 Pod size

2.1.12 Pod weight

2.1.13 Number of seeds per pod

2.1.14 Weight of 100 seeds

2.1.15 Yield per plant

2.1.16 Yield per bed

2.2 Biochemical parameters

2.2.1 Total phenol content

2.2.2 Antioxidant activity

2.2.3 Ascorbic acid

2.2.4 Protein content

2.2.5 Total soluble sugar

3. Statistical analysis: Replicated data from each treatment will be subjected to statistical analysis by using software SPSS.20 (SPSS. Inc, Chicago, USA)

Table 1 : Pea genotypes to be used in study

Sr. no.	Genotypes	Source
T1	Vasundra	Tycoon seed, Ludhiana
T2	Ali-89	Arman seed farms, Ludhiana
T3	Vasundhra-10	Tycoon, Ludhiana
T4	Ronak-10	Ronak seeds, Ludhiana
T5	PS-10	North east hybrid seeds, Phagwara
T6	Nirali	Agro seeds, Phagwara
T7	JK-Special	Jk agro hybrid seeds,Phagwara

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