STUDY ON GENETIC DIVERSITY IN VEGETABLE PEA
(*Pisum sativum* L. var. *hortense*)

POOJA TETARWAL

Thesis

Master of Science in Horticulture

(VEGETABLE SCIENCE)

DEAPARTMENT OF VEGETABLE SCIENCE

COLLEGE OF HORTICULTURE AND FORESTRY

RANI LAKSHMI BAI CENTRAL AGRICULTURALUNIVERSITY
JHANSI – 284003, UTTAR PRADESH, INDIA

August 2022

STUDY ON GENETIC DIVERSITY IN VEGETABLE PEA
(*Pisum sativum* L. var. *hortense*)

THESIS

Submitted to the

Rani Lakshmi Bai Central Agricultural University
Jhansi – 284 003 (U.P.) India

By

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B.Sc. (Hons.) Horticulture

IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE DEGREE OF

Master of Science in Horticulture
(Vegetable Science)

August, 2022

College of Horticulture and Forestry

Rani Lakshmi Bai Central Agricultural University

Jhansi -284003

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CERTIFICATE - I

Certified that Ms. Pooja Tetrawal ID.No. RLBCAU/H/PG/007 has satisfactorily pursued her course of research for not less than IV semesters and that the thesis entitled "**Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)**" submitted by her to the Rani Lakshmi Bai Central Agricultural University, Jhansi 284003 (U.P.) in partial fulfillment of the requirements for the award of the degree of **Master of Science in Horticulture** in the subject of Vegetable Science is the result of original research work conducted by her under my supervision and is sufficiently of a high standard to warrant its presentation to the examination.

I also certify that the thesis or part thereof has not been previously submitted by her for a degree/diploma of any University.

Date: 13-09-2022

Chairperson
(A.K. Pandey)

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CERTIFICATE- II

This is to certify that the thesis entitled **"Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)."** submitted by Ms. Pooja Tetarwal ID. No. RLBCAU/H /PG/007submitted to the Rani Lakshmi Bai Central Agricultural University, Jhansi 284003 (U.P.) for partial fulfillment of the requirements for the award of the degree of **Master of Science in Horticulture** in the subject of Vegetable Science has been approved by the Student's Advisory Committee after the viva voce examination.

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ACKNOWLEDGEMENT

Fervently and modestly, I take this opportunity to thank ***Dr. A. K. Pandey****, Dean College ofHorticulture & Forestry, RLBCAU, Jhansi and Chairman of my advisory committee, who has the attitude and substance of genius: for his valuable support, constant inspiration, delighted affection, and humble advice. Generous kindness extended by him from the start of my course and research work till the completion of the final manuscript is heartily acknowledged. I take this opportunity to thank* ***Dr. Arvind Kumar****, Honorable Vice-Chancellor, RLBCAU,Jhansi, for providing me the platform to study and research in addition to positive environment during the tenure of my master's study. I would like to express my deepest gratitude to* ***Dr. S. K. Chaturvedi****, Dean, College of Agriculture, RLBCAU, Jhansi, for his constant support, inspiration and intellectual guidance during my study and researchwork. His constructive ideas were always limelight to my valuable work. With endless pleasure, I extol my sincere gratitude to* ***Dr. Anil Kumar****, Director Education, RLBCAU, Jhansi, a great thinker and influential mentor. I thank him for his valuable motivation and perfect guidance.*

I am highly indebted to ***Dr. A. R. Sharma****, Director Research, RLBCAU, Jhansi, for his inestimable Knowledge, useful comments, remarks, and engagement through the learning process of this master thesis, and* ***Dr. Sati Shankar Singh****, Director Extension Education, RLBCAU, for his support and guidance for scientific writing. I would also like to express my gratitude to* ***Dr. Mukesh Srivastava****, Registrar, RLBCAU, Jhansi for giving me the wonderful opportunity to study in this University and granting the institutional fellowship during the tenure of my master's programme. I feel immense pleasure to thank* ***Dr. Gaurav Sharma****, and Head, Department of Fruit Science, RLBCAU, Jhansi, and member of my advisory committee for his invaluablesuggestions, innovative thoughts and consistent help.*

Dr. Arjun Lal Ola*, Assistant Professor, Department of Vegetable Science, RLBCAU, Jhansi, and member of my advisory committee for his constructive suggestions and* *generous advice. I feel pleasure thank to **Dr. Rumana Khan**, Assistant Professor, Department of Genetics and Plant breeding, RLBCAU, Jhansi, and member of my advisory committee for his invaluable suggestions, innovative thoughts and help. I feel immense pleasure thank to **Dr. Shailendra Kumar**, Assistant Professor-Agricultural Statistics, RLBCAU, Jhansi for their valuable guidance and tirelessness help.*

*Solely no one is able to do anything. The work to be accomplished requires technical expertise and practical experience, which was not possible for a new bud-like me. Therefore, I thank to **Dr. S. S. Kushwaha**, Head Librarian, **Dr. Maneesh Pandey**, Teaching Associate-Vegetable Science, **Dr. Ranjeet Pal**, Assistant Professor-Fruit Science, **Dr. Govind Vishavakarma**, Teaching Associate-Fruit Science, **Dr. Priyanka Sharma**,Assistant Professor-Floriculture, **Dr. Ghan Shyam Abrol**, Assistant Professor- Post Harvest Technology, RLBCAU, Jhansi for their valuable guidance and tirelessness help. I feel great thank to **Dr. Saurabh Singh** (Teaching Associate-Vegetable Science) RLBCAU, Jhansi for their support during my field experimentation.*

*Great work has never been accomplished in a day, and it also requires perseverance and a positive environment. Therefore, I take this opportunity to thanks my colleagues **Rajkumar, Sreenidhi, Suman, Amita, Mamta, Anil, Satyanarayana, Mukesh, Sarvan, Davendra, Amogha, Charita, Bharat, Shruti, Karan** and my seniors **Arjun,Narendra, Bhawar, Siddesh, Chetan** and my juniors **Sneha, Kiran, Lalchand, Rajeev, Rakesh, Priyanka, Jhabar, Himanshu, Ganesh**, **Manoj, Hariom Urmila, Tcenet, Amna**, for their support by various means during my study.*

*Diction is not enough to express my unboundful gratitude and affection to my beloved parents **Smt. Bhanwari Devi** and **Shri Sitaram Tetarwal** for bringing me up in the best of ways, for rendering me the best of education, for nurturing in me the best of ideals, and forhelping me to see the best of times. There is too love that much I can show for my brother **Kamlesh** and **Sanjay** and sisters **Monika, Manisha, Priyanka, Lalita** who made my lifethe happiest throughout.*

August 2022 *Pooja Tetarwal*

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LIST OF ABBREVIATIONS AND SYMBOLS

S. No.	Symbols	Abbreviation
1	Cm	Centimeter
2	M	Meter
3	%	Percentage
4	Mg	Miligram
5	G	Gram
6	Df	Degree of freedom
7	Ph	Hydrogen ion concentration
8	DAS	Days after sowing
9	SEm(±)	Standard error of mean
10	ANOVA	Analysis of variance
11	CV	Coefficient of variation
12	PV	Phenotypic variance
13	GV	Genotypic variance
14	PCV	Phenotypic coefficient of variation
15	GCV	Genotypic coefficient of variation
16	GA	Genetic advance
17	H^2	Heritability
18	EMS	Error mean sum of square
19	GMS	Genotypic mean sum of square
20	NBPGR	National Bureau of Plant Genetic Resources
21	*i.e.*	That is
22	Fig.	Figure
23	*a.i.*	Active ingredient
24	@	at the rate
25	*et al.*	and co-workers
26	°C	Degree Celsius
27	$Ha\text{-}^{1}$	Per Hectare
28	L	Litre
29	m^2	Meter square
30	Max	Maximum
31	Kg	Kilogram
32	kg/ha	Kilogram per hectare
33	*viz.*,	Namely

LIST OF ABBREVIATIONS AND ACRONYMS

S. No.	Trait Abbreviation	Acronyms
1	DF1	DF1-Days to first flowering
2	DF50	Days to 50% flowering
3	NPB	Number of primary branches
4	NNP	Number of nodes per plant
5	PH	Plant height
6	PL	Pod length
7	PW	Pod width
8	NSP	Number of seed per pod
9	SW	100 seed weight
10	PR	Protein content
11	INL	Internodal length
12	M	Moisture percentage
13	TSS	Total soluble solid
14	SHL	Shelling percentage
15	DS1	Days to first pod setting
16	DP1	Days to first pod picking
17	APW	Average pod weight
18	NPP	Number of pods per plant
19	PYP	Pod yield per plant
20	PYH	Yield per hectare

1. INTRODUCTION

Vegetable Pea is botanically known as *Pisum sativum* L. var. *hortense* Its chromosome number (2n) is 14 and belongs to the family Fabaceae, sub family Faboideae, sub tribe Phaseolineae and tribe Phaseoleae. It is famous plant species in which G.H. Mendel worked out Genetic principles and Mendel's Law. It is the second important legume vegetable worldwide after *Phaseolus vulgaris* (Taran *et al.,* 2005). According to Blixt *et al.,* (1970), the Mediterranean region is the primary centre of diversity with secondary origin in Ethiopia. According to (Zohary and Hopf, 1973) Archaeological evidences dates the existence of pea back to 10,000 B.C. in Near East and Central.

It is an annual herb which self-pollinated and grows as a bush or climbing plant. Pinnately compound leaves have two to many leaflets. A simple or complex branched tendril emerges from the rachis's end. Large stipules present at the base of the leaves. Its inflorescence is raceme arising from leaves axil. The typical papilionaceous flowers have a green calyx that consists of five joined petals and five sepals. For consumption during the off-season tender and immature seeds are processed (canned, frozen, or dehydrated). Pea plants is raised for its dried seeds and green pods, which are valued for their high-quality protein content mainly lysine content. Vegetable pea generally has white flowers. Its round seeds are predominated over wrinkled seeds. Pea seeds are generally harvested from the pods when they are young and succulent stage. Pea pods are inedible due to a parchment layer on the inside of the pods and fibers along the suture lines

Vegetable pea is nutritive vegetable crops which have high quantity of protein (amino acid, methionine and cysteine), carbohydrate, vitamin C, vitamin A and minerals like calcium, potassium, phosphorus and iron. Increasing the demand of protein and mineral rich food has led interest in the pea as protein rich source (Santalla *et al.,* 2001). Hundred grams edible portion on fresh weight basis contain 308 k cal energy, 18.44 g protein, 1.4 g fats, 42.4 g carbohydrate, 2.6 g fiber, 295 mg phosphorus, 3.5 mg iron, 116 mg magnesium, and 138 μg vitamin B_9 (FAO, 2016). The dry pea seeds are rich in protein (19-21%) and free of anti-nutritional substances (Petterson *et al.,* 1997).

It is adapted to cool moist climate and moderate temperature. Pea is grown as winter season vegetable in plains and summer season in hills. Legumes can interact symbiotically with the soil-borne bacteria called Rhizobium and allow them to fix atmospheric nitrogen then improve the physical property of the soil and protect them against fungal pathogens (Chakraborty *et al*., 2003). It improves soil fertility by providing nitrogen to successive crop (nitrogen fixation by *Rhizobium leguminosarum*) without the added expense of supplemental fertilizer. In India, garden pea is grown in an area of 0.55 million hectares with an annual production of 5.52 million tonnes and productivity of 10.03 t/ha (NHB, 2018-19). The major pea producing states are Uttar Pradesh, Madhya Pradesh, Punjab, Jharkhand, and Himachal Pradesh.

The main objectives of pea breeding are more yield, regional adaptability, suitable plant type, shattering and lodging resistance as well as resistance towards biotic and abiotic stresses, quality and genotypes with nitrogen fixing capacity.

According to Nath (1976) the yield potential of vegetable pea for green pod is low and there is a scope for its improvement. When developing genotypes for pod yield, it is important to be knowledge of the environmental factor influencing the yield. The quantity and quality of vegetable peas are directly influenced by the seed and pod attributes. The traits such as well-filled medium-sized pods with high shelling percentages and wrinkled-type seeds are taken account since they are expected to produce superior quality and yield

Complete biological knowledge and an understanding of genetic variation for yield and its component are required for the development of an improvement programme and intensive breeding. There must be a thorough knowledge of the existence of genetic variability, the mode of inheritance of economic characters, the mode of gene action, heritability and the relative values of dominance, additive and total genotypic and phenotypic variance of the population. Considering the availability of genetic variability, there is vital scope of yield and quality traits improvement and develop export potential of garden peas.

According to (Azmat *et al.*, 2011) selection for quality and yield characters can be find to best possible extent if information about correlation coefficient between such traits is available followed by better understanding of the association among the related traits provided by path coefficient analysis. Genetic variability is an important criterion for effective improvement programme of any crop. Yield is the result of several correlated traits and selection of such traits which are positively correlated and highly heritable is more desirable. Presence of more variability in the pea germplasm provides more scope for its improvement. A great amount of diversity is present in vegetable pea that may be used to develop new high yielding varieties. A high amount of variability has been observed in different agronomic characters of pea. Local and exotic germplasms can be useful in hybridization programme for genetic improvement of vegetable pea.

Knowing the role and relationships between various yield and yield related components is essential for a successful breeding programme. The correlation coefficient would indicate the relationship among independent and dependent variables without specifying cause and effect (Akinnola, 2012). A positive association between desirable traits is favorable to plant breeder because it is useful simultaneous improvement of both the parameters and a negative correlation will hinder the simultaneous expression of both the characters with high values.

The genetic improvement in dependent parameters can be achieved by applying strong selection to a character which is genetically correlated with dependent parameters. This is called as correlated response (Al-Jibouri *et al.*, 1958). Using path coefficient analysis, it is possible to resolve the correlations, by subjecting the correlation co-efficient to path analysis for splitting the correlation magnitudes into direct and indirect effect through alternate ways. It has been widely used to identify characters that have significant effect to yield for potential use in selection. Pea yield could be enhanced by an understanding the relationship of yield and other parameters at both phenotypic and genotypic levels. Losses from various biotic causes are one of the main restrictions, along with the absence of cultivars with stable and high yield. In order to develop high yielding varieties, it is important to analyse genetic diversity

Genetic diversity has been considered as an important factor which is a necessary in the crop improvement programmmes for achieving high yielding progenies. Evaluation of genetic diversity is important to know the source of genes for a particular character within available germplasm (Pandey, 2009). In any crop species the genetic diversity assessment is a good first step toward crop improvement it provides baseline data that may be used to assist parental line selection and breeding scheme design. (Van der Maesen, 1990).

Genetic diversity among germplasm is important for genetic development of any crop since it makes it allows to detect the most divergent parents based on the contribution of various qualitative and quantitative parameters. Which can then be used in any hybridization programme. In order to select the best genotypes in a breeding programme, genetic diversity in the germplasm must be evaluated. (Goyal and Bisen, 2017).

The genetically diverse parents are always able to produce a high frequency and high heterotic of desirable segregants in subsequent generations. Genetic variability and diversity are in prime interest to the plant breeder as it plays an important role in successful breeding program. The genetically diverse parents are always able to produce great frequency and high heterotic of desirable segregants in further generation as already observed by earlier (Kumar and Nadarajan 1994). D^2 statistic is a helpful tool to estimate genetic divergence among genotypes in crop developed by Mahalanobis (1936).

Keeping above facts in the view, the present investigation entitled "Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)" was under taken during *rabi* season 2021-2022, with the following objectives.

1.To assess the genetic variability, heritability and genetic advance in vegetable pea.

2. To estimate the correlation coefficient among the yield and yield components.

3. Path coefficient analysis for yield and yield components.

4. To study the genetic divergence in vegetable pea for growth, yield and quality attributes.

2. REVIEW OF LITERATURE

A brief review of available literature in consonance with the objectives of the present investigation in respect of garden pea crop are reviewed and presented under the following heads.

2.1 Genetic variability

2.2 Coefficient correlation

2.3 Heritability and Genetic advance

2.4 Path analysis

2.5 Genetic divergence

2.1. Genetic variability and heritability

Improvement in any crop is based on the level of genetic variation and the degree of improvement depends upon the magnitude of available useful genetic variability (Shirshat *et al*., 2007). The genetic improvement in any crop is proportional to the extent of its genetic variability present in the germplasm. Greater the variability in a population has greater chance for effective selection for desirable types (Vavilov, 1931). A wide range of variability is available in vegetable pea genotypes which provide more scope for improvement in pod yield through systematic breeding. The variability observed in a population could be due to two factors i.e., genetic and environmental. which was discussed in early part of last century by Johannsen (1909) who attributed the genetic variation in a segregating population to both heritable and non-heritable factors and variation within pure line to only environmental factors. For the any breeding program initiation, it is necessary to assess the genetic variability present in the indigenous genotypes for yield and its components. Parameter of phenotypic and genotypic coefficient of variations is helpful in detecting the amount of variability present in the germplasm (Datta and Das, 2013).

Kumar *et al*. (2022) studied genetic variability and association among agronomic characters of pea (*Pisum sativum* L.) genotypes. Highly significant differences were found among the tested pea genotypes. The results obtained revealed that genotypes (G6) were best for 50% flowering, fresh pod shelling percentage and days to maturity. Genotype (G2) had highest plant height, number of pods plant per plant and seed yield per plant. Genotype (G9) had maximum 100-seed fresh and dry weight. Genotype (G5) had more primary branches per plant whereas genotype (G8) showed maximum pod length and seeds pod per plant.

Tasnim *et al*. (2022) studied the genetic relationship between different quantitative traits for commercial cultivation and to assess selection criteria in pea breeding program in five inbred parents. Phenotypic coefficients of variation (PCV) were close to genotypic coefficients of variation (GCV) for all the characters indicating less impact of the environment and potentiality of selection.

Ali *et al*. (2021) conducted an experiment to study the variability, heritability, genetic advance and correlation coefficient for yield and yield related traits in 10 pea (*Pisum sativum* L.) genotypes. Highly significant differences were observed for days to 50% flowering, primary branches per plant, plant height days to maturity, pods plant per plant, pod length, fresh pod shelling percentage, 100-seeds fresh and dry weight, number of seeds per pod and seed yield per plant. Among the genotypes, Sultan was observed best for 50% flowering, days to maturity and fresh pod shelling percentage. Genotype PL-4 had maximum plant height, number of pods plant per plant and seed yield per plant.

Pujari *et al*. (2021) evaluated genetic parameters for eleven characters with 21 genotypes of field pea. The analysis of variance had large variability present among the genotypes studied. High to moderate PCV and GCV estimates for the traits viz; number of primary branches per plant, pods per plant, and plant height (cm) was noted.

Yadav *et al*. (2021) reported the phenotypic coefficients of variations (PCV) were higher than genotypic coefficients of variations (GCV) for all the characters of vegetable pea. The highest phenotypic as well as genotypic coefficients of variation were observed in case of primary branches per plant followed by pod yield per plant, pods per plant, nodes to first flower appears and nodes to first pod appears. The highest phenotypic and genotypic coefficient of variations were observed for node to first pod appear followed by number of seeds per 250 g, number of pods per 250 g and total soluble solid.

Kanwar *et al*. (2020) studied the genetic variability, heritability and genetic gain in the 30 genotypes of pea. The results from experiment revealed that pea genotype JP-54 recorded maximum pod yield per plant and maximum number of pods per plant. Swarna Mukti recorded maximum number of branches per plant and plant height. Maximum protein content, pod length and plant spread were recorded in genotype Arka Karthik. AP-5 recorded highest average pod weight and moisture content in pod. Pusa Pragati recorded minimum days to first flowering. Rachna recorded maximum fiber content. Analysis of variance revealed significant difference for all the characters under study, indicating more scope for selection of promising genotypes

Long Kumar and Chaturvedi (2020) observed significant variation among the genotypes for all the character studied in pea. The studies also revealed that the PCV were higher than the GCV for all the characters studied indicating the influence of environmental effect.

Gupta *et al.* (2020) reported that the analysis of variance showed the significant variability for all the characters studied in vegetable pea. High GCV and PCV were recorded in seed yield per plant and number of pods per plant which indicates the presence of high genetic variation among pea genotype.

Thapa *et al*. (2020) reported high GCV and PCV for total chlorophyll content followed by green pod yield and number of leaves per plant.

Yumkhaibam *et al*. (2019) reported that magnitude of phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters studied which is an indicator of additive gene effect of environment on the expression of the traits.

Lal *et al.* (2018) while studying the genetic variability in pea observed moderate to high level of genotypic coefficient of variance (GCV) and phenotypic coefficient of variance (PCV). The magnitudes of phenotypic coefficient of variance (PCV) for all the characters were slightly higher than their corresponding genotypic coefficient of variance (GCV), showed very less environmental influence on the expression of the characters. Higher estimate of GCV was recorded for number of seeds per pod followed by seed yield per plant.

Devi *et al.* (2017) recorded high PCV, GCV (>30%) estimates for days to fifty per cent flowering, days to marketable maturity and total soluble solids expressing significant variability among the genotypes.

Gudadinni *et al*. (2017) conducted an experiment to study the analysis of variance and observed the significant variability for all the studied characters except number of primary branches per plant. High values of GCV and PCV were observed for characters viz., pod yield per plant, pod yield per plot and days to first flowering and which indicates the presence of high genetic variation.

Rajbhar *et al*. (2017) reported the estimates of phenotypic coefficients of variation (PCV) were higher than genotypic coefficients of variation (GCV) for all the traits. High magnitudes of variability were observed in number of pods per plant, pod yield per plant and primary branches per plant pod yield per plant.

Bhuvaneswari *et al*. (2017) conducted an experiment and evaluated 51 diverse field pea genotypes for nine yield related quantitative traits and four morphological qualitative traits for improvement. The combined analysis of variance of genotypes for all the nine traits was observed to be significant. The amount of variability in one variable as a linear function of another variable was also estimated through genotypic and phenotypic correlation among nine quantitative traits.

Toppo *et al*. (2017) conducted an experiment to estimate the variability and character association of different qualitative characters on seed yield of 29 field pea genotypes. The analysis of variance showed that the sufficient variability was present in the material studied for all the qualitative characters. Among the different quality parameters, the moderate genotypic coefficient of variation was observed for swelling index.

Tambolkar *et al*. (2016) observed significant difference among the pea genotypes for the characters. Estimates of phenotypic and genotypic co-efficient of variance were significant for plant height, number of branches, number of leaves, leaf area, days to initiation of first flowering, number of clusters per plant, pod length, number of seeds per green pod, green pod yield per plant, pod yield per plot, pod yield per hectare and crop duration.

Toppo *et al*. (2017) conducted an experiment to estimate the variability and character association of different qualitative characters on seed yield of 29 field pea genotypes. The

analysis of variance showed that the sufficient variability was present in the material studied for all the qualitative characters. Among the different quality parameters, the moderate genotypic coefficient of variation was observed for swelling index.

Singh *et al*. (2017) reported that quantitative traits had promising variability in germplasm collected from different location of tropical, sub-tropical and temperate regions of India. A wide range of quantitative characters and high coefficient of variation and maximum standard deviation was observed for all quantitative traits among the 32 genotypes for primary branches per plant, secondary branches per plant, pods per plant, ten pod weight, pod width, pod yield per plant, shelling percentage, seeds/pod and plant height. However, for green pod length expressed low coefficient of variability (9.93 cm).

Georgieva *et al*. (2016) conducted an experiment for genetic evaluation of five genotypes of pea. Analysis of variance showed significant differences among genotypes for the traits like pod width, seeds per plant, seed weight per plant and 1000 seed weight. The estimates of genetic parameters of five varieties showed a good amount of genetic variation in the experimental materials under investigation. Moderate genotypic and phenotypic coefficients of variation were observed for all the traits except pod length and pod width.

Jeberson *et al*. (2016) estimated the genetic parameters in 12 genotypes of field pea. High to moderate GCV and PCV estimates and high heritability with high genetic advance as percent of mean were observed for the characters namely plant height, cluster per plant, no of seed per pod, 100 seed weight and yield.

Katoch *et al.* (2016) recorded the wide range of variability for most of the characters under study. The magnitude of phenotypic coefficient of variation (PCV) was recorded higher than the genotypic coefficient of variability (GCV) for all the traits. High genotypic and phenotypic coefficient of variations were recorded for protein content, plant height ascorbic acid and pod yield per plant for both the years.

Kumar *et al*. (2015) studied the parameters of variability and association of important characters with yield in 54 garden pea genotypes including four checks. Analysis of variance had significant differences among the genotypes for all the morphological characters studied. The genotypic and phenotypic coefficient of variation was high for total soluble solids, total sugars, pod yield per hectare and total phenols.

Pandey *et al*. (2015) found phenotypic coefficient of variation (PCV) was invariably higher than their corresponding genotypic coefficient of variation (GCV) for most of the characters. High genotypic coefficient of variation (GCV) as well as phenotypic coefficient of variation (PCV) was observed for plant height, pod yield per plant, number of pods per plant and pod yield per hectare.

Ahmad *et al*. (2014) conducted an experiment to observe the genetic variability in 12 genotypes of peas during growing season. Analysis of variance was observed highly significant for all characters studied except plant height. The highest genotypic and phenotypic co-efficient of variation were recorded for pod per plant followed by seed yield per plant and lowest was noted for days to maturity.

Dar *et al.* (2013) conduct an experiment and found considerable genetic variability for pod yield and other traits in pea.

Basaiwala *et al*. (2013) estimated genotypic and phenotypic coefficients of variation, heritability, expected genetic advance, correlation and path analysis for yield and yield contributing traits in 32 genotypes of field pea. Moderate to high PCV and GCV were recorded for pod bearing length, plant height, seed yield per plant, pods per plant, harvest index, seeds per pod and hundred seed weight.

Habtamu and Million (2013) evaluated in thirteen pea genotypes to estimate the genetic variability and identify superior genotypes that generate putative transgressive segregates. Genotypes differed significantly in case of phonological, yield and some yield related traits, and were highly influenced by the environment. Large magnitude of variability among the genotypes was observed to pod length and reaction to Ascochyta blight.

Jaiswal *et al*. (2015) found moderate to high level of genotypic coefficient of variability (GCV), phenotypic coefficient of variability (PCV), heritability and genetic advance for days to 50% flowering, plant height, number of pods per plant, days to maturity, number of seed per pod, pod length, 100-seed weight and grain yield per plant in pea. The magnitudes of the phenotypic variance of these traits were higher than the genotypic variance, indicated that the phenotypic component was the major contributor to total variance. Among all traits, plant height exhibited high estimates of GCV and PCV followed by seed yield per plant and number of seed per pod in pea.

Karnwal *et al*. (2013) studied 23 diverse genotypes of garden pea collected from diversified areas for mean, genetic variability, heritability, genetic advance. The four genotypes were found promising for future breeding program on the basis of their superior performance with respect to number pod per plant and green pod yield per plant in both summer and winter season under rained and dry temperate condition.

Pal and Singh (2013) found maximum shelling percentage in genotype VRP-86 (55.84%). Phenotypic variance and coefficient of variance were higher as compared to genotypic variance and coefficient of variance for all the characters under studied. Maximum GCV and PCV were recorded for plant height followed by number of pods per plant and green pod yield/plant.

Fikreselassie *et al*. (2012) conducted an experiment in different pea genotypes and observed that the mean squares due to genotypes were highly significant for all the characters in pea. The genotypic coefficient of variation (GCV) ranged from 11.19% for days to mature to 25.72% for number of seeds per plant.

Choudhary *et al.* (2010) found considerable amount of genotypic and phenotypic coefficient of variation for number of pods per plant, green pod yield per plant and plant height.

Lavanya *et al*. (2010) conducted an experiment to study variability and characters association among attributes in field pea crosses in F3 generation. High PCV and GCV estimates were recorded for seed yield per plant, number of pods per plant and 100 seed weight.

Nawab *et al*. (2008) observed highly significant differences among genotypes for days to emergence, days to 50 percent flowering, number of pods per plant, weight of pods per plant, pod length, 100-seed weight, number of seeds per pod and green pod yield. Green pod yield per plot, number of pods per plant, 100-seed weight and weight of pods per plant showed high GCV with high heritability and genetic advance indicating good scope for selection.

2.2 Coefficient correlation

The term correlation coefficient was given by Karl Pearson in 1902 and denoted by “r”. It is used to measure association between yield and it’s contributing traits to determine the component trait on which selection can be based for genetic improvement in yield. For a plant breeder, it is essential to know the degree of relationship between yield and its contributing traits to facilitate the improvement in desirable traits. Correlation coefficient provides information on inter-character association of various yield components but when more characters are involved in the association analysis it becomes challenging to ascertain which trait actually contributes more towards yield.

Tiwari *et al*. (2020) reported the correlation pod yield per hectare exhibited highly significant and positive correlation with pod yield (g/plant), pod yield (q/ha), average pod weight (g), total sugar, T.S.S., number of seeds per pod, pod length (cm), number of leaves per plant, number of pods per plant, protein content, shelling percent, plant height(cm), number of primary branch per plant and expressed negative association with days to first flower appearance, days to 50% flowering and days to first picking. Phenotypic correlation coefficient revealed that the pod yield per hectare had the maximum significant positive correlation with pod yield (g/plant), pod yield (q/ha), average pod weight (g), total sugar, TSS, number of seeds per pod, protein content, number of leaves per plant, number of pods per plant, pod length (cm), shelling percent, Plant height and number of primary branches per plant.

Tasnim *et al*. (2022) observed that pod length had a highly significant positive correlation with pod width and hundred seeds weight, however, days to first flowering showed a highly negative correlation with pod length and hundred seed weight

Ali *et al*. (2021) recorded the significant and positive phenotypic coefficient of correlation was exhibited by seed yield per plant with plant height, days to 50% flowering, days to maturity, pods per plant, pod length, fresh pod shelling percentage, 100-seed fresh weight and 100-seed dry weight. Significant and positive genotypic coefficient of correlation was exhibited by seed yield per plant with plant height, days to maturity and number of pods per plant.

Kalapchieva *et al*. (2021) reported that most of the quantitative indicators, the phenotypic relationships were found insignificantly lower than the values of their genetic correlation coefficients. The next correlation coefficients were found with significant genotype dependencies: among the plant height and internode length, height to first fertile node and average number of grains per pod, two pods per fruiting handle with pod weight per plant, number of tillers with average number of grains per pod, total number of pods per plant with two pods per fruiting handle. Strong to average was found the dependence on the green grains weight with the pods weight, percent of unfilled grains.

Raj *et al*. (2020) in correlation studies reported that height of plant, number of branches per plant, moisture per cent, number of nodes per plant and number of pods per plant exhibited significant correlation for pod yield and these attributes can be considered for identification of high yielding genotypes. The path analysis revealed that focusing on number of branches per plant and height of plant could improve breeding efficiency of pea.

Thapa *et al*. (2020) conducted an experiment and found the pod yield was significantly and positively correlated with pod weight, pod girth, pericarp thickness, seed weight per pod, number of pods per plant and weight of 100 seeds.

Longkumer and Chaturvedi (2020) conducted an experiment and observed the analysis of variance revealed significant variation among the genotypes for all the character studied. Correlation analysis had significant positive association with seeds per pod and shelling percentage.

Kumar *et al*. (2019) found that pod yield per plant was significantly and positively correlated with plant height, number of leaves per plant, days to first flowering, days to first picking, number of pods per plant, number of pods per axil, pod width, pod length, pod yield per plot, number of seeds per pod, weight of 100 seeds at both genotypic and phenotypic level.

Singh *et al*. (2019) reported that seed yield per plant had positive and significant association with green pod yield per plant, shell weight per plant, number of pods per plant and length of pod both at genotypic and phenotypic levels. Path coefficient analysis revealed direct positive effect on seed yield per plant by green pod yield per plant, number of first fruiting node, length of pod, days to 50% flowering and plant height. Hence, from correlation and path analysis it can be inferred that green pod yield per plant and pod length had significant and positive correlation and direct positive effect on seed yield and these traits can used as key indices towards the direct selection of genotypes for yield improvement of pea germplasm.

Lal *et al*. (2018) observed in correlation analysis that seed yield per plant had highly significant and positive correlation with harvest index, seeds per pod, pod length and 100-seed weight.

Srivastava *et al*. (2018) observed that seed yield per plant had highly significant and positive correlation with 100 seed weight, number of pods per plant, harvest index, number of seeds per pod and biological yield. The highest positive direct effect on seed yield per plant was exerted by harvest index followed by biological yield, 100 seed weight, number of seeds per pod and number of pods per plant.

Bhuvaneswari *et al*. (2017) studied combined analysis of variance of genotypes for all the nine traits was found to be significant. The amount of variability in one variable as a linear function of another variable was also estimated through genotypic and phenotypic correlation among nine quantitative traits. The pod number per plant, 100 seed weight and seed number per pod showed significant positive correlation with seed yield per plant both at genotypic and phenotypic levels.

Khan *et al*. (2017) observed the phenotypic variance was higher than the genotypic variance for all the characters studied. All the characters showed moderate to low genotypic and phenotypic coefficient of variation. Genotypic coefficient of variation recorded highest for hundred seed weight followed by number of branches plant and seeds plant. Hundred seed weight had the highest heritability. Pod length, hundred seed weight, pods plant and seeds plant showed significant positive genotypic and phenotypic correlation with seed yield.

Devi *et al*. (2017) conducted an experiment and observed the pod length had maximum positive direct effect on pod yield per plot followed by number of pods per plant, number of seeds per pod, harvest duration, 100-pod weight, TSS and pod width.

Toppo *et al*. (2017) studied the correlation analysis in pea and revealed that seed yield per plant exhibited a significant positive association with protein at genotypic level. The number of pods per plant, number of seeds per pod and 100 seed weight showed significant positive correlation with seed yield per plant both at genotypic and phenotypic levels.

Jeberson *et al*. (2016) studied the correlation coefficients and it revealed positive and highly significant association of yield with plant height, cluster per plant, pods per plant, pod length, seeds per pod and 100 seed weight in pea. The number of pods per plant exhibited highly positive and direct effect on grain yield followed by pod length and days to maturity.

Katoch *et al*. (2016) conducted an experiment and found the pod yield had a positive and significant correlation with number of pods per plant, pod length and number of seeds per pod both the years. Path analysis showed that pod length and number of pods per plant have highest positive direct effect both the years and thus it may be treated as selection criteria for isolating higher yielding genotypes in vegetable peas.

Kumar *et al*. (2015) studied correlation among different genotypes of pea reported 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 peas yield.

Pandey *et al*. (2015) conducted an experiment and reported significant association of yield per hectare with pod yield per plant, total soluble solids, number of pods per plant, and days to 50% flowering at phenotypic and genotypic level (PCV and GCV) respectively.

Tofiq *et al*. (2015) studied simple correlation coefficient among characters of pea and reported that weight of seeds was positively and highly significantly correlated with number of pods per plant, weight of pods per plant, biological weight plant^{-1} and harvest index respectively

Kumar *et al*. (2014) reported in their study that the association of the seed yield per plant was found to be significant and positively correlated with plant height, days to maturity, number of primary branches, pods per plant, pod length and seed index.

Basaiwala *et al.* (2013) conducted an experiment and estimated correlations to study the strength of association between yield and ten other characters of pea. Seed yield per plant was positive and significantly correlated with plant height, pod bearing length, pods per plant, seed setting %, seeds pod-1 and harvest index. Plant height, pods plant-1 and seed setting % had positive direct effect and exhibited significant positive correlation with seed yield, indicating a true relationship of these traits with seed yield.

Siddika *et al*. (2013) conducted an experiment for the characters association of 26 advanced lines of vegetable pea and they found significant positive genotypic and phenotypic correlation between seed yield per plant and days to 50% harvest, pod length, pod breadth and seeds per pod.

Dhama *et al*. (2010) conducted an experiment to observe the character associations and their mode of direct and indirect effect on pod yield in 30 genotypes of pea to pick up the best character contribution under irrigated and rainfed environments. The value of genotypic correlations was higher than phenotypic correlations for all the characters studied in the environments. Number of pods per plant showed significant and positive association with pod yield per plant in all the environments.

Ghobary (2010) observed the relationship among yield and some yield components using correlation. Positive and significant relationship was found among seed yield per plant and number of pods per plant, pod length, 100 seed weight and number of branches per plant.

Guleria *et al*. (2009) found in correlation studies that the characters like flower number, pod number and seeds per pod not only contributed positively to the pod yield but also had strong correlation coefficient with yield. Thus, genotypes with higher number of flowers, pods and seeds per pod should be selected to increase the pod yield

Nawab *et al*. (2008) conducted an experiment and reported that correlation studies revealed that in general, estimates of genotypic correlation coefficient were higher than corresponding phenotypic correlation coefficient. Green pod yield per plot exhibited positive and significant correlation with number of seeds per pod and weight of pods per plant at phenotypic and genotypic levels.

2.3 Heritability and Genetic advance

Heritability shows the proportion of phenotypic variance that is due to genotype which is heritable (Hanson *et al*. 1956). Selection of a trait should fairly be easy if heritability of that trait is very high. This is because there would be a close correspondence between phenotype and genotype due to a relatively smaller contribution of environment to the phenotype. High heritability shows the existence of additive genes in the expression of traits that could be easily exploited (Bharadwaj *et al.* 2007) and high broad sense heritability estimate indicate genetic variances with less influence of the environment and the potential effectiveness of selection of the hybrids for traits of interest (Allard, 1960). The estimates of heritability are influenced by various factors, such as type of genetic material, sample size, sampling method, conduct of experiment, method of calculation and effect of linkage (Fehr, 1987). It is necessary to split the overall variability into heritable and nonheritable components.

Kumar *et al*. (2022) reported high the heritability and genetic advance for days to 50% flowering, plant height and seed yield per plant. High heritability with moderate genetic advance were observed for days to maturity, pod length fresh pod shelling percentage, 100-seed fresh and dry weight.

Tasnim *et al*. (2022) observed high heritability relationship with high genetic advance for plant height, pod per plant, hundred seed weight, and seed yield per plot in pea.

Ali *et al.* (2021) estimated high heritability and genetic advance for days to 50 percent flowering, plant height and seed yield per plant. High heritability with moderate genetic advance were observed for days to maturity, pod length, fresh pod shelling percentage, 100-seed fresh and dry weight.

Pujari *et al.* (2021) analyzed genetic parameters for 11 characters with 21 diverse genotypes of field pea and observed high heritability coupled with high genetic advance as percent of mean for the characters like plant height (cm), number of pods per plant, number of primary branches per plant, and seed yield per plant (g).

Yadav *et al*. (2021) found the high heritability for almost all the character except number of seeds per pod, and shelling percentage in pea. High heritability coupled with high genetic advance in percent of mean were observed for primary branches per plant, number of pods per plant, pod yield per plant and number of seeds per 250 g indicating that these traits were little influenced of environment.

Longkumar and Chaturvedi (2020) conducted an experiment and observed high heritability coupled with high genetic advance as percent of mean for days to 50 percent flowering and diameter of pods indicating that these characters are controlled by additive gene effects and phenotypic selection of these traits would be effective for further breeding purpose.

Thapa *et al.* (2020) observed the heritability (>60 %) for all the characters in garden pea except pod set per inflorescence, protein content and shelling percentage which exhibited medium heritability.

Gupta *et al*. (2020) found high heritability coupled with high genetic advance for the traits viz. plant height, seed yield per plant, number of pods per plant, length of first fruiting node, days to 50% flowering, number of first fruiting node, length of pod and number of seeds per pod which indicates presence of additive gene action and needs for improvement through selection.

Yumkhaibam *et al.* (2019) found the heritability exerts at high degree for all the plant characters studied viz. plant height, days to first flowering, days to first pod harvesting, pod weight, ascorbic acid, protein content, shelling percentage, internodal length, pod yield per plant, number of primary branches per plant, pod yield per hectare as well for other yield attributing traits. Plant height, number of primary branches plant^{-1} and internodal length had highest genetic advance and lowest for days to first pod picking. High heritability coupled with high genetic advance was found for plant height, internodal length and number of primary branches per plant.

Devi *et al*. (2017) observed the high heritability (>80%) coupled with high to moderate genetic gain for days to fifty per cent flowering, days to marketable maturity and 100-pod weight indicating prominent role of additive gene effects.

Gudadinni *et al*. (2017) recorded high heritability for all characters except protein content. Further, high heritability coupled with high genetic advance was observed for the traits *viz*., pod yield, pod yield per plot, plant height and days to first flowering which indicates presence of additive gene action and useful for population improvement by selection.

Khan *et al*. (2017) conducted an experiment and observed for highest heritability (95.97) the hundred seed weight. Pod length, hundred seed weight, pods plant and seeds plant showed significant positive genotypic and phenotypic correlation with seed yield.

Rajbhar *et al*. (2017) reported high magnitudes of variability for number of pods per plant, pod yield per plant, primary branches per plant and width of pod. They recorded high heritability coupled with high genetic advance in per cent of mean for number of pods per plant, primary branches per plant and pod yield per plant showed scope of high selection response. High heritability along with high genetic advance in per cent of mean provides ample scope for further improvement in advance generations.

Katoch *et al*. (2016) reported that the pod yield per plant and plant height exhibited high heritability associated with high genetic advance indicating the additive gene action for their expression and are likely to respond better to selection.

Jeberson *et al*. (2016) observed high heritability along with high genetic advance as percent of mean were observed for the characters namely plant height, number of clusters per plant, 100 seed weight, number of seeds per pod and yield. The correlation coefficients had positive and highly significant association of yield with plant height, number of clusters per plant, pods/plant, pod length, number of seeds per pod and 100 seed weight. The number of pods per plant exhibited highly positive and direct effect on grain yield followed by pod length and days to maturity. Therefore, these traits can be considered for selecting genotypes to improve the seed yield in the field pea.

Pandey *et al*. (2015) observed high heritability with high genetic advance in percent of mean for plant height (99, 53.36), total soluble solid (TSS) (99, 53.36) and pod yield per plant (99, 51.99), which showed that these traits were under additive gene control and selection for phenotypic and genotypic improvement for these traits would be effective.

Kumar *et al*. (2014) reported that genotypic and phenotypic coefficient variations for all the characters were more or less similar for all the traits. The heritability in broad sense was observed to be high 87.6% to 95.7% for all characters which had significant difference among the genotype. The path coefficient analysis indicated that number of pods per plant, pod length, number of primary branches, seed weight and number seeds per pod had high direct influence on enhancing the yield per plant resulting in positive and strong correlation between these traits.

Dar *et al*. (2013) reported high heritability measured for all the characters. High genetic advance coupled with high heritability for number of pods per plant, pod width, seeds per pod and pod yield per plant indicated that selection for these characters should be effective for improving economic yield.

Pal and Singh (2013) noted the highest heritability for green pod yield per plant and days to 50 % flower emergence and its higher value may be attributed to additive gene action. The estimate of genetic advance ranged from 0.07 to 73.3 and it was highest for pod yield per plant.

Choudhary *et al*. (2010) observed the high estimates of heritability, genotypic coefficient of variation (GCV) and genetic advance for plant height(cm), number of pods per plant and green pod yield per plant.

Guleria *et al*. (2009) observed that heritability estimation couple with the knowledge of genetic gain are more helpful than the heritability alone in predicting the value of selection. High genetic advance as percent of mean was observed in seeds per plant, shoot height and internodal length, which indicated that fix ability of heritable characters was high.

Kumar *et al.* (2007) observed the high to moderate heritability coupled with high to moderate genetic advance for yield per plant, 100-seed weight and biological yield in pea.

Sharma *et al*. (2007) found that the heritability and genetic advance were high for plant height and moderate for number of pods per plant and pod yield per plant showed the additive and non-additive gene action for their expression.

Gupta *et al*. (2006) reported that genetic advance was observed highest for green pod yield per plant. High heritability along with high genetic advance was observed for days to first flowering nodes, plant height, number of first flowering nodes, green pod yield per plant, dry matter weight per plant and number of primary branches per plant, showing the preponderance of additive gene effect and the potential of selection for these traits to improve vegetable pea yield.

Rai *et al*. (2006) observed high genetic advance along with moderate estimates of heritability for the plant height and high heritability couple with low genetic advance for number of seeds per pod and number of pods per plant. Genetic advance as per cent of mean exhibited maximum value for yield per plant followed by number of pods per plant in pea.

2.4 Path Analysis

Path coefficient is the estimation of direct influence of one variable on another which permits the separation of correlation coefficient into component of direct and indirect effects. The path coefficient term was coined by Wright (1921). In plant breeding this technique was first introduced by Dewey and Lu (1959). The use of path coefficient analysis requires a cause-and-effect situation among variables. Path analysis helps in partitioning correlation coefficients into direct and indirect effects of component characters in yield. Wright (1921) provided effective means of finding out direct and indirect causes of association and permits a critical examination of the 16 specific forces acting to produce a given correlation and measures the relative importance of each casual factor through path analysis technique.

Tasnim *et al.,* (2022) observed the path coefficient analysis revealed that plant height, pod per plant, and seeds per pod had a highly positive effect on yield per plant. Therefore, associating and selecting those characters, improvement in pea yield must be possible.

Raj *et al*. (2020) conducted an experiment and observed the path analysis revealed that focusing on height of plant and number of branches per plant could improve breeding efficiency of pea.

Longkumer and Chaturvedi (2020) reported that the path analysis revealed that seeds per pod contributed maximum positive direct effect on pod yield per plant and also exhibited positive correlation with yield. This shows true relationship between these traits and selection emphasis should be given on this attribute - seeds per pod.

Thapa *et al*. (2020) recorded the path coefficient analysis using the phenotypic correlation coefficient among the pair of characters which showed that number of pods per plant had the highest positive direct effect on yield.

Kumar *et al*. (2019) while analyzing path coefficient analysis observed positive effect on pod yield per plant was exhibited by plant height, number of pods per plant, pod length and pod yield per plot and these traits shall be considered for direct selection of genotypes for the successful breeding program.

Singh *et al*. (2019) observed the path coefficient analysis revealed direct positive effect on seed yield per plant by green pod yield per plant, number of first fruiting node, length of pod, days to 50% flowering and plant height. Hence, from correlation and path analysis it can be inferred that green pod yield per plant and pod length had significant and positive correlation and direct positive effect on seed yield and these traits can used as key indices towards the direct selection of genotypes for yield improvement of pea germplasm.

Srivastava *et al*. (2018) observed the seed yield per plant exhibited highly significant and positive correlation with 100 seed weight (0.37), number of pods/plant (0.35), harvest index (0.32), number of seeds per pod (0.32) and biological yield (g) (0.28). The occurrence of positive as well as negative indirect effects on yield by one or another character presents a complex situation where a compromise balance is used to attain proper balance of different yield components for analyzing the ideotype of seed yield in field pea. The highest positive direct effect on seed yield per plant was exhibited by harvest index (0.79) followed by biological yield (g) (0.78), 100 seed weight (0.34), number of seeds per pod (0.27) and number of pods per plant (0.26).

Lal *et al*. (2018) reported the path analysis indicated the highest positive and direct effect on seed yield per plant exerted by harvest index and seeds per pod. Highly positive indirect effect on seed yield per plant was showed by harvest index *via* pod length, seeds per pod and biological yield per plant. The traits identified above as direct and indirect yield components can be used in formulation of selection strategy in field pea for selection of high yielding genotypes.

Devi *et al*. (2017) observed the high heritability (>80%) coupled with high to moderate genetic gain for days to fifty per cent flowering, days to marketable maturity and 100-pod weight indicating prominent role of additive gene effects.

Khan *et al*. (2017) observed the path analysis, plant height, internode length, hundred seed weight, number of seeds per pod showed positive direct effect on yield. Considering genetic variability, correlation and path analysis, emphasis should be given on pod length, seeds pod, seeds per plant and hundred seed weight during breeding program to improve seed yield of pea.

Toppo *et al*. (2017) studied the path coefficient analysis for seed yield and its components. The studied showed that protein content had the negligible positive direct effect on seed yield. Direct selection for quality traits would likely not be effective in decreasing or increasing seed yield in field pea.

Katoch *et al*. (2016) conducted an experiment and observed the path analysis revealed that number of pods per plant and pod length have highest positive direct effect on yield of both the years which may be treated as selection criteria for isolating higher yielding genotypes in garden peas.

Tofiq *et al*. (2015) studied the path analysis between weight of seeds per plant and other characters in pea. The characters viz; biological weight per plant and harvest index exhibited the maximum positive direct effect in weight of seeds per plant, the character number of pods per plant showed the highest positive indirect effect on weight of seeds per plant via harvest index.

Jeberson *et al*. (2016) observed that number of pods per plant exhibited highly positive and direct effect on grain yield followed by pod length and days to maturity.

Therefore, these traits can be considered for selecting genotypes to improve the yield in the field pea.

Kumar *et al.* (2014) studied the association of yield attributes traits and their direct and indirect influences of the seed yield in pea. Results of the path coefficient analysis showed that number of pods per plant, seed weight, pod length, number of primary branches and seed per pod had high direct influence on enhancing yield per plant resulting in positive and strong correlation between these characters.

Karnwal *et al.* (2013) studied 23 diverse genotype of garden pea collected from diversified areas of country for mean, genetic variability, heritability, genetic advance, in respect of horticultural traits. Path analysis exhibited the highly positive direct effects through number of grains per pod, number of green pods per plant and pod length. Therefore, these characters may be considered as the most reliable selection indices for effective improvement of green pod yield in vegetable pea.

Siddika *et al.* (2013) conducted an experiment to study the genetic variability and character association in 26 genotypes of vegetables pea. Path coefficient analysis revealed that days to 50% flowering, days to 50% harvest, number of branches per plant, pods per plant, seeds per plant and 100 seed weight had positive direct effect on seed yield per plant.

Kosev and Mikic (2012) reported the strongest and direct positive effect on seed yield was found with branch length, 1000-seed weight and number of seeds per pod. The highest positive indirect contribution was in branch length to number of seeds per pod, number of fertile nodes per plant and number of seeds per plant in pea.

Fikreselassie (2012) observed in path analysis at genotypic level that the harvest index and biomass yield contributed major positive direct effect on seed yield in pea.

Lal *et al*. (2011) in path coefficient analysis found that pod per plant, harvest index and biological yield but pod per plant and harvest index were the most important yield components that could be used as selection for further improvement in field pea.

Nawab *et al*. (2008) evaluated twelve pea genotypes and observed 100-seed weight, number of pods per plant, number of seeds per pod and days to 50 percent flowering had maximum positive direct effect on green pod yield per plot. It showed that these characters are main contributors towards pea yield.

Togay *et al*. (2008) carried out an experiment to determine the relationship among yield and yield components using correlation and path coefficient analysis in twelve pea genotypes. Biological yield and numbers of pods per plant recorded the highest positive and direct effects on seed yield followed by first pod harvest and number of seeds per pod.

2.5 Genetic Divergence

Evaluation of genetic diversity is important to know the source of genes for a particular trait within the germplasm (Farhad *et al*. 2010). The plant breeders always want to know the genetic divergence among the available varieties due to reasons that crosses between genetically diverse parents are likely to produce high heterotic effect (Ramanujam *et al*. 1974)

Kumar *et al.* (2022) collected of 47 lines sorted into seventeen clusters after a genetic divergence analysis using Mahalanobis's D^2 analysis. Cluster XII and XIII (43.6) had the greatest average inter-cluster distance, while cluster VII had the greatest intra-cluster distance (12.6). The highest percentage contribution of features to divergence was biological yield per plant followed by the number of primary branches per plants. For most of the genotypes, clusters XV and XVII had higher cluster means.

Jaiswal *et al*. (2021) based on cluster analysis, groped pea genotypes into three cluster. The maximum and minimum genotypes grouped in cluster I (50) and minimum were in Cluster II (1) and cluster III (1) respectively. The maximum intra-cluster distance was shown by cluster I (D^2=5.07) indicating maximum difference among the genotypes within and the minimum value was shown by cluster II and cluster III. Maximum value of inter-cluster distance (D^2=16.7) was recorded between cluster I and cluster III revealing that the genotypes of these clusters were highly diverse from others and can be used as divergent parents for hybridization and selection. Therefore, for getting high heterosis for recovering transgressive segregants, genotypes from cluster I and III can be used as distant parents in a breeding program for successful improvement in pea.

Aman *et al*. (2020) reported grouped pea genotypes into five clusters at a dissimilarity level of 0.61 which also exhibiting the presence of high magnitude of variation among the genotypes studied. On the basis of superior performance for maturity, yield and yield-related characters, pea genotypes Leena Pak, UAP-47, UAP-29 and Green Gold are recommended for testing across locations and for onward use in pea breeding programs.

Bijalwan *et al.* (2018) studied genetic diversity among 23 pea genotypes and these genotypes were grouped into 5 clusters. Cluster IV was largest, consisting of 8 genotypes followed by cluster I with 7 genotypes, cluster III with 4 genotypes, cluster II with 3 genotypes while cluster V contained one genotype. There was no parallelism among genetic diversity and geographical distribution. Cluster IV (PSM-3, Pea 901, CHP-2, AP-2, AP-5, VRP-6, PSM-4 and Pea 902) and cluster V (Pb-89) had highest value of inter-cluster distance (377.6) followed by cluster III (PC-531, AP-1, VRP-7 and VL-7) and cluster V (284.1), cluster II (PSM-5, E-6 and Pant Uphar) and cluster V (214.09) and cluster I (PM-2, Pea-801, Arkel, Arka Ajeet, AP-3, JM-1 and AP-4) and cluster V (168.02). The maximum intra-cluster distance was noted for cluster IV (25.8). Cluster V showed maximum mean values for pod yield for plant, pod length, TSS, number of pods plant per plant, root length, fresh weight of root nodules per plant, number of flowers per cluster and days to 50% flowering.

Srivastava *et al.* (2018) in cluster analysis of pea found that cluster VI had highest number of genotypes, followed by cluster IV, IX and XI. Lowest genotypes were recorded in cluster VIII. The 11 clusters in divergence analysis contained genotypes of heterogeneous origin by indicating no parallelism between genetic and geographic diversity. Cluster pairs showing very high inter-cluster distance were showed between clusters V and X and cluster III and X. The highest intra cluster distance was found in cluster II followed by cluster I and cluster VII. The lowest values were found in cluster X.

Gupta *et al.* (2017) using D^2 analysis grouped pea genotypes in four clusters showing the existence of considerable amount of variation among the genotypes. Maximum pod yield 73.2 q/ha was found in PB-89 genotype. Cluster pattern exhibited that, cluster III had largest number of genotypes (10) followed by cluster II (5 genotypes), cluster IV (3 genotypes) and cluster I had only (2 genotypes). Highest intra cluster distance was found cluster II (D2 =1.9) whereas, highest inter cluster distance was observed between cluster III and I (D2 = 6.6).

Kumar and Kumar (2016) grouped 54 genotypes of pea into 4 clusters and maximum number of genotypes was accommodated in cluster II. The average intra-cluster distance was observed maximum in cluster II and minimum in cluster III. Maximum inter-cluster between cluster II and III exhibiting that hybridization between genotypes from cluster II and III useful for getting the superior recombinants in segregating generations. On the basis of cluster means of different traits studied, cluster II was found superior for number of pods per plant, number of seeds per pod, shelling percentage, pod yield, pod length, total sugars and total soluble solids, whereas cluster III was found superior for plant height and total phenols.

Saxesena *et al.* (2013) studied the intra-cluster D^2 value which ranged from 0.00 to 65.1 while inter-cluster D^2 value ranged from 101.3 to 763.2 indicated that the selected advance breeding lines were highly divergent. The maximum intra cluster distance was recorded for cluster I (65.1) while cluster IV and V (0.0) showed no intra-cluster distance values had homogenous nature of the genotypes within the cluster. The genetically high divergent advanced breeding lines present in cluster II and V as indicated by inter-cluster distance value (763.2). Selecting lines of these clusters probably give promising recombinants and better segregants for future breeding programme.

Singh *et al.* (2007) grouped pea genotypes into 6 clusters. To get the desirable segregants the hybridization among the genotypes of cluster III and VI, cluster V and VI and cluster I and VI as the inter cluster distances were greater between these clusters. Association studies indicated that pods per plant, clusters per plant, seeds per pod and days to 50% flowering were significantly correlated with grain yield. Pods per plant, seeds per pod, 100-seed weight and days to maturity had positive direct effect on grain yield, while plant height, pod length and number of pods per cluster had negative direct effect on grain yield.

3. MATERIALS AND METHOD

The present investigation on the "Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)" was implemented during the *Rabi* season of 2021-22. The details of the experimental materials, observations and methods or techniques adopted during the course of the investigation are presented in this chapter.

3.1 Experimental material and other details

Experimental site

Rani Lakshmi Bai Central Agricultural University (RLBCAU) is situated in the Bundelkhand agro-climatic zone (6) of Uttar Pradesh. The experiment was conducted in the Vegetable Research Farm of RLBCAU, Jhansi. The experimental site is situated at 25.31° N latitude and 78.33° E longitude at an altitude of 227 m above mean sea level.

Climate and weather

Bundelkhand is a sub-tropical and semi-arid place subjected to the severe warm summer season and cold wintry weather.

Soil condition of the experimental field

A soil sample was taken from a depth of 15 cm below the surface of the experimental field, before raising the crop for experiment. The sample was placed to laboratory analysis to determine the physical and chemical compositions by using various standard methods. It was observed that soil of the experimental plot was sandy loam having pH 6.8 which show the neutral nature of experimental soil. The electrical conductivity was 0.4dS/m and organic carbon content of soil was 2.04g/kg of soil.

Experimental material

The experimental material comprises 30 vegetable pea genotypes collected from different sources CAUs, SAUs and ICAR-Institutions. IPFD11-5, IPFD10-12 and Aman are dual purpose variety of pea. The experimental genotypes were grown in the Vegetable Research Farm near the College of Horticultural and Forestry RLBCAU, Jhansi which are shown in Table (3.1)

Table (3.1): Genotypes of Pea and their sources of collections.

Treatment	Name of Genotype	Source
T1	Kashi Uday	ICAR - IIVR, Varanasi
T2	Kashi Nandani	ICAR - IIVR, Varanasi
T3	Kashi Ageti	ICAR - IIVR, Varanasi
T4	Kashi Samarth	ICAR - IIVR, Varanasi
T5	Kashi Mukti	ICAR - IIVR, Varanasi
T6	AP-3	CSAU&T,Kanpur
T7	Arka Priya	ICAR - IIHR, Bangalore
T8	AP-1	CSAU&T,Kanpur
T9	Pusa Sree	ICAR - IARI, New Delhi
T10	Pusa Pragati	ICAR - IARI, New Delhi
T11	Arkel	ICAR - IIVR, Varanasi
T12	PSM-3	GBPUAT, Pantnagar
T13	PSM-2	GBPUAT, Pantnagar
T14	NDVP -1	ANDUA&T, Ayodhya
T15	VL-7	VPKAS, Almora, UK
T16	PB-89	PAU, Punjab
T17	AS-10	Anvay Seed Company
T18	PC-531	ICAR - IIVR, Varanasi
T19	IC 208366	ICAR - IIVR, Varanasi
T20	IC 395309	ICAR - IIVR, Varanasi
T21	EC 6621	ICAR - IIVR, Varanasi
T22	EC 243642	ICAR - IIVR, Varanasi
T23	EC 302842	ICAR - IIVR, Varanasi
T24	IPFD-10-12	ICAR - IIPR, Kanpur
T25	IPFD-11-5	ICAR - IIPR, Kanpur
T26	Aman	ICAR - IIPR, Kanpur
T27	Pencil Matar	Haryali Seed Company
T28	Pea TS -10	Tycoon Seed Tech Pvt. Ltd., Delhi
T29	Ganga -10	Malwa Agritech Pvt. Ltd.
T30	GS -10	Advanta Golden Seed Company

Table (3.2) Experimental Design:

1.	**Title of the Experiment**	**Study on genetic diversity in vegetable pea *(Pisum sativum* L. *var. hortense*)**
2.	**Location**	Vegetable Research Farm, College of Horticulture and Forestry, RLBCAU, Jhansi
3.	**Year of commencement**	*Rabi*, 2021-2022
4.	**Experimental design**	RBD
5.	**Crop**	Pea
6.	**Seed rate**	90-100 kg per ha.
7.	**Sowing date**	9/11/2021
8.	**Spacing**	30 cm x 10 cm
9.	**Number of replications**	3
10.	**Number of genotypes**	30

3.2 Cultural practices

The standard cultural practices were followed in experimental field during the research work.

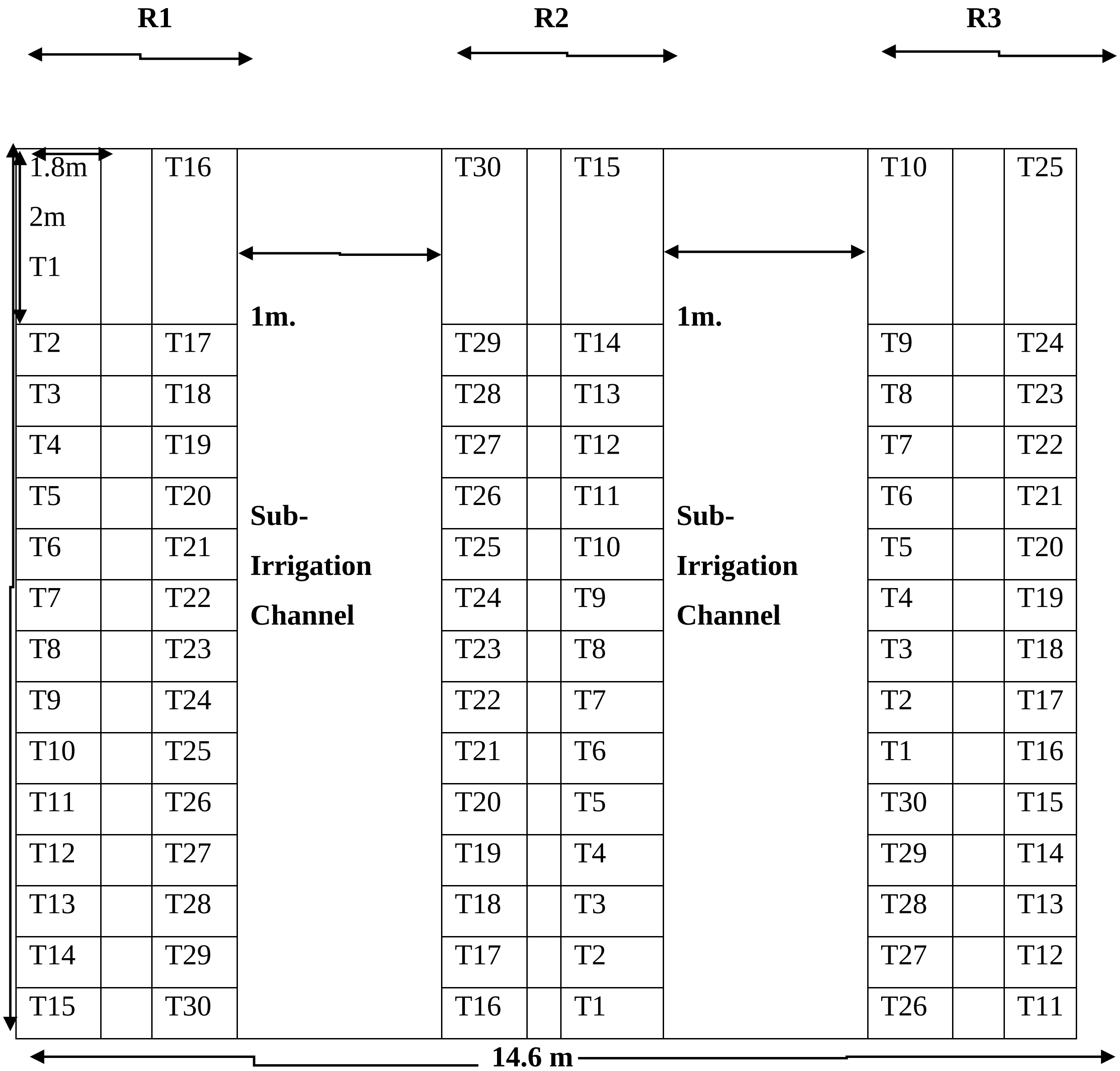
Land preparation

land was prepared well before sowing the seed. The experimental field was uniformly ploughed to a fine tilth. Ploughing the field with soil turning plough followed by one or two harrowing.

Manures and fertilizers

The Experimental area was be ploughed repeatedly and brought to a fine tilth. The recommended dose (10 t/ha) of farm yard manure was given as basal dose and recommended dose of fertilizers (30:60:50 kg NPK/ha) was incorporated in the soil before final harrowing and treatments were assigned to different plot in each replication by using random table. The main and sub-irrigation channels were laid out taking into account the gradient of the site.

Layout of experimental field



R1		R2		R3	
T1	T16	T30	T15	T10	T25
T2	T17	T29	T14	T9	T24
T3	T18	T28	T13	T8	T23
T4	T19	T27	T12	T7	T22
T5	T20	T26	T11	T6	T21
T6	T21	T25	T10	T5	T20
T7	T22	T24	T9	T4	T19
T8	T23	T23	T8	T3	T18
T9	T24	T22	T7	T2	T17
T10	T25	T21	T6	T1	T16
T11	T26	T20	T5	T30	T15
T12	T27	T19	T4	T29	T14
T13	T28	T18	T3	T28	T13
T14	T29	T17	T2	T27	T12
T15	T30	T16	T1	T26	T11

Fig 3.1 Layout of experimental field

Sowing

After planning the layout of field experiment the genotypes were sown to different sub-plots in each replication randomly following the principle of RBD. Seeds were sowed at a spacing of 30 cm between the lines and 10 cm within the lines. Seeds were sown about 2.5cm deep. The seeds of different genotypes were sown manually.

3.3 Intercultural operations

3.3.1 Weeding

Hand weeding was carried with the help of the khurpi and spade.

3.3.2 Irrigation

During the experiment, irrigation was given at 7-10 days intervals based upon the moisture requirement of field soil. The flowering stage and pod development stage are important stages for irrigation in the pea.

3.3.3 Harvesting

Green and tender pods were harvested manually without damage. Pods were harvested in morning hours.

3.4 Observations recorded

Following observations were recorded for the study.

A. Growth parameter

1. Plant height (cm)

At the time of last picking, height of plants of the main stems of each selected plant were measured from the ground level to the tip portion and the average plant height was calculated.

2. Number of primary branches per plant

The number of pods bearing primary branches arising from the main shoot were counted at maturity from the selected plants and averaged.

3. Number of nodes per plant

All the nodes of five randomly selected plants were counted separately before last harvest, summed and mean values were calculated.

4. Inter nodal length (cm)

It was measured as the length between two central nodes of 5 randomly selected plants in centimeter.

B. Flowering

1. Days to first flowering

Number of days taken from sowing to the appearance of first flower on the randomly selected plants in each plot was noted and average days to first flowering were calculated.

2. Days to 50% flowering

The number of days taken from sowing to appearance of 50% flowers of pants in each experimental plot was recorded and average was calculated

C. Yield parameter

1. Days to first pod setting

The number of days taken from sowing of seeds to the first appearance of pods set of the plant in each experimental plot was recorded and average was calculated.

2. Days to first pod picking

It was observed as number of days taken from sowing of seeds to the first picking of pods.

3. Number of pods per plant

Ten pods from each experimental plot were randomly picked and seeds were extracted manually. The number of seeds was counted and average number of seeds per ten pods were calculated.

4. Pod length (cm)

Pod length was measured from base to the tip of the pods using Digimatic vernier calipers. Pods were harvested during second picking from all the experimental plots from a single line were bulked and 10 pods were taken randomly to calculate average pod length.

5. Pod width(cm)

The pods taken randomly for measuring its diameter were considered for observing its diameter. The pod diameters of ten (10) pods were measured with the help of Digimatic venires caliper and its average pod width were calculated.

6. Average pod weight (g)

The weight of ten pods was observed separately with the help of weighing balance and average pod weight was worked out for each genotype for one pod.

7. Pod yield per plant (g)

The pods which had attained marketable size were picked and weighed. Pod weight was observed in grams up to two decimal places of all the pickings for each of selected plants and average pod yield per plant was calculated.

8.Yield (q/ha)

The weight of pods obtained at all pickings was recorded and average yield per hectare was calculated by multiplication of the number of plants per plot and per hectare.

9. 100 seed weight (g)

The pods from second picking were shelled out, 100 seeds were taken randomly and weight was observed with the help of weighing balance in grams.

10. Number of seed per pod

Five pods from each of the selected plants were taken randomly, shelled and their seeds were counted. The average number of seeds was taken to represent the number of seeds per pod.

11. Shelling percentage

100-gram fresh pods from each experimental line were taken for this purpose. The weight of the pods was taken and then shelled. On the same way the weight of seeds of the same pods were taken.

$$\text{Shelling percentage} = \frac{weight\ of\ \ seed}{weight\ of\ seed\ with\ pod} \times 100$$

D. Quality Parameters

1. Protein Content (%)

Method: Kjeldahl method

Procedure:

0.2 g samples of dry pea seed were taken for weighed then transfer them into the digestion tube of the Gerhardt digestor in the duplicated sample and two spatulas from each sodium and copper sulphate were added to each tube. Then 10 ml of sulphuric acid was also added with sample digested until the tubes were seen in green colour and each the digested materials were dissolved into distilled water then transfers into a 100 ml of volumetrics flaked then made the mark. Each sample (10 ml) was transferred into the distillation tube then 20 ml of 4% of boric acid to added into 3-4 drops of mixed for the indicator. The indicator was placed in the collected conical flask to trap the safe rate of ammonium. The unit was equipped with 31- 40% of NaOH then the facilitated operation for distilled water. Distillation was done only for 5 minutes the ammonium was collected with captured by the boric acid. The unit of distillation unit was rinsed with distilled water for 3 minutes. The boric acid turned from reddish to pink with green during the collection of the ammonium. The green color was titrated against the HCl until the appearance of the color turned to pink color and blank sample run simultaneously. The titrate values obtain put on the formula the multiply the factor 6.25 for get to protein percentage.

$$\text{Total Protein} = \frac{A}{AS} \times \text{Concentration of standard}$$

Where,

A = absorbance of sample,

As = absorbance of standard

2. Total Soluble Solid (ºBrix)

Method: Hand Refractometer

Procedure –

- firstly, clean the prism with tissue paper.
- The fresh pea seed crush by mottle and pestle for the extract of juice.
- The juice is squeezed with the help of a muslin cloth and drop on the one place prism.
- Thereafter the value direct by the eye piece of refractometer towards the light at room temperature.

3. Moisture Content (%)

One hundred grams of pods were collected at random from each plot. They were weighed before and after drying and the moisture content recorded.

Moisture content (%) = $\frac{\text{Weight of dried seed}}{\text{Weight of green seed}} \times 100$

3.5 Statistical Analysis:

1. Analysis of Variance (Panse and Shukhatme, 1967)
2. Coefficient of Variation (Burton and De Vane, 1953)
3. Heritability Broad Sense (Burton and De Vane, 1953)
4. Correlation Coefficient Analysis (Al-Jibouri *et al.*, 1958)
5. Path coefficient analysis (Dewey and Lu, 1959)

3.5.1 Analysis of Variance

Analysis of variance was done to estimate total variance into total variation due to the treatments and replications according to procedure described by Panse and Sukhatme (1957). Structure of analysis of variance is given below:

Table (3.3) ANOVA table for randomized block design

Source of variation	Degree of freedom	Mean sum of square	F ratio
Replication	r-1	MSR	MSR/MSE
Treatments	t-1	MST	MST/MSE
Error	(r-1) (t-1)	MSE	
Total	rt-1		

Where,

r = Number of replications

t=Number of treatments/genotypes

MSR = Mean square due to replications

MST = Mean square due to treatments

MSE = Mean square due to error

Standard Error of Mean (SEm)

Standard error of mean was calculated by formula

$SEm = \sqrt{EMS/r}$

Critical difference

Critical difference was calculated by the following formula

Critical difference = $\sqrt{2} \times SEm/r \times t$ value at 5% level of significance

Where,

SEm = Standard error of mean

r = Number of replications

t = Table value of 't' distribution at error d. f. on $P<0.05$ and 0.01.

Test of significance

If the variance of F-calculated value of (MSS (T)/ EMS) for treatment was greater than the F-table value at 5% and 1% level of significance, the variance between treatments was considered to be significant. If the F-calculated value is less than F-tabulated value, the differences between treatments were considered to be non-significant. Statistical significance of variation due to genotype was tested by comparing calculated values to Table F values at the one per cent and five per cent level of probability.

Mean

Mean value of each character was worked out by dividing the totals by the corresponding number of observations.

Mean = $\Sigma X/N$

Where,

ΣX = Sum of all the observations for each character in each replication.

N = Corresponding number of observations.

Range

Lower and upper limits of mean values for each character was arrange to measure the range of variation for the character.

Range = R2 - R1

Where,

R2 = Highest mean

R1= Lowest mean

3.5.2 Coefficient of variation

Genotypic and phenotypic coefficients of variation were computed according to Burton and De Vane (1953) based on the estimate of genotypic and phenotypic variance as follows:

$$GCV = \sqrt{GV} / \bar{x} \quad x\ 100$$

$$PCV = \sqrt{PV} / \bar{x} \quad x\ 100$$

Where,

GV = Genotypic variance

PV = Phenotypic variance

$\bar{X}$ = Grand mean

PCV and GCV were classified as suggested by Robinson *et al*. (1949)

Less than 10%: Low

10 to 20%: Moderate

More than 20%: High

Phenotypic variance ($\sigma 2$ p) Phenotypic variance ($\sigma 2$ p) denotes the total variance present in a population for particular character and is calculated by following formula

$\sigma 2 p = \sigma 2 g + \sigma 2 e$

Where,

$\sigma 2 g$ = Genotypic variance

$\sigma 2 e$ = Error variance

3.5.3 Heritability (h^2)

Heritability in broad sense is the ratio of genotypic variance to total or phenotypic variance. It is that portion of total variability or phenotypic variability which is heritable and due to the genotype. It was calculated by the formula given by Lush (1949) and Burton and De Vane (1953).

$h^2 (bs) = \sigma \frac{2g}{\sigma 2p}\ X\ 100$

Where,

$\sigma 2 g$ = genotypic variance

$\sigma 2 p$ = phenotypic variance

h^2 (bs) = Heritability in broad sense

Heritability- The higher the value of heritability more is the genetic advance.

As suggested by Johnson *et al*. (1955), heritability values are categorized as follows:

Less than 30%: Low

30 to 60%: Moderate

More than 60%: High

The heritability percentage is observed as high then it indicates that characters are least influenced by the environment and selection for this type of characters are fruitful for improvement purpose. If the heritability percentage is found to be low indicates that characters are highly influenced by the environment and genetic improvement through selection is difficult for these characters.

Genetic Advance

The genetic advance that is, expected genetic gain was worked out by using the formula suggested by Lush (1949) and Johnson *et al*. (1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection that heritability estimates alone.

GA = K. h^2. σp

Where, GA = Genetic advance

K= Selection coefficient, which assumes the value of 2.06 for 50% selection intensity.

h^2 = Heritability

σp = Phenotypic standard deviation

Genetic advance as % of mean

It was calculated by the following formula:

Genetic advance as % mean = Genetic advance / General mean X 100

The range of genetic advance as percent of mean is classified as suggested by Johnson *et al.* (1955)

Less than 10 percent = Low

10-20 percent = Moderate

More than 20 percent = High

3.5.4 Correlation coefficient analysis

Correlation coefficient analysis reveals the association of characters i.e., a change in one character brought about by a change in the other character. Phenotypic and genotypic correlation coefficients between different variables were calculated by using the covariance technique (Al-Jibouri *et al.* 1958). The correlation coefficients among all possible traits combinations at genotypic (rg) and phenotypic (rp) level were estimated using formula by Johnson *et al.* (1955).

$$r_{xy} = \frac{\surd\ \Sigma\,(Xi - \bar{X}_{)}\,(Y_i - \bar{Y})}{\surd\sum\,(Xi - \bar{X})^2 \sum\,(Yi - \bar{Y})^2}$$

Rxy – the correlation coefficient of the linear relationship among the variables x and y

$\bar{x}$– the mean of the values of x-variable

$\bar{y}$ – the mean of the values of y-variable

xi – the values of the x-variable in sample

yi – the values of the y-variable in sample

$$\text{Correlation} = \frac{Cov(x,y)}{\sigma x.\sigma y}$$

$rg = Covg(xy) / \surd\sigma\ 2rg\ 1\ x\ \sigma\ 2\ rg\ 2$

$rp = Covp\ (xy) / \surd\sigma\ 2\ rp\ 1\ x\ \sigma\ 2\ rp\ 2$

Where,

rp (xy)= phenotypic correlation coefficient

rg (xy)= genotypic correlation coefficient

Covp, Covg are the phenotypic and genotypic covariance of y and x, respectively

σ 2p and σ 2g are the phenotypic and genotypic variance of y and x, respectively.

Test of significance

To test the significance of correlation coefficient, the estimated values were compared with table value of correlation coefficient prescribed by Fisher and Yates (1938) at (n-2) treatment degree of freedom at 5% and 1% level of significant. If the calculated value of correlation coefficient is greater than tabulated value, it is considered to be significant and vice-versa.

3.5.5 Path Coefficient Analysis

Path coefficient analysis term coined by Wright (1921) and explained by Dewey and Lu (1959) was executed separately to know the direct and indirect effects of the important component traits on yield per plant. Standard path coefficients which are the standardized partial regression coefficient were obtained by solving the following set of "P" simultaneous equations through the use of Do-little technique as given by Goulden (1959).

$P_{01} + P_{02}r_{12} + \dots \dots + P_{op}r_{1p} = r_{01}$

$P_{01}r_{12} + P_{02} + \dots \dots + P_{op}r_{2p} = r_{02}$

$P_{0p}r_{1p} + P_{02}r_{2p} + \dots \dots + P_{op} = r_{op}$

Where P_{01}, P_{02}, … are the direct path effects of 1, 2, ……, P variables on zero variables r_{12}, r_{13}, ……$r_{1p}r_{p}$, (p-1) are the possible coefficients between dependent variable and independent variables and r_{01}, r_{02}, ……r_{op} are the correlation coefficients between dependent variable and independent variables.

The indirect effect of ith variable through jth variable was worked out as (Poj x rij).

The contribution of the remaining unknown was measured as the residual factor and was calculated as:

$P\ 2\ ox = 1 - (P^{2}{}_{01} + 2P_{01}P_{02}r_{12} + 2P_{01}P_{03}r_{13} + \dots \dots + P^{2}{}_{02} + 2P_{02}P_{03}r_{23} + P^{2}{}_{op})$

Residual factor = P^{2}_{ox}

Later the path coefficients were rated based on the scales given below (Lenka and Mishra, 1973).

More than 1.00 = Very high

0.3-0.99 = High

0.2-0.29 = Moderate

0.1-0.19 = Low

0.0-0.09 = Negligible

3.5.6 Genetic Divergence

Mahalanobis D^2 analysis

Mahalanobis (1936) the generalized distance between two populations is calculated by formula.

$D^2 = \Sigma\Sigma\lambda ijSiSj$

Where, D^2 = Square of generalized distance

λij= Reciprocal of the common dispersal matrix

Si = (μi 1 – μi 2)

Sj = (μj 1 – μj 2)

μ = General mean

Transformation of correlated variables

The original means were subjected to get the un-correlated transformed variable with the standard deviation unity. The correlated values (Xs) were first transformed to uncorrelated ones (Ys), following the pivotal condensation method (Rao 1952). The Yi was then transformed to Yjs by division of the corresponding standard deviation with relation.

$Yi = Yj/Y_{ar}(y_j)0.5$

So, as to make the variance of Yi =1

Calculation of D^2 values

D^2 between any two populations or genotypes was calculated as the sum of squares of differences in the values between pairs of corresponding mean values of the transformed characters.

$\sum(Yi^2 - Yj^2)^2 = D^2$

Where, i=1,2, 3...p

Contribution of individual characters towards divergence

In the combinations each character was ranked on the basis of $di = yi^j - yi^k$ values. Rank 1 was given to highest mean difference and ranked p to the lowest mean differences, where P is the total number of characters.

Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as the calculated value of X^2 and is tested against the tested value D^2 for ‘p’ degrees of freedom, where p is number of characters considered.

Group constellation

The D^2 values were arranged in increasing order of magnitude. Tocher’s method of clustering was used for clustering of genotypes (Rao, 1952). The 2 most closely associated genotypes were chosen and then a 3 genotype was found which had the smaller average D^2 from the first three and so on.

Cluster mean

The cluster mean for a particular trait is the summation of mean values of the genotypes included in a cluster divided by number of genotypes in the cluster.

Intra and inter-cluster distances

The intra cluster D^2 was calculated by the formula $\sum Di^2$ /n, where Di^2 is the sum of the distances between all possible combinations [n = i (i-1)/2] of the genotypes (i) includes in a cluster. All possible D^2 values between the genotypes of two clusters were added then divided by n_1 x n_2 for computing inter -cluster distance.

Where, n_1 and n_2 = the number of genotypes in 2 clusters.

The square root of average D^2 value was used to calculate the average intra and inter-cluster D values. Average intra and inter cluster (D) = $\sqrt{}$ D^2 value.

Cluster diagram

Using intra (D) and inter cluster (D^{2}) values between and within clusters, cluster diagram showing the relationship between different populations was drawn.

4. RESULTS AND DISCUSSION

The experimental findings of the present investigation entitled “Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)” was carried out with thirty genotypes of pea. Germplasm accessions of pea were grown in three replications in Randomized Block Design 2021-2022.The results obtained for genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance, and genetic advance as percent of mean, correlation coefficient analysis, path coefficient analysis have been described under the following sub-heads:

4.1 Analysis of variance,
4.2 Mean performance of genotypes,
4.3 Genetic variability, heritability, Genetic advance,
4.4 Correlation coefficient analysis,
4.5 Path coefficient analysis
4.6 Genetic divergence

4.1 Analysis of variance

Analysis of variance showed significant differences among the 30 genotypes for the 21 characters studied. Analysis of variance showed significant differences among the genotypes at 1% and 5% level of significance. The mean sum squares are given in table (4.1) for different characters. The highly significant mean sum of squares was recorded for the traits viz., days of first flowering, days to 50% flowering, plant height, number of primary branches per plant, number of nodes per plant, internodal length, days to first pod setting, days to first pod picking, number of pods per plant, pod length, average pod weight, pod yield per plant, yield per ha, 100 seed weight, number of seed per pod, shelling percentage, protein Content, Total Soluble Solid, moisture content. Among all the traits pod width was found to be not significant. Pujari *et al*. (2021), Kumar *et al*. (2019), Yadav *et al*. (2021**),** Gudadinni *et al.* (2017), Jaiswal *et al*. (2015), Yadav *et al*. (2021**)** and Kumar *et al*. (2015) also recorded highly significant differences among the garden peas genotypes with respect most of the characters under their studies.

Table 4.1 ANOVA analysis of pea genotypes for different characters

S. No.	Characters	Source of variation		
		Replications Mean sum of squares	Treatments Mean sum of squares	Error
1.	**D.F.**	2	29	58
2	**Plant height**	584.77	765.33**	53.07
3	**Number of primary branches per plant**	0.67600	0.57595*	0.17623
4	**Number of nodes per plant**	0.0560	0.0560**	0.5251
5	**Inter nodal length**	3.4397	1.9600**	0.4529
6	**Days of first flowering**	3.244	154.981**	0.693
7	**Days to 50% flowering**	1.433	177.397**	1.606
8	**Days to first pod setting**	17.8	193.603**	1.892
9	**Days to first pod picking**	2.678	90.090**	0.827
10	**Number of pods per plant**	0.0490	11.0067**	0.4361
11	**Pod length**	0.0048	3.2366**	0.1470
12	**Pod width**	0.00357	0.02347	0.01452
13	**Average pod weight**	0.0191	1.17211**	0.1575
14	**Pod yield per plant**	9.68	337.94**	22.81
15	**Yield per ha**	26.88	938.71**	63.37
16	**100 seed weight**	18.900	90.132**	4.601
17	**Number of seed per pod**	0.103	5.7920**	0.092
18	**Shelling percentage**	9.411	129.27**	4.813
19	**Protein Content**	2.1523	21.618**	0.8827
20	**Total Soluble Solid**	0.10533	0.9456**	0.1471
21	**Moisture content**	3.721	26.087**	2.199

***Significant at 5% level of probability, ** Significant at 1% level of probability**

4.2 Mean performance of genotypes

The wide range of genetic variability inherent in the experimental materials allows superior genotypes to be selected based on many characters. Mean values and ranges for 21 characters of different genotypes are shown in table (4.2) and fig. (4.1), (4.2), (4.3), (4.4)

4.2.1 Plant height

The plant height ranged from 42.9 cm to 119.2 cm with mean of 63.8 cm. The maximum plant height was statistically observed in Aman (119.27 cm) followed by IC 208366 (96.00 cm) and Pusa Pragati (95.37 cm), whereas the minimum plant height was statistically observed in Kashi Nandani (42.93 cm) followed by PSM-3 (48.53 cm).

4.2.2 Number of primary branches per plant

Number of branches per plant ranged from 1.33 to 2.93 with mean of 2. The maximum branches per plant was statistically recorded in IPFD -11-5 (2.93) followed by Kashi Samarth (2.73) and Arka Priya (2.53), IC 208366 (2.53) whereas, the minimum primary branches recorded in Kashi Uday (1.33), PSM-3 (1.33), IC 305309(1.33).

4.2.3 Number of nodes per plant

Number of nodes per plant ranged from 10.20 to 15. Minimum number of nodes was in Arkel (10.20) and maximum number of nodes per plant was found in Aman (15). The mean of this trait was 12.44.

4.2.4 Inter nodal length

The internodal length ranged from 3.39 cm to 6.9 cm. The grand mean for internodal length was 4.42 cm. The maximum internodal length was recorded in Aman (6.94 cm) followed by IC 208366 (6.5 cm) and Pusa Pragati (5.5 cm). Whereas, minimum internodal length observed in PSM-2 (3.39cm).

4.2.5 Days of first flowering

Days to first flowering ranged from 32.6 to 59.00 days with mean of 44.2 days. The minimum days to first flowering was recorded in Pusa Sree (32.67 days), whereas the maximum days to first flowering was recorded in Aman (59.00 days) followed by IPFD 11-5 (54.00 days).

4.2.6 Days to 50% flowering

Days to 50 % flowering ranged from 36.6 to 72.6 days with mean of 49.8 days. The minimum days to first flowering was recorded in Pusa Sree and Kashi Uday (36.7 days), whereas the maximum days to 50% flowering was recorded in Aman (72.66 days) followed by IPFD 10-12 (59.33 days).

4.2.7 Days to first pod setting

Days to first pod setting ranged from 39 to 68.3 days with mean of 50.95 days. The maximum days to first flowering was recorded in Aman (68.33 days) followed by IPFD-11-5 (63.00 days), whereas the minimum days to first pod setting was recorded in Kashi Nandani (39.00 days) followed by Pusa Sree and PSM-3(39.67 days).

4.2.8 Days to first pod picking

Days to first pod harvesting ranged from 55.6 to 77.6 days with a general mean of 69.42 days. The earliest pod maturity for harvest was in AP-3 (55.6 days) followed by Pusa Pragati (62.33 days), Pusa Pragati and Pusa Sree, Kashi Nandani and Kashi Uday. Whereas, late pod maturity was shown in Aman (77.6 days) followed by EC 302842 (77.3 days).

4.2.9 Number of pods per plant

Number of pods per plant ranged from 8.8 to 17.2 with mean of 12.6. The maximum number of pods per plant observed in Kashi Samarth (17.2) followed by Pea TS-10 (16.13). whereas minimum number of pods per plant recorded in Kashi Uday (8.80).

4.2.10 Pod length (cm)

Pod length per plant ranged from 6.39 to 10.30 with mean of 8.02. The maximum pod length was recorded in GS-10 (10.30 cm) followed by Pusa Pragati (9.60 cm), Pencil Matar (9.52 cm) and PB-89 (9.473 cm). Whereas the minimum pod length was recorded in Aman (6.393 cm) followed by AP-1 (6.49 cm) and IC 208366 (6.54 cm).

4.2.11 Pod width (cm)

Pod width (cm) ranged from 0.96 cm to 1.25 cm with mean of 1.09 cm. The maximum pod width was observed in Kashi Nandani and Kashi Uday (1.24 cm) followed by Kashi Ageti (1.21 cm) and PSM-2 (1.21 cm). whereas, the minimum pod width (0.96 cm) was observed in Arka Priya followed by IC 208366 and EC 6621.

4.2.12 Average pod weight(g)

Average Pod Weight ranged from 3.5g to 6.03g with mean of 4.79g. The maximum average Pod weight was observed in AS-10(6.03g) followed by Pencil Matar (5.80g), GS-10 (5.56). Whereas the minimum Average Pod Weight was observed in IC 395309 (3.5g).

4.2.13 Pod yield per plant (g)

Pod yield per plant (g/plant) ranged from 43.4 g to 77.2 g with mean of 55.70 g. The maximum pod yield per plant (g/plant was recorded in GS-10 (79.633 g) followed by Pea TS-10 (77.23 g), Kashi Samarth (76.433 g), whereas the minimum pod yield per plant (g/plant) was recorded in Kashi Nandani (43.4 g).

4.2.14 Yield per plot (kg)

Pod yield per plant (kg) ranged from 2.61 kg to 5.03 kg with mean of 3.34 kg. The maximum pod yield per plot was recorded in GS-10 (4.78 kg) followed by Pea TS-10 (4.63 kg) and Kashi Samarth (4.59 kg), whereas the minimum pod yield per plot found in IC208366 (2.62 kg).

4.2.15 Yield per ha

Pod yield (q/ha) ranged from 72.83 q to 132.7 q with mean of 92.83. The maximum pod yield (q/ha) was recorded in GS-10 (132.72 q) followed by Pea TS-10 (128.72 q) and Kashi Samarth (127.38 q) and AS-10 (117.22 q). Whereas the minimum pod yield (q/ha) was recorded in IC 208366 (72.83 q).

4.2.16 100 seed weight(g)

100 seed weight ranged from 28.60 g to 50.3 g with mean of 35.8. The maximum 100 seed weight observed in PSM-3 (50.3 g). Whereas the minimum 100 seed weight observed in PSM-2 (28.67 g) and VL 7 (28.67g).

4.2.17 Number of seed per pod

The number of seed per pod ranged from 4.00 to 10.20 seeds with a general mean of 6.73 seeds. The highest number of seed per pod was observed in GS-10 (10.20 seeds), followed by AS-10(9.07) and Pencil Matar (9.67 seeds). Whereas the minimum number of seeds per pod was counted in the Aman (4.00 seeds) genotype.

4.2.18 Shelling percentage

Shelling percentage ranged from 34.33% to 57% with mean of 44.88%. The maximum shelling percentage were observed in Pusa Sree (57%) followed IPFD-10-12 (55.66%), Aman (55%), EC 243642(55%), PSM-3(53.00%), Whereas the minimum Shelling Percentage were observed in PSM-2 (34.33%).

4.2.19 Protein content (%)

Protein content ranged from 12.8% to 21.3% with mean of 17.5%. The maximum protein content observed in IC 208366 (21.3%) and minimum protein content observed in Pea TS-10 (12.88%).

4.2.20 Total Soluble Solid (°Brix)

The total soluble solid ranged from 13.8 to 16.5 °Brix with a general mean of 15.33 °Brix. The maximum total soluble solid was shown in VL – 7 (16.5 °Brix) followed by AP-3 (16.33°Brix) and PC-531 (16.10°Brix. Whereas, lowest total soluble solid was observed in the EC 6621 (13.8 °Brix) genotype.

4.2.21 Moisture content (%)

Moisture Percentage ranged from 70.9% to 81.9% with mean of 74.84%. The maximum moisture percentage was observed in Pencil Matar (81.9%) followed by AS-10 (81.8%). Whereas the minimum Moisture Percentage was observed in IC 395309 (70.9%).

4.3 Genetic Variability, Heritability and Genetic advance

21 characters under study were analyzed for genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), genetic advance as percent of mean and heritability (broad sense). In the present study, it was found that magnitude of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters. The pod yield is the key objective in garden pea improvement. Absolute variability of different character does not reveal which of the particular characters were showing the highest variability. This could only be accessed through standardizing the phenotypic and genotypic variances and by obtaining coefficient of variability. The estimate of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (h^2) in broad sense, genetic advances and genetic advances as per cent of mean were estimated for 21 characters and presented in table (4.3**)** and fig (4.5), (4.6).

Table 4.2 Mean performance of vegetable pea genotypes

S. No.	Genotypes	DF1	DF50	NPB	INL	NNP	PH	PL	PW	NSP	SW	PR	M	TSS	SHL	DS1	DP1	APW	NPP	PYPT	PYP
1.	**Kashi Uday**	33.67	36.67	1.33	4.61	11.73	49.73	8.73	1.24	6.80	42.3	20.0	74.0	15.3	44.3	40.3	63.3	5.43	8.80	2.63	43.8
2.	**Kashi Nandani**	33.67	38.67	1.53	3.73	11.27	42.93	8.24	1.25	6.43	38.0	15.4	76.5	15.0	40.3	39.0	62.6	5.40	9.33	2.61	43.4
3.	**Kashi Ageti**	36.33	44.33	1.47	3.97	14.93	65.60	8.51	1.21	7.40	33.0	19.6	77.4	15.7	37.3	42.3	65.6	4.80	9.87	2.70	45.0
4.	**Kashi Samarth**	36.67	44.00	2.73	4.91	12.80	65.40	6.81	1.09	6.40	35.3	14.1	75.9	14.9	49.0	43.0	66.3	4.43	17.2	4.59	76.4
5.	**Kashi Mukti**	36.00	40.00	2.27	4.21	12.20	51.73	8.59	1.19	6.57	39.3	15.2	73.1	15.1	42.0	41.6	66.6	4.70	11.8	3.09	51.5
6	**AP-3**	38.67	43.33	2.20	4.48	13.40	68.80	8.27	1.08	7.07	37.6	20.5	71.6	16.3	46.6	42.0	55.6	5.03	11.5	3.27	54.5
7.	**Arka Priya**	48.33	54.00	2.53	4.17	13.47	73.40	8.19	0.96	7.27	32.3	21.1	75.5	14.9	44.0	51.6	70.3	5.20	13.2	3.95	65.9
8.	**AP-1**	45.33	49.00	2.40	3.64	13.83	58.40	6.49	1.15	4.77	42.0	20.0	77.6	15.5	43.0	48.3	67.3	4.90	10.5	3.04	50.7
9.	**Pusa Sree**	32.67	36.67	1.40	4.23	10.87	51.20	7.35	1.11	5.90	41.3	17.5	73.3	15.1	57.0	39.6	63.3	3.70	11.8	2.75	45.8
10.	**Pusa Pragati**	49.67	54.33	1.93	5.57	15.00	95.37	9.60	1.17	7.60	44.6	19.5	76.8	14.8	49.6	52.3	62.3	5.03	11.8	2.92	48.7
11.	**Arkel**	35.00	44.00	1.60	4.83	10.20	48.60	7.67	1.18	6.10	41.6	19.0	72.8	15.4	44.0	41.3	64.6	4.93	9.20	2.83	47.1
12.	**PSM-3**	33.67	40.67	1.33	3.87	10.93	48.53	8.12	1.14	6.20	50.3	18.4	73.5	15.8	53.0	39.6	64.0	5.03	11.8	3.11	51.9
13.	**PSM-2**	50.33	54.33	2.40	3.39	13.13	50.67	8.66	1.21	7.73	28.6	15.6	77.7	15.3	34.3	56.0	72.3	4.67	12.7	2.96	49.2
14.	**NDVP -1**	36.00	44.67	1.80	4.39	12.73	57.13	8.07	1.16	6.70	34.3	15.5	72.9	15.9	42.3	42.3	64.3	4.40	12.0	2.82	47.0
15.	**VL-7**	48.00	54.33	2.07	4.27	11.87	56.60	6.90	1.15	5.87	28.6	18.2	74.4	16.5	34.6	55.6	73.3	4.80	14.6	3.78	63.0
16.	**PB-89**	46.33	51.33	1.73	3.80	12.87	53.53	9.47	1.10	7.20	38.6	15.7	74.9	14.9	46.0	52.6	69.3	5.03	12.9	3.07	51.1
17.	**AS-10**	48.33	52.00	2.27	3.69	12.00	51.33	8.62	1.01	9.07	41.3	14.9	81.8	15.4	42.6	55.3	74.6	6.03	12.8	4.22	70.3
18.	**PC-531**	41.33	46.33	2.47	4.43	12.13	61.70	8.66	0.96	7.13	31.0	13.4	75.7	16.1	40.3	48.6	65.6	5.37	14.4	3.82	63.7
19.	**IC 208366**	47.67	55.00	2.53	6.52	13.87	96.00	6.54	0.96	6.53	32.6	21.3	71.3	15.8	52.3	54.6	72.6	4.03	12.8	2.62	43.7
20.	**IC 395309**	48.33	54.33	1.33	4.01	13.13	61.80	8.00	1.12	5.67	31.0	16.7	70.9	14.5	41.3	55.0	72.0	3.50	13.5	3.49	58.1
21.	**EC 6621**	47.67	52.67	1.67	4.45	12.23	59.60	7.03	0.96	6.63	30.0	13.8	73.2	13.8	35.3	56.3	76.6	3.90	14.2	2.99	49.9
22.	**EC 243642**	50.67	55.67	2.20	4.03	13.20	68.93	6.87	1.10	4.93	33.0	20.1	72.7	14.9	55.0	58.6	76.6	4.10	13.6	2.81	46.8
23.	**EC 302842**	49.00	53.00	1.93	4.40	12.13	68.27	8.29	1.13	6.07	33.3	18.5	71.1	15.1	34.6	57.6	77.0	4.30	11.8	2.68	44.6

24.	**IPFD-10-12**	53.00	59.33	2.40	4.89	12.27	71.36	6.75	1.04	6.00	34.0	20.0	72.0	15.8	55.6	62.0	72.6	4.33	13.2	3.41	56.8
25.	**IPFD-11-5**	54.00	58.33	2.93	5.36	12.13	71.27	6.83	1.06	5.33	29.0	19.5	73.0	15.9	45.3	63.0	73.3	4.10	14.4	3.89	64.8
26.	**Aman**	59.00	72.67	1.93	6.94	15.00	119.27	6.39	1.02	4.00	29.3	19.1	71.9	14.9	55.0	68.3	77.6	4.60	14.0	3.65	60.7
27.	**Pencil Matar**	48.00	51.67	1.73	4.05	12.98	60.67	9.53	1.00	9.07	41.3	14.2	81.9	14.9	50.6	55.6	73.6	5.80	12.5	3.76	62.7
28.	**Pea TS -10**	47.33	52.00	2.00	4.21	12.80	61.33	8.99	1.00	8.53	31.0	12.8	79.7	15.1	47.6	56.0	70.6	5.10	16.1	4.63	77.2
29.	**Ganga -10**	47.00	52.33	2.00	3.39	14.33	59.07	8.19	1.09	8.33	35.6	21.2	74.3	15.0	43.0	54.6	73.6	5.53	13.4	3.38	56.3
30.	**GS -10**	46.00	49.33	2.07	4.35	13.92	68.70	10.30	0.99	10.20	34.0	14.2	76.6	15.5	40.0	54.0	74.0	5.57	13.2	4.78	79.6
	Mean	44.25	49.83	2.00	4.42	12.44	63.77	8.02	1.09	6.73	35.8	17.5	74.8	15.3	44.8	50.9	69.4	4.79	12.6	3.34	55.7
	C.V	1.88	2.54	20.92	15.20	5.67	11.42	4.78	11.01	5.14	5.98	5.35	1.98	2.50	4.88	2.70	1.31	8.28	5.21	8.5	8.57
	S.E.	0.48	0.73	0.24	0.39	0.42	4.21	0.22	0.07	0.18	1.24	0.54	0.86	0.22	1.27	0.79	0.53	0.23	0.38	0.17	2.76
	C.D. 5%	1.36	2.07	0.69	1.10	1.18	11.90	0.63	0.20	0.50	3.51	1.54	2.42	0.63	3.59	2.70	1.48	0.65	1.08	0.47	7.81
	Lowest Range	32.67	36.67	1.33	3.39	10.20	42.93	6.39	0.96	4.00	28.6	12.8	70.9	13.8	34.3	39.0	55.6	3.50	8.80	2.61	43.4
	Highest Range	59.00	72.60	2.93	6.94	15.00	119.2	10.30	1.25	10.20	50.3	21.3	81.9	16.5	57.0	68.3	77.6	6.03	17.2	4.78	79.6

DF1-Days to first flowering, DF50-Days to 50% flowering, NPB- Number of primary branches per plant, INL-Internodal length, NNP-Number of nodes per plant, PH-Plant height, PL-Pod length, PW-Pod width, NSP-Number of seed per pod, SW-100 seed weight, PR-Protein content, M-Moisture percentage, TSS- Total soluble solid, SHL- Shelling percentage, DS1-Days to first pod setting, DP1-Days to first pod picking, APW-Average pod weight, NPP-Number of pod per plant, PYPT- Pod yield per plot, PYP-Pod yield per plant

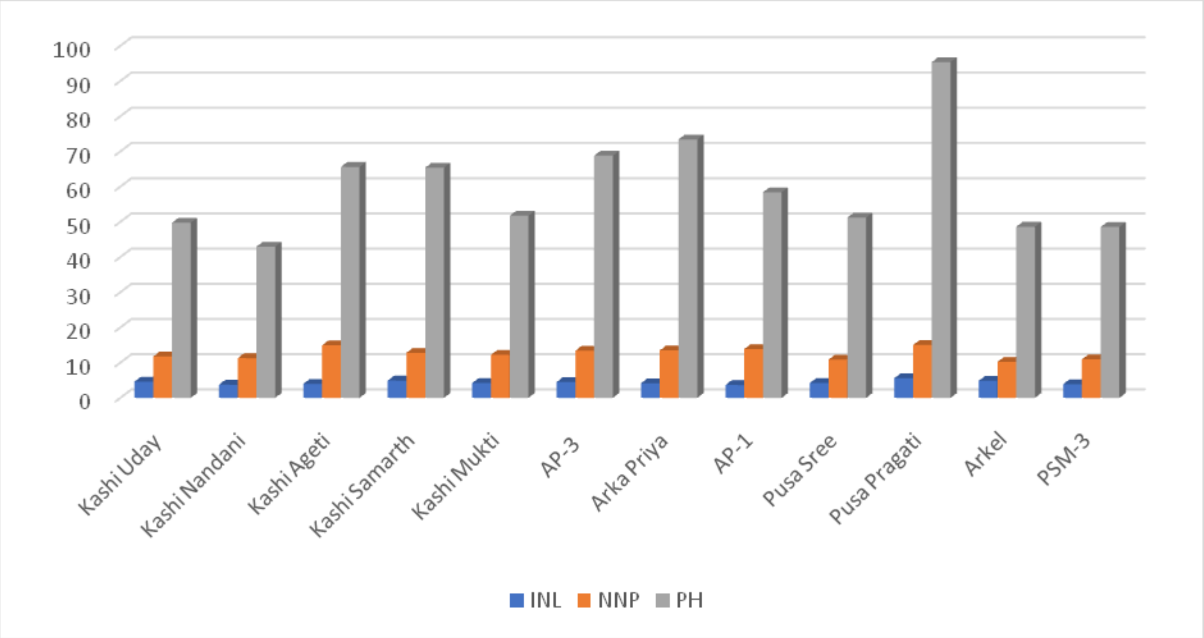


Fig. 4.1 Mean performance of different pea genotype for Internodal length, Number of nodes per plant, Plant height

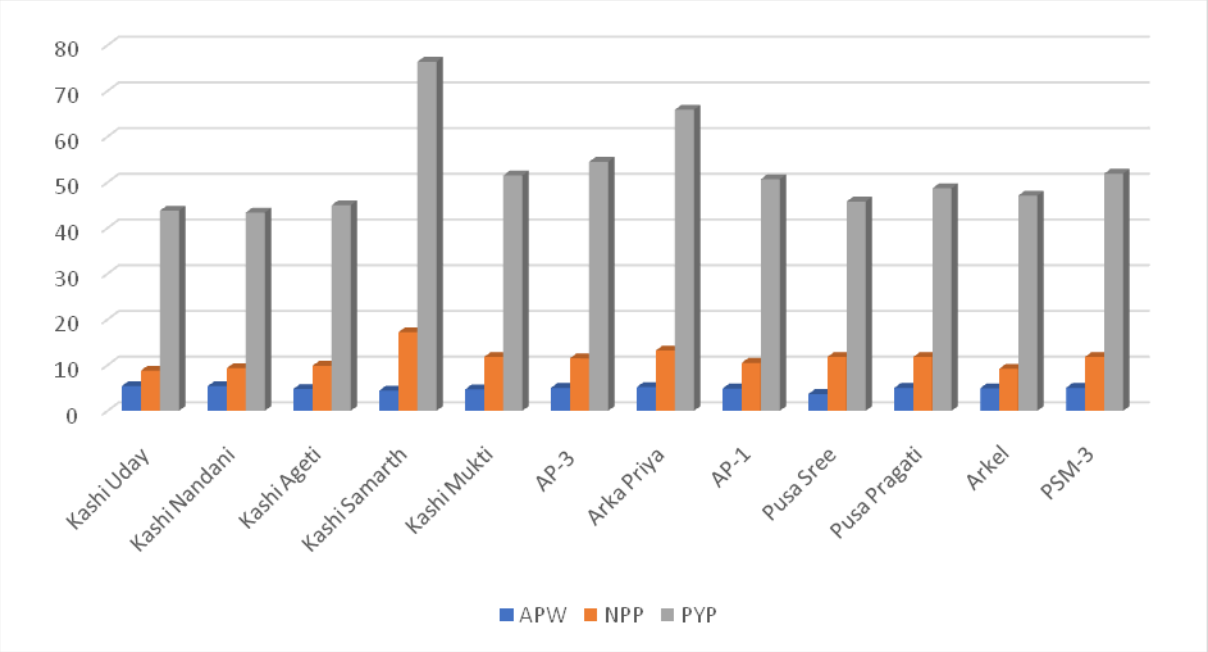


Fig. 4.2 Mean performance of pea genotypes for Average pod weight, Number of pods per plant, Pod yield per plant

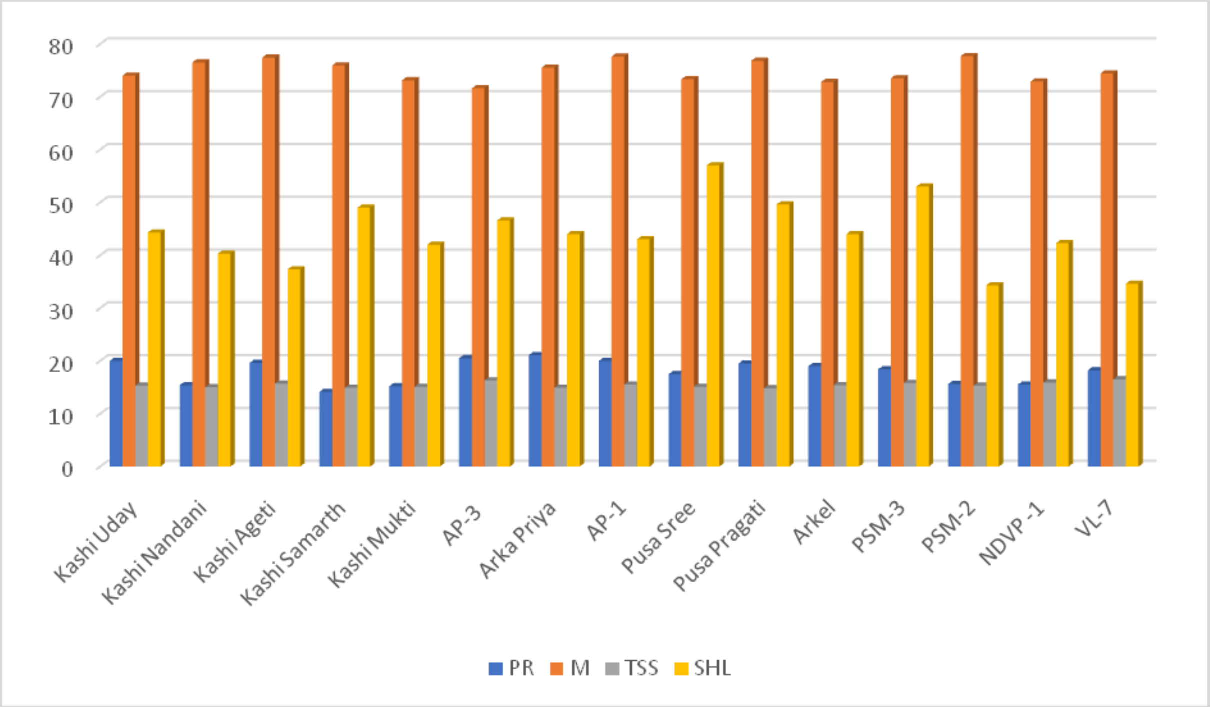


Fig. 4.3 Mean performance of vegetable pea genotypes for protein content, moisture content, total soluble solids, shelling percentage

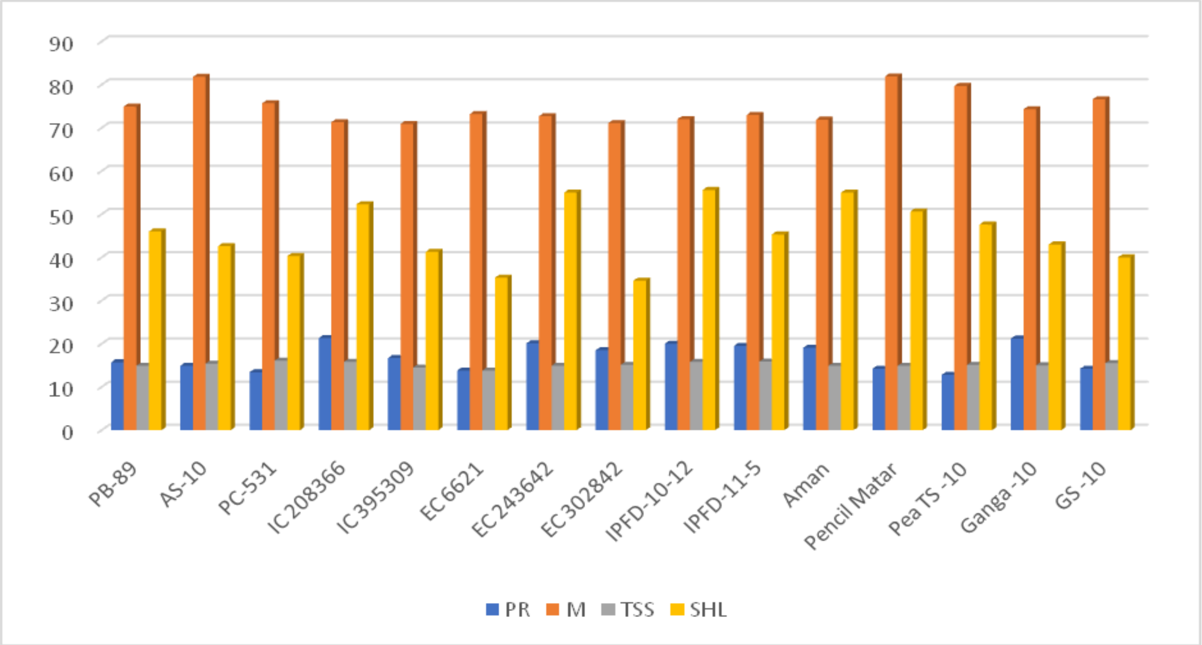


Fig. 4.4 Mean performance of vegetable pea genotypes for protein content, moisture content, total soluble solids, shelling percentage

Genotypic coefficient of variation

The variability, heritability and genetic advance parameters are explained below.

4.3.1 Plant height

Plant height showed phenotypic variance 290.48 and genotypic variance 237.41. The high value of phenotypic coefficient of variation was (26.72%) and genotypic coefficient of variation was (24.16%). It exhibited high broad sense heritability (81%) coupled with high genetic advance as percent of mean (44.99%).

4.3.2 Number of primary branches per plant

Number of primary branches per plant under study exhibited phenotypic variance and genotypic variance values as 0.31 and 0.13, respectively. Whereas, phenotypic coefficient of variation was (27.71%) and genotypic coefficient of variation (18.18%). Moderate broad sense heritability (43.05%) coupled with high genetic advance as percent of mean (24.58%).

4.3.3 Number of nodes per plant

Number of nodes per plant showed phenotypic variance 1.81 and genotypic variance 1.29. The value of phenotypic coefficient of variation was (10.54%) and genotypic coefficient of variation was (8.89%). It exhibited high heritability (71.1%) coupled with high genetic advance as percent of mean (15.44%).

4.3.4 Inter nodal length

Internodal length showed phenotypic variance 0.96 and genotypic variance 0.50. The high value of phenotypic coefficient of variation was (22.08%) and genotypic coefficient of variation was (16.01%). It exhibited moderate heritability (52.59%) coupled with high genetic advance as percent of mean (23.92%).

4.3.5 Days of first flowering

In respect to this trait, the observed values of genotypic variance and phenotypic variance 51.42 and 52.12 respectively. It expressed moderate phenotypic coefficient of variation (16.31%) and genotypic coefficient of variation (16.20%) and high broad-sense heritability (98%) combined with high genetic advance as percent of mean (33.15%).

4.3.6 Days to 50% flowering

Days to 50% flowering under study exhibited phenotypic variance and genotypic variance values as 60.20 and 58.59, respectively. The assessed moderate phenotypic coefficient of variation was (15.57%) and genotypic coefficient of variation (15.36%). Moderate broad sense heritability (97.3%) coupled with high genetic advance as percent of mean (31.21%).

4.3.7 Days to first pod setting

Days to first pod setting under study exhibited phenotypic variance and genotypic variance values as 65.79 and 63.90, respectively. The assessed moderate value for phenotypic coefficient of variation was (15.91%) and genotypic coefficient of variation (15.68%). High broad sense heritability (97.1%) coupled with high genetic advance as percent of mean (31.84%).

4.3.8 Days to first pod picking

Days to first pod picking under study exhibited phenotypic variance and genotypic variance values as 30.58 and 29.75, respectively. The assessed low phenotypic coefficient of variation was (7.96%) and genotypic coefficient of variation (7.85%). High broad sense heritability (97.3%) coupled with moderate genetic advance as percent of mean (15.96%).

4.3.9 Number of pods per plant

Number of pods per plant under study exhibited phenotypic variance and genotypic variance values as 3.95 and 3.52, respectively. The assessed moderate phenotypic coefficient of variation was (15.71%) and genotypic coefficient of variation (14.82%). High broad sense heritability (88.95%) coupled with high genetic advance as percent of mean (28.80%).

4.3.10 Pod length

Pod length showed phenotypic variance 1.18 and genotypic variance 1.03. The moderate value of phenotypic coefficient of variation was (13.52%) and genotypic coefficient of variation was (12.65%). It exhibited high heritability (87.5%) coupled with high genetic advance as percent of mean (24.37%).

4.3.11 Pod width

The estimated value of phenotypic variance 0.02 was comparatively high as compared to value of genotypic variance 0.0046. This trait expressed moderate phenotypic coefficient of variation (12.09%) and low genotypic coefficient of variation (5.00%). It also expressed low moderate heritability (17.14%) coupled with low genetic advance as percent of mean (4.268%).

4.3.12 Average pod weight

The character showed phenotypic variance as 0.50 and genotypic variance value 0.34. It expressed moderate phenotypic coefficient of variation as (14.69%) and genotypic coefficient of variation as (12.13%). High heritability (68.23%) coupled with high genetic advance as percent of mean (20.64%) was accessed for this character.

4.3.13 Pod yield per plant

The value of phenotypic variance 127.8 and genotypic variance105.04 for this attribute was recorded. It expressed comparatively high PCV (20.29%) and moderate GCV value (18.39%) for pod yield per plant. High heritability (82.1%) coupled with high genetic advance percent of mean (34.35%) was observed for this trait.

4.3.14 Pod yield per plot

The value of phenotypic variance (0.379) and genotypic variance (0.461) was recorded for pod yield per plot. High PCV (20.33%) and moderate GCV (18.42%) were noted for pod yield per plot. High heritability (82.1%) coupled with high genetic advance as percent of mean (34.41%) was recorded for pod yield per plot.

4.3.15 Yield per ha

The value of phenotypic variance 355.1 and genotypic variance 291.7 for this attribute was recorded. It expressed comparatively high PCV (20.29%) and moderate GCV value (18.39%) for pod yield per plant. High heritability (82.1%) coupled with high genetic advance percent of mean (34.35%) was observed for this trait.

4.3.16 100 seed weight

The value of phenotypic variance 33.11 and genotypic variance 28.51 for this attribute was recorded. It expressed comparatively moderate PCV (16.05%) and GCV value (14.90%) for 100 seed weight. High heritability (86.1%) coupled with high genetic advance percent of mean (28.48%) was observed for this trait.

4.3.17 Number of seed per pod

The recorded value for genotypic variance 1.90 and phenotypic variance was value 1.99 for number of seed per pod. This attribute expressed high phenotypic coefficient of variation

(20.97%) and genotypic coefficient variation (20.48%). This character exhibited high heritability (95.3%) coupled with genetic advance as percent of mean (41.19%)

4.3.18 Shelling percentage

Genotypic variance 41.48 and phenotypic variance 46.29 value were accessed showed for shelling percentage. Whereas moderate phenotypic coefficient of variation (15.15%) and genotypic coefficient of variation (14.38%) were observed for this trait. The broad sense heritability (89.6%) coupled with high genetic advance as percent of mean (27.97%) was noted for shelling percentage.

4.3.19 Protein content (%)

Genotypic variance (6.91) and phenotypic variance (7.79) values were recorded. This estimated moderate genotypic coefficient of variation (14.98%) for protein content as well as and phenotypic coefficient of variation (15.91%) for protein content. Highest heritability (88%) coupled with high genetic advance as percent of mean (29.06%) was noticed.

4.3.20 Total Soluble Solid (^{o}Brix)

Genotypic variance 0.27 and phenotypic variance 0.41 value were accessed showed for the total soluble solid. Whereas low phenotypic coefficient of variation (4.19 %) and genotypic coefficient of variation (3.36%) were observed for this trait. The broad sense heritability (64.3%) coupled with low genetic advance as percent of mean (5.55%) was noted for total soluble solid.

4.3.21 Moisture content (%)

The value of phenotypic variance 10.16 and genotypic variance 7.96 for this attribute was recorded. It expressed comparatively low PCV (4.25%) and moderate GCV value (3.77%) for moisture percentage. High heritability (78.3%) coupled with low genetic advance percent of mean (6.87%) was observed for this trait.

Range, variance, PCV, GCV, heritability and genetic advance as % of mean are biometrical components that can be used to measure the genetic variation in a germplasm collection. Pod yield per plant is a complex trait controlled by polygenes and highly impacted by environmental influences, it cannot be utilized as a character for genotype selection. In measuring the genetic diversity present in the experimental materials, PCV and GCV are more useful.

The phenotypic coefficient of variation was observed higher than the genotypic coefficient of variation for all 21 characters in this study, indicated that the apparent variation was not only due to genotype but also to favorable environmental influences and that genotyping based on these traits can be misleading at times. This environmental influence is enhanced by heterogeneity in soil fertility status field and other uncontrollable factors.

High estimated GCV and PCV for the parameters like plant height number of seed per pod and moderate GCV and PCV for pod length, pod width, protein content, shelling percentage, days to first pod picking days to 50% flowering, pod width, days to first pod setting, number of nodes per plant have been reported by Yumkhaibham *et al*. (2019).

Genotypic coefficient of variation (GCV) ranged from 3.36 to 24.16%. Higher magnitude of GCV was recorded for plant height (24.16), number of seed per pod (20.48%), Similar findings were also reported by Yumkhaibam *et al*. (2019), Katoch *et al*. (2016), Afreen *et al.* (2017), Jaiswal *et al*. (2015), Kumar *et al*. (2015), Kumar *et al.* (2013), Pal and Singh (2013), Ahmad *et al*. (2014), The moderate amount of GCV were recorded for days to 50% flowering (15.16%), pod length (12.65%), pod yield q/ha (18.39 %), pod yield per plant (18.39%), average pod weight (12.13%), pod width, shelling percentage. The results are in conformity with the findings of Georgieva *et al*. (2016). The low amount of GCV were recorded for primary branches per plant (6.58%), plant spread (5.74%).

The moderate amount of PCV was recorded for days to 50% flowering (15.57%), average pod weight (14.69%), average pod length (13.52%), pod width (12.09%), shelling percentage (15.15%). Similar finding was also reported by Georgieva *et al.* (2016). In the present investigation it was observed that extent of phenotypic coefficient of variation were higher than genotypic coefficient of variation for all the traits studied which indicates the additive effect of the environment on the expression of the traits. Similar results were also reported by Katoch *et al*. (2016), Siddika *et al*. (2013), Kumar *et al*. (2013), Siddika *et al*. (2013) and Ahmad *et al*. (2014).

High PCV were observed for number of branches per plant (27.7%), pod yield per plant (20.29%). which would be amenable for further selection. The similar results were also reported by Pal and Singh (2012), Pandey *et al*. (2015).

High heritability (broad sense) was recorded for all the characters like shelling % (89.6%), moisture percentage (78.3 %), pod yield q/ha (82.10%), pod yield per plant (g)

(82.10), days to first flowering (98.6%), days to first pod set (97.37%), days to 50% flowering (97.3%), plant height (cm) (81.70%), pod length (87.5%), days to first pod picking (97.3%), average pod weight (68.23%). Results were noticed by Yumkhaibham *et al.* (2019), Gudadinni *et al*. (2017), Georgieva *et al*. (2016), Jaiswal *et al.* (2015), Ahmad *et al*. (2014), Siddika *et al*. (2013), Kumar *et al*. (2015), Pal and Singh (2013), Guleria et *et al*. (2009), Afreen *et al*. (2017) and Kumari *et al.* (2008).

The estimates of genetic advance for 21 characters studied. High genetic advance was recorded for, plant height (28.69). The moderate estimates of genetic advance were observed for days to first pod set (16.22), days to first flowering (14.67), pod yield/plant (g) (19.13), days to first pod picking (11.08). The low genetic advances were observed in pod length (1.96), no of seeds per pod (1.39), average pod weight (0.99), pod width (0.05), primary branches per plant (0.49). High heritability coupled with high genetic advance were noted for characters like plant height, days to 50% flowering. These results indicated that these traits could be considered as reliable indices for selection. Similar findings were also reported by Yumkhaibam *et al*. (2019), Georgieva *et al.* (2016), Jaiswal *et al*. (2015), Ahmad *et al*. (2014), Katoch *et al*. (2016).

The genetic advance (as per cent per mean) varied from 4.27% to 44.99%. The higher genetic advance (as per cent of mean) was reported for plant height (44.9%) followed by days to first flowering (33.15%), days to first pod setting (31.8), days to 50% flowering (31.2%), pod yield q/ha (34.3%), days to first pod picking (15.9%), pod length (24.7%), average pod weight (20.6%) and shelling percentage (27.9%). Similar findings were reported by Georgieva *et al*. (2016), Ahmad *et al*. (2014), Katoch *et al.* (2016), Jaiswal *et al*. (2015), Guleria *et al.* (2009) and Akhilesh *et al*. (2007).

Kashi Ageti **Kashi Uday** **Pusa Pragati**

Plate (4.1) Pod length and number of seed per pod

Kashi Nandani **Ganga -10** **PSM -3**

Plate (4.2) Pod length and number of seed per pod

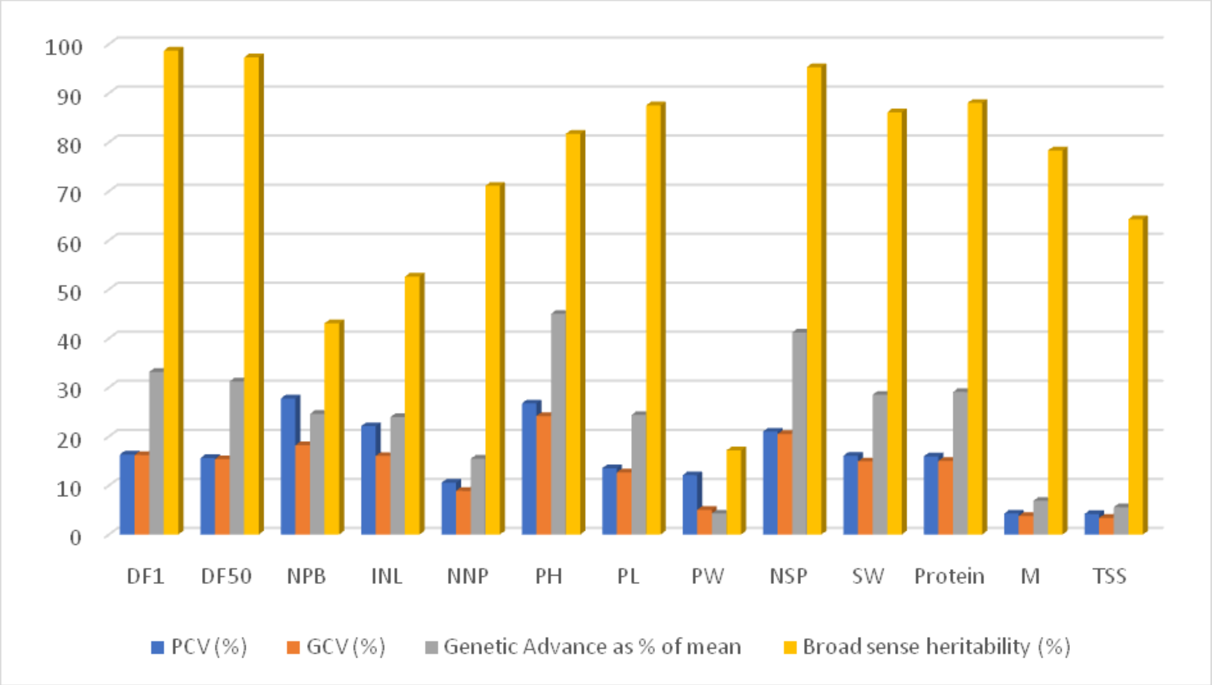


Fig. 4.5 Genetic variability for different characters in vegetable pea genotypes

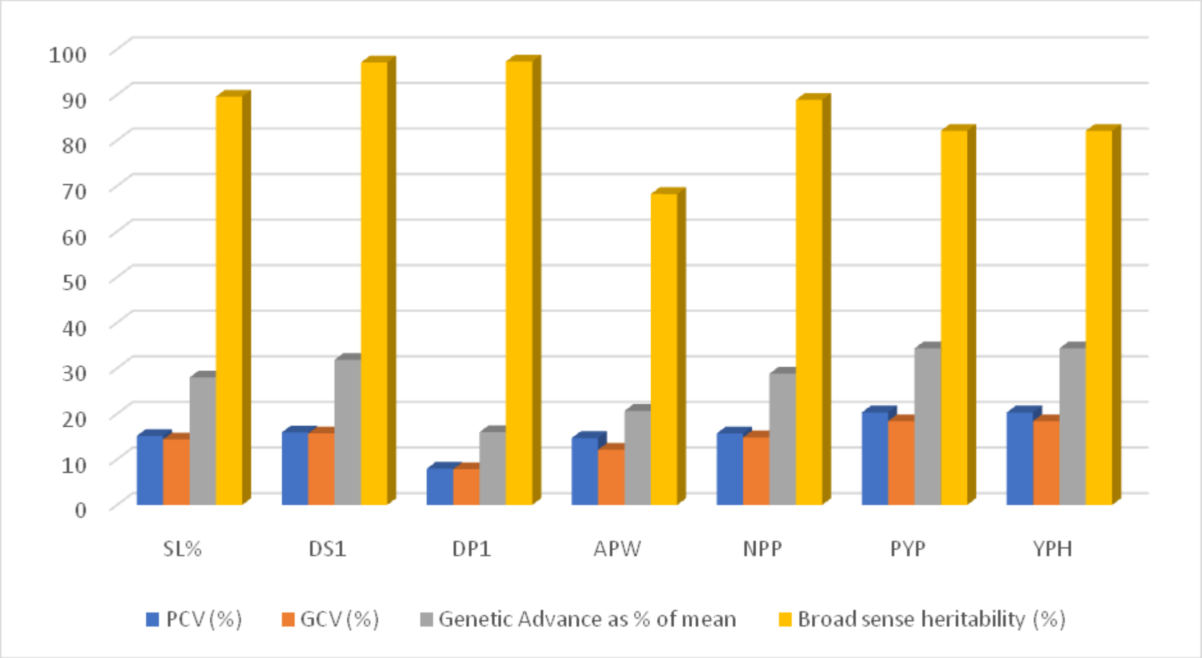


Fig. 4.6 Genetic variability for different characters in vegetable pea genotype

Table 4.3: Mean, Range, Coefficient of variations (GCV and PCV), Genetic Advance, Genetic Advance as Per cent of mean and Heritability, for 21 Characters of vegetable Pea genotypes.

Characters	Range	Mean	Vp	Vg	PCV (%)	GCV (%)	Genetic Advance	Genetic Advance as % of mean	Broad sense heritability (%)
DF1	32.67- 59.00	44.25	52.12	51.42	16.31	16.20	14.67	33.15	98.67
DF50	36.67-72.60	49.83	60.20	58.59	15.57	15.36	15.55	31.21	97.30
NPB	1.33-2.93	2.00	0.31	0.13	27.71	18.18	0.49	24.58	43.05
INL	3.39-6.94	4.42	0.96	0.50	22.08	16.01	0.53	23.92	52.59
NNP	10.20-15.00	12.77	1.81	1.29	10.54	8.89	1.97	15.44	71.10
PH	42.9-119.20	63.77	290.48	237.41	26.72	24.16	28.69	44.99	81.70
PL	6.39-10.30	8.02	1.18	1.03	13.52	12.65	1.96	24.37	87.50
PW	0.96-1.25	1.09	0.02	0.00	12.09	5.01	0.05	4.27	17.14
NSP	4.00-10.20	6.73	1.99	1.90	20.97	20.48	2.77	41.19	95.30
SW	28.6-50.3	35.83	33.11	28.51	16.05	14.90	10.20	28.48	86.10
Protein	12.8-21.3	17.54	7.79	6.91	15.91	14.98	5.10	29.06	88.00
M	70.9-81.9	74.84	10.16	7.96	4.26	3.77	5.15	6.87	78.30
TSS	13.8-16.5	15.33	0.41	0.27	4.19	3.36	0.85	5.56	64.30
SL%	34.3-57.00	44.88	46.29	41.48	15.15	14.38	12.55	27.97	89.60
DS1	39.00-68.3	50.95	65.79	63.90	15.91	15.68	16.22	31.84	97.10
DP1	55.6-77.6	69.42	30.58	29.75	7.96	7.85	11.08	15.96	97.30
APW	3.50-6.03	4.79	0.50	0.34	14.69	12.13	0.99	20.64	68.23
NPP	8.8-17.2	12.66	3.95	3.52	15.71	14.82	3.65	28.80	88.90
PYP	43.4-79.6	55.70	127.8	105.04	20.29	18.39	19.13	34.35	82.10
YPH	72.8-132.7	92.83	355.1	291.78	20.29	18.39	31.89	34.35	82.10

4.4 Correlation Coefficient Analysis

Correlation coefficient is a parameter which is used to find out the direction of relationship between two or more variables. In selection process, it is very essential to have details on the nature of the association of characters with economic yield. The genotypic correlation coefficients were higher than the phenotypic correlation coefficients for most of the pair of traits. A positive value of correlation shows that the changes in two variables were in the same directions, i.e., high value of one variable is associated with high value of other and *vice- versa*. When correlation is negative, the movement are in opposite directions, i.e., high value of one variable is associated with low value of other. The correlation coefficient is represented by *"r",* whose value ranged from -1 to +1. The extent of the correlation coefficient is applicable, only when these values (*r*) are significantly different from zero. Otherwise, the values are suggesting the absence of correlation. The estimates of simple correlation coefficient among 21 genotypes of pea under study are presented in table- (4.4) and (4.5)

4.4. A Genotypic correlation coefficient analysis

The inherent association between two variables is known as genotypic correlation. This type of correlation may be either due to linkage or pleiotropic action of gene or more likely both. The main genetic cause of such correlation is pleiotropy, which refers to many effects of a gene (Falconer, 1981). Genotypic correlation coefficient parameters are given below

4.4.1 Plant height

Plant height showed significant positive association with primary branches per plant (0.4332 *), internodal length (0.9504 **), number of nodes per plant (0.7508 **), shelling percentage (0.4032 *), protein (0.3799 *), while non-significant and positive association with number of pods per plant (0.3106) and pod yield per plant (0.1254). while remaining all characters showed non-significant negative association with plant height.

4.4.2 Number of primary branches per plant

Primary branches per plant showed positive and highly significant association with plant height (0.4332 *), pod yield per plant (0.5447 **), number of pods per plant (0.6137 **), while non-significant positive association with total internodal length (0.3167), number of nodes per plant (0.2884), protein (0.0705), moisture (0.025), total soluble solids (0.3556) and significant negative association was found with no of seeds per pod (-0.546**), average pod weight (-0.433**) and non-significant and negative association with remaining characters.

4.4.3 Number of nodes per plant

Number of nodes per plant showed significant positive association with plant height (0.7508 **), days to first flowering (0.5211 **), days to 50% flowering (0.5525 **), days to first pod setting (0.4315 *) and showed significant negative association width (-0.4306 *). While non-significant and negative association with 100 seed weight (-0.3084) and total soluble solids (-0.1424). The remaining all characters showed non-significant positive association was found with number of nodes per plant.

4.4.4 Inter nodal length

Internodal length showed significant positive association with plant height (0.9504 **), days to 50% flowering (0.5205 **), days to first pod setting (0.3934 *), shelling percentage (0.4968 **) and showed significant negative association moisture content (-0.4449 *), pod length (-0.4615 *), pod width (-0.4362 *), average pod weight (-0.3803 *), number of seed per pod (-0.4187 *). The non-significant and negative association was found with 100 seed weight (-0.2486). The remaining all characters showed non-significant positive association with internodal length.

4.4.5 Days to first flowering

Days to first flowering displayed positive and high significant correlation with days to 50% flowering (0.9647 **) followed by days to first pod setting (0.9843 **), days to first pod picking (0.7812 **), number of primary branches (0.5321 **), plant height (0.6215 **), number of nodes per plant (0.5211 **), number of pods per plant. Whereas, 100 seed weight (-0.5474 **) and pod width (-0.8171 **) showed high significant and negative correlation with days to first flowering. Average pod weight (-0.133), number of seed per pod (-0.0406), total soluble solids (-0.1923) expressed non-significant and negative correlation with days to first flowering, whereas remaining characters showed non-significant and positive association with days to first flowering.

4.4.6 Days to 50% flowering

Days to 50% flowering exhibited highly significant positive correlation with days to first pod setting (0.9538 **) followed by days to first pod picking (0.7512 **), plant height (0.7333

**) and number of primary branches (0.4777 **), internodal length (0.5205 **), number of nodes per plant (0.5525 **), number of pods per plant (0.5053 **), whereas 100 seed weight (-0.5777 **) and pod width (-0.7745 **) had significant and negative correlation. The days to shelling percentage (0.1261), protein content (0.1898) and pod yield per plant (0.2921) showed non-significant and positive correlation with days to 50% flowering. Remaining characters showed non-significant and negative correlation with days to 50% flowering.

4.4.7 Days to first pod setting

Days to first pod setting indicated positive and highly significant correlation with days to first pod picking (0.8512 **), plant height (0.592 **), number of primary branches (0.4761 **), internodal length (0.3934 *), number of nodes per plant (0.4315 *), number of pods per plant (0.554 **) days to first flowering (0.9843 **), days to 50% flowering (0.9538 **), while non-significant positive association with shelling percentage (0.0738), protein (0.072). The significant negative association exhibited with 100 seed weight (-0.5967 **), pod width (-0.8649 **). The non-significant and negative association with remaining all characters.

4.4.8 Days to first pod picking

Days to first pod picking indicated significant and positive correlation with days to first flowering (0.7812 **). Days to 50% flowering (0.7512 **), days to first pod setting (0.8512 **), number of pods per plant (0.4941 **). The 100 seed weight (-0.5581 **) and pod width (-0.7735 **) showed significant negative association width days to first pod picking. Whereas protein content (-0.0817), total soluble solid (-0.3517) and pod length (-0.2246), average pod weight (-0.179) and number of seed per pods (-0.0135) exhibited non-significant and negative association with days to first pod picking. The remaining characters showed non-significant positive association width days to first pod setting.

4.4.9 Number of pods per plant

Number of pods per plant showed significant positive association with yield per plant (0.7311 **), days to first flowering (0.5117 **), days to 50% flowering (0.5053 **), days to first pod setting (0.5544 **), days to first pod picking (0.4941 **),100 seed weight (0.5628 **), number of primary branches (0.6137 **) and showed significant negative association pod width (-1.000 **), protein (-0.3832 *). The non-significant and negative association was found with total soluble solid (-0.1334), pod length (-0.2099) and average pod weight (-

0.2531). The remaining all characters showed non-significant positive association with number of pods per plant.

4.4.10 Pod length

Pod length showed significantly and positive correlation with number of seed per pod (0.8351 **) average pod weight (0.6892 **) and moisture content (0.533 **). Whereas internodal length (-0.4615 *), protein content (-0.4152 *) exhibited highly significant negative correlation with pod length. Number of nodes per plant (0.1282), 100 seed weight (0.215), pod yield per plant (0.1849), showed non-significant positive correlation with pod length, while remaining characters showed non-significant and negative correlation with pod length.

4.4.11 Pod width

Pod width showed highly significant and positive association with 100 seed weight (0.5182 **), protein content (0.3781 *). The days to first flowering (-0.81 **), days to 50% flowering (-0.7745 **), days to first pod setting (-0.8649 **), days to first pod picking (-0.7735 **), plant height (-0.6585 **), number of primary branches (0.7518 **), internodal length (-0.4362 *), number of nodes per plant (-0.4306 *), shelling percentage (-0.39 *) expressed highly significant negative correlation with pod width. Total soluble solids (0.278) showed non-significant positive association with pod width. Remaining characters showed non- significant negative association with pod width.

4.4.12 Average pod weight

Average pod weight showed highly significant positive association with 100 seed weight (0.419 *), pod length (0.6892 **), moisture percentage (0.7662 **), while non-significant positive association was found with number of nodes per plant (0.0584), total soluble solid (0.2144), number of seed per pod (0.0742), pod yield per plant (0.3542). The significant negative association with internodal length (-0.3803) and the remaining characters shows non-significant negative association.

4.4.13 Pod yield per plant

Pod yield per plant exhibited significantly positive correlation with number of primary branches (0.5447 **), number of pods per plant (0.7311 **), 100 seed weight (0.2822*) and number of seed per pod (0.4439 *). Whereas pod width (-0.935**), protein content (-0.4567 *) showed significant negative correlation with pod yield per plant. While remaining characters showed non-significant positive correlation with pod yield per plant.

4.4.14 100 seed weight

100 seed weight showed significant positive association with average pod weight (0.419 *), pod width (0.5182 **), pod yield per plant (0.22*). While significant negative association with days to first flowering (-0.5474 **), days to 50% flowering (-0.5777 **), days to first pod setting (-0.5967 **), days to first pod picking (-0.5581 **), number of primary branches (-0.4963 **), number of pods per plant (-0.562**). The non-significant and negative association with plant height (-0.3266), internodal length (-0.2486), number of nodes per plant (-0.3084) and total soluble solid (-0.0146). The remaining all characters showed non-significant positive association with 100 seed weight.

4.4.15 Number of seed per pod

Number of seed per pod exhibited significant positive association with moisture (0.7005 **), pod width (0.8351 **) and pod length (0.8351 **), pod yield per plant (0.4439 *). Whereas internodal length (-0.4187 *), protein content (-0.4148 *), pod width (-0.3754*) showed high significant and negative correlation with number of seeds per pod. Number of seed per pod (0.0742), number of nodes per plant (0.197), 100 seed weight (0.136), total soluble solid (0.0028) had showed non-significant and positive association with number of seed per pod. Remaining characters showed non-significant negative association with number of seed per pod.

4.4.16 Shelling percentage

Shelling percentage shows positive and highly significant association with characters plant height (0.4032 *), internodal length (0.4968 **), while non-significant negative association with days to first flowering (-0.103), number of primary branches (-0.0133), TSS (-0.0229), moisture content (-0.1642), pod length (-0.2784), average pod weight (-0.166), number of seed per pod (-0.2268). The significant negative association with pod width (-0.3943 *). While the remaining characters showed non-significant negative association.

4.4.17 Protein Content

Protein content exhibited positively significant correlation with pod width (0.3781 *), plant height (0.3799 *). While moisture content (-0.4883 **), pod length (-0.4152 *), number of seed per pod (-0.4148 *), number of pods per plant (-0.3832 *), pod yield per plant (-0.4567 *) showed significant negative correlation. Days to first pod picking (-0.081) and average pod weight (-0.166) showed non-significant negative correlation and remaining characters showed non-significant positive correlation with protein content.

4.4.18 Total Soluble Solid

Total soluble solid showed non-significant and positive correlation with number of primary branches (0.3556), internodal length (0.1009), protein content (0.274), pod width (0.278), average pod weight (0.214), number of seed per pod (0.0028), pod yield per plant (0.0425). Whereas remaining all characters showed non-significant negative correlation with total soluble solid.

4.4.19 Moisture Content

Moisture percentage showed highly significant positive association with pod length (0.533 **), average pod weight (0.7662 **), number of seed per pod (0.7005 **), while non-significant negative association with pod width (-0.1291), shelling percentage (-0.1642), plant height (-0.2464), days to first pod setting (-0.0284) days to 50% flowering (-0.0907), while significant negative association with internodal length (-0.4449 *), protein content (-0.4883 **). The remaining characters showed non-significant positive association.

4.4.B. Phenotypic correlation coefficient

The phenotypic correlation coefficient was computed to know the nature and magnitude of relationship existing between yield and its component characters as well as the association among the component characters. The relationship between two variables which can be directly observed is termed as phenotypic correlation. It includes both genotypic and environmental effects therefore, differs under different environmental conditions. Phenotypic correlation coefficient parameters are given below –

4.4.1 Plant height

Plant height (cm) showed positive association with internodal length (0.6697 **), number of nodes per plant (0.5889 **), shelling percentage (0.3292 **), protein content (0.3272 **), number of pods per plant (0.2555 *). Average pod weight (-0.236 *), pod width (-0.2891 **), pod length (-0.2135 *), moisture content (-0.2381 *), 100 seed weight (-0.2962 **) showed significant negative association with plant height. Whereas pod yield per plant

(0.0976) and number of primary branches showed non-significant positive association width plant height. while non-significant and negative association with remaining all characters.

4.4.2 Number of primary branches per plant

Primary branches per plant showed highly significant positive correlation with number of pod per plant (0.4201 **), pod yield per plant (0.317 **), days to first flowering(0.3486 **), days to 50% flowering(0.2872 **), days to first pod setting (0.3066 **), whereas non-significant negative association with number of seed per pod (-0.0223), while significant and negative association with 100 seed weight,(-0.2994 **), pod length (-0.235 *), pod width (-0.2562 *).Remaining all characters showed non-significant positive association with number of primary branches per plant.

4.4.3 Number of nodes per plant

Number of nodes per plant exhibited highly significant positive correlation with plant height (0.5889 **), days to first pod setting (0.35 **), days to first flowering (0.4315 **), days to 50% flowering (0.4466 **), protein content (0.2119 *). Whereas non-significant negative association with pod width (-0.0506). while significant and negative association with 100 seed weight (-0.2443 *), pod length (-0.235 *), pod width (-0.2562 *). Remaining all characters showed non-significant positive association with number of nodes per plant.

4.4.4 Inter nodal length

Internodal length indicated positive and highly significant correlation with plant height (0.6697 **), days to first flowering (0.2509 *), days to 50% flowering (0.3692 **), days to first pod setting (0.2571 *). The non-significant negative association with 100 seed weight (-0.1368), pod yield per plant (-0.013). The significant negative association exhibited with no of seeds per pod (-0.2683 *), moisture percentage (-0.3623 **), average pod weight (-0.2286 *), pod length (-0.2981 **), pod width (-0.24 *). The non-significant and positive association with remaining all characters.

4.4.5 Days of first flowering

Days to first flowering shows positive and highly significant correlation with days to 50% flowering (0.9464 **), days to first pod setting (0.9704 **), days to first pod picking (0.7662 **), plant height (0.558 **), number of primary branches (0.3486 **), internodal length (0.2509 *), number of nodes per plant (0.4315 **), number of pods per plant (0.4725

**) and pod yield per plant (0.2909 **). The non-significant and positive association with shelling percentage (0.0555), protein content (0.1325), moisture percentage (0.0256), while significant negative association found with 100 seed weight and pod width (-0.3332 **). The non-significant and negative association with remaining all characters.

4.4.6 Days to 50% flowering

Days to 50 % flowering show positive and highly significant correlation with plant height (0.6509 **), days to first pod picking (0.7311 **), days to first pod setting (0.9365 **), number of pods per plant (0.4723 **) and pod yield per plant (0.2909 **), while non-significant and positive association found with shelling percentage (0.1352), protein content (0.1814). The significant negative association with pod length (-0.2777 **), pod width (-0.3193 **), 100 seed weight (-0.5259 **), while non-significant and negative association with remaining all characters.

4.4.7 Days to first pod setting

Days to first pod setting exhibited positive and highly significant correlation with days to first flowering (0.9704 **), days to 50% flowering (0.9365 **), days to first pod picking (0.8294 **), total number of leaves (0.2884*), plant height (0.5155 **), number of primary branches (0.3066 **), internodal length (0.2571 *), number of nodes per plant (0.35 **), while non-significant positive association with shelling percentage (0.0721), protein content (0.063), moisture content (0.0019). The significant negative association showed with 100 seed weight (-0.5409 **), pod width (-0.3489 **), while non-significant and negative association with remaining all characters.

4.4.8 Days to first pod picking

Days to first pod picking indicated positive and highly significant correlation with days to first flowering (0.7662 **), days to 50 % flowering (0.7311 **),days to first pod set (0.8294 **), plant height (0.2706 **), number of pod per plant (0.4637 **), pod yield per plant (0.2603 *).while non-significant and positive association found with moisture content (0.0387), number of nodes per plant (0.1916), internodal length (0.0796), number of primary branches (0.1899), while significant negative association with 100 seed weight (-0.5143 **), TSS (-0.2841 **), pod width(-0.3107 **). The non-significant and negative association found with remaining all characters.

4.4.9 Number of pods per plant

Number of pods per plant showed highly significant positive association with number of primary branches (0.4201 **), pod yield per plant (0.6764 **), plant height (0.2555 *), days to first pod picking (0.4637 **), days to 50% flowering (0.4723 **), days to first pod setting (0.5178 **), days to first flowering (0.4725 **). The non-significant negative association with pod length (-0.1855), total soluble solids (-0.1207). While significant negative association with pod width (0.4335 **), protein content (-0.341 **), 100 seed weight (-0.5254 **), while the remaining characters showed non-significant negative association.

4.4.10 Pod length

Pod length showed highly significant positive association with number of seed per pod (0.761 **), moisture % (0.4271 **), average pod weight (0.492 **), 100 seed weight (0.2539 *), while non-significant negative association with number of nodes per plant (0.0814). The significant negative association with total plant height (-0.2135 *), days to 50% flowering (-0.2777 **), number of primary branches (-0.235 *), internodal length (-0.2981 **), shelling percentage (-0.2468 *), protein content (-0.3806 **). The remaining characters shows non-significant negative association.

4.4.11 Pod width

Pod width shows highly significant positive association with 100 seed weight (0.252 *), while non-significant positive association with protein content (0.0737), TSS (0.0038), pod length (0.0377). The significant negative association with number of pods per plant (-0.4335 **), pod yield per plant (- 0.398 **), days to first flowering (-0.3332 **), days to 50% flowering (-0.3193 **) days to first pod setting (-0.3489 **), days to first pod picking (-0.3107 **), plant height (-0.2891 **), number of primary branches (-0.2562 *), internodal length (-0.24 *). The remaining characters shows non-significant negative association with pod width.

4.4.12 Average pod weight

Average pod weight showed highly significant positive association with 100 seed weight (0.3276 **), moisture % (0.5587 **), pod length (0.492 **), number of seed per pod (0.5758 **), pod yield per plant (0.2713 **). The non-significant positive association with number of primary branches (0.0148), number of nodes per plant (0.0508), total soluble solid

(0.1599), while significant negative association with plant height (-0.236 *), internodal length (-0.2286 *). The remaining characters show non-significant negative association.

4.4.13 Pod yield per plant

Pod yield per plant showed highly significant positive association with 100 seed weight (0.2345 *), number of primary branches, moisture content (0.3587 **), average pod weight (0.2713 **), number of seed per pod (0.3966 **), number of pods per plant (0.6764 **), days to first flowering (0.2909 **), days to 50% flowering (0.2909 **), days to first pod setting (0.3074 **), days to first pod picking (0.2603 *). The non-significant negative association with internodal length (-0.013), while highly significant negative association with protein content (-0.3874 **), pod width (0.398 **). The remaining characters shows non-significant positive association with pod yield per plant.

4.4.14 100 seed weight

100 seed weight showed highly significant positive association with shelling percentage (0.3461 **), average pod weight (0.3276 **), pod length (0.2539 *), pod width (0.252 *), while non-significant positive association with plant spread (0.017), pod width (0.1975), moisture percentage (0.0167), average pod length (0.0642). The highly significant negative association with number of pods per plant (-0.5254 **), primary branches per plant (-0.2994 **), number of nodes per plant (-0.2443 *), plant height (-0.2962 **), days to first flowering (-0.5053 **), days to first pod set (-0.5409 **), days to 50% flowering (-0.5259 **), days to first pod picking (-0.5143 **). The remaining characters show non-significant negative association.

4.4.15 Number of seed per pod

Number of seeds per pod exhibited highly significant positive association with, pod yield per plant (0.3966 **), pod length (0.761 **), average pod weight (0.5758 **), moisture content (0.5787 **) while non-significant positive association with plant spread (0.017), pod width (0.1975), moisture percentage (0.0167), average pod length (0.0642). The non-significant positive association with number of nodes per plant (0.1384), 100 seed weight (0.112), number of pods per plant (0.0747), while highly significant negative association with internodal length (-0.2683 *), shelling percentage (-0.2229 *), protein content (-0.3873 **).

The remaining characters showed non-significant negative association with number of seed per pod.

4.4.16 Shelling percentage

Shelling percentage showed positive and highly significant association with characters 100 seed weight (0.3461 **), protein content (0.2719 **), plant height (0.3292 **), internodal length (0.3471 **), while non-significant negative association with days to first pod picking (-0.0937), total soluble solid (-0.0036), moisture percentage (-0.116), while significant negative association with pod length (-0.2468 *), number of seed per pod (-0.2229 *). The remaining characters showed non-significant positive association with shelling percentage.

4.4.17 Protein Content

Protein content showed highly significant positive association with plant height (0.3272 **), internodal length (0.2328 *), shelling percentage (0.2719 **), number of nodes per plant (0.2119 *) while non-significant positive association with pod width (0.0737), TSS (0.2051), number of primary branches (0.0798), days to first flowering (0.0798), days to 50% flowering (0.1814), days to first pod setting (0.0636). The significant negative association with moisture percentage (-0.4255 **), pod length (-0.3806 **), yield per plant (-0.3874 **), number of pods per plant (-0.341 **), number of seed per pod (-0.3873 **). The remaining characters show non-significant negative association.

4.4.18 Total Soluble Solid

Total soluble solid showed highly significant negative association with days to first picking (-0.2841 **), while non-significant positive association with average pod weight (0.1599), yield per plant (0.0575), pod width, number of primary branches (0.1923), internodal length (0.0208), number of nodes per plant (0.0208), 100 seed weight (0.0266), protein content (0.2051). While the remaining characters shows non-significant negative association total soluble solids.

4.4.19 Moisture content

Moisture percentage showed highly significant positive association with average pod weight (0.5587 **), number of seed per pod (0.5787 **), pod yield per plant (0.3587 **), while non-significant negative association with shelling percentage (-0.116), TSS (-0.0687), pod width (-0.0777), while significant negative association with plant height (-0.2381 *), internodal length (-0.3623 **), protein content (-0.4255 **). The remaining characters show non-significant positive association with moisture content.

Pod yield per plant was found to be significantly and positively correlated with number of seeds per pod and number of pods per plant, number of primary branches per plant similar findings reported by Pal and Singh (2012)

Strong genotypic correlation relationships were found between the plant height and internodal length (0.950**), number of nodes per plants (0.750**). Similar observations were reported by Kalapchieva *et al*. (2021)

Green pod yield per plot showed highly significant positive association with number of seeds per pod and weight of pods per plant at genotypic and phenotypic levels. These observations are in agreement with the report of Navab *et al.* (2008) who obtained strong association between pod length and number of seed per pod in pea.

Green pod yield per plant had highly significant positive association with number of primary branches per plant, number of seeds per pod and number of pods per plant at phenotypic and genotypic level Pal and Singh (2012).

Khan *et al*. (2017) reported the yield showed significant positive correlation with number of primary branches, number of seed per pod, number of pods per plant.

Very high phenotypic correlation coefficients showed between length of internode (0.588**) with plant height (0.669**). There is a weak to medium and statistically significant phenotypic relationship of 0.132 between the pod width and plant height (-0.256*) similar findings reported by Kalapchieva *et al*. (2021).

Phenotypic correlation revealed positive and highly significant association of yield per plant with 100 seed weight (0.234*) and genotypic correlation showed positive and highly significant association for yield per plant with number of pods per plant (0.731*), 100 seed weight (0.282*), number of seeds per pod (0.443*) and number of primary branches (0.544**) similar findings reported by Kumar *et al*. (2014).

The correlation coefficients recorded positive and highly significant association of yield per plant, width number of pods per plant (0.731*), number of seed per pod (0.443*) and 100 seed weight (0.282*). These results reported by Jeberson *et al*. (2016) and Yadav *et al*. (2010).

Table 4.4 Estimation of genotypic correlation coefficients for different characters of pea

Traits	**DF1**	**DF50**	**DS1**	**DP1**	**PH**	**NPB**	**INL**	**NNP**	**SHL**	**SW**	**PR**	**TSS**	**M**	**PL**	**PW**	**APW**	**NSP**	**NPP**	**PYP**
DF1	1	0.964**	0.98 **	0.781**	0.62 **	0.53 **	0.3606	0.52 **	0.0633	-0.54 **	0.1396	-0.1923	0.0171	-0.1802	-0.81 **	-0.1335	-0.0406	0.511**	0.3253
DF50		1	0.95 **	0.75 **	0.73**	0.47**	0.520**	0.55 **	0.1261	-0.57 **	0.1898	-0.1594	-0.0907	-0.3048	-0.77**	-0.1981	-0.1671	0.505**	0.2921
DS1			1	0.85 **	0.59**	0.476**	0.393 *	0.431 *	0.0738	-0.59 **	0.0727	-0.2044	-0.0284	-0.2081	-0.86 **	-0.1729	-0.0479	0.5544 **	0.3487
DP1				1	0.3056	0.2944	0.1326	0.215	-0.103	-0.55 **	-0.0817	-0.3517	0.0154	-0.2246	-0.77 **	-0.1797	-0.0135	0.49 **	0.2961
PH					1	0.433 *	0.95**	0.75 **	0.403*	-0.3266	0.379 *	-0.0763	-0.2464	-0.2788	-0.65 **	-0.1945	-0.2169	0.3106	0.1254
NPB						1	0.3167	0.2884	-0.0133	-0.49 **	0.0705	0.3556	0.025	-0.3499	-0.75**	-0.0365	-.040	0.613**	0.54 **
INL							1	0.327	0.49 **	-0.2486	0.3105	0.1009	-0.444*	-0.461 *	-0.436 *	-0.38*	-0.418*	0.1996	0.0339
NNP								1	0.0391	-0.308	0.2825	-0.142	0.1282	0.1081	-0.430 *	0.0584	0.1975	0.2087	0.1481
SHL									1	0.3486	0.284	-0.022	-0.164	-0.278	-0.394 *	-0.166	-0.226	0.1162	0.0175
SW										1	0.1077	-0.014	0.215	0.3082	0.518**	0.419 *	0.136	-0.56**	0.282*
PR											1	0.2748	-0.48**	-0.415 *	0.378 *	-0.166	-0.414 *	-0.383*	-0.456 *
TSS												1	-0.062	-0.113	0.278	0.2144	0.0028	-0.133	0.0425
M													1	0.533**	-0.129	0.766**	0.700**	0.0528	0.0425
PL														1	0.1196	0.689**	0.835**	-0.209	0.1849
PW															1	-0.058	-0.375 *	-1.00**	-0.93 **
APW																1	0.0742	-0.253	0.3542
NSP																	1	0.0742	0.4439*
NPP																		1	0.73 **
PYP																			1

****Significance at 5% level, *Significance at 1% level**

Table 4.5 Estimation of phenotypic correlation coefficients for different characters of vegetable pea

Traits	DF1	DF50	DS1	DP1	PH	NPB	INL	NNP	SHL	SW	PR	TSS	M	PL	PW	APW	NSP	NPP	PYP
DF1	1	0.946**	0.97**	0.766**	0.558 **	0.348 **	0.250*	0.431**	0.055	-0.50 **	0.1325	-0.1556	0.0256	-0.1731	-0.33**	-0.1074	-0.0455	0.472 **	0.290 **
DF50		1	0.93**	0.73**	0.65**	0.28 **	0.369**	0.446**	0.1352	-0.52**	0.1814	-0.120	-0.0756	-0.27 **	-0.31 **	-0.1652	-0.1667	0.472**	0.29**
DS1			1	0.829**	0.515**	0.30 **	0.2571 *	0.35 **	0.0721	-0.54 **	0.0636	-0.135	0.0019	-0.1927	-0.34 **	-0.1414	-0.0483	0.517 **	0.307 **
DP1				1	0.27**	0.1899	0.0796	0.1916	-0.0937	-0.51 **	-0.0743	-0.28 **	0.0387	-0.1971	-0.31 **	-0.1408	-0.0176	0.463**	0.2603 *
PH					1	0.1899	0.66 **	0.58 **	0.32 **	-0.29 **	0.327 **	-0.0503	-0.238 *	-0.213*	-0.28**	-0.236 *	-0.173	0.2555 *	0.0976
NPB						1	0.1552	0.1728	0.0785	-0.29 **	0.0798	0.1923	0.119	-0.235 *	-0.256 *	0.0148	-0.0223	0.420 **	0.317 **
INL							1	0.1621	0.347**	-0.1368	0.2328 *	0.0208	-0.36**	-0.29 **	-0.24 *	-0.22 *	-0.268*	0.142	-0.013
NNP								1	0.039	-0.244 *	0.2119 *	0.0208	0.1228	0.0814	-0.0506	0.0508	0.1384	0.144	0.0986
SHL									1	0.346**	0.271 **	-0.0036	-0.116	-0.24 *	-0.1487	-0.1256	-0.222*	0.108	0.0159
SW										1	0.1057	0.0266	0.1802	0.2539 *	0.252 *	0.327 **	0.112	-0.52 **	0.2345 *
PR											1	0.2051	-0.42**	-0.38 **	0.0737	-0.1571	-0.38**	-0.34**	-0.38**
TSS												1	-0.068	-0.044	0.0038	0.1599	-0.012	-0.120	0.0575
M													1	0.4271 **	-0.077	0.558 **	0.578 **	0.049	0.358 **
PL														1	0.0377	0.492 **	0.761 **	-0.1855	0.1436
PW															1	-0.0173	-0.1954	-0.43**	-0.39 **
APW																1	0.575 **	-0.1597	0.271 **
NSP																	1	0.0747	0.396 **
NPP																		1	0.676 **
PYP																			1

****Significance at 5% level, *Significance at 1% level**

4.5 Path analysis

Correlation coefficient values do not reveal the real association pattern of the independent variables with the dependent one. The path coefficient analysis is the standardized partial regression coefficient which divides the correlation coefficient into the measures of direct and indirect effect of independent variables on the genetic makeup of independent traits. To know these various effects, the correlation coefficient of different characters with pod yield per plot was grouped into their direct and indirect effects. This helps the selection of genotypes based on those traits which will accurately contribute more towards yield, the results of path coefficient analysis given in table (4.6) and (4.7)

4.5.1 Plant height

The plant height (0.407) showed positive direct effect on pod yield per plant. Found highly positive indirect effect of days to 50% flowering (0.118), number of pods per plant (0.243), 100 seed weight (0.080), number of primary branches (0.044), shelling percentage (0.040) and indirect negative effect of days to first pod setting (-0.128), internodal length (-0.172), number of nodes per plant (-0.275), average pod weight (-0.114) on pod yield per plant.

4.5.2 Number of primary branches per plant

Number of primary branches per plant (0.1024) showed positive direct effect on pod yield per plant. Number of primary branches showed positive indirect effect of plant height (0.176), 100 seed weight (0.122), number of pods per plant (0.148), and indirect negative effect of days to first pod setting (-0.103), number of nodes per plant (-0.105) on pod yield per plant.

4.5.3 Internodal length

Internodal length (-0.181) showed negative direct effect on pod yield per plant. The character showed positive indirect effect of days to 50% flowering (0.084), plant height (0.387), number of pods per plant (0.156) and indirect negative effect of number of nodes per plant (-119), pod length (-0.037), average pod weight (-0.223) on pod yield per plant.

4.5.4 Number of nodes per plant

Number of nodes per plant (-0.336) showed negative direct effect on yield per plant. The character showed positive indirect effect of plant height (0.306), number of pods per plant

(0.163), days to 50% flowering (0.089), 100 seed weight (0.076) and indirect negative effect of days to first pod setting (-0.093), internodal length (-0.059) on pod yield per plant.

4.5.5 Days to first flowering

Days to first flowering (-1145) showed direct negative effect on pod yield per plant and highly positive indirect effect of days to 50% flowering (0.156), plant height (0.253), 100 seed weight (0.135), number of pods per plant (0.401) and indirect negative effect via days to first pod setting (-0.213), number of nodes per plant (-0.190), average pod weight (-0.078).

4.5.6 Days to 50% flowering

Days to 50% flowering (0.162) showed positive direct effect on pod yield per plant and positive indirect effect of plant height (0.298), 100 seed weight (0.142), number of pods per plant (0.396) and negative indirect effect via number of nodes per plant (-0.202), internodal length (-0.094), pod length (-0.025) on pod yield per plant.

4.5.6 Days to first pod setting

Days to first pod setting (-0.217) showed negative direct effect on pod yield per plant and have a highly positive indirect effect of days to 50% flowering (0.154), plant height (0.241), 100 seed weight (0.147), number of pods per plant (0.435) and indirect negative of days to first flowering (-0.11), number of nodes per plant (-0.158), average pod weight (-0.101) on pod yield per plant.

4.5.7 Days to first pod picking

Days to first pod picking (0.0088) showed positive direct effect on pod yield per plant. The character showed positive indirect effect of days to 50% flowering (0.121), plant height (0.124),100 seed weight (0.138), number of nodes per plant (0.387) and indirect negative effect of days to first pod setting (-0.18), average pod weight (-0.105), number of nodes per plant (-0.078) on pod yield per plant.

4.5.8 Pod length

Pod length (0.0822) showed positive direct effect on pod yield per plant. The character showed positive indirect effect of average pod weight (0.404), internodal length (0.083), and indirect negative effect via plant height (-0.113) 100 seed weight (-0.076), number of primary branches per plant (-0.035) on pod yield per plant.

4.5.9 Pod width

Pod width (0.029) showed direct positive effect on pod yield per plant. Pod width showed positive indirect effect of days to first flowering (0.0936), days to first pod setting (0.188), number of nodes per plant (0.157) and negative indirect effect of days to 50% flowering (-0.125), plant height (-0.268), number of primary branches (-0.077) on pod yield per plant.

4.5.10 Average pod weight

Average pod weight (0.587) showed positive direct effect on pod yield per plant. Average pod weight showed indirect positive effect of days to first flowering (0.015), moisture percentage (0.038) and negative indirect effect of 100 seed weight (-0.103), plant height (-0.07), days to first flowering (-0.032) on pod yield per plant.

4.5.11 Number of seed per pod

Number of seed per pod (0.0331) showed direct positive effect on pod yield per plant. The number of primary branches highly positive indirect effect of internodal length (0.076), moisture percentage (0.069), number of pods per plant (0.0582) and indirect negative effect of plant height (-0.088) number of nodes per plant (-0.072) on pod yield per plant.

4.5.12 Number of pods per plant

Number of pods per plant (0.784) showed direct positive effect on pod yield per plant. The character showed indirect positive effect via days to 50% flowering (0.081), plant height (0.126), internodal length (0.062), number of seed per pod (0024) and indirect negative effect via number of nodes per (-0.076), days to first pod setting (-0.120), internodal length (-0.036) on pod yield per plant.

Path coefficient which achieved from genotypic correlation coefficient are referred to as genotypic path coefficient analysis. It measures the direct and indirect contribution of various independent characters towards a dependent character say yield in plant breeding experiment.

4.5.13 Shelling percentage

Shelling percentage (0.099) showed positive direct effect on yield per plant. The character showed highly positive indirect effect of plant height (0.164), number of pods per plant (0.091), days to 50% flowering (0.020) and indirect negative effect of internodal length (-0.090), 100 seed weight (-0.085), average pod weight (-0.097) on green pod yield.

4.5.14 100 seed weight

100 seed weight (0.247) showed positive direct effect on pod yield per plant. The character showed positive indirect effect of days to first pod setting (0.129), average pod weight (0.245), internodal length (0.045) and indirect negative effect of number of primary branches (-0.050) on pod yield per plant.

4.5.15 Protein content

Protein content (0.0164) showed positive direct effect on pod yield per plant. The character showed positive indirect effect of plant height (0.154), shelling percentage (0.028) and indirect negative effect of number of nodes per plant (-0.103), average pod weight (-0.097) on pod yield per plant.

4.5.16 Total soluble solid

Total soluble solid (-0.056) showed negative direct effect on pod yield per plant. The character highly positive indirect effect of days to first flowering (0.022), days to first pod setting (0.044) and indirect negative effect of number of pods per plant (-0.104) on pod yield per plant.

4.5.17 Moisture content

Moisture content (0.499) showed positive direct effect on pod yield per plant. The character showed indirect positive effect of average pod weight (0.449), internodal length (0.080), number of seed per pod (0.023), number of pods per plant (0.0414) and indirect negative effect of number of nodes per plant (-0.046), 100 seed weight (-0.0531), shelling percentage (-0.0163) on pod yield per plant.

Path coefficient which achieved from genotypic correlation coefficient are referred to as genotypic path coefficient analysis. It measures the direct and indirect contribution of various independent characters towards a dependent character say yield in plant breeding experiments. It breaks the genotypic correlation coefficient analysis. It breaks the genotypic correlation coefficient into the measures of direct and indirect effect. A perusal of genotypic path coefficient analysis showed that number of pods per plant (0.784) had maximum positive direct effect on pod yield per plant followed by average pod weight (0.587), plant height

Table 4.6 Direct (diagonal) and indirect diagonal (above and below diagonal genotypic path effects of different characters towards yield in vegetable pea

Traits	DF1	DF50	DS1	DP1	PH	NPB	INL	NNP	SHL	SW	PR	TSS	M	PL	PW	APW	NSP	NPP
DF1	**-0.1145**	0.1563	-0.2139	0.0069	0.2532	0.0545	-0.0655	-0.1908	0.0062	0.1354	0.0023	0.0109	0.0008	-0.0148	-0.0237	-0.0783	-0.0013	0.4016
DF50	-0.1105	**0.162**	-0.2073	0.0066	0.2988	0.0489	-0.0946	-0.2023	0.0125	0.1429	0.0031	0.0090	-0.0045	-0.0250	-0.0224	-0.1162	-0.0055	0.3966
DS1	-0.1127	0.1546	**-0.217**	0.0075	0.2412	0.0487	-0.0715	-0.1580	0.0073	0.1476	0.0012	0.0116	-0.0014	-0.0171	-0.0251	-0.1014	-0.0015	0.4351
DP1	-0.0895	0.1217	-0.1850	**0.0088**	0.1245	0.0301	-0.0241	-0.0787	-0.0102	0.1380	-0.0013	0.0200	0.0007	-0.0184	-0.0224	-0.1055	-0.0004	0.3878
PH	-0.0712	0.1188	-0.1286	0.0027	**0.407**	0.0443	-0.1727	-0.2750	0.0401	0.0808	0.0062	0.0043	-0.0123	-0.0229	-0.0191	-0.1141	-0.0071	0.2438
NPB	-0.0609	0.0774	-0.1034	0.0026	0.1765	**0.1024**	-0.0575	-0.1056	-0.0013	0.1228	0.0011	-0.0202	0.0012	-0.0287	-0.0218	-0.0214	0.0000	0.4817
INL	-0.0413	0.0843	-0.0855	0.0011	0.3873	0.0324	**-0.181**	-0.1198	0.0494	0.0615	0.0051	-0.0057	-0.0222	-0.0379	-0.0126	-0.2232	-0.0138	0.1567
NNP	-0.059	0.089	-0.0937	0.0019	0.306	0.029	-0.059	**-0.36**	0.003	0.076	0.0046	0.008	0.006	0.008	-0.012	0.034	0.006	0.1637
SHL	-0.007	0.0204	-0.016	-0.0009	0.164	-0.001	-0.090	-0.014	**0.099**	-0.086	0.00468	0.0013	-0.0082	-0.0229	-0.011	-0.097	-0.0075	0.0912
SW	0.06273	-0.093	0.1297	-0.004	-0.133	-0.050	0.0452	0.11296	0.03468	**0.247**	0.00177	0.00083	0.01073	0.02536	0.01504	0.24597	0.00451	-0.44172
PR	-0.016	0.03077	-0.015	-0.0007	0.15485	0.00722	-0.056	-0.103	0.0282	-0.026	**0.0164**	-0.0156	-0.024	-0.034	0.0109	-0.097	-0.013	-0.300
TSS	0.02203	-0.025	0.04443	-0.0031	-0.0311	0.03644	-0.0183	0.05216	-0.0022	0.00362	0.00453	**-0.056**	-0.003	-0.009	0.008	0.125	0.00009	-0.1047
M	-0.0019	-0.014	0.00617	0.00014	-0.1004	0.0025	0.0808	-0.0469	-0.0163	-0.053	-0.008	0.0035	**0.049**	0.0438	-0.0037	0.4498	0.0232	0.0414
PL	0.02064	-0.0494	0.04525	-0.0019	-0.1136	-0.0358	0.0839	-0.0396	-0.0277	-0.0762	-0.0068	0.00644	0.02661	**0.0822**	0.00347	0.40465	0.0277	-0.16473
PW	0.0936	-0.1256	0.1881	-0.0068	-0.2685	-0.0770	0.0793	0.1578	-0.0392	-0.1282	0.0062	-0.0158	-0.0064	0.0098	**0.029**	-0.0344	-0.0124	-0.7853
APW	0.0153	-0.0321	0.0375	-0.0015	-0.0792	-0.0037	0.0691	-0.0214	-0.0165	-0.1036	-0.0027	-0.0122	0.0382	0.0567	-0.0017	**0.587**	0.0237	-0.1986
NSP	0.0046	-0.0270	0.0104	-0.0001	-0.0884	0.0000	0.0761	-0.0723	-0.0225	-0.0336	-0.0068	-0.0001	0.0349	0.0687	-0.0108	0.4196	**0.033**	0.0582
NPP	-0.0586	0.08191	-0.1205	0.0043	0.1265	0.0628	-0.036	-0.0764	0.01156	0.13923	-0.0063	0.0076	0.00264	-0.0172	-0.029	-0.148	0.00246	**0.784**

Residual effect - 0.147

Table 4.7 Direct (diagonal) and indirect (above and below diagonal) phenotypic path effects of different characters towards yield in vegetable pea

Traits	DF1	DF50	DS1	DP1	PH	NPB	INL	NNP	SHL	SW	PR	TSS	M	PL	PW	APW	NSP	NPP
DF1	0.2901	-0.0459	-0.262	0.0254	0.0671	-0.0082	-0.0070	-0.0352	-0.00009	-0.0191	-0.0092	-0.0223	0.0031	0.0006	0.0158	-0.0219	-0.0062	0.3261
DF50	0.2745	-0.0485	-0.2528	0.0242	0.0783	-0.0068	-0.0104	-0.0364	-0.0002	-0.0198	-0.0126	-0.0173	-0.0092	0.001	0.0151	-0.0338	-0.0228	0.3261
DS1	0.2815	-0.0454	-0.2699	0.0275	0.0620	-0.0072	-0.0072	-0.0285	-0.0001	-0.0204	-0.0044	-0.0195	0.0002	0.0007	0.0165	-0.0289	-0.0066	0.3574
DP1	0.2223	-0.0354	-0.2239	0.0331	0.0325	-0.0045	-0.0022	-0.0156	0.0001	-0.0194	0.0051	-0.0408	0.0047	0.0007	0.0147	-0.0287	-0.0024	0.3201
PH	0.1619	-0.0315	-0.1391	0.0089	0.1203	-0.0039	-0.0189	-0.0481	-0.0005	-0.0111	-0.0227	-0.0072	-0.029	0.0007	0.0137	-0.0482	-0.0237	0.1763
NPB	0.1011	-0.0139	-0.0827	0.0063	0.0200	-0.0236	-0.0043	-0.0141	-0.0001	-0.0113	-0.0055	0.0277	0.0145	0.0008	0.0122	0.0031	-0.0031	0.2900
INL	0.0727	-0.0179	-0.0694	0.0026	0.0805	-0.0036	-0.0282	-0.0132	-0.0005	-0.0051	-0.0161	0.0029	-0.0441	0.0010	0.0113	-0.0469	-0.0367	0.0979
NNP	0.12522	-0.02167	-0.0945	0.00636	0.07086	-0.00411	-0.00457	-0.08172	-0.00006	-0.00923	-0.01473	-0.01892	0.01495	-0.00029	0.0024	0.01035	0.01894	0.09934
SHL	0.0161	-0.00656	-0.01947	-0.00311	0.03961	-0.00186	-0.0098	-0.00319	-0.00163	0.01308	-0.01891	-0.00049	-0.01413	0.00089	0.00706	-0.02571	-0.03055	0.07456
SW	-0.14661	0.02553	0.14604	-0.01706	-0.03564	0.00709	0.00387	0.01996	-0.00056	0.03779	-0.00734	0.00385	0.02195	-0.00092	-0.01196	0.06698	0.01534	-0.3627
PR	0.03844	-0.0088	-0.01717	-0.00247	0.03937	-0.00189	-0.00657	-0.0173	-0.00044	0.00399	-0.06955	0.02948	-0.05185	0.00138	-0.00347	-0.03215	-0.05307	-0.23533
TSS	-0.04515	0.00586	0.03667	-0.00942	-0.00605	-0.00457	-0.00058	0.01075	0.00001	0.00101	-0.01426	0.1437	-0.00838	0.00016	0	0.03254	-0.00166	-0.08312
M	0.00743	0.00367	-0.00051	0.00128	-0.02865	-0.00282	0.01024	-0.01002	0.00019	0.00681	0.0296	-0.00989	0.12182	-0.00155	0.00371	0.11426	0.07931	0.03383
PL	-0.05022	0.01347	0.05203	-0.00653	-0.02569	0.00557	0.00842	-0.00665	0.0004	0.00959	0.02648	-0.00638	0.05203	-0.00362	-0.00198	0.10068	0.10427	-0.12826
PW	-0.09662	0.01551	0.09436	-0.01029	-0.0348	0.00612	0.00677	0.00413	0.00024	0.00953	-0.00508	0.0023	-0.00954	-0.00015	-0.04879	-0.0044	-0.02642	-0.29898
APW	-0.03116	0.00802	0.0382	-0.00467	-0.0284	-0.00036	0.00649	-0.00413	0.00021	0.01238	0.01093	0.02288	0.06806	-0.00178	0.00102	0.20463	0.07889	-0.1099
NSP	-0.01317	0.00809	0.01304	-0.00058	-0.02082	0.00054	0.00758	-0.01129	0.00036	0.00423	0.02693	-0.00174	0.0705	-0.00275	0.00915	0.11771	0.13709	0.05164
NPP	0.1370	-0.0229	-0.1398	0.0153	0.0307	-0.0099	-0.0040	-0.0117	-0.0001	-0.0198	0.0237	-0.0173	0.0059	0.0006	0.0205	-0.0325	0.0102	0.6904

Residual effect - 0.3403

(0.407), primary branches per plant (0.102) shelling percentage (0.099), moisture percentage (0.0499, no of seeds per pod (0.033), pod length (0.0822), pod width (0.029), days to first pod picking (0.0088). Days to first flowering (-0.114), days to 50% flowering (-0.097), showed negative direct effect on pod yield per plant. These observations are in conformity with the report of Afreen *et al*. (2017), Toppo *et al*. (2017), Katoch *et al*. (2016), Jaiswal *et al.* (2015), Kumar *et al*. (2015), Ahmad *et al*. (2014).

4.6 Genetic divergence

Genetic divergence is desirable to select suitable genetically divergent parents, based on information about the genetic diversity and genetic variations present in the available germplasm. In plant breeding, genetic diversity plays an important role as it helps in selecting the suitable parents for hybridization programme resulting in desirable recombinants and superior hybrids.

Thirty genotypes of garden peas taken for multivariate analysis were differed significantly with regards to the character under study and displayed marked divergence, when taking 19 characters together. Thus, it would be worthwhile to classify gene pools into different groups on the basis of characters studied. Similar findings were also reported by Srivastava *et al*. (2018), Gupta *et al*. (2017), Jaiswal *et al*. (2021), Kumar *et al* (2016), Saxesena *et al*. (2013).

The genetic diversity in 30 genotypes of garden pea was estimated by using D^2 statistics. Based on (D^{2}) statistics of Mahalanobis (1936) and also by the use of non-hierarchical Euclidean cluster analysis, 30 genotypes were grouped into six divergent cluster. Cluster 1 have 10 genotypes, 7 genotypes in cluster 2, 10 genotypes in cluster 3, one genotype in cluster 4, one genotype in cluster 5 and one genotype in cluster 1.

4.6.1 Cluster distance

The inter cluster D2 value was maximum (2502.5) between cluster 6 and 3. The minimum (367.1) distance was observed between cluster 4 and 3 which indicated close relationship among the 2 genotypes. table (4.8)

Intra cluster distance

Intra cluster distance was observed only in the cluster 1, 2 and 3 as the remaining clusters contained only one constituent genotype. Intra cluster distance was highest in the cluster 3 (229.6) followed by cluster 1 (211.02).

Table (4.8) Inter and Intra Cluster Distance: Tocher Method

	Cluster 1	**Cluster 2**	**Cluster 3**	**Cluster 4**	**Cluster 5**	**Cluster 6**
Cluster	211.02	401.0	799.3	393.8	390.3	1170.9
Cluster 2		152.4	1016.1	390.2	790.9	580.8
Cluster 3			229.6	367.1	888.0	2502.5
Cluster 4				0.000	496.7	1298.1
Cluster 5					0.000	1520.8
Cluster 6						0.000

Table (4.9) Percentage contribution of different characters towards diversity in vegetable pea genotypes

Source	**Contribution %**	**Source**	**Contribution %**
DF1	24.6	PYP	2.1
DP1	15.8	NPP	2
DF50	15.2	PH	1.9
NSP	10.6	APW	1.5
DS1	5.2	SW	1.5
PL	4.1	NPB	1.2
SHL	3.9	TSS	1.1
M	3	INL	0.9
NPP	2.7	PW	0.3
PR	2.4		

4.6.2 Percent contribution of characters

Percent contribution of 19 characters to total genetic diversity is presented table (4.9) and fig. (4.7). The characters namely, days to first flowering (24.6%) contributed maximum to the manifestation of genetic divergence. The characters like days to first pod picking (15.8%), days to 50% flowering (15.2%), number of seed per pod(10.6%), days to first pod setting(5.2%), pod length (4.1%), shelling percentage (3.9%), moisture content (3%), number of pod per pod(2.7), protein content (2.4%), pod yield per plant (2.1%), number of pod per plant(2%), plant height (1.9%), average pod weight(1.5%), 100 seed weight(1.5%), number of primary per plant(1.2%), total soluble solids(1.1%), internodal length(0.9%), pod width(0.3).

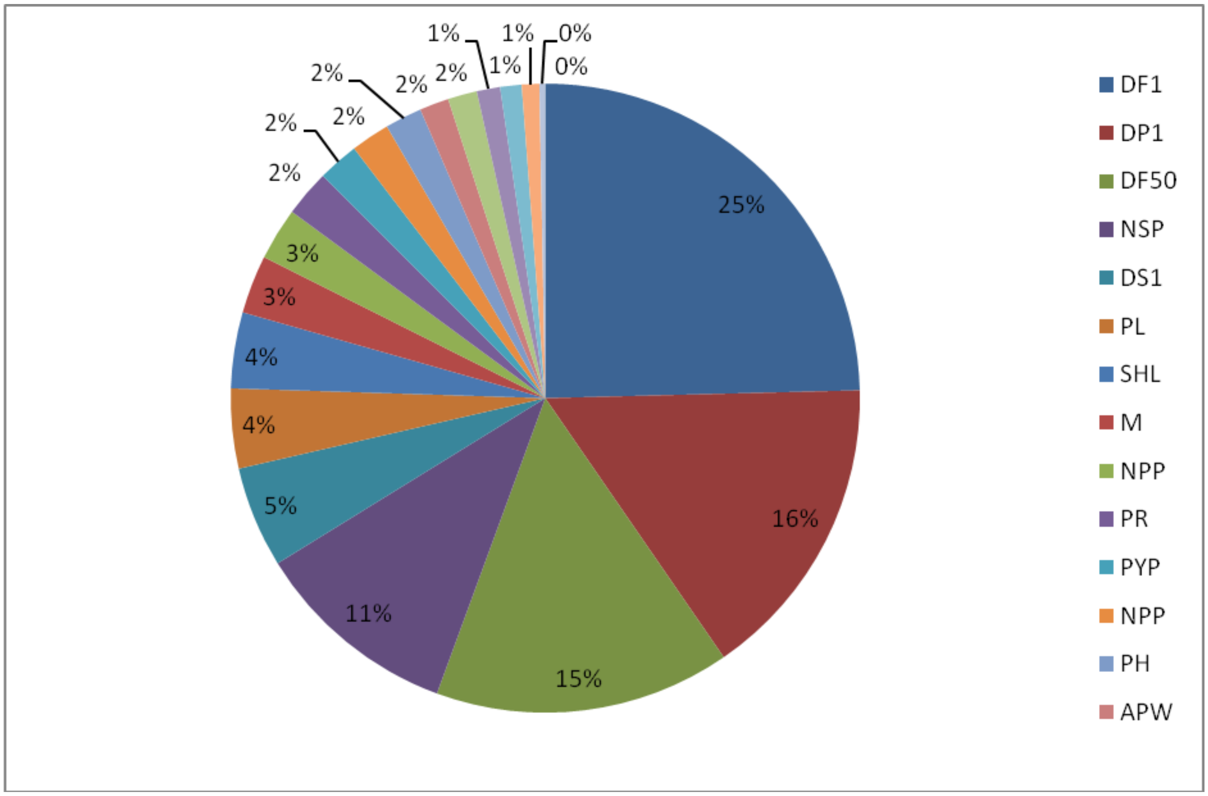


Fig. (4.7) Contribution percent towards divergence

Table (4.10) Clustering pattern of 30 vegetable pea genotypes by Tocher's method

Group	Number of genotypes	Genotypes
Cluster 1	10	AS 10, Pencil Matar, GS 10, Pea TS- 10, Ganga-10, Arka Priya, PSM-2, PB-89, PC-531, VL-7
Cluster 2	7	IPFD-10-12, IPFD-11-5, EC 243642, IC 208366, IC 395309, EC 302842, EC 6621
Cluster 3	10	Kashi Mukti, NDVP-1, Arkel, Kashi Nandani, PSM-3, Kashi Uday, Kashi Uday, AP-3, Pusa Shree, Kashi Samarth,
Cluster 4	1	AP-1
Cluster 5	1	Pusa Pragati
Cluster 6	1	Aman

5. SUMMARY AND CONCLUSION

The present investigation on “Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)” using thirty genotypes of pea were conducted in Randomized Block Design with three replications at the Experimental Farm in Vegetable Research Farm of the College of Horticulture and Forestry, RLBCAU, Jhansi during *Rabi* season 2021-2022 with the following objectives:

1. To assess the genetic variability, heritability and genetic advance in vegetable pea.
2. To estimate the correlation coefficient among the yield and yield components.
3. Path coefficient analysis for yield and yield components.
4. To study the genetic divergence in vegetable pea for growth, yield and quality attributes.

The results of the experiment have been briefed and salient findings are given as under:

1. The minimum days required to first flowering was noticed in Pusa Sree (32.67 days) followed by Kashi Uday (33.67 days) and Kashi Nandani (33.67 days).
2. Among the genotype, Aman showed highest plant height (199.2 cm) followed by IC 208366 (96 cm), IPFD -10-12(71.3cm), and IPFD 11-5(71.2 cm).
3. Pusa Sree and Kasi Uday expressed earliest 50 % flowering (36.67 days) followed by Kashi Nandani (38.6 days).
4. IPFD-11-5 had highest number of primary branches (2.9) followed by Kashi Samarth (2.7) and Arka Priya (2.5).
5. Highest internodal length was noted in Aman (6.9 cm) followed by IC 208366(6.5 cm), Pusa Pragati (5.5 cm), IPFD-11-5(5.3 cm) and Kashi Samarth (4.9 cm).
6. Number of nodes per plant was counted highest in Aman and Pusa Pragati (15) followed by Kashi Samarth (14.9), Ganga-10(14.3).
7. Highest pod length was measured in GS-10 (10.3 cm) followed by Pusa Pragati (9.6 cm), Pencil Matar (9.5 cm), PB-89 (9.4 cm).

8. Number of seed per pod was counted maximum in GS-10 (10.2) followed by AS-10 (9) and Pencil Matar (8.5).
9. Maximum 100 seed weight was found in PSM-3(50 g) and highest protein content in Ganga-10(21.2%) followed by IC 208366(21.3) and Arka Priya (21.1%).
10. Highest moisture content was measured in Pencil Matar (81.1%) and highest Total soluble solid in VL-7(16.5°Brix).
11. Highest shelling percentage was recorded in IPFD-10-12(55.6 %) followed by EC 6621 (55.3 %) whereas, average pod weight was found maximum in Pencil Matar (5.8 g).
12. GS-10(79.6g) had highest pod yield per plant followed by Pea TS-10(77.2g), Kashi Samarth (76.4).
13. High value of PCV was noted for internodal length (22.08%), yield per plant (20.2%), number of seed per pod (20.7%). Whereas, GCV for yield per plant (20.2%), number of seed per pod (20.7%). Moderate GCV and PCV were observed for number of primary branches, days to first flowering, days to 50% flowering.
14. High heritability found for majority of traits viz., the number of primary branches, days to first pod setting, days to 50% flowering, number of nodes per plant, plant height, moisture content, total soluble solid, days to first pod setting, days to first pod picking, internodal length, shelling percentage, average pod weight, number of seed per pod, number of pods per plant and pod yield per plant.
15. Except moisture content, pod width and total soluble solids all other characters expressed high genetic advance percent mean.
16. Pod yield per plant exhibited highly significant positive association with 100 seed weight, number of primary branches, moisture content, average pod weight, number of seed per pod, number of pods per plant, days to first flowering, days to 50% flowering, days to first pod setting, days to first pod picking.
17. Pod yield per plant had maximum positive direct effect of number of pods per plant (0.784) followed by average pod weight (0.587), 100 seed weight (0.2474), number of primary branches (0.1024), pod length (0.082) and number of seeds per pod (0.033).
18. Based on (D^2) statistics of Mahalanobis (1936) and also by the use of non-hierarchical Euclidean cluster analysis, thirty genotypes were grouped into six highly divergent

cluster based on similarity in traits. Cluster first have 10 genotypes, 7 genotypes in cluster second, 10 genotypes in cluster third, one genotype in cluster fourth, one genotype in cluster fifth and one genotype in cluster first. Grouping of genotypes into different clusters showed considerable amount of diversity present in genotypes. Intra cluster distance was observed only in the cluster first, second and third as the remaining clusters contained only one constituent genotype. Intra cluster distance was highest in the cluster third (229.6) followed by cluster one (211.02) and inter cluster D^2 value was maximum (2502.5) between cluster six and third. The minimum (367.1) distance was observed between cluster fourth and third which indicated close relationship among the two genotypes.

Conclusion

1. AP-3(55 days), Kashi Nandani (62 days), Pusa Pragati (62 days), Pusa Sree (63 days), Kashi Uday (63 days) are variety of early maturity group. Whereas, Aman (77 days), EC 302842(77 days), EC 243642(76 days), EC 6621(76 days) are varieties of early maturity group.
2. Analysis of variance had significant for all characters under study. It Indicates that there is ample scope for selection of promising genotypes for yield improvement.
3. In the study highest PCV, GCV was shown for plant height (26.72%), (24.16%) and heritability broad sense in days to first flowering (98.6%). Whereas highest genetic advance as % of mean was observed for plant height (44.9%).
4. Number of pods per plant (0.784) and average pod weight (0.587) had highest positive direct effect on pod yield per plant.
5. Number of primary branches per plant (0.1024) and number 100 seed weight (0.247) had direct positive association to pod yield per plant.
6. Most promising varieties on the basis of yield per plant were GS-10(79.6 g), Pea TS-10(77.2 g), Kashi Samarth (76.4 g), Ganga- 10(73.6 g), AS-10 (70 g) and these varieties are recommended to grow at commercial level.

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APPENDIX I.

Weekly meteorological data for the Rabi season

Month	Max. Temp.	Min. Temp.	Max. R.H.	Min. R.H.	Wind velocity	Rainfall mm	Evaporation
Oct 2021	31.8	17.1	83.75	55.75	3.725	30.8	4.625
Nov 2021	28.6	10.5	83.75	50.5	3.05	0	3.875
Dec 2021	23.3	12.5	88.75	60.5	3.05	3	2.5
Jan 2022	19.6	7.9	91	71.25	2.85	11.35	1.725
Feb 2022	26.1	8.5	87	49.5	3.65	0	3.5
March 2022	32.9	14.3	81	41.25	4.625	0.1	5.575

Appendix II. Mean performance of pea genotype for different characters

S. No.	Genotypes	DF1	DF50	NPB	INL	NNP	PH	PL	PW	NSP	SW	PR	M	TSS	SHL	DS1	DP1	APW	NPP	PYPT	PYP
1.	**Kashi Uday**	33.67	36.67	1.33	4.61	11.73	49.73	8.73	1.24	6.80	42.3	20.0	74.0	15.3	44.3	40.3	63.3	5.43	8.80	2.63	43.8
2.	**Kashi Nandani**	33.67	38.67	1.53	3.73	11.27	42.93	8.24	1.25	6.43	38.0	15.4	76.5	15.0	40.3	39.0	62.6	5.40	9.33	2.61	43.4
3.	**Kashi Ageti**	36.33	44.33	1.47	3.97	14.93	65.60	8.51	1.21	7.40	33.0	19.6	77.4	15.7	37.3	42.3	65.6	4.80	9.87	2.70	45.0
4.	**Kashi Samarth**	36.67	44.00	2.73	4.91	12.80	65.40	6.81	1.09	6.40	35.3	14.1	75.9	14.9	49.0	43.0	66.3	4.43	17.2	4.59	76.4
5.	**Kashi Mukti**	36.00	40.00	2.27	4.21	12.20	51.73	8.59	1.19	6.57	39.3	15.2	73.1	15.1	42.0	41.6	66.6	4.70	11.8	3.09	51.5
6	**AP-3**	38.67	43.33	2.20	4.48	13.40	68.80	8.27	1.08	7.07	37.6	20.5	71.6	16.3	46.6	42.0	55.6	5.03	11.5	3.27	54.5
7.	**Arka Priya**	48.33	54.00	2.53	4.17	13.47	73.40	8.19	0.96	7.27	32.3	21.1	75.5	14.9	44.0	51.6	70.3	5.20	13.2	3.95	65.9
8.	**AP-1**	45.33	49.00	2.40	3.64	13.83	58.40	6.49	1.15	4.77	42.0	20.0	77.6	15.5	43.0	48.3	67.3	4.90	10.5	3.04	50.7
9.	**Pusa Sree**	32.67	36.67	1.40	4.23	10.87	51.20	7.35	1.11	5.90	41.3	17.5	73.3	15.1	57.0	39.6	63.3	3.70	11.8	2.75	45.8
10.	**Pusa Pragati**	49.67	54.33	1.93	5.57	15.00	95.37	9.60	1.17	7.60	44.6	19.5	76.8	14.8	49.6	52.3	62.3	5.03	11.8	2.92	48.7
11.	**Arkel**	35.00	44.00	1.60	4.83	10.20	48.60	7.67	1.18	6.10	41.6	19.0	72.8	15.4	44.0	41.3	64.6	4.93	9.20	2.83	47.1
12.	**PSM-3**	33.67	40.67	1.33	3.87	10.93	48.53	8.12	1.14	6.20	50.3	18.4	73.5	15.8	53.0	39.6	64.0	5.03	11.8	3.11	51.9
13.	**PSM-2**	50.33	54.33	2.40	3.39	13.13	50.67	8.66	1.21	7.73	28.6	15.6	77.7	15.3	34.3	56.0	72.3	4.67	12.7	2.96	49.2
14.	**NDVP -1**	36.00	44.67	1.80	4.39	12.73	57.13	8.07	1.16	6.70	34.3	15.5	72.9	15.9	42.3	42.3	64.3	4.40	12.0	2.82	47.0
15.	**VL-7**	48.00	54.33	2.07	4.27	11.87	56.60	6.90	1.15	5.87	28.6	18.2	74.4	16.5	34.6	55.6	73.3	4.80	14.6	3.78	63.0

16.	**PB-89**	46.33	51.33	1.73	3.80	12.87	53.53	9.47	1.10	7.20	38.6	15.7	74.9	14.9	46.0	52.6	69.3	5.03	12.9	3.07	51.1
17.	**AS-10**	48.33	52.00	2.27	3.69	12.00	51.33	8.62	1.01	9.07	41.3	14.9	81.8	15.4	42.6	55.3	74.6	6.03	12.8	4.22	70.3
18.	**PC-531**	41.33	46.33	2.47	4.43	12.13	61.70	8.66	0.96	7.13	31.0	13.4	75.7	16.1	40.3	48.6	65.6	5.37	14.4	3.82	63.7
19.	**IC 208366**	47.67	55.00	2.53	6.52	13.87	96.00	6.54	0.96	6.53	32.6	21.3	71.3	15.8	52.3	54.6	72.6	4.03	12.8	2.62	43.7
20.	**IC 395309**	48.33	54.33	1.33	4.01	13.13	61.80	8.00	1.12	5.67	31.0	16.7	70.9	14.5	41.3	55.0	72.0	3.50	13.5	3.49	58.1
21.	**EC 6621**	47.67	52.67	1.67	4.45	12.23	59.60	7.03	0.96	6.63	30.0	13.8	73.2	13.8	35.3	56.3	76.6	3.90	14.2	2.99	49.9
22.	**EC 243642**	50.67	55.67	2.20	4.03	13.20	68.93	6.87	1.10	4.93	33.0	20.1	72.7	14.9	55.0	58.6	76.6	4.10	13.6	2.81	46.8
23.	**EC 302842**	49.00	53.00	1.93	4.40	12.13	68.27	8.29	1.13	6.07	33.3	18.5	71.1	15.1	34.6	57.6	77.0	4.30	11.8	2.68	44.6
24.	**IPFD-10-12**	53.00	59.33	2.40	4.89	12.27	71.36	6.75	1.04	6.00	34.0	20.0	72.0	15.8	55.6	62.0	72.6	4.33	13.2	3.41	56.8
25.	**IPFD-11-5**	54.00	58.33	2.93	5.36	12.13	71.27	6.83	1.06	5.33	29.0	19.5	73.0	15.9	45.3	63.0	73.3	4.10	14.4	3.89	64.8
26.	**Aman**	59.00	72.67	1.93	6.94	15.00	119.27	6.39	1.02	4.00	29.3	19.1	71.9	14.9	55.0	68.3	77.6	4.60	14.0	3.65	60.7
27.	**Pencil Matar**	48.00	51.67	1.73	4.05	12.98	60.67	9.53	1.00	9.07	41.3	14.2	81.9	14.9	50.6	55.6	73.6	5.80	12.5	3.76	62.7
28.	**Pea TS -10**	47.33	52.00	2.00	4.21	12.80	61.33	8.99	1.00	8.53	31.0	12.8	79.7	15.1	47.6	56.0	70.6	5.10	16.1	4.63	77.2
29.	**Ganga -10**	47.00	52.33	2.00	3.39	14.33	59.07	8.19	1.09	8.33	35.6	21.2	74.3	15.0	43.0	54.6	73.6	5.53	13.4	3.38	56.3
30.	**GS -10**	46.00	49.33	2.07	4.35	13.92	68.70	10.30	0.99	10.20	34.0	14.2	76.6	15.5	40.0	54.0	74.0	5.57	13.2	4.78	79.6

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ABSTRACT

The present experiment entitled "**Study on genetic diversity in vegetable pea (*Pisum sativum* L. var. *hortense*)**" was carried out during *rabi* 2021-22 at Vegetable Research Farm, RLBCAU, Jhansi. In current investigation, a total of 30 genotypes of pea were sown in a randomized block design with three replications to estimate genetic variability, heritability and genetic advance and also correlation studies and path coefficient analysis among the genotypes. Observations were recorded on 21 characters. Analysis of variance and mean performance for pod yield and its components showed significant differences among all the genotypes for all characters except pod width, indicating the presence of wide range of variability in genotypes. PCV values were slightly greater than GCV, indicates very little influence of environment on their expression. High estimates of genotypic and phenotypic coefficient of variation were found for the characters *viz*., plant height, number of seeds per pod, number of primary branches. High heritability coupled with genetic advance as per cent of mean was observed for plant height, pod length, number of seed per pods, 100 seed weight, protein content, shelling percentage, days to first pod setting, average pod weight, number of pods per plant, pod yield per plant, days to first flowering, days to 50% flowering, number of primary branches per plant. In correlation studies, it was observed that pod yield per plant had a significant positive association with number of pods per plant, number of seed per pod, 100 seed weight and number of primary branches per plant. The positive direct effect on pod yield per plant was exhibited by number of seed per pod, number of pods per plant, 100 seed weight, average pod weight, pod length, seed moisture content, protein content, shelling percentage, number of primary branches, plant height, days to first pod picking, days to 50% flowering. While total soluble solids, internodal length, days to first pod setting, days to first flowering, number of nodes per plant showed a negative direct effect on yield. Based on yield performance, GS- 10, Pea TS-10, Kashi Samarth, AS-10, Arka Priya were found to be the superior yielding genotypes.

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सलाहकार- डॉ. ए. के. पांडे

सारांश

"सब्जी मटर आनुवंशिक विविधता पर अध्ययन शीर्षक पर सब्जी अनुसंधान फार्म आर एल बी सी एयू झांसी में प्रयोग रबी मौसम 2021-22 के दौरान किया गया था। वर्तमान जांच में आनुवंशिक विविधता आनुवंशिकता और आनुवंशिक उन्नति का अनुमान लगाने के लिए और आनुवांशिक रूप के बीच सहसंबंध अध्ययन और पथ गुणांक विश्लेषण के लिए तीन प्रतिकृति के साथ एक यादृच्छिक ब्लॉक डिजाइन (आर बी डी) में मटर के कुल 30 आनुवांशिक प्रारूप उगाये गए थे। कुल 21 लक्षणों पर दर्ज किए गए थे। फली की उपज और उसके घटकों के लिए विचरण और औसत प्रदर्शन के विश्लेषण ने फली की चौड़ाई को छोड़कर सभी वर्णों के लिए सभी आनुवांशिक प्रारूप के मध्य महत्वपूर्ण अंतर पाया गया जो आनुवांशिक रूप में विभिन्नता की विस्तृत श्रृंखला की उपस्थिति को दर्शाता है। अभिलक्षित विभिन्नता (पी सी वी) का मान आनुवंशिकता विभिन्नता (जी सी वी) गुणांक के मान से थोड़े अधिक थे जो ये संकेत करता है इन परिणाम पर पर्यावरण का प्रभाव बहुत सीमित था। विभिन्नता के जीनोटाइपिक और प्ररूपी गुणांक के उच्च अनुमान जैसे पौधे की ऊंचाई प्रति फली में बीजों की संख्या प्राथमिक शाखाओं की संख्या पाए गए थे। पौधे की ऊंचाई फली की लंबाई प्रति फली में बीज की संख्या 100 बीज वजन प्रोटीन सामग्री शेलिंग प्रतिशत पहली फली समायोजन तक के दिन औसत फली वजन प्रति पौधे फली की संख्या प्रति पौधे फली की उपज पहले फूल आने तक का समय 50% फूल आने तक के दिन प्रति पौधे प्राथमिक शाखाओं की संख्या के प्रति प्रभावी पाया। सहसंबंध अध्ययन में यह देखा गया कि प्रति पौधे फली की उपज का प्रति पौधे फली की संख्या प्रति फली में बीज की संख्या 100 बीज वजन और प्रति पौधे प्राथमिक शाखाओं की संख्या के साथ सकारात्मक संबंध था। प्रति पौधे फली की उपज पर प्रति फली बीज की संख्या प्रति पौधे फली की संख्या 100 बीज वजन औसत फली वजन फली की लंबाई नमी प्रतिशत, प्रोटीन की मात्रा शेलिंग प्रतिशत प्राथमिक शाखाओं की संख्या था। पौधे की ऊंचाई पहली फली तुड़ाई के दिन 50 प्रतिशत फूल आने तक के दिन का सकारात्मक प्रत्यक्ष प्रभाव प्रदर्शित किया गया था। जबकि कुल घुलनशील ठोस पदार्थ गांठ की लंबाई पहली फली बनने तक के दिन पहले फूल आने तक के दिन प्रति पौधे गांठ की संख्या ने उपज पर नकारात्मक सीधा प्रभाव दिखाया। उपज प्रदर्शन के आधार पर जीएस-10 मटर टीएस-10 काशी समर्थ एएस-10 अर्का प्रिया बेहतर उपज देने वाले आनुवांशिक रूप पाए गए थे|

ए.के. पाण्डेय

डॉ ए.के. पांडे
सलाहकार

पूजा तेतरवाल

पूजा तेतरवाल
विद्यार्थी

CURRICULUM VITAE

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Present Address - Manu Hostel, RLBCAU campus, Rani Lakshmi Bai Central Agricultural University, Gwalior Road Near, Pahuj Dam, IGFRI, Jhansi Uttar Pradesh 284003.

Permanent Address-Village- Ramjipura Khurd, Post- Kishangarh Renwal, Tehsil- Kishangarh Renwal, District- Jaipur, Rajasthan 303603.

Academic Qualification:

Degree	**Board/University**	**Institution/School**	**Year of Passing**	**Percentage**
M.Sc. (Hort.) Vegetable Science	Rani Lakshmi Bai Central Agricultural University	College of Horticulture & Forestry	2022	84.3
B.Sc. (Hons.) Horticulture	Agriculture University Kota	College of Horticulture & Forestry, Jhalawar	2020	77.8
Intermediate/10+2	BSER	Beniwal Bal Bharti SRSS, Jaipur, Raj.	2016	73.8
High School/10th	BSER	Adarsh Girls Vidhya Mandir SRSS, Jaipur, Raj.	2014	69

DECLARATION

I do hereby declare that the information given above is true to the best of my knowledge and belief.

Your truly,
पूजा तेतरवाल
Pooja Tetarwal