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Genetic variability and correlation analysis in F_2 segregating population of cross Him Palam Matar-1 × L-40-1014 of garden pea (*Pisum sativum* L.)

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Abstract

The present study was carried out in 184 F_2 progenies derived Him Palam Matar-1 × L-40-1014 following augmented block design in four blocks with five check varieties, replicated in each block. Analysis of variance revealed significant differences for all morpho-physiological traits. High PCV and GCV vis-à-vis high heritability and genetic advance were observed for primary branches/plant, peduncle length, stipule width and pods/plant indicating the predominance of additive gene action. Correlation studies showed positive association of pods/plant with stipule length, leaf length, leaf width, seeds/pod, nodes/plant, internodal length, plant height, pod length and pod width, signifies their importance in selection process. F_2 progenies namely, P-49, P-125, P-34, and P-84 were the most diverse along with P-1, P-23, P-29, P-40, P-67, P-115, P-98, P-63 and P-35 based on PCA and yield attributes, and needs focus to identify superior progenies in segregating generations which will help to strengthen garden pea germplasm.

Keywords: *Pisum sativum* L., variability, heritability, genetic advance, correlation, PCA

Garden pea (*Pisum sativum* L.) is an important leguminous crop worldwide belonging to the family Fabaceae and is cultivated for its fresh-shelled green seeds. The use of green-shelled seeds in canned, frozen, or dehydrated products signifies its coveted position in the processing industry (Sharma *et al.* 2022a). It is an essential winter vegetable in the north western Himalayas of India and is particularly abundant in proteins, vitamins, minerals and vital amino acids, mainly lysine that help to maintain health (Sharma *et al.* 2022b; Sharma *et al.* 2025a). In addition, fresh pea pods are exceptionally good sources of folic acid, vitamin C, vitamin K, and β-sitosterol (Rana *et al.* 2021). It is also a nitrogen-fixing legume crop that is suggested for crop rotation because of its abilities to improve soil quality, short growing seasons and higher yields (Sharma *et al.* 2014; 2024 & 2025).

Owing to diverse agro-climatic conditions in Himachal Pradesh, it is mostly grown as an off-season cash crop during summer at higher altitudes, providing the farmers with lucrative returns while it is grown in mid and low elevation areas during winter (Sharma *et al.* 2013). The consumers have a unique affinity for hill-grown peas because of their characteristic flavour, sweetness and freshness (Bhardwaj *et al.* 2020). To fulfil the increasing need of the changing production ecology, phenotypic and genotypic partitioning of current germplasm is required on a regular basis in order to identify genetically varied lines with desirable features (Srishti *et al.* 2023). The lack of genetic diversity often obstructs breeding efforts for subsequent improvement. The genetic variability present in a crop provides the basis for effective selection vis-à-vis an opportunity to improve the yield and quality through strategic breeding programme (Sekhon *et al.* 2019; 2019a).

Majority of the desirable traits are quantitative in nature, exhibiting continuous variation *i.e* heritable and non-heritable, implying the influence of environment. Selection is the traditional method for improvement of those traits that show additive and additive × additive type of gene action, but traits with non-additive gene action do not respond to selection, and hence, needs efforts to partition this into additive

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variance following hybridization of parents with desirable attributes, which can be achieved through genetic variability studies (Sharma *et al*. 2017). The response to selection mainly depends upon the relative proportion of the heritable component. Therefore, it would be imperative to partition variability into heritable and non-heritable components with the help of genetic parameters *viz*., coefficient of variation, heritability and genetic advance. The knowledge of correlation between yield and its contributing traits is the most endeavour and fundamental basis for indirect selection or to find out guidelines for plant selection. Correlation analysis could be an imperative tool to fetch information about the suitable cause-and-effect relationship between the yield and component traits (Sharma *et al*. 2014). The assessment of genetic divergence helps in reducing the number of breeding lines from the large germplasm. The progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants (Sharma *et al*. 2013). PCA provides important information about the most significant traits contributing to the variation and is used to identify significant relationship between traits. Keeping this in view, the present investigation has been planned to assess the genetic variability in F_2 progenies of an intervarietal cross to design breeding strategy for further utilization in segregating generations to identify the desirable pea lines.

Materials and Methods

The experimental material consisted of 184 F_2 progenies derived from a cross between Him Palam Matar-1 × L-40-1014 of garden pea which were evaluated for different morpho-physiological traits by following Augmented Block Design by formulating four blocks wherein five check varieties *viz*., Him Palam Matar-1, L-40-1014, AP-0.3-129, Pb-89 and Lincoln were replicated in each block during *rabi* 2023-24 under polyhouse conditions at Research Farm, Department of Vegetable Science and Floriculture, Chaudhary Sarwan Kumar Himachal Pradesh Krishi Vishvavidyalaya, Palampur. Each progeny was sown at 70 cm between rows and 10 cm within rows on raised beds. The recommended package of practices was followed for healthy growth of the crop and drip irrigation was applied at every alternate day. Data were recorded on each F_2 plant for yield attributing characters namely, primary branches/plant, first flower node, peduncle length (cm), stipule length (cm), stipule width (cm), leaf length (cm), leaf width (cm), nodes/plant, internodal length (cm), plant height (cm), pod length (cm), pod width (cm), seeds/pod, and pods/plant.

Statistical analysis

Augmented block design which estimates the error variance of unreplicated treatment that uses replicated check to estimate the genetic parameters was used in the analysis using RStudio (v.1.3.1056) software. The adjusted means of treatments were calculated before ANOVA. The total variation for each of the character was partitioned into variation due to blocks and unassignable causes (error), according to the model given by Federer and Wolfinger (2003). Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the method suggested by Burton and De Vane (1953). Heritability for the present study was calculated in broad sense while genetic advance for each trait was estimated by adopting the method suggested by Johnson *et al*. (1955). The correlation analysis was performed by RStudio (v.1.3.1056) software using methodology suggested by Pearson (1948). Principal component analysis was computed by using Past 4.03 software.

Results and Discussions

The analysis of variance based on 184 F_2 progenies and five checks revealed that mean sum of squares due to treatment ignoring block and treatment test were significant for all the traits (Table 1) indicating the wide range of genetic variability in the germplasm and a scope of effective selection for these traits. Further, it was found that mean sum of squares due to treatment check and treatment test vs check were significant for most of the traits except treatment check for internodal length (cm), pod width (cm) and treatment test vs check for seeds/pod, internodal length.

The mean performance of 184 F_2 progenies revealed variation ranging from 1.00-4.00 with a mean of 2.35 for primary branches/plant, and that of 9.00-15.00 and 11.90 for first flower node, 2.40-11.90 cm cm and 8.17 cm for peduncle length, 3.00-9.80 cm and 7.18 cm for stipule length, 3.02-7.80 cm and 6.07 cm for stipule width, 3.40-6.20 cm and 4.92 cm for leaf

Table 1. Analysis of variance for different traits in F_2 population of an intervarietal cross of garden pea

Source	df	Mean sum of squares						
		Primary branches/ plant	**First flower node**	**Peduncle length (cm)**	**Stipule length (cm)**	**Stipule width (cm)**	**Leaf length (cm)**	**Leaf width (cm)**
Treatment (ignoring Blocks)	188	0.34*	1.80*	61.90*	0.90*	14.94*	0.31*	0.15*
Treatment: Check	4	1.20*	5.56*	2.50*	2.16*	0.74*	1.16*	0.49*
Treatment: Test	183	0.31*	1.73*	62.77*	0.83*	15.30*	0.28*	0.13*
Treatment: Test vs. Check	1	3.26*	0.17*	139.64*	8.72*	5.66*	3.00*	2.29*
Block (eliminating Treatments)	3	0.00	0.01	0.06	0.04	0.09	0.04	0.06
Residuals	12	0.00	0.02	0.02	0.04	0.07	0.02	0.04
		Seeds/ pod	**Nodes/ plant**	**Internodal length (cm)**	**Plant height (cm)**	**Pod length (cm)**	**Pod width (cm)**	**Pods/ plant**
Treatment (ignoring Blocks)	188	1.03*	4.20*	0.68	247.66*	0.65*	0.01*	27.83*
Treatment: Check	4	5.00*	14.01*	1.25	314.65*	4.09*	0.00	15.60*
Treatment: Test	183	0.94*	3.99*	0.67	203.38*	0.56*	0.01*	27.87*
Treatment: Test vs. Check	1	0.08	4.68*	0.55	8083.25*	3.01*	0.04*	69.53*
Block (eliminating Treatments)	3	0.02	0.18	0.20	0.78	0.07	0.00	1.50
Residuals	12	0.03	0.39	0.41	4.54	0.15	0.00	0.53

*Significant at P=0.05

length, 2.00-4.20 cm and 2.89 for leaf width, 4.67-10.33 and 7.82 for seeds/pod, 10.00-22.00 and 16.14 for nodes/plant, 3.67-7.70 cm and 5.59 cm for internodal length, 52.22-129.50 cm and 83.99 cm for plant height, 6.90-11.00 cm and 9.17 cm for pod length, 1.00-1.43 cm and 1.15 cm for pod width and 5.00-41.00 and 17.26 for pods/plant (Table 2). This indicated that parents used in hybridization *i.e.* Him Palam Matar-1 and L-40-1014 were diverse with respect to different traits and resulted in creating good genetic diversity in F_2 population. Out of 184 F_2 progenies, 70 progenies showed significantly more amount of pods/plant over best check variety Him Palam Matar-1.

Table 2. Descriptive statistics and components of genetic variability for various traits in garden pea

Trait	Mean	Range	Phenotypic variance	Genotypic variance	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%) broad sense	Genetic advance (% of mean)
Primary branches/plant	2.35±0.04	1.00-4.00	0.31	0.30	23.46	23.63	98.53	48.04
First flower node	11.90±0.09	9.00-15.00	1.73	1.71	10.97	11.04	98.78	22.50
Peduncle length (cm)	8.17±0.57	2.40-11.90	62.77	62.75	96.97	96.98	99.97	200.01
Stipule length (cm)	7.18±0.07	3.00-9.80	0.83	0.80	12.43	12.72	95.42	25.04
Stipule width (cm)	6.07±0.28	3.02-7.80	15.30	15.23	64.27	64.42	99.55	132.30
Leaf length (cm)	4.92±0.04	3.40-6.20	0.28	0.26	10.26	10.71	91.82	20.28
Leaf width (cm)	2.89±0.03	2.00-4.20	0.13	0.09	10.54	12.47	71.43	18.38
Nodes/plant	16.14±0.14	10.00-22.00	3.99	3.60	11.75	12.37	90.24	23.03
Internodal length (cm)	5.59±0.06	3.67-7.70	0.67	0.26	9.05	14.62	38.32	11.56
Plant height (cm)	83.99±1.06	52.22-129.50	203.38	198.84	16.79	16.98	97.77	34.25
Pod length (cm)	9.17±0.06	6.90-11.00	0.56	0.41	7.01	8.15	74.02	12.44
Pod width (cm)	1.15±0.01	1.00-1.43	0.01	0.00	5.90	7.01	70.75	10.24
Seeds/pod	7.82±0.07	4.67-10.33	0.94	0.92	12.25	12.43	97.04	24.89
Pods/plant	17.26±0.38	5.00-41.00	27.87	27.34	30.29	30.58	98.10	61.88

Where, ± is SE(m)

Parameters of genetic variability

The observation on magnitude of genetic variability present in a crop provides the basis for effective selection and an opportunity to improve the yield and its attributes through planned breeding programme. The knowledge of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) is helpful to assess the amount of variation present in the germplasm of a particular crop, which in turn helps in framing an effective breeding programme (Sharma *et al*. 2016). The estimates of PCV were higher than corresponding GCV for all the characters studied (Tables 2) which revealed that the apparent variation is not the cause of genotypes only but environment has influence on the expression of the traits. However, the differences between the genotypic and phenotypic variances were comparatively low for all the traits which points towards the highly heritable and relatively stable nature of the attributes that supports the effective selection based on phenotypic performance of these traits (Sharma *et al*. 2007).

The magnitude of PCV and GCV was high for primary branches/plant, peduncle length, stipule width and number of pods/plant (Table 2) which indicated that there is substantial variability ensuring ample scope for improvement of these traits through selection. The moderate estimates of PCV and GCV were observed for first flower node, stipule length, leaf length, leaf width, seeds/pod, nodes/plant and plant height except low GCV for internodal length. The moderate estimates suggested careful approach to be followed for direct selection for these traits. Bhardwaj *et al*. (2020) have also reported the moderate estimates for plant height in garden pea.

Heritability and genetic advance

The magnitude of heritability in broad sense (%) guides the reliability with which a genotype can be predicted by its phenotypic expression. Heritability is a measure of heritable variation and is supportive in envisaging expected amount of improvement to be realized through selection along with the GCV. The evidence on heritability estimates is helpful in studying the inheritance of quantitative traits as well as for planning breeding programmes with desirable degree of expected general progress. In the present study, high heritability estimates were observed for all the characters (Table 2) which indicated the lesser influence of environment and greater role of genetic component of variation.

The knowledge of estimates of heritability alone is not sufficient for an effective selection programme and it is therefore beneficial to study genetic advance along with heritability. Genetic advance may or may not be in proportion to genetic variability and heritability estimates because both high estimates of heritability and genetic variability are important to obtain higher genetic gain (Sharma *et al*. 2007). Accordingly, high heritability coupled with high genetic advance was observed for primary branches/plant, peduncle length, stipule width, plant height and pods/plant. The inheritance of these characters indicated the importance of additive gene action and possibility of selection in the early generation. Earlier workers have also reported high heritability and genetic advance for primary branches/plant, plant height and pods/plant (Singh and Sharma 2019; Bhardwaj *et al*. 2020). High heritability along with moderate genetic advance was observed for first flower node, stipule length, leaf length, leaf width, seeds/pod, nodes/plant, pod length and pod width, which indicated the preponderance of additive and non-additive gene effects for their inheritance suggesting that their improvement can be achieved by following hybridization and selection in the later generations (Sharma *et al*. 2020).

Correlation coefficient analysis

The effectiveness of any breeding or selection programme depends upon the nature of association between yield and other component characters, as more directly a character is associated with yield in the desirable direction, more will be the success of the selection programme (Sharma *et al*. 2016). Therefore, after getting the knowledge on the nature and magnitude of genetic variation, it is also important to gather information on association of yield with other characters and among themselves, and their basis to identify characters for increasing the efficiency of both direct and indirect selection and thereby, defining an ideal plant type (Negi and Sharma 2019). The effective yield improvement would be achieved through the characters, which have significant and positive/desirable correlation with each other.

Pods/plant showed a positive and significant association with stipule length, leaf length, leaf width, seeds/pod, nodes/plant, internodal length, plant height, pod length and pod width (Table 3). This reflected that selection based on these traits might lead to higher yield. Earlier reports of many research workers have also indicated significant and positive association of pods/plant with seeds/pod and pod length (Sharma *et al*. 2025) with different breeding materials at different locations and thereby, pointing towards emphasis on these traits to obtain improvement in garden pea. Further, critical scrutiny of correlation between different traits revealed that peduncle length, stipule length, stipule width, leaf length, leaf width, seeds/pod, internodal length, plant height and pod length are invariably associated with one another indicating that they supplement one another and resulted in better manifestation of pea attributes. Therefore, due consideration should be given to these traits during selection for effective isolation of plants with high pod yield.

Principal component analysis (PCA)

A genetically diverse origin plays a significant role in crop improvement programme based on economic characters because it generates baseline data to guide selection of parental lines and strategy of a breeding programme. The progenies derived from diverse parents are expected to show a broad spectrum of genetic variability and provide better scope to isolate superior recombinants. PCA provides important information about the most significant traits contributing to the variation and is used to identify significant relationship between traits. This multivariate analysis technique explains the association between many variables using a smaller number of underlying independent factors. Principal components with eigen values ≥1.0 were considered significant. As a result, the first four significant principal components explained 56.41 of the variation (Table 4).

The first principal component (PC1) was the most significant and explained 29.97% of the total variance and the variation was mainly due to plant height followed by stipule length, leaf length, internodal length, pod length, leaf width and pods/plant. Similarly, PC2 accounted for 9.93% variation which was attributed mainly due to first flower node followed by nodes/plant, pods/plant and plant height. PC3 contributed 8.92%, which was mainly due to primary branches/plant followed by seeds/pod, peduncle length and first flower node. PC4 contributed 7.59%, which was mainly due to first flower node followed by pod width, leaf width, stipule width and leaf length. In all the principal components, first flower node resulted in the highest positive value followed by primary branches/plant, pod width and nodes/plant indicating maximum contribution towards genetic divergence and focus should be given to these traits for effective selection to increase pea yield. PC1 had the high positive loading for all characters.

The loading plots for PC1 and PC2 also demonstrated the significance of various attributes and genotypes in explaining genotype variance when

Table 3. Pearson correlation among yield attributes during 2023-24

Trait	First flower node	Peduncle length (cm)	Stipule length (cm)	Stipule width (cm)	Leaf length (cm)	Leaf width (cm)	Nodes/ plant	Internodal length (cm)	Plant height (cm)	Pod length (cm)	Pod width (cm)	Seeds/ pod	Pods/ plant
Primary branches/plant	0.15*	0.09	0.00	0.09	0.07	-0.01	0.08	0.07	0.05	0.01	-0.12	0.05	0.11
First flower node		0.06	0.01	0.06	0.09	0.08	0.26*	0.06	0.17*	-0.01	0.03	0.07	0.09
Peduncle length (cm)			0.20*	0.06	0.17*	0.14	0.11	0.17*	0.28*	0.18*	-0.02	0.21*	0.12
Stipule length (cm)				0.27*	0.53*	0.42*	0.26*	0.41*	0.60*	0.45*	0.18*	0.29*	0.40*
Stipule width (cm)					0.27*	0.18*	0.06	0.20*	0.20*	0.18*	0.07	0.26*	0.13
Leaf length (cm)						0.70*	0.24*	0.47*	0.40*	0.39*	0.15*	0.33*	0.25*
Leaf width (cm)							0.20*	0.31*	0.24*	0.36*	0.14	0.31*	0.17*
Nodes/plant								0.35*	0.45*	0.26*	0.05	0.20*	0.38*
Internodal length (cm)									0.54*	0.34*	0.01	0.24*	0.29*
Plant height (cm)										0.38*	0.17*	0.21*	0.64*
Pod length (cm)											0.02	0.40*	0.32*
Pod width (cm)												-0.01	0.20*
Seeds/pod													0.16*

*Significant at 5% level

Table 4. Eigenvectors of different traits in 184 F_2 progenies of garden pea including check varieties and correlation between factors and variables

	PC1	PC2	PC3	PC4
Eigenvalue	4.20	1.39	1.25	1.06
Variability (%)	29.97	9.93	8.92	7.59
Cumulative %	29.97	39.90	48.82	56.41
Primary branches/plant	0.05	0.29	0.51	0.16
First flower node	0.09	0.40	0.25	0.58
Peduncle length (cm)	0.17	0.06	0.26	-0.35
Stipule length (cm)	0.37	-0.11	-0.16	-0.09
Stipule width (cm)	0.19	-0.18	0.16	0.24
Leaf length (cm)	0.36	-0.30	0.05	0.24
Leaf width (cm)	0.30	-0.38	0.05	0.30
Nodes/plant	0.26	0.40	0.00	0.04
Internodal length (cm)	0.33	0.06	0.04	-0.13
Plant height (cm)	0.38	0.31	-0.19	-0.16
Pod length (cm)	0.31	-0.16	0.06	-0.26
Pod width (cm)	0.10	-0.03	-0.58	0.41
Seeds/pod	0.25	-0.23	0.32	-0.07
Pods/plant	0.29	0.36	-0.27	-0.13

Note: The values which are bold represent the maximum contribution to the respective PC

plotted against two PCs and grouped according to their quantitative measures [Fig. 1]. Scattered diagram construed that significant number of the progenies were unique as they fall in different corners of four quadrants of the biplot which inferred that all the variables, involved in variance, were taken into

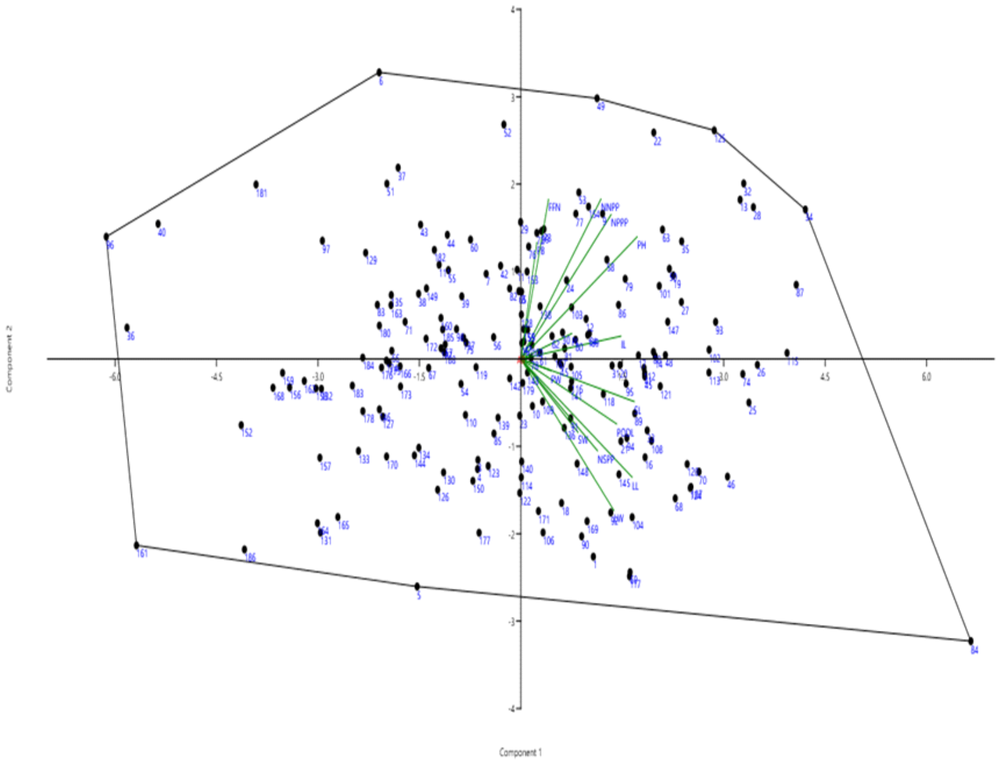

Figure 1. Biplot of different variables and lines on principal components

consideration but suggested that addition of variables may have resulted into clear and informative biplot. Further, it was observed that the progenies namely, P-49, P-125, P-34, and P-84 were the most diverse as were placed on the vertices of the polygon while the other progenies placed within their respective performance. The other promising and diverse progenies were P-22, P-32, P-13, P-28, P-87, P-115, P-98, P-63, and P-35, and may be suitable for garden pea improvement programme. The distribution of accessions based on the first and second principal components showed phenotypic variations among the populations and explained their wide dispersion along both the axes.

Conclusion

Based on mean performance, lines P-1, P-27, P-8, P-23, P-29, P-120, P-17, P-21, P-40 and P-67 were top ranked ten progenies for pods/plant and showed better performance for other attributes and therefore, may have potential to identify superior progenies from them in the following generations. The PCV and GCV vis-a-vis high heritability and high genetic advance were recorded for primary branches/plant, peduncle length, stipule width, plant height and pods/plant indicating ample scope of improvement through selection. Pods/plant showed a positive and significant association with stipule length, leaf length, leaf width, seeds/pod, nodes/plant, internodal length, plant height, pod length and pod width implying the significance of these traits in garden pea improvement. The first four significant components of PCA explained about 56.41% of the total variation with major contribution of first flower node followed by primary branches/plant, pod width and nodes/plant towards genetic divergence. The progenies namely, P-49, P-125, P-34, and P-84 were the most diverse along with P-1, P-23, P-29, P-40, P-67, P-115, P-98, P-63 and P-35 indicating due consideration for identify superior lines in the advanced generations.

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