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Genetic variability, heritability, correlation, path analysis and genetic divergence studies for yield and yield contributing traits in pea (*Pisum sativum* L.)

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Abstract

The present study was conducted to assess genetic variability, heritability, correlation, path coefficient and genetic divergence among nineteen pea (*Pisum sativum* L.) genotypes for yield and yield contributing traits, with objective of identifying superior genotypes for prospective breeding programs. The experiment was conducted during *Rabi* season of 2025-2026 at Prof. Rajendra Singh (Rajju Bhaiya) University, Prayagraj, Uttar Pradesh, India. These were used to evaluate in Randomized Block Design (RBD) with three replications. Statistical analyses such as ANOVA, GCV, PCV, heritability, genetic advance, correlation, path coefficient and Mahalanobis D² analysis were achieved. Analysis of variance showed significant differences among genotypes for all traits studied. High GCV, PCV and heritability were reported for plant height at 90 DAS. Seed yield plant⁻¹ showed positive association with pod length, number of seeds pod⁻¹, seed yield plot⁻¹ and seed index. Path analysis indicated that harvest index and seed yield plot⁻¹ showed positive direct effects on seed yield plant⁻¹. Genetic divergence analysis grouped the genotypes into three clusters. The study confirmed the presence of substantial genetic variability among pea genotypes. Genotypes AP-3, AP-2 and Kashi Uday were identified as suitable in improving seed yield and related traits for pea breeding programs.

Keywords: *Pisum sativum*, yield, genetic variability, path coefficient analysis, correlation, genetic divergence

Introduction

The Pea (*Pisum sativum* L.) is one of the most important cool-season vegetable crops in the Fabaceae family. Its dry seeds, which are high in protein, vitamins, and minerals, and green pods are the main reasons it is produced (Anonymous, 2021). Pea growing is important for India's agricultural economy and nutritional security. Is an essential and nutritious winter food that is cultivated all throughout the country. India produces 5524 thousand metric tonnes of peas annual on an area of approximately 563 thousand hectares (Anonymous 2019). The first cultivation of peas appears to have been in western Asia, from where it spread to Europe, China and India. India is the second largest producer of pea in the world after Russia (Vasanthrao *et al.*, 2025). Currently pea is being produced in more than 95 Countries across the world, with an annual production of around 15.7 million tons (FAO, 2023). The evaluation of genetic variability is important to know the source of genes for a particular trait within the available germplasm. There was no common criterion for selection of genotypes based on specific objectives among the plant materials (Kumar *et al.*, 2022). Pea provided protein and fiber for human and livestock diets (Hood-Nieferet *et al.*, 2012), Variability indices such GCV and PCV, heritability (h²), and genetic advance (GA) are necessary when creating an ideal breeding program targeted at utilizing the inherent variability found in the original population (Raj *et al.*, 2020). According to the assumption that yield components are mutually related, path coefficient analysis determines the direct and indirect contributions of different independent characters on a dependent component (Jeberson *et al.*, 2016; Sharma *et al.*, 2023). Any crop needs to have genetic variability, heritability, and genetic advancement in order to identify superior genotypes and enhance any attributes (Prabhu M *et al.*, 2009). The activities and interactions of different component characteristics culminate in [4, 3, 32, 10, 15, 11, 21, 12, 25, 10]

the complex character that is called yield (Uhlarik *et al.*, 2022). Along with to functioning as a method for identifying a genotype with a high yield potential, path analysis permits breeders to analyze the nature of forces interacting to form the given relationship. Therefore, the results of correlation and path analysis for yield and yield contributing traits in pea are the primary objective of this analysis. (Kumar *et al.*, 2014). Genetic divergence can be used to identify desirable parents for the aim of improving a specific trait through hybridization when selection is ineffective. Mahalanobis developed D2 statistics, that is a useful tool to estimate how much genetic diversity is present in a population (Sharma M. 2023). The experiment was also conducted to evaluate the yield performance of different pea genotypes in order to identify superior genotypes for higher productivity. In addition, genotypic and phenotypic correlation coefficients were estimated to determine the association among yield and yield contributing traits, which would help in understanding the nature and magnitude of relationships among different characters influencing seed yield in pea [21, 17, 23].

Materials and Methods

Experimental Location and Plant Material

The current research investigation was carried out at the Agricultural Research Farm of Prof. Rajendra Singh (Rajju Bhaiya) University in Naini, Prayagraj, Uttar Pradesh, India, during the Rabi season of 2025-2026. The present study, a total of 19 pea genotypes used as experimental material. Kashi Mukti (V1), Kashi Ageti (V2), AP-3 (V3), AP-1 (V4), AP-2 (V5), K-6 (V6), AP-4 (V7), Kashi Uday (V8), GS-10 (V9), M-7 (V10), AP-5 (V11), Kali Naina (V12), Anzel (V13), Pant Matar-155 (V14), IPFD 9-2 (V15), Swami Aparna (V16), Phool Bahar (V17), Rachna (V18), and Kashi Nandini (V19) were among the genotypes.

Experimental Design

The experiment was laid out in a Randomized Block Design (RBD) with three replications. A total of 19 field pea genotypes (18 genotypes along with one check variety) were evaluated. Each plot measured 2 × 1.5 m², maintaining a spacing of 30 cm between rows and 10 cm between plants.

Data collection

Data were collected for a range of yield and related traits which included plant height at 30, 60 and 90 days after sowing (DAS), DAS to first flowering, DAS to 50% flowering, DAS to first pod setting, number of branches per plant, pod length (cm), number of pods per plant, number of seeds per pod, DAS to maturity, seed yield per plot (kg), biological yield (kg), seed index, seed yield (q/ha), harvest index (%), and seed yield per plant (g).

2.4. Statistical analysis

The data thus collected were statistically analysed using method proposed by (Steel *et al.*, 1980). To find actual differences in traits between plant types (genotypes), we used ANOVA testing.

Mean Performance

Arithmetic mean was calculated using the formula:

$$\bar{X} = \frac{\sum n}{n} \quad (\text{Source: Steel et al., 1980})$$

Analysis of Variance (ANOVA)- The ANOVA was performed according to Randomized Block Design (RBD).

$$F\text{-test: } F = \frac{MSE}{MST}$$

Where

- MST = Mean sum of squares due to treatments
- MSE = Mean sum of squares due to error
- (Source: Steel *et al.*, 1980)

$$\text{Genotypic coefficient of variation (GCV): } GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV): } PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

(Source: Falconer & Mackay, 1996)

$$\text{Heritability (Broad Sense): } h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

(Source: Falconer & Mackay, 1996)

$$\text{Genetic Advance: } GA = k \times \sigma_p \times h^2$$

(Source: Johnson *et al.*, 1955)

Correlation Coefficient

$$\text{Genotypic correlation: } r_g = \frac{\text{Cov}_g(xy)}{\sqrt{\sigma_g^2(x)\sigma_g^2(y)}}$$

$$\text{Phenotypic correlation: } r_p = \frac{\text{Cov}_p(xy)}{\sqrt{\sigma_p^2(x)\sigma_p^2(y)}}$$

(Source: Johnson *et al.*, 1955)

$$\text{Path Coefficient Analysis: } r_{ij} = P_{ij} + \sum r_i P_{kj}$$

(Source: Dewey & Lu, 1959)

Cluster Analysis

Cluster analysis was performed using Mahalanobis D2 statistics to assess genetic divergence among genotypes and to classify them into different clusters.

$$D^2 = (X_i - X_j)' V^{-1} (X_i - X_j)$$

(Source: Mahalanobis, 1936)

Results and Discussion

3.1. Mean Performance of Genotypes

Genotype V17 recorded the highest plant height at 30 DAS (27.3 cm), whereas V14 showed maximum plant height at 60 DAS (99.1 cm) and V18 at 90 DAS (174.7 cm). The earliest flowering was observed in V17 for days to first flowering (41.0 days), while V19 showed the earliest 50% flowering (48.7 days). Genotypes V10 and V13 recorded the earliest first pod setting (53.7 days), whereas V16 was identified as the latest flowering and maturing genotype with maximum days to maturity (99.3 days). Among the yield attributing traits, genotype V14 produced the highest number of branches per plant (3.6) and maximum number of pods per plant (15.5). The longest pod

length (10.7 cm) and highest number of seeds per pod (8.9) were recorded in genotype V9. For yield traits, genotypes V3 and V11 recorded the highest seed yield per plot (0.8 kg), while genotype V5 showed maximum biological yield (1.7 kg). Genotype V3 recorded the highest seed index (26.7 g), seed yield per hectare (27.8 q/ha), harvest index (55.0%) and seed yield per plant (18.0

g). Overall, genotype V3 exhibited superior mean performance for most of the yield and yield contributing traits, indicating its potential usefulness in future pea breeding programmes. Similar results were obtained by Abdulla *et al.*, (2014); Bueckert *et al.*, (2015). Table 1. showed the mean values of different traits of nineteen genotypes of pea ^[1].

Table 1: Mean Performance of Genotypes

Genotypes	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	DAS to First Flowering	DAS to 50% Flowering	DAS to First pod setting	Number of branches per plant	Pod length (cm)	Number of pods per plant	Number of Seed Per Pod	DAS to maturity	Seed yield per plot (kg)	Biological yield (kg)	Seed index	Seed yield q/h	Harvest index (%)	Seed yield Per plant (g)
V1	20	45.7	58.6	46.3	50.7	54.3	2.8	9.7	12.9	8.8	79.7	0.7	1.3	22	23.3	51.3	15.2
V2	20.9	57.7	69.6	48	52.7	55.7	2.8	10	9.7	7.5	76.7	0.7	1.4	22.7	22.6	52.2	15.1
V3	22.4	55	78.7	46.7	52	56.7	3	8.8	11.9	7.9	77.7	0.8	1.6	26.7	27.8	55	18
V4	21.3	59.1	75.1	46.7	50	54.7	2.8	9.2	12.7	7.5	82.3	0.6	1.3	26	20.8	51.6	16.6
V5	24.9	94	157.7	55.3	59.3	63.3	3	7.1	14.8	6.4	96.3	0.7	1.7	23	22.3	40.1	14
V6	21.5	63.2	73.5	46.3	50.7	54	2.6	9.4	12.4	7.7	74.7	0.6	1.3	23.3	21.9	46.4	14.4
V7	21.6	58.3	84.2	49.7	55.7	60.3	2.7	9.7	11.1	8.5	82.3	0.6	1.2	23.7	19.6	46.9	15.7
V8	18.4	53.7	59.9	45.7	50	54.3	3.5	9.7	12.5	8.7	75.3	0.6	1.2	23	19.9	50.2	14.9
V9	21.6	60.4	77.9	53	57.3	60	3.2	10.7	10.2	8.9	85.7	0.6	1.4	19.7	21	44.6	13.3
V10	22.6	56.9	71.7	46	50	53.7	3	9.2	9	7.7	77.3	0.6	1.3	23	20.4	47.4	12.9
V11	19.4	56.3	71.7	47.7	51.3	59.7	2.4	9.5	9.7	8.3	80.7	0.8	1.6	22.3	24.1	50.5	14.1
V12	22.9	92.1	149.9	59	62	68	2.9	8	12.1	6.8	97.7	0.6	1.5	22.7	18.9	36.6	14.7
V13	21.6	46.3	69.7	44.7	49.7	53.7	2.8	10	10	7.8	78.7	0.6	1.4	22	22.1	46.7	13.3
V14	25.7	99.1	166.4	47	54	62	3.6	6.2	15.5	6.1	97.3	0.5	1.5	23	17.7	33.2	12
V15	24.8	88.9	156.9	56.7	62.7	67	2.1	8.2	14.1	6.8	96.3	0.5	1.2	22.7	17.6	36.4	13.3
V16	16.6	53.9	90.5	65.7	68.3	73	2.5	7.1	9.8	5.6	99.3	0.6	1.4	21.7	19.2	42.1	13.5
V17	27.3	68.1	134.5	41	52	55	2.6	6.6	10.9	5.3	74.7	0.5	1.3	22.3	15.8	34.4	11.7
V18	22.3	92.2	174.7	57	63.7	69	2.9	6.2	12.7	5.8	92.7	0.5	1.4	19.3	15.7	33.6	13.2
V19	20.6	45.5	55.7	41.7	48.7	54.3	3	9.2	11.6	8	80.7	0.7	1.3	24	22.4	47.3	15.7
Mean	21.9	65.6	98.8	49.7	54.8	59.4	2.8	8.7	11.8	7.4	84.5	0.6	1.4	22.8	20.7	44.6	14.3
SEd (±)	0.8381	2.902	1.9225	0.6291	1.0999	1.5868	0.0527	0.5272	0.8753	0.2051	0.492	0.0169	0.1057	0.5544	0.8836	3.1071	0.785
CD (5%)	1.6997	5.8856	3.8991	1.2758	2.2308	3.2181	0.107	1.0692	1.7751	0.4159	1.003	0.0342	0.2143	1.1243	1.792	6.3016	1.592
CV	4.6815	5.4169	2.3425	1.5463	2.4564	3.2677	2.2572	7.47	8.4629	3.4102	0.713	3.3458	9.2486	2.9657	5.2319	8.5392	6.728
Max	27.3	99.1	174.7	65.7	68.3	73	3.6	10.7	15.5	8.9	99.3	0.8	1.7	26.7	27.8	55	18
Min	16.6	45.5	55.7	41	48.7	53.7	2.1	6.2	9	5.3	74.7	0.5	1.2	19.3	15.7	33.2	11.7

V1	V2	V3	V4	V5	V6	V7	V8	V9	V10	V11	V12	V13	V14	V15	V16	V17	V18	V19
Kashi Mukti	Kashi Ageti	AP - 3	AP - 1	AP - 2	K - 6	AP - 4	Kashi uday	GS - 10	M - 7	AP - 5	Kali Naina	Anzel	Pant Matar -155	IPFD 9 -2	Swami Aparna	Phool Bahar	Rachna	Kashi Nandini

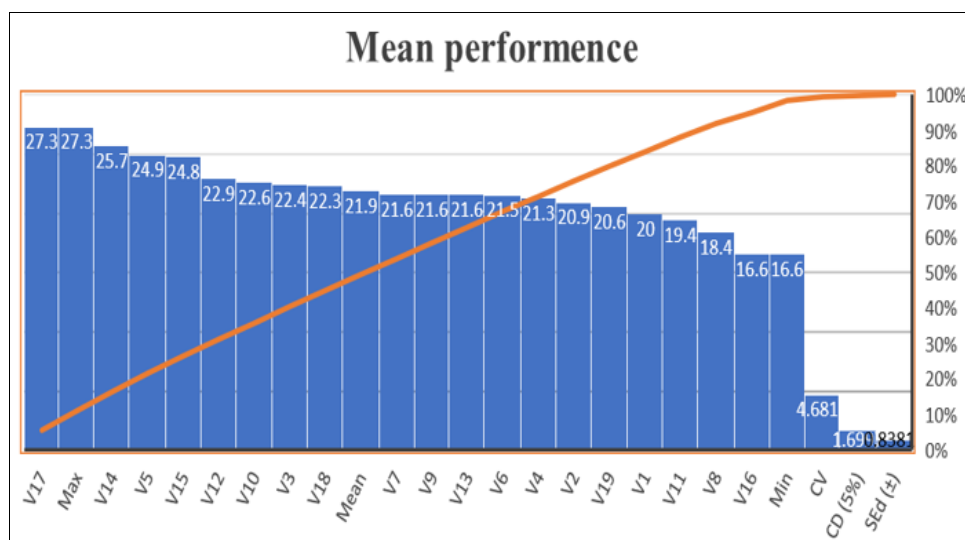


Fig 1: Mean performance

Analysis of variance

The significant genetic variability in the experimental material was indicated by the analysis of variance, that showed substantial differences among the genotypes for each characteristic examined. In line with earlier findings, this suggests that additive genetic effects predominate and that simple selection can be useful for improvements (Maurya *et al.*, 2018) ^[22]. The magnitude of variance due to genotypes was

particularly high for plant height at 90 DAS (5592.888), plant height at 60 DAS (967.823), days to maturity (239.864) and harvest index (144.452), reflecting substantial differences among the genotypes for these traits. The analysis of variance for a Randomized Block Design was carried out for the data recorded on each character as per standard procedure given by Panse and Sukhatme (1967) ^[19] for individual characters for each environment. The ANOVA skeleton is given below:

Table 2: Analysis of variance

Traits	Mean sum of squares		
	Replications	Genotypes	Error
	(d.f=2)	(d.f=18)	(d.f=36)
Plant height 30 DAS	0.777	19.391 **	1.053
Plant height 60 DAS	88.636	967.823 **	12.633
Plant height 90 DAS	10.203	5592.888 **	5.544
DAS to First Flowering	0.649	121.532 **	0.594
DAS to 50% Flowering	1	98.68 **	1.815
DAS to First pod setting	6.684	109.271 **	3.777
Number of branches per plant	0.005	0.332 **	0.004
Pod length (cm)	0.055	5.787 **	0.417
Number of pods per plant	0.649	14.556 **	1.149
Number of Seed Per Pod	0.051	3.758 **	0.063
DAS to maturity	0.214	239.191 **	0.726
Seed yield per plot (kg)	0.001	0.028 **	0
Biological yield (kg)	0.027	0.054 **	0.017
Seed index	0.368	8.78 **	0.461
Seed yield q/h	1.085	26.218 **	1.171
Harvest index (%)	14.059	144.452 **	14.481
Seed yield Per plant (g)	0.316	7.456 **	0.924

* indicates significance at 5% level, ** indicates significance at 1% level

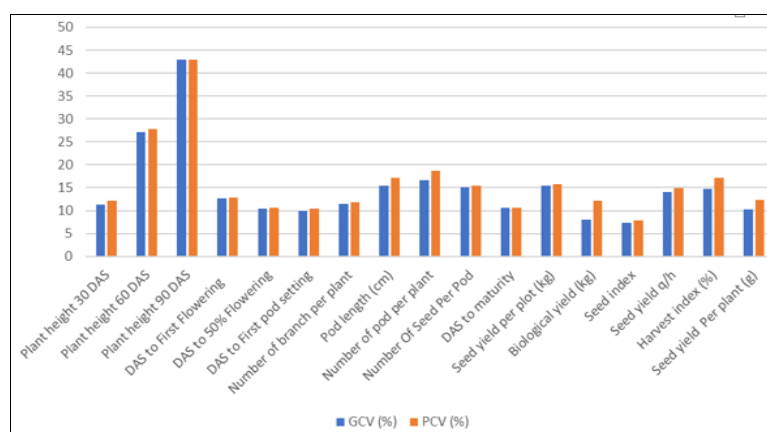
Heritability, coefficient of variation and genetic advance

The genetic parameters presented in Table 03 indicated that the higher genotypic variance was found for the Plant height 90 DAS (1866.14) and lowest for Seed yield per plot (kg) (0.01). The highest values of phenotypic variance were obtained for trait Plant height 90 DAS (1871.69) and lowest for Seed yield per plot (kg) (0.01). The highest genotypic coefficients of variability were obtained for Plant height 90 DAS. (42.93%) followed by Plant height 60 DAS (27.20%) while the lowest for Seed index (7.27%) followed by Biological yield (kg) (8.02%). The highest value of the PCV was found for Plant height 90

DAS (43.00%) followed by Plant height 60 DAS (27.73%) while lowest value was obtained for the Seed index (7.86%). followed by DAS to maturity (10.60%). Similar results were also obtained by Kosev *et al.*, (2016); Zanutto *et al.*, (2025). The highest heritability values were found for Plant height 90 DAS (99.70%) followed by number of seeds per pod (99.55%), DAS to first flowering (98.55%) and number of branches per plant (96.32%) while the Biological yield (kg) showed the lowest heritability value (42.89%). Similar results were also obtained by Tiwari *et al.*, (2025); Singh *et al.*, (2024); Vennela *et al.*, (2024) [13, 36, 30, 26, 33].

Table 3: Genotypic variance (Vg), phenotypic variance (Vp), heritability (h²) and genetic advance for different traits in Pea (*Pisum sativum* L.)

Traits	Vg	Vp	GCV (%)	PCV (%)	HERTI (%)	GA	GA AS%
Plant height 30 DAS	6.81	7.87	11.28	12.21	85.30	4.70	21.46
Plant height 60 DAS	326.82	339.45	27.20	27.73	96.18	36.05	54.94
Plant height 90 DAS	1866.14	1871.69	42.93	43.00	99.70	88.77	88.31
DAS to First Flowering	40.71	41.30	12.74	12.84	98.55	12.98	26.06
DAS to 50% Flowering	33.50	35.31	10.36	10.65	94.68	11.39	20.77
DAS to First pod setting	37.68	41.46	9.97	10.49	90.30	11.61	19.52
Number of branch per plant	0.11	0.12	11.55	11.77	96.32	0.67	23.36
Pod length (cm)	2.07	2.49	15.48	17.19	81.11	2.48	28.72
Number of pod per plant	.24	6.38	16.69	18.71	79.55	3.88	30.66
Number of Seed Per Pod	1.27	1.34	15.07	15.45	95.13	2.23	30.27
DAS to maturity	80.08	80.44	10.57	10.60	99.55	18.36	21.73
Seed yield per plot (kg)	0.01	0.01	15.44	15.80	95.51	0.19	31.08
Biological yield (kg)	0.02	0.04	8.02	12.24	42.89	0.15	10.81
Seed index	3.08	3.54	7.27	7.86	85.74	3.18	13.87
Seed yield q/h	9.13	10.30	13.97	14.92	87.70	5.57	26.95
Harvest index (%)	52.98	67.46	14.77	17.06	74.95	11.74	26.34
Seed yield Per plant (g)	2.79	3.72	10.33	12.33	70.20	2.55	17.82

**Fig 2:** GCV&PCV

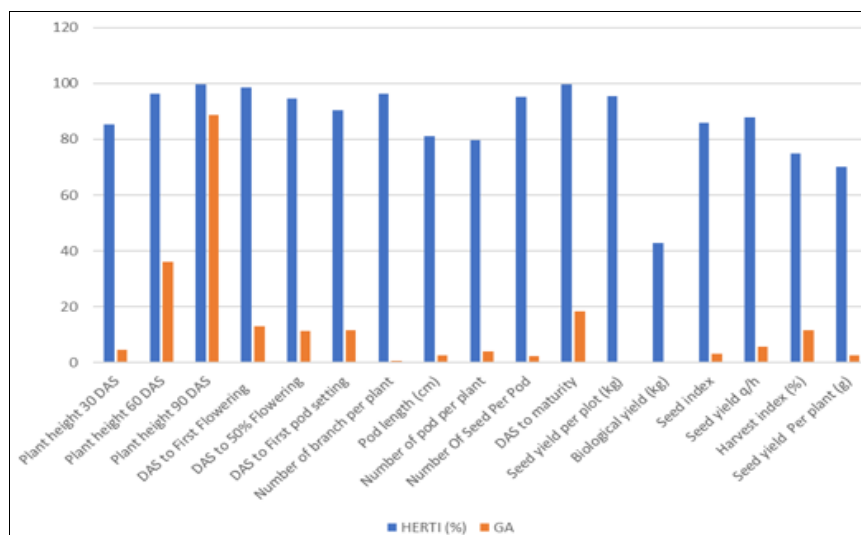


Fig 3: Heritability & Genetic advance

Correlation Analysis

Identifying the type and level of association between yield and its parts is made easier by the correlation coefficient, which gives a fair evaluation of the degree of relationship between two traits (Singh *et al.*, 2018). It is evident from the correlation analysis that several yield contributing traits exhibited positive and significant association with harvesting index at both genotypic and phenotypic levels. Harvesting index (%) showed a strong and positive significant correlation with seed yield per plant (0.78 & 0.67) at both levels. Similarly, seed yield q/ha. exhibited a positive and significant association with total yield (0.764 & 0.576), indicating its direct contribution towards productivity. Seed yield per plot (kg) and seed index (g) showed strong and positive significant correlation with seed yield per plant (0.668 & 0.553; 0.649 & 0.505) at genotypic and phenotypic levels, respectively. Pod length (cm) also exhibited positive and significant association with seed yield per plant (0.489 & 0.417) at both levels. These results agree with the findings of Yadav *et al.*, (2025) who also reported similar associations in pea. Number of branches per plant a positive

relationship with total yield (0.043 & 0.052), though the magnitude was comparatively lower. On the other hand, plant height 30,60,90 DAS, and maturity days exhibited negative and significant correlation with seed yield per plant (-0.431 & -0.357; -0.445 & -0.37; -515 & -424; -0.324 & -0.266) at genotypic and phenotypic levels, respectively. This indicates that short plant height genotypes are more productive compared to long height. These findings are in conformity with the reports of Kumar *et al.*, (2022). Number of pods per plant showed a positive and significant association with seed yield per plant (489 & 0.031). First flowering, 50% flowering and first pods setting showed a negative association with total yield at genotypic level (-0.155 & -0.142; -0.293 & -0.142; -0.291 & -0.229). In general, genotypic correlation coefficients were higher than phenotypic correlations for most of the traits, indicating that the observed associations are largely governed by genetic factors with minimal environmental interference. These findings are in close agreement with earlier reports of Kumar *et al.*, (2022).

Table 4: Genotypic correlation coefficient among various traits of 19 pea genotypes evaluated

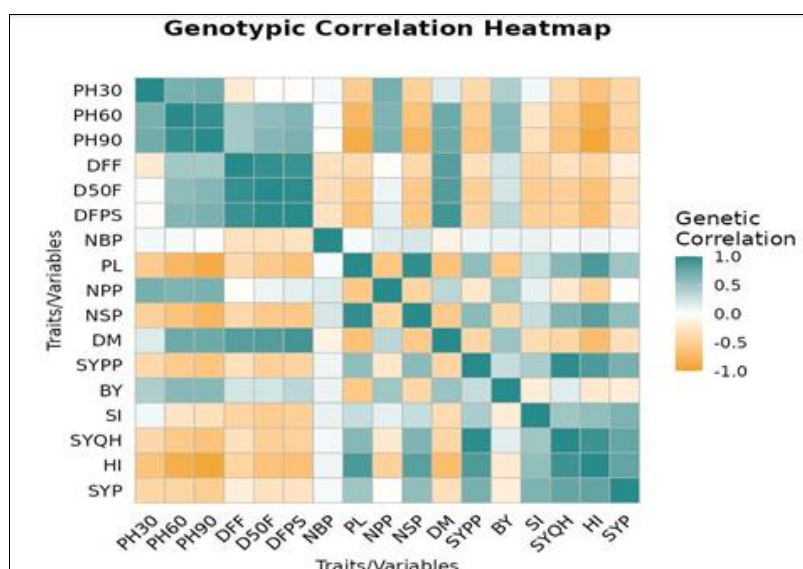
Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	DAS to First Flowering	DAS to 50% Flowering	DAS to First pod setting	Number of branch per plant	Pod length (cm)	Number of pod per plant	Number Of Seed Per Pod	DAS to maturity	Seed yield per plot (kg)	Biological yield (kg)	Seed index	Seed yield q/h	Harvest index (%)	Seed yield Per plant (g)
Plant height 30 DAS	1.00	0.671**	0.705**	-0.206	-0.018	-0.03	0.05	-0.536*	0.684**	-0.478*	0.163	-0.397	0.411	0.067	-0.409	-0.625**	-0.431
Plant height 60 DAS		1.00	0.962**	0.466*	0.568*	0.624**	0.041	-0.753**	0.643**	-0.633**	0.726**	-0.534*	0.599*	-0.272	-0.569*	-0.852**	-0.445
Plant height 90 DAS			1.00	0.461*	0.616**	0.662**	-0.026	-0.875**	0.666**	-0.766**	0.726**	-0.6**	0.605*	-0.317	-0.633**	-0.937**	-0.515*
DAS to First Flowering				1.00	0.962**	0.943**	-0.31	-0.384	-0.024	-0.396	0.827**	-0.31	0.221	-0.451	-0.309	-0.444	-0.155
DAS to 50% Flowering					1.00	0.988**	-0.32	-0.559*	0.082	-0.563*	0.845**	-0.494*	0.217	-0.527*	-0.492*	-0.644**	-0.293
DAS to First pod setting						1.00	-0.292	-0.635**	0.133	-0.579*	0.911**	-0.455	0.338	-0.494*	-0.477*	-0.664**	-0.291
Number of branch per plant							1.00	0.035	0.17	0.208	-0.122	0.075	0.098	0.107	0.057	0.076	0.043
Pod length (cm)								1.00	-0.583*	0.966**	-0.645**	0.556*	-0.573	0.285	0.606**	0.877**	0.489*
Number of pod per plant									1.00	-0.445	0.338	-0.241	0.482	0.117	-0.22	-0.476	-0.012
Number Of Seed Per Pod										1.00	-0.557*	0.58*	-0.413	0.279	0.643**	0.82**	0.561*
DAS to maturity											1.00	-0.43	0.506	-0.36	-0.43	-0.705**	-0.324
Seed yield per plot (kg)												1.00	0.29	0.424	0.986**	0.87**	0.668**
Biological yield (kg)													1.00	-0.184	0.148	-0.217	-0.18
Seed index														1.00	0.48*	0.55*	0.649**
Seed yield q/h															1.00	0.932**	0.764**
Harvest index (%)																1.00	0.78**
Seed yield Per plant (g)																	1.00

* indicates significance at 5% level, ** indicates significance at 1% level

Table 5: Phenotypic correlation coefficient among various traits of 19 pea genotypes evaluated

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	DAS to First Flowering	DAS to 50% Flowering	DAS to First pod setting	Number of branches per plant	Pod length (cm)	Number of pods per plant	Number of Seed Per Pod	DAS to maturity	Seed yield per plot (kg)	Biological yield (kg)	Seed index	Seed yield q/h	Harvest index (%)	Seed yield Per plant (g)
Plant height 30 DAS	1.00	0.602**	0.652**	-0.192	-0.02	-0.013	0.052	0.407**	0.596**	-0.457**	0.155	-0.336*	0.371**	0.091	-0.311*	-0.574**	-0.357**
Plant height 60 DAS		1.00	0.945**	0.447**	0.539**	0.579**	0.033	0.681**	0.568**	-0.612**	0.712**	-0.505**	0.415**	-0.243	0.515**	-0.738**	-0.37**
Plant height 90 DAS			1.00	0.456**	0.599**	0.631**	-0.027	0.784**	0.598**	-0.746**	0.724**	-0.581**	0.397**	-0.29*	0.589**	-0.805**	-0.424**
DAS to First Flowering				1.00	0.94**	0.896**	-0.295*	0.356**	-0.019	-0.386**	0.82**	-0.305*	0.125	0.422**	-0.292*	-0.373**	-0.142
DAS to 50% Flowering					1.00	0.928**	-0.303*	-0.5**	0.078	-0.532**	0.819**	-0.479**	0.123	0.483**	0.469**	-0.536**	-0.267*
DAS to First pod setting						1.00	-0.285*	0.528**	0.085	-0.528**	0.861**	-0.415**	0.222	0.428**	-0.42**	-0.546**	-0.229
Number of branches per plant							1.00	0.036	0.161	0.191	-0.116	0.073	0.065	0.097	0.057	0.065	0.052
Pod length (cm)								1.00	-0.481**	0.836**	-0.582**	0.528**	-0.275*	0.261*	0.571**	0.68**	0.417**
Number of pods per plant									1.00	-0.379**	0.307*	-0.216	0.23	0.112	-0.189	-0.329*	0.031
Number of Seed Per Pod										1.00	-0.549**	0.537**	-0.287*	0.248	0.57**	0.694**	0.46**
DAS to maturity											1.00	-0.418**	0.333*	-0.33*	-0.4**	-0.609**	-0.266*
Seed yield per plot (kg)												1.00	0.294*	0.382**	0.96**	0.7**	0.553**
Biological yield (kg)													1.00	-0.153	0.285*	-0.466**	-0.222
Seed index														1.00	0.415**	0.473**	0.505**
Seed yield q/h															1.00	0.657**	0.576**
Harvest index (%)																1.00	0.67**
Seed yield Per plant (g)																	1.00

* indicates significance at 5% level, ** indicates significance at 1% level.

**Fig 4:** Genotypic Correlation Heatmap

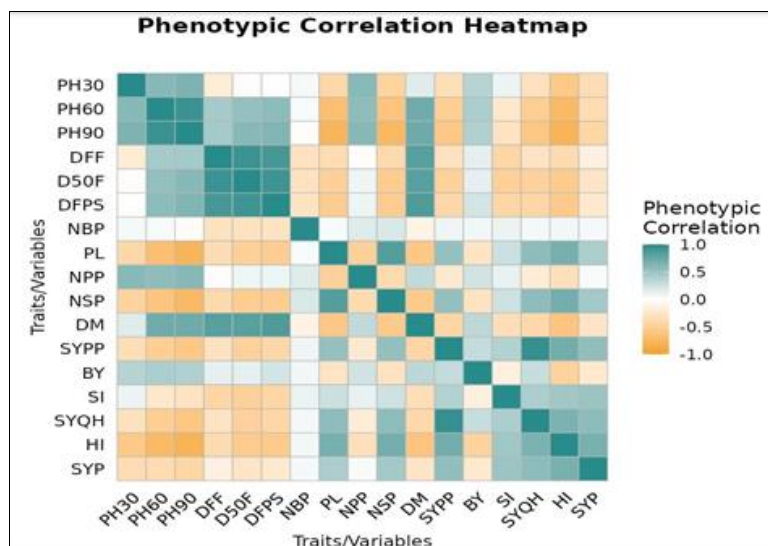


Fig 5: Phenotypic Correlation Heatmap

Path Coefficient Analysis: Path coefficient analysis is broken down correlations into direct effects (straight impact of one trait) and indirect effects (through other traits). This helps uncover the real causes behind relationships between variables. It provides a comprehensive picture of how characteristics affect one another and the main goal, such as seed yield, when combined with routine correlation studies. These findings are in conformity with the reports of (Verma *et al.*, 2021). Pod length ranged from 6.2-10.7 cm (avg. 8.7 cm), pods per plant from 9.0-15.5 (mean 11.8), seed yield per hectare from 15.7-27.8 q/ha, seed index

from 19.3-26.7 g, seed yield per plant from 11.7-18.0 g, and harvest index from 33.2-55.0%. These traits correlated positively with seed yield, boosting it directly or indirectly. Days to first flowering and maturity had negative direct effects, so early-flowering, early-maturing genotypes performed better here. Plant height indirectly influenced yield via other traits. Path analysis highlights prioritizing seed yield per plot, harvest index, pods per plant, pod length, and seed index when selecting top pea genotypes for higher output. Early same results found by Kumar *et al.*, (2014) and Ali *et al.*, (2021).

Table 6: Genotypic path

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	DAS to First Flowering	DAS to 50% Flowering	DAS to First pod setting	Number of branches per plant	Pod length (cm)	Number of pods per plant	Number of Seed Per Pod	DAS to maturity	Seed yield per plot (kg)	Biological yield (kg)	Seed index	Seed yield q/h	Harvest index (%)	GC with SYP
Plant height 30 DAS	-0.496	0.891	-0.683	0.295	-0.02	-0.023	0.006	-0.17	0.368	0.186	-0.033	-0.6	-0.582	0.017	-0.506	0.918	-0.431
Plant height 60 DAS	-0.333	1.327	-0.931	-0.667	0.644	0.475	0.005	-0.238	0.346	0.246	-0.146	-0.807	-0.848	-0.068	-0.703	1.252	-0.445
Plant height 90 DAS	-0.35	1.277	-0.968	-0.66	0.699	0.504	-0.003	-0.277	0.359	0.298	-0.146	-0.906	-0.857	-0.079	-0.782	1.377	-0.515
DAS to First Flowering	0.102	0.619	-0.446	-1.431	1.091	0.718	-0.038	-0.122	-0.013	0.154	-0.166	-0.468	-0.313	-0.112	-0.382	0.652	-0.155
DAS to 50% Flowering	0.009	0.754	-0.596	-1.376	1.134	0.752	-0.04	-0.177	0.044	0.219	-0.17	-0.746	-0.307	-0.131	-0.608	0.946	-0.293
DAS to First pod setting	0.015	0.828	-0.641	-1.349	1.121	0.761	-0.036	-0.201	0.072	0.225	-0.183	-0.687	-0.479	-0.123	-0.59	0.975	-0.291
Number of branches per plant	-0.025	0.054	0.025	0.444	-0.363	-0.222	0.124	0.011	0.092	-0.081	0.025	0.113	-0.139	0.027	0.07	-0.112	0.043
Pod length (cm)	0.266	-1	0.847	0.549	-0.634	-0.483	0.004	0.317	-0.314	-0.376	0.13	0.84	0.811	0.071	0.749	-1.288	0.489
Number of pods per plant	-0.34	0.854	-0.645	0.034	0.093	0.101	0.021	-0.185	0.539	0.173	-0.068	-0.364	-0.682	0.029	-0.272	0.699	-0.012
Number of Seed Per Pod	0.237	-0.84	0.742	0.567	-0.639	-0.441	0.026	0.306	-0.24	-0.389	0.112	0.876	0.585	0.069	0.795	-1.205	0.561
DAS to maturity	-0.081	0.964	-0.703	-1.183	0.959	0.693	-0.015	-0.204	0.182	0.217	-0.201	-0.649	-0.716	-0.089	-0.531	1.036	-0.324
Seed yield per plot (kg)	0.197	-0.709	0.581	0.444	-0.56	-0.346	0.009	0.176	-0.13	-0.226	0.086	1.51	-0.411	0.105	1.219	-1.278	0.668
Biological yield (kg)	-0.204	0.795	-0.586	-0.316	0.246	0.257	0.012	-0.181	0.26	0.161	-0.102	0.438	-1.416	-0.046	0.183	0.319	-0.18

Seed index	-0.033	-0.361	0.307	0.645	-0.598	-0.376	0.013	0.09	0.063	-0.108	0.072	0.64	0.261	0.248	0.593	-0.808	0.649
Seed yield q/h	0.203	-0.755	0.613	0.442	-0.558	-0.363	0.007	0.192	-0.119	-0.25	0.086	1.489	-0.21	0.119	1.236	-1.369	0.764
Harvest index (%)	0.31	-1.131	0.907	0.635	-0.731	-0.505	0.009	0.278	-0.256	-0.319	0.142	1.314	0.307	0.137	1.152	-1.469	0.78

(GC = Genotypic Coefficient, PC = Phenotypic Coefficient DAS = Days after sowing, SYP = Seed yield plant-1)

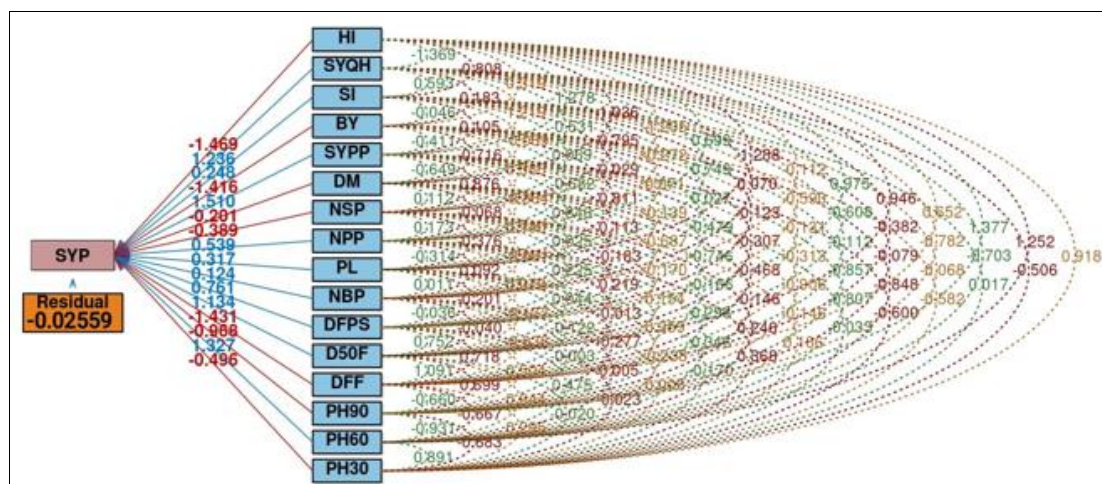


Fig 6: Genotypic path

Table 7: Phenotypic path

Traits	Plant height 30 DAS	Plant height 60 DAS	Plant height 90 DAS	DAS to First Flowering	DAS to 50% Flowering	DAS to First pod setting	Number of branches per plant	Pod length (cm)	Number of pods per plant	Number of Seed Per Pod	DAS to maturity	Seed yield per plot (kg)	Biological yield (kg)	Seed index	Seed yield q/h	Harvest index (%)	PC with SYP
Plant height 30 DAS	-0.306	0.104	0.084	0.021	0.001	-0.005	0.005	-0.105	0.242	0.039	-0.014	-0.558	-0.541	0.021	0.086	0.741	-0.357
Plant height 60 DAS	-0.184	0.173	0.121	-0.05	-0.014	0.227	0.003	-0.176	0.231	0.052	-0.065	-0.839	-0.605	0.056	0.142	0.953	-0.37
Plant height 90 DAS	-0.199	0.164	0.128	-0.051	-0.016	0.248	-0.002	-0.203	0.243	0.063	-0.067	-0.965	-0.578	0.066	0.162	1.04	-0.424
DAS to First Flowering	0.059	0.077	0.058	-0.111	-0.025	0.352	-0.026	-0.092	-0.008	0.033	-0.075	-0.507	-0.182	0.096	0.081	0.482	-0.142
DAS to 50% Flowering	0.006	0.093	0.077	-0.105	-0.026	0.364	-0.026	-0.129	0.032	0.045	-0.075	-0.796	-0.179	-0.11	0.129	0.692	-0.267
DAS to First pod setting	0.004	0.1	0.081	-0.1	-0.025	0.393	-0.025	-0.137	0.035	0.045	-0.079	-0.689	-0.323	0.098	0.116	0.705	-0.229
Number of branches per plant	-0.016	0.006	-0.003	0.033	0.008	-0.112	0.087	0.009	0.065	-0.016	0.011	0.121	-0.095	0.022	0.016	-0.084	0.052
Pod length (cm)	0.124	-0.118	-0.101	0.04	0.013	-0.207	0.003	0.259	-0.196	-0.071	0.053	0.877	0.401	0.06	0.157	-0.878	0.417
Number of pods per plant	-0.182	0.098	0.077	0.002	-0.002	0.033	0.014	-0.125	0.407	0.032	-0.028	-0.359	-0.335	0.026	0.052	0.425	0.031
Number of Seed Per Pod	0.14	-0.106	-0.096	0.043	0.014	-0.207	0.017	0.216	-0.154	-0.084	0.05	0.892	0.418	0.057	0.157	-0.896	0.46
DAS to maturity	-0.047	0.123	0.093	-0.091	-0.022	0.338	-0.01	-0.151	0.125	0.046	-0.092	-0.694	-0.485	0.075	-0.11	0.787	-0.266
Seed yield per plot (kg)	0.103	-0.088	-0.075	0.034	0.013	-0.163	0.006	0.137	-0.088	-0.045	0.038	1.661	-0.428	0.087	0.265	-0.904	0.553
Biological yield (kg)	-0.113	0.072	0.051	-0.014	-0.003	0.087	0.006	-0.071	0.094	0.024	-0.031	0.488	-1.457	0.035	0.079	0.602	-0.222
Seed index	-0.028	-0.042	-0.037	0.047	0.013	-0.168	0.008	0.068	0.046	-0.021	0.03	0.634	0.223	0.229	0.114	-0.611	0.505
Seed yield q/h	0.095	-0.089	-0.076	0.033	0.012	-0.165	0.005	0.148	-0.077	-0.048	0.037	1.594	-0.415	0.095	0.276	-0.849	0.576
Harvest index (%)	0.175	-0.128	-0.103	0.042	0.014	-0.214	0.006	0.176	-0.134	-0.059	0.056	1.163	0.679	0.108	0.181	-1.292	0.67

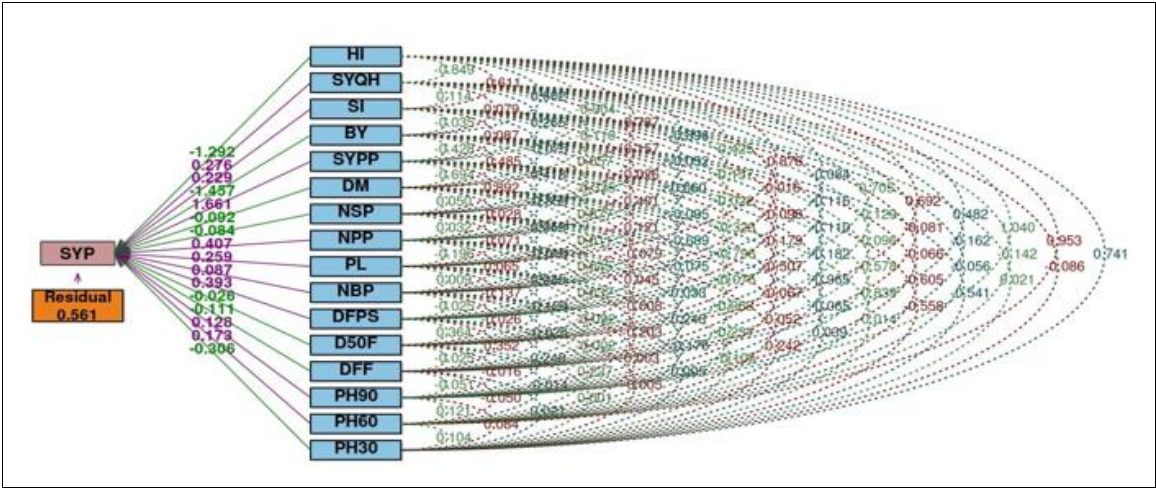


Fig 7: Phenotypic path

Genetic Divergence Analysis

Table 11. showed the Representing Cluster means values of different traits of nineteen genotypes of pea. We did the clustering with Tocher's method and Mahalanobis D² distance. The estimates of cluster contribution of traits for different characters of pea genotypes are presented in (Table 12.). Cluster I ended up with 12 genotypes, the biggest bunch. Cluster (II) 6, and Cluster 3 just had one. Plant height (PH)90 was the big driver of diversity 42.77% (Singh *et al.*,1981). DAS to maturity (DM) came second at 21.63%. On plant height (PH)30, Cluster III was highest at 27.33, while Cluster I sat at 21.0. plant height 60 varied from 86.72 in Cluster II down to 54.85 in Cluster I. Plant height 90 really stood out at 152.3 in Cluster II, but dropped to 71.47 in Cluster I. DAS to first flowering (DFF) maxed at 56.94 in Cluster II and was lowest at 41.0 in Cluster

III. DAS to 50% flowering (D50F) went 61.67 in Cluster II to 51.67 in Cluster I. DAS to first flowering (DFPS) hit 67.06 in Cluster II, 55.0 in Cluster III. Number of branches plant-1 (NBP) was 2.91 in Cluster I, down to 2.67 in Cluster III. Pod length (PL) ranged 9.58 in Cluster I to 6.63 in Cluster III. Number of pod plant-1 (NPP) peaked at 15.67 in Cluster III, lowest 11.78 in Cluster I. NSP got to 8.1 in Cluster I, 5.27 in Cluster III. DM spanned 96.61 (Cluster II) to 74.67 (Cluster III). SYPP was 0.66 in Cluster I, only 0.48 in Cluster III. BY topped 1.49 in Cluster II, 1.36 in Cluster I. SI from 23.42 (Cluster I) to 21.94 (Cluster II). SYQH at 22.16 in Cluster I, 15.80 in Cluster II. HI reached 49.19 in Cluster I, fell to 34.45 in Cluster III. SYP was 14.93 in Cluster I down to 11.7 in Cluster III. These findings are in close agreement with earlier reports of Azam *et al.*, (2024); Sharma *et al.*, (2022); Brhane *et al.*, (2024)^[5, 6].

Table 8: List of genotypes under various cluster.

Cluster	Total Genotypes	Genetic Material
cluster I	12	V ₁ , V ₁₁ , V ₁₂ , V ₁₃ , V ₁₄ , V ₁₆ , V ₁₇ , V ₁₈ , V ₁₉ , V ₂ , V ₃ , V ₅
cluster II	6	V ₁₀ , V ₁₅ , V ₄ , V ₆ , V ₇ , V ₈
cluster III	1	V ₉

Table 9: Intra and Inter cluster distance

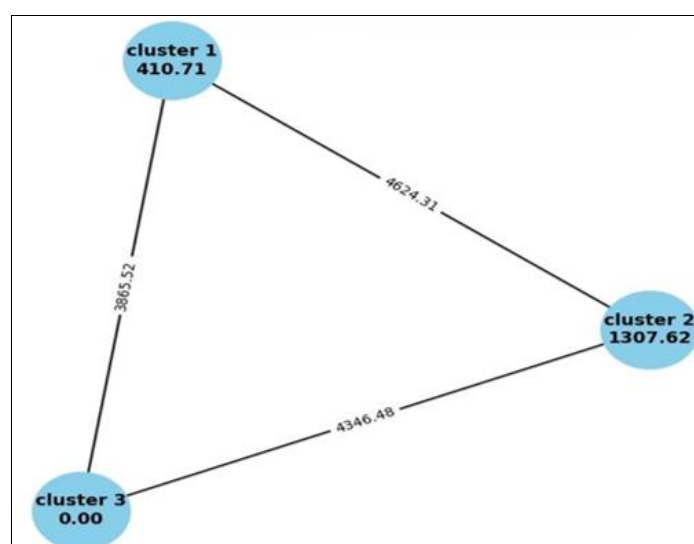
Cluster Number	cluster.1	cluster.2	cluster.3
cluster I	410.7115402	4624.306836	3865.519244
cluster II		1307.619513	4346.480954
Cluster III			0

Table 10: Representing Cluster means: Tocher method

Trait	cluster 1	cluster 2	cluster 3
PH30	21.00	22.87	27.33
PH60	54.85	86.72	68.13
PH90	71.47	152.30	138.47
DFF	47.00	56.94	41.00
D50F	51.67	61.67	52.00
DFPS	56.06	67.06	55.00
NBP	2.91	2.81	2.67
PL	9.58	7.12	6.63
NPP	11.78	13.94	15.67
NSP	8.10	6.24	5.27
DM	79.31	96.61	74.67
SYPP	0.66	0.55	0.48
BY	1.36	1.49	1.38
SI	23.42	21.94	22.33
SYQH	22.16	18.55	15.80
HI	49.19	37.00	34.45
SYP	14.93	13.43	11.70

Table 11: Contribution of traits

Traits	Singh statistic	Percentage Contribution	Cumulative proportion
PH90	1916407.356	42.77	42.77
DM	968995.2259	21.63	64.40
SYPP	609995.5088	13.61	78.01
DFF	427178.6905	9.53	87.54
NBP	155843.1886	3.48	91.02
NSP	148551.4228	3.32	94.34
HI	82899.22744	1.85	96.19
PL	39162.09756	0.87	97.06
PH30	32187.63406	0.72	97.78
DFPS	26750.34585	0.60	98.38
SI	24933.13737	0.56	98.93
BY	19040.19104	0.42	99.36
SYP	12854.15686	0.29	99.64
PH60	7955.356376	0.18	99.82
D50F	3924.554326	0.09	99.91
NPP	3526.51125	0.08	99.99
SYQH	563.6970229	0.01	100.00

**Fig 8:** Cluster distances by Tocher method**Table 12:** Abbreviations

PH30	Plant height 30 DAS
PH60	Plant height 60 DAS
PH90	Plant height 90 DAS
DFF	DAS to First Flowering
D50F	DAS to 50% Flowering
DFPS	DAS to First pod setting
NBP	Number of branches per plant
PL	Pod length (cm)
NPP	Number of pods per plant
NSP	Number of Seed Per Pod
DM	DAS to maturity
SYPP	Seed yield per plot (kg)
BY	Biological yield (kg)
SI	Seed index
SYQH	Seed yield q/h
HI	Harvest index (%)
SYP	Seed yield Per plant (g)

Conclusion

Phool Bahar (74.7 days), K-6 (75 days), Kashi Uday (75.3 days), and Kashi Ageti (76.7 days) are variety of early maturity. Analysis of variance had significant for all characters under study. In the study highest GCV, PCV was shown for plant height 90 DAS (cm) (42.93%), (43.00%) and heritability broad

sense in plant height 90 DAS (cm) (99.70%). Whereas highest genetic advance was observed for plant height 90 DAS (88.9%). Seed yield per plant (g) exhibited highly significant positive association with number of branches, pod length (cm), number of seeds per pod, seed yield per plot (kg), seed index (g), harvest index (%). Seed yield per plant had maximum positive direct

effect at genotypic level viz. harvest index (%) (0.780) followed by seed yield q/ha. (0.764), seed yield per plot (0.668), seed index (g) (0.649), number of pod (0.561), pod length (0.489), number of branches per plant (0.043). AP-3, GS-10, AP-2, AP-5, Kashi Uday these varieties are recommended to farmers on the basis of seed yield per plant, seed yield per plot, number of seeds per pod, biological yield per plot, number of pods per plant seed yield q/ha.

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- **Data availability:** No datasets were generated or analyzed during the current study.
- **Clinical Trial Number:** Not applicable
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