

Evaluation of Pea (*Pisum sativum* L.) genotypes in Nagaland ecosystem for yield and yield-related traits

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ABSTRACT

Pea is an authenticated vegetable crop in the ethnic tribes of Nagaland and plays a major role in their traditions. Developing high-yielding elite variants of pea can be achieved by leveraging the genetic variability present within the population. Hence, the present study was aimed at understanding the genetic variability and trait association of grain quality and yield traits in 29 pea accessions. Observations were recorded for eleven yield-contributing traits. Analysis of variance revealed significant variation for all the parameters under study. In this present study, high genotypic and phenotypic variation was observed for traits, seed yield per plant followed by plant height, number of pods per plant, seed index and number of branches per plant indicating the presence of ample variation for these traits in the present material. In the present study, all yield and yield related traits exhibit high (>60%) heritability except pod length. High heritability coupled with high genetic advance percentage of the means was observed for all traits except pod length, pod diameter and shelling percentage. Seed yield per plant exhibited positive and significant correlations with various traits, viz., no. of pods per plant, pod length, 100 seed weight and no. of seeds per pod at genotypic and phenotypic level. Plant height showed positive and significant correlations at phenotypic level. Path analysis revealed that pod length has the highest positive direct effect and also exhibited significant positive correlation with yield indicating a true relationship between the traits. The existing variability identified can be further exploited in crop improvement of field pea.

Keywords: Pea, Variability, Correlation and Path analysis.

INTRODUCTION

Field pea (*Pisum sativum* L.) is an important legume crop grown during the cool season. As a cool-season crop, it is most extensively grown in temperate regions throughout the world (Pratap *et al.*, 2024). Field pea is highly nutritious, a rich source of digestible proteins (7%), along with carbohydrates and minerals and mainly used as a pulse, but are also consumed in vegetable form (Singh *et al.*, 2024). The potential of pea as a fresh vegetable is not fully exploited due to lack of proper knowledge about the cultivars best suited to the agro-climatic condition (Uhlarić *et al.*, 2022). Hence proper emphasis on the aspects of genotype suitability and yield is necessary. Before recommending any cultivars suitable for the region, it is pertinent to evaluate cultivars emphasizing the aspects of genotype suitability and yield (Sanwal *et al.*, 2024). Northern states of India led the cultivation and production of pea, while productivity is lower in range and didn't meet the per capita requirement

of pulses (Pratap *et al.*, 2024). Hence, a challenge has arisen to increase pulse production to meet the growing demand caused by India's progressively increasing population. Therefore, exploiting the genetic variability in field pea germplasm is essential for developing high-yielding and high-quality seed varieties. Genetic variability serves as an essential foundation for the enhancement of crops, offering critical insights into trait heritability and informing the implementation of effective selection strategies for the development of high-yielding varieties (Anand *et al.*, 2024). Assessment of genetic variability present in the genetic material is important to estimate the magnitude of improvement that can be achieved in breeding material for various characters (Punyo and Chaturvedi, 2020; Deshmukh, 2022). The complexity of yield in genotypes arises from the fact that the expression of yield traits is influenced by environmental and soil conditions. Therefore, relying solely on direct heritability for the selection of these traits may not be beneficial.

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Employing a combined approach of correlation and path coefficient analysis facilitates the identification of key traits that significantly impact yield. Consequently, the current study was conducted on 29 pea germplasm accessions in the foothills of Nagaland to characterise, assess variability, and examine trait associations to identify elite lines with high yield potential.

MATERIALS AND METHODS

Experiment location and Plant material

The study was conducted during the *Rabi* season-2022, at the Research Farm of the Department of Genetics and Plant Breeding, School of Agricultural Sciences, Nagaland University, Medziphema, India. A total of 29 pea germplasm accessions were procured from the Indian Institute of Pulses Research (IIPR), Kanpur-U.P. The complete list of the 29 genotypes is presented in Table 1.

Table 1: List of genotypes used in the experiment

Sl. No.	Genotype	Sl. No.	Genotype
1	Field Pea IVT(D) NHZ FPD 22-95	16	Field Pea IVT(T) NHZ FPT 22-18
2	Field Pea IVT(D) NHZ FPD 22-96	17	Field Pea IVT(T) NHZ FPT 22-19
3	Field Pea IVT(D) NHZ FPD 22-97	18	Field Pea IVT(T) NHZ FPT 22-20
4	Field Pea IVT(D) NHZ FPD 22-98	19	Field Pea IVT(T) NHZ FPT 22-21
5	Field Pea IVT(D) NHZ FPD 22-99	20	Field Pea IVT(T) NHZ FPT 22-22
6	Field Pea IVT(D) NHZ FPD 22-101	21	Field Pea IVT(T) NHZ FPT 22-23
7	Field Pea IVT(D) NHZ FPD 22-102	22	Field Pea IVT(T) NHZ FPT 22-24
8	Field Pea IVT(D) NHZ FPD 22-103	23	Field Pea IVT(T) NHZ FPT 22-25
9	Field Pea IVT(D) NHZ FPD 22-104	24	Field Pea IVT(T) NHZ FPT 22-26
10	Field Pea IVT(D) NHZ FPD 22-105	25	Field Pea IVT(T) NHZ FPT 22-27
11	Field Pea IVT(D) NHZ FPD 22-106	26	Field Pea IVT(T) NHZ FPT 22-28
12	Field Pea IVT(D) NHZ FPD 22-107	27	Field Pea IVT(T) NHZ FPT 22-29
13	Field Pea IVT(D) NHZ FPD 22-108	8	Field Pea IVT(T) NHZ FPT 22-30
14	Field Pea IVT(T) NHZ FPT 22-16	29	Field Pea IVT(T) NHZ FPT 22-31
15	Field Pea IVT(T) NHZ FPT 22-17		

Experimental design and field layout

The study employed a randomized complete block design (RCBD) with three replications across the experimental area to account for differences in site fertility. Within each replication, there were 29 plots measuring 2m x 1m, spaced at intervals of 20cm. Plant spacing within rows was 10cm, while row spacing was 30cm. Recommended agricultural practices were adhered consistently throughout the experiments.

Data collection:

A total of 11 quantitative characters of pea were taken for experimentation. These characteristics were chosen based on descriptions and guidelines provided by PPV&FR in 2001 (DUS). For each characteristic, data were gathered from five randomly sampled plants from each genotype and in each replication. The quantitative data encompassed

various traits, including, day to 50% flowering (DF50%), days of maturity (DM), number of primary branches per plant (NPBPP), plant height (PH) (cm), length of pods (LP) (cm), diameter of pods (DP) (cm), number of pods per plant (NPPP), number of seeds per pod (NSPP), 100 seeds weight (SI) (g), shelling percentage (SP%) and seed yield per plant (SYPP)(g).

Statistical analysis

The analysis of variance (ANOVA) was conducted using the OPSTAT open-source software to assess the data. The phenotypic, genotypic and environmental coefficient of variation was calculated according to Burton and De Vane (1953). Heritability was calculated according to Allard (1960). Genetic advance possible through selection was calculated according to Johnson *et al.*, (1955). Phenotypic and genotypic correlation coefficients were worked out as suggested by Al-Jibouri *et al.*,

(1958). The partitioning of genotypic correlation coefficient of traits into direct and indirect effects was carried out using the procedure suggested by Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance

The mean squares obtained from the

combined analysis of variance for yield traits were presented in Table 2. These results indicated significant effects ($P < 0.05$) were observed among the genotypes. These significant differences suggest that there is a substantial amount of genetic variation among the evaluated genotypes. Comparable findings are presented in studies conducted by Winther *et al.* (2023) and Tun *et al.* (2022).

Table 2: Analysis of variance for yield traits in Pea

Source of variance	Replication	Genotype	Error
DF	2	28	56
Daysto50% Flowering	0.05	198.95**	2.85
Days to Maturity	3.13	42.56**	2.44
No. of branches /plant	0.09	5.21**	0.04
Plant height (cm)	411.71	2300.44**	40.97
Pod Length (cm)	0.63	0.59*	0.3
No. of pods /plant	17.78	25.75**	1.32
Diameter of pod (cm)	0.001	0.02**	0.002
No. of seed/pod	0.028	2.37**	0.026
100 seed weight (g)	1.27	46.97**	0.067
Shelling %	18.9	38.70**	1.4
Seed yield (g / plot)	0.94	54.75**	0.125

** indicates 1% significant, * indicates 5% significant

Genetic Variability Analysis

Crop breeding success depends on the existing genetic variability in the population and rate of heritability of concerned traits. A plant breeder needs to analyse the genetic variation in

existing population for the selection of desirable traits for trait modeling. Genetic variance components for yield and yield related traits were presented in Table 3.

Table 3: Genetic variance components for yield and yield-related traits of Pea

Traits	GCV	PCV	h^2	G.A.	GAM
Days to50% Flowering	14.96	15.28	95.82	16.28	30.13
Days to Maturity	12.24	13.44	84.51	6.91	23.35
No. of branches /plant	16.31	16.50	97.72	2.65	32.96
Plant height (cm)	35.76	36.72	94.84	55.05	71.74
No. of pods /plant	24.57	26.49	86.04	5.44	46.85
Pod Length (cm)	4.60	9.94	21.46	0.27	4.39
Diameter of pod (cm)	6.27	7.56	68.81	0.136	10.72
No. of seed/pod	15.27	15.53	97.50	1.80	31.1
100 seed weight (g)	24.52	24.58	99.50	8.11	50.34
Shelling %	7.47	7.88	89.87	6.84	14.5
Seed yield (g / plot)	36.62	36.78	99.28	8.66	75.01

GCV - genotypic coefficient of variation; PCV - phenotypic coefficient of variation, h^2 - broad sense heritability (%), G.A.- genetic advance, GAM- genetic advance as percentage mean

Present study result revealed that phenotypic coefficient of variance (PCV) was higher than genotypic coefficient of variance (GCV) for yield and yield related traits. Hence this study suggests that environment influences the expression of these variables. High

genotypic and phenotypic coefficient of variation (>20%) among yield parameter was observed for the characters, plant height followed by seed yield per plant, 100 seed weight and number of pods per plant. These traits demonstrated the higher genetic variability, hence these traits

Table 4(a): Estimate of genotypic (r_g) correlation coefficient between yield traits of field pea

	Days to 50% Flowering	Days to Maturity	No. of branches /plant	Plant height (cm)	No. of pods/plant	Pod Length (cm)	Diameter of pod (cm)	No. of seed/pod	100 seed weight (g)	Shelling %	Seed yield (g / plot)
Days to 50% Flowering	1										
Days to Maturity	-0.1387	1									
No. of branches /plant	0.5543 **	-0.253	1								
Plant height (cm)	-0.169	0.5996 **	-0.3666	1							
No. of pods /plant	-0.0232	0.2366	0.0435	0.357	1						
Pod Length (cm)	0.1453	0.0335	-0.2268	0.1005	0.5037 **	1					
Diameter of pod (cm)	0.2403	-0.2459	0.2666	-0.4826 **	-0.1905	0.1843	1				
No. of seed/pod	-0.006	0.1195	-0.1497	0.2288	0.3126	0.8843 **	-0.1394	1			
100 seed weight (g)	-0.1203	-0.0024	-0.2758	0.0591	-0.133	0.0645	0.0509	0.2461	1		
Shelling %	-0.0953	-0.1213	0.0225	0.0085	-0.2231	-0.3063	-0.2527	0.0093	-0.0144	1	
Seed yield (g / plot)	-0.0618	0.2004	-0.1926	0.3329	0.6231 **	0.5508 **	-0.0953	0.6922 **	0.6006 **	-0.0955	1

* = Significant at 5% level. ** = Significant at 1% level

Table 4(b): Estimate of Phenotypic (r_p) correlation coefficient between yield traits of field pea

	Days to 50% Flowering	Days to Maturity	No. of branches /plant	Plant height (cm)	No. of pod /plant	Pod Length (cm)	Diameter of pod (cm)	No. of seed/pod	100 seed weight (g)	Shelling %	Seed yield (g / plot)
Days to 50% Flowering	1										
Days to Maturity	-0.1402	1									
No. of branches /plant	0.529 **	-0.2241*	1								
Plant height (cm)	-0.1665	0.5356**	-0.3556**	1							
No. of pods /plant	-0.0073	0.1813	0.0396	0.3192 **	1						
Pod Length (cm)	0.0549	0.0459	-0.1043	0.0479	0.249 *	1					
Diameter of pod (cm)	0.2274 *	-0.2054	0.2121 *	-0.4056 **	-0.0965	0.143	1				
No. of seed/pod	0.0011	0.1043	-0.1483	0.2179 *	0.3031 **	0.4058 **	-0.1029	1			
100 seed weight (g)	-0.1231	0.004	-0.2695*	0.0502	-0.1234	0.0294	0.0342	0.2391*	1		
Shelling %	-0.0838	-0.1131	0.0209	0.0035	-0.1788	-0.1936	-0.2062	0.0093	-0.0131	1	
Seed yield (g / plot)	-0.0568	0.1839	-0.1899	0.319 **	0.5709 **	0.2388 *	-0.0776	0.6758**	0.5974 **	-0.0863	1

* = Significant at 5% level. ** = Significant at 1% level

Table 5: Direct and indirect effect of different characters' genotypic level on seed yield per plant of pea

	Days to 50% Flowering	Days to Maturity	No. of branches /plant	Plant height (cm)	No. of pods/plant	Pod Length (cm)	Diameter of pod (cm)	No. of seed/pod	100 seed weight (g)	Shelling %	Seed yield (g / plot)
Days to 50% Flowering	-0.1901	-0.01661	0.20262	-0.01627	-0.00763	0.12431	-0.05023	0.00223	-0.09212	-0.018	-0.0618
Days to Maturity	0.02636	0.11976	-0.09249	0.05772	0.07782	0.02867	0.05139	-0.0441	-0.00182	-0.02292	0.2004
No. of branches /plant	-0.10538	-0.0303	0.36552	-0.03529	0.01429	-0.19403	-0.05572	0.05528	-0.21125	0.00425	-0.1926
Plant height (cm)	0.03213	0.07181	-0.13399	0.09627	0.11743	0.08595	0.10087	-0.08448	0.0453	0.0016	0.3329
No. of pods /plant	0.00441	0.02833	0.01589	0.03437	0.32891	0.43085	0.03982	-0.11541	-0.10189	-0.04215	0.6231 **
Pod Length (cm)	-0.02762	0.00401	-0.08291	0.00967	0.16566	0.85542	-0.03854	-0.32644	0.04938	-0.05786	0.5508 **
Diameter of pod (cm)	-0.0457	-0.02946	0.09747	-0.04647	-0.06267	0.15776	-0.209	0.05147	0.03898	-0.04776	-0.0953
No. of seed/pod	0.00115	0.01431	-0.05473	0.02203	0.10283	0.75641	0.02913	-0.3692	0.18846	0.00175	0.6922 **
100 seed weight (g)	0.02286	-0.00028	-0.10081	0.00569	-0.04375	0.05515	-0.01063	-0.09083	0.76594	-0.00271	0.6006 **
Shelling %	0.01811	-0.01453	0.00822	0.00082	-0.07338	-0.262	0.05282	-0.00343	-0.01101	0.18892	-0.0955

Residual effect = 0.1201

suited to simple selection. Moderate magnitude of genotypic and phenotypic coefficient of variation (10-20%) was observed for days to 50% flowering, days to maturity, no. of branches per plant and number of seeds per pod, while remaining traits exhibited low magnitude of genotypic and phenotypic coefficient of variation. Traits exhibiting lowest variance values demonstrate that selection among them will not be effective. Similar studies reported by Kumar *et al.*, (2022) and Kumar *et al.*, (2023).

In the present study all yield and yield related traits exhibited high (>60%) heritability except for pod length, which indicates proper correlation between phenotypic and genotypic values and low environmental impact on the expression of these traits. Heritability alone doesn't show how much genetic improvement can be achieved from selecting a specific genotype. The success of selection depends not only on heritability but also on genetic advance (GA) (Luthra *et al.*, 2023). High heritability coupled with high genetic advance percentage of the means was observed for all traits except pod length, poddiameter and shelling percentage. These traits predominantly exhibit additive gene action, hence simple selection methods might help improve these traits. The remaining yield traitsexhibit high heritability coupled with moderate genetic advance which implies the influence of both additive and non-additive gene actions.

Correlation Studies:

Correlation studies reveal the magnitude of association between the yield and its attributing trait which is essential for planning a sound breeding programme. Correlation coefficients (both genotypic and phenotypic) for yield traits were presented in Table 4(a) & (b). In the present study, seed yield per plant exhibited positive and significant correlations with various traits, namely number of pods per plant, pod length, 100 seed weight and number of seeds per pod at genotypic and phenotypic level. Trait like plant height showed positive and significant

correlations at phenotypic level. Similar results were reported by Winther *et al.*, (2023) and Pratap *et al.*, (2024).

Path coefficient analysis

Path coefficient analysis was carried out at the genotypic level to separate the direct and indirect effects of different yield-contributing characters and it was presented in Table 5. The number of pods per plant, seed index (100 seed weight) and pod length showed positive significant correlation as well as positive direct effect hence, while selection emphasis should be given on these traits. These results are in agreement with Jagadeesh *et al.*, (2023). The residual effect estimated was 0.12 indicating that the traits under study are not sufficient to account for variability and there might be a few more pertinent characters other than those studied in the present investigation. Similar results reported by Singh *et al.*, (2024) and Jagadeesh *et al.*, (2023).

CONCLUSION

In the present study, seed yield per plant exhibited the highest genetic and phenotypic coefficient of variation, followed by plant height, number of pods per plant, seed index, and number of branches per plant, indicating ample variation in these traits. Broad sense heritability was highest in seed index, pod yield per plant, number of primary branches, and number of seeds per plant, indicating their potential for selection and further improvement. In general, genotypic correlation coefficient was higher than phenotypic correlation indicating a true relationship among the characters. The number of pods per plant, pod length and seed index showed positive significant correlation as well as positive direct effect. Hence, selection emphasis should be given on these traits. Among the 29 genotypes evaluated, superior performance genotype was IVT NHZ FPT 22-30 followed by IVT NHZ FPD 22-96, IVT NHZ FPT 22-27, IVT NHZ FPT 22-19 and IVT NHZ FPD 22-10.

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