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GENETIC VARIABILITY AND ASSOCIATION ANALYSIS OF YIELD AND QUALITY TRAITS IN GARDEN PEA (*Pisum sativum* L. var. *hortense*)

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ABSTRACT

The present study assessed genetic variability and trait associations to identify effective selection criteria for improving productivity in garden pea (*Pisum sativum* L. var. *hortense*). Analysis of variance revealed significant genotypic variation for most yield, earliness and quality traits. Genotypic coefficient of variation (GCV) ranged from 5.37% for single pod weight to 24.94% for total protein content, while phenotypic coefficient of variation (PCV) ranged from 5.42% to 497.31%. The relatively close GCV and PCV estimates for most traits indicated limited environmental influence on trait expression. Broad-sense heritability ranged from 59.69% for total soluble solids to 99.85% for total sugar content, with high heritability observed for most traits. Genetic advance as percentage of mean ranged from 1.38% to 50.36%, with high estimates for total protein, total sugar, 100-seed weight, plant height, number of seeds per pod, pod length, number of pods per plant and pod yield. High heritability coupled with high genetic advance indicated good prospects for selection. Correlation analysis revealed positive associations of pod yield with number of pods per plant, pod weight per plant, weight of 20 pods, single pod weight and pod length, whereas 100-seed weight showed negative associations with major yield components. Path analysis further identified these traits as important contributors to pod yield. Overall, the results demonstrated substantial exploitable genetic variability and highlighted pod number and pod-weight-related traits as reliable selection criteria for improving yield in garden pea.

Key words : Garden pea, Genetic variability, Heritability, Genetic advance, Correlation, Path analysis.

Introduction

Garden pea (*Pisum sativum* L. var. *hortense*, 2n = 2x = 14) is an economically important leguminous vegetable crop widely cultivated for its tender pods and nutritious seeds. It belongs to the family Fabaceae and subfamily Papilionoideae. In India, pea is grown over approximately 4.30 lakh ha, with a production of 41.13 lakh MT and productivity of 9.70 t ha^{-1} (Anonymous, 2023). Uttar Pradesh is the major pea-producing state, covering about 2.18 lakh ha with a production of 24.81 lakh tonnes, followed by Madhya Pradesh and Jharkhand. The crop is mainly cultivated during the *rabi* season in northern India, where cool climatic conditions prevailing from October to February favour its growth and development. Seed germination is optimum around 22°C, while crop growth performs best under mean temperatures of 13–18°C.

Pea is an annual, herbaceous and predominantly self-pollinated crop with considerable nutritional and agronomic significance. Besides serving as an important vegetable and pulse, it enhances soil fertility through symbiotic nitrogen fixation (Anushka *et al*., 2025). Green peas are nutritionally rich, containing proteins, carbohydrates, minerals, vitamins and essential amino acids such as lysine and tryptophan (Akin *et al*., 2025). Fresh seeds and immature pods are consumed as vegetables, while green peas are also suitable for canning, freezing and dehydration. Their nutritional properties contribute to a healthy diet and may help reduce the risk of various lifestyle-related disorders (Kumari *et al*., 2015). Pea

foliage is additionally utilized as livestock fodder, increasing its overall economic value.

With increasing consumer demand for garden pea, enhancement of yield and associated quality traits remains a major breeding objective. Development of superior genotypes requires the exploitation of available genetic variability and identification of traits that can serve as reliable selection criteria. Correlation analysis is useful for determining the direction and magnitude of associations among yield and its component traits and can assist in identifying characters suitable for indirect selection. However, correlation coefficients alone cannot distinguish between the direct contribution of a trait and its association arising through other characters. Path coefficient analysis therefore provides a more comprehensive understanding by partitioning correlations into direct and indirect effects, thereby identifying the traits with the greatest contribution to yield.

Considering the importance of garden pea and the need for increased productivity, an integrated assessment of genetic variability, correlation and path relationships can provide valuable information for crop improvement. Such an approach facilitates the identification of promising parents and cross combinations and helps formulate effective selection strategies for improving yield and quality traits in garden pea.

Materials and Methods

Experimental materials

The experiment was conducted at the Vegetable Research Farm, Department of Vegetable Science, Kalyanpur, C.S. Azad University of Agriculture and Technology, Kanpur, Uttar Pradesh, India. The experimental material comprised 13 diverse garden pea (*Pisum sativum* L. var. *hortense*) genotypes, including 10 female lines and three testers selected for variation in morphological, yield and quality attributes. The parental genotypes were crossed following the Line × Tester mating design of Kempthorne (1957), generating 30 F_1 hybrids. The F_1 hybrids were subsequently selfed to develop corresponding F_2 populations. Thus, the study involved 73 genotypes comprising 13 parents, 30 F_1 hybrids and 30 F_2 populations.

Experimental design

The experiment was conducted during three consecutive winter seasons of 2022–23, 2023-2024 and 2024–25. In the first season, the selected parents were grown in a crossing block and artificial hybridization was performed by emasculation and hand pollination to obtain F_1 seed. In the second season, the parents and F_1 hybrids were grown and F_1 plants were self-pollinated to generate F_2 seed. During the third season, the parents, F_1 hybrids and F_2 populations were evaluated in a Randomized Block Design (RBD) with three replications. Observations were recorded on five randomly selected plants per genotype per replication, except for plot-based measurements. Eighteen traits covering phenology, growth, yield components and quality were evaluated: days to flowering, number of pods plant^{-1}, pod length, pod width, number of seeds pod^{-1}, weight of 20 pods, single pod weight, weight of 20 pod seeds, plant height at edible stage, days to maturity, days to first pod picking, days to first fruiting knot, total soluble solids (TSS), total protein content (TPC), total sugar content (TSC), 100-seed weight, pod yield ha^{-1} and pod weight plant^{-1}.

Statistical analysis

Analysis of variance was performed to determine the significance of differences among genotypes. Genetic variability was assessed using genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (h^2), genetic advance (GA) and genetic advance as percentage of mean (GAM). Genotypic and phenotypic correlation coefficients were estimated to assess associations among traits, while path coefficient analysis was performed to partition the correlations with pod yield into direct and indirect effects. All statistical analyses were performed using R software. The results were used to identify important yield-associated traits and potential selection criteria for genetic improvement of garden pea.

Results and Discussion

Analysis of Variance

The analysis of variance revealed significant genetic variability among genotypes for most of the yield and quality traits evaluated in garden pea (Table 1). Highly significant differences among genotypes were observed for days to flowering, number of pods per plant, pod length, pod width, number of seeds per pod, weight of 20 pods, single pod weight at edible stage, weight of 20 pod seeds, days to maturity, 100-seed weight, pod yield per hectare, days to first pod picking, days to first fruiting knot, total soluble solids, total protein content and total sugar content, indicating the existence of substantial genetic variation within the experimental material. In contrast, comparatively lower variability was observed for plant height at edible stage, days to first harvesting and pod weight per plant, which exhibited non-significant differences.

Table 1 : Analysis of variance (ANOVA) for different Yield and Quality traits in garden pea.

Source	df	DAFMF	DAFFF	NNBFFF	SR	NSP	W20P	SPW	W20S	PH	DM	DFPP	DFFH	TSS	TPC	TSC	PWP	HSW	PYH
Replication	2	1.23	0.03	0.09	0.028	0.44	0.12	0.53	0.9	2293.24	1.63	0.45	12648.67	0.43	0.38	0.43	1229.75	0.71	4.2
Genotypes	42	56.09**	2.85**	3.08**	0.07**	6.91**	154.48**	0.38**	193.48**	2359.22	173.63**	117.13**	12843.46	12.11**	1.39**	1.04**	1276.1	134.78**	462.25**
Hybrids (H)	29	43.33**	2.84**	3.69**	0.04**	6.4**	104.9**	0.26**	134.88**	334.76	188.28**	127.29**	18375.14	5.7**	0.79**	0.67**	1772.58	126.03**	397.46**
Parents (P)	12	73.04**	3.08**	1.4**	0.13**	7.33**	285.29**	0.71**	293.35**	7267.89	133.88**	102.31**	5.64	7.64**	1.56**	0.94**	126.2	166.92**	651.06**
Line (L)	9	79.43**	2.5**	1.18**	0.15**	2.18*	296.77**	0.73**	128.77**	9656.77*	154.14**	61.03**	2.88	8.9**	1.85**	1.09**	141.07	38.7**	731.74**
Tester (T)	2	80.76**	2.72**	2.44**	0.09**	22.19**	184.86**	0.52**	259.47**	133.23	105.16**	331**	9.44	3.04**	0.48**	0.37**	57.84	775.05**	285.82**
L vs T	1	0.06	9.05**	1.27**	0.01**	24.01**	382.87**	0.94**	1842.4**	37.3	8.89**	16.4**	22.89	5.48**	1.05**	0.69**	129.12	104.61**	655.47**
H vs P	1	222.61**	0.05	5.46**	0.01*	16.52**	22.67**	0.03*	694.47**	2164.37	225.75**	0.25	6478.66	251.67**	16.7**	13.22**	677.01	2.9	75.39*
Error	84	0.578	0.042	0.064	0.001	0.521	0.528	0.008	1.63	2348.256	0.884	0.951	12768.556	0.001	0.001	0.043	1206.98	1.864	11.116
Total	128	18.8	0.96	1.05	0.02	2.62	51.04	0.13	64.57	2350.99	57.58	39.06	12791.26	3.98	0.46	0.35	1230.02	45.46	159.04

Estimation of Genetic parameters of variability

The success of any crop improvement programme largely depends upon the extent of genetic variability present in the breeding material. The estimates of genotypic variance (GV), phenotypic variance (PV), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2), genetic advance (GA) and genetic advance as percentage of mean (GAM) provide valuable information regarding the nature and magnitude of genetic variation governing different traits. The estimates of these genetic parameters for yield and quality traits in garden pea are presented in Table 2 and discussed under the following headings.

Coefficient of Variation

The phenotypic coefficient of variation (PCV) was slightly higher than the corresponding genotypic coefficient of variation (GCV) for all the traits studied, indicating a relatively low influence of environmental factors on the expression of these traits. The close correspondence between GCV and PCV values suggested that most of the observed variation was genetic in nature and selection based on phenotypic performance would be effective.

The PCV ranged from 5.42 per cent for weight of single pod at edible stage (SPW) to 497.31 per cent for days to first pod picking (DFPP). High PCV (>20%) was recorded for Days to First Pod Picking (497.31%), pod weight per plant (85.05%), total protein content (25.45%) and total sugar content (16.36%). Moderate PCV (10–20%) was observed for number of seeds per pod (17.89%), total soluble solids (18.52%), plant height at edible stage (13.80%), pod yield per hectare (11.94%), number of pods per plant (11.93%), pod length (12.44%), 100-seed weight at edible stage (16.14%), days to flowering (8.10%), days to maturity (8.62%) and days to first pod picking (8.71%). Low PCV (<10%) was observed for weight of 20 pods (5.45%), weight of single pod at edible stage (5.42%), weight of 20 pod seeds (9.42%) and pod width (8.66%).

The GCV ranged from 5.37 per cent for weight of single pod at edible stage (SPW) to 24.94 per cent for total protein content (TPC). High GCV (>20%) was observed for total protein content (24.94%). Moderate GCV (10–20%) was recorded for days to first pod picking (18.24%), total sugar content (16.34%), 100-seed weight at edible stage (15.87%), number of seeds per pod (15.23%), total soluble solids (14.31%), plant height at edible stage (13.75%), pod length (12.11%), number of pods per plant (11.71%) and pod yield per hectare (11.36%). Low GCV (<10%) was observed for days to

Table 2 : Estimation of different genetic variability parameter for different in garden pea.

Trait	Mean	Range	GV	PV	GCV	PCV	Heritability	GA	GAM
DF	47.39	38.8 - 56.3	14.2959	14.7375	7.98	8.1	97	7.67	16.19
NPP	8.26	6.4 - 10.8	0.9359	0.9721	11.71	11.93	96.27	1.96	23.67
PL	9.08	7.22 - 12.81	1.207	1.2742	12.11	12.44	94.72	2.2	24.27
PW	1.4	1.25 - 1.91	0.0136	0.0147	8.35	8.66	92.89	0.23	16.57
NSP	9.04	6.7 - 18.8	1.8938	2.6133	15.23	17.89	72.47	2.41	26.71
W20P	109.07	90.8 - 123.2	34.783	35.3308	5.41	5.45	98.45	12.05	11.05
SPW	5.45	4.54 - 6.16	0.0857	0.0874	5.37	5.42	98.09	0.6	10.96
W20S	71.54	56.8 - 88.3	44.7465	45.3892	9.35	9.42	98.58	13.68	19.13
PH	76.72	61.4 - 103.2	111.3127	112.1348	13.75	13.8	99.27	21.65	28.22
DM	92.38	74.3 - 105.2	62.4203	63.441	8.55	8.62	98.39	16.14	17.48
DFPP	75.48	63.9 - 88.4	42.0351	43.2234	8.59	8.71	97.25	13.17	17.45
DFFK	27.22	8.33 - 1297	24.6402	18325.8563	18.24	497.31	0.13	0.37	1.38
TSS	15.52	12.8 - 18	3.3243	5.5689	14.31	18.52	59.69	2.9	22.77
TPC	7.78	6.7 - 8.5	45.451	47.3173	24.94	25.45	96.06	13.61	50.36
TSC	6.82	5.8 - 7.5	1.3226	1.3246	16.34	16.36	99.85	2.37	33.65
PWP	49.11	32.72 - 438	14.0833	1744.4138	7.64	85.05	0.81	0.69	1.41
HSW	40.61	28.15 - 57.37	41.5344	42.9656	15.87	16.14	96.67	13.05	32.14
PYH	99.59	72.64 - 132.09	128.0845	141.2871	11.36	11.94	90.66	22.2	22.29

flowering (7.98%), pod width (8.35%), weight of 20 pods (5.41%), weight of single pod at edible stage (5.37%), weight of 20 pod seeds (9.35%), days to maturity (8.55%), days to first pod picking (8.59%) and pod weight per plant (7.64%). The present findings corroborate earlier reports by Devi *et al*. (2018), Mamatha *et al*. (2022), Verma *et al*., (2023) and Kaur *et al*. (2023).

The close proximity of GCV and PCV values for most of the traits such as days to flowering, number of pods per plant, pod length, pod width, weight of 20 pods, weight of single pod at edible stage, weight of 20 pod seeds, plant height, days to maturity, days to first pod picking, total sugar content, 100-seed weight and pod yield per hectare indicated lesser environmental influence on their expression.

Heritability

Heritability provides information regarding the proportion of total phenotypic variation that is attributable to genetic causes and helps in predicting the effectiveness of selection.

The estimates of broad-sense heritability ranged from 0.13 per cent for Days to First Pod Picking (DFPP) to 99.85 per cent for total sugar content (TSC). Very high heritability (>80%) was observed for total sugar content (99.85%), plant height at edible stage (99.27%), weight of 20 pod seeds (98.58%), weight of 20 pods (98.45%), days to maturity (98.39%), weight of single pod at edible stage (98.09%), days to flowering (97.00%), days to first pod picking (97.25%), 100-seed weight at edible stage (96.67%), number of pods per plant (96.27%), total protein content (96.06%), pod length (94.72%), pod width (92.89%) and pod yield per hectare (90.66%).

Moderately high heritability was observed for number of seeds per pod (72.47%) and total soluble solids (59.69%). However, very low heritability was recorded for Days to First Pod Picking (0.13%) and pod weight per plant (0.81%), indicating a greater influence of environmental factors on these traits. The high heritability estimates for most of the traits suggested that selection based on phenotypic performance would be reliable and effective for improving these characters in garden pea. Similar findings have been reported by Devi *et al*. (2018), Pathak *et al*. (2019), Gupta *et al*. (2020), Mamatha *et al*. (2022), Prajapati *et al*. (2022) and Kaur *et al*. (2023).

Genetic Advance and Genetic Advance as per cent of Mean

Genetic advance along with heritability provides a better understanding of the nature of gene action controlling a trait. High heritability coupled with high genetic advance as percentage of mean generally indicates the predominance of additive gene action and greater effectiveness of selection.

The genetic advance (GA) ranged from 0.23 for pod width (PW) to 22.20 for pod yield per hectare (PYH). Higher genetic advance values were observed for pod yield per hectare (22.20), plant height at edible stage

Table 3a : Genotypic and Phenotypic correlation coefficients analysis of F_{1s}(Hybrids) for different Yield traits in garden pea.

Traits		DF	NPP	PL	PW	NSP	W20P	SPW	W20S	PH	DM	DFPP	DFFK	TSS	TPC	TSC	PWP	HSW	PYH
DF	P	1.000	0.399*	0.078	-0.055	0.165	-0.183	-0.240	-0.064	0.143	0.365*	0.490**	0.184	0.249	0.252	0.255	0.034	-0.235	0.146
	G	1.000	0.403*	0.079	-0.056	0.167	-0.184	-0.255	-0.065	0.144	0.368*	0.493**	0.187	0.250	0.253	0.256	0.039	-0.237	0.146
NPP	P	0.399*	1.000	0.558**	-0.160	0.479**	-0.183	-0.349	-0.178	-0.026	0.065	0.159	0.151	0.146	0.133	0.129	0.483**	-0.606***	0.606***
	G	0.403*	1.000	0.562**	-0.163	0.484**	-0.184	-0.372*	-0.179	-0.026	0.066	0.160	0.154	0.147	0.134	0.129	0.568**	-0.611***	0.610***
PL	P	0.078	0.558**	1.000	-0.436*	0.689***	-0.060	-0.143	0.000	0.404*	0.227	0.399*	-0.008	0.471**	0.477**	0.475**	0.320	-0.608***	0.360
	G	0.079	0.562**	1.000	-0.444*	0.695***	-0.061	-0.151	0.000	0.405*	0.227	0.401*	-0.008	0.472**	0.478**	0.476**	0.375*	-0.612***	0.361*
PW	P	-0.055	-0.160	-0.436*	1.000	-0.229	0.065	0.175	-0.017	-0.185	-0.440*	-0.590***	0.121	-0.147	-0.144	-0.143	-0.115	0.199	-0.035
	G	-0.056	-0.163	-0.444*	1.000	-0.234	0.066	0.189	-0.017	-0.188	-0.448*	-0.603***	0.125	-0.150	-0.146	-0.145	-0.137	0.203	-0.036
NSP	P	0.165	0.479**	0.689***	-0.229	1.000	0.008	-0.097	0.249	0.267	0.093	0.274	-0.055	0.250	0.234	0.236	0.305	-0.674***	0.350
	G	0.167	0.484**	0.695***	-0.234	1.000	0.008	-0.103	0.251	0.268	0.094	0.277	-0.056	0.251	0.235	0.237	0.360	-0.680***	0.353
W20P	P	-0.183	-0.183	-0.060	0.065	0.008	1.000	0.879***	-0.177	-0.052	0.023	-0.039	0.012	-0.115	-0.105	-0.113	0.619***	-0.117	0.665***
	G	-0.184	-0.184	-0.061	0.066	0.008	1.000	0.933***	-0.177	-0.052	0.023	-0.039	0.012	-0.115	-0.105	-0.113	0.726***	-0.118	0.667***
SPW	P	-0.240	-0.349	-0.143	0.175	-0.097	0.879***	1.000	-0.084	-0.007	-0.021	-0.091	0.027	-0.084	-0.070	-0.080	0.429*	0.043	0.475**
	G	-0.255	-0.372*	-0.151	0.189	-0.103	0.933***	1.000	-0.090	-0.008	-0.023	-0.097	0.029	-0.089	-0.074	-0.085	0.532**	0.046	0.504**
W20S	P	-0.064	-0.178	0.000	-0.017	0.249	-0.177	-0.084	1.000	0.388*	-0.094	-0.091	-0.376*	0.232	0.196	0.207	-0.256	0.537**	-0.279
	G	-0.065	-0.179	0.000	-0.017	0.251	-0.177	-0.090	1.000	0.389*	-0.094	-0.092	-0.381*	0.232	0.197	0.208	-0.301	0.541**	-0.280
PH	P	0.143	-0.026	0.404*	-0.185	0.267	-0.052	-0.007	0.388*	1.000	0.068	0.184	-0.085	0.635***	0.606***	0.610***	-0.232	0.057	-0.090
	G	0.144	-0.026	0.405*	-0.188	0.268	-0.052	-0.008	0.389*	1.000	0.068	0.184	-0.086	0.635***	0.606***	0.611***	-0.272	0.057	-0.090
DM	P	0.365*	0.065	0.227	-0.440*	0.093	0.023	-0.021	-0.094	0.068	1.000	0.713***	0.242	0.198	0.204	0.199	0.005	-0.178	0.049
	G	0.368*	0.066	0.227	-0.448*	0.094	0.023	-0.023	-0.094	0.068	1.000	0.717***	0.246	0.198	0.204	0.199	0.006	-0.179	0.049
DFPP	P	0.490**	0.159	0.399*	-0.590***	0.274	-0.039	-0.091	-0.091	0.184	0.713***	1.000	0.181	0.172	0.154	0.155	0.079	-0.322	0.068
	G	0.493**	0.160	0.401*	-0.603***	0.277	-0.039	-0.097	-0.092	0.184	0.717***	1.000	0.184	0.172	0.155	0.156	0.092	-0.325	0.068
DFFK	P	0.184	0.151	-0.008	0.121	-0.055	0.012	0.027	-0.376*	-0.085	0.242	0.181	1.000	-0.086	-0.073	-0.075	0.117	-0.256	0.117
	G	0.187	0.154	-0.008	0.125	-0.056	0.012	0.029	-0.381*	-0.086	0.246	0.184	1.000	-0.087	-0.074	-0.076	0.139	-0.260	0.119
TSS	P	0.249	0.146	0.471**	-0.147	0.250	-0.115	-0.084	0.232	0.635***	0.198	0.172	-0.086	1.000	0.980***	0.984***	-0.171	-0.023	0.002
	G	0.250	0.147	0.472**	-0.150	0.251	-0.115	-0.089	0.232	0.635***	0.198	0.172	-0.087	1.000	0.980***	0.984***	-0.200	-0.023	0.002
TPC	P	0.252	0.133	0.477**	-0.144	0.234	-0.105	-0.070	0.196	0.606***	0.204	0.154	-0.073	0.980***	1.000	0.999***	-0.122	-0.045	0.001
	G	0.253	0.134	0.478**	-0.146	0.235	-0.105	-0.074	0.197	0.606***	0.204	0.155	-0.074	0.980***	1.000	0.999***	-0.143	-0.045	0.001

Table 3a continued....

Table 3a continued....

TSC	P	0.255	0.129	0.475**	-0.143	0.236	-0.113	-0.080	0.207	0.610***	0.199	0.155	-0.075	0.984***	0.999***	1.000	-0.135	-0.036	-0.009
	G	0.256	0.129	0.476**	-0.145	0.237	-0.113	-0.085	0.208	0.611***	0.199	0.156	-0.076	0.984***	0.999***	1.000	-0.158	-0.037	-0.009
PWP	P	0.034	0.483**	0.320	-0.115	0.305	0.619***	0.429*	-0.256	-0.232	0.005	0.079	0.117	-0.171	-0.122	-0.135	1.000	-0.481**	0.865***
	G	0.039	0.568**	0.375*	-0.137	0.360	0.726***	0.532**	-0.301	-0.272	0.006	0.092	0.139	-0.200	-0.143	-0.158	1.000	-0.566**	1.015***
HSW	P	-0.235	-0.606***	-0.608***	0.199	-0.674***	-0.117	0.043	0.537**	0.057	-0.178	-0.322	-0.256	-0.023	-0.045	-0.036	-0.481**	1.000	-0.540**
	G	-0.237	-0.611***	-0.612***	0.203	-0.680***	-0.118	0.046	0.541**	0.057	-0.179	-0.325	-0.260	-0.023	-0.045	-0.037	-0.566**	1.000	-0.543**
PYH	P	0.146	0.606***	0.360	-0.035	0.350	0.665***	0.475**	-0.279	-0.090	0.049	0.068	0.117	0.002	0.001	-0.009	0.865***	-0.540**	1.000
	G	0.146	0.610***	0.361*	-0.036	0.353	0.667***	0.504**	-0.280	-0.090	0.049	0.068	0.119	0.002	0.001	-0.009	1.015***	-0.543**	1.000

(21.65), days to maturity (16.14), weight of 20 pod seeds (13.68), pod weight per plant (13.61), days to first pod picking (13.17), 100-seed weight at edible stage (13.05) and weight of 20 pods (12.05).

The genetic advance as percentage of mean (GAM) ranged from 1.38 per cent for Days to First Pod Picking (DFPP) to 50.36 per cent for total protein content (TPC). High GAM (>20%) was recorded for total protein content (50.36%), total sugar content (33.65%), 100-seed weight at edible stage (32.14%), plant height at edible stage (28.22%), number of seeds per pod (26.71%), pod length (24.27%), number of pods per plant (23.67%), total soluble solids (22.77%) and pod yield per hectare (22.29%).

Moderate GAM (10–20%) was observed for days to flowering (16.19%), pod width (16.57%), weight of 20 pods (11.05%), weight of single pod at edible stage (10.96%), weight of 20 pod seeds (19.13%), days to maturity (17.48%) and days to first pod picking (17.45%). Low GAM (<10%) was recorded for days to first fruiting knot (1.38%) and pod weight per plant (1.41%). The present estimates are broadly in accordance with previous reports of Gudadinni *et al*. (2017), Pathak *et al*. (2019), Gupta *et al*. (2020) and Kaur *et al*. (2023).

The combination of high heritability along with high GAM observed for number of pods per plant, pod length, number of seeds per pod, plant height at edible stage, total protein content, total sugar content, 100-seed weight and pod yield per hectare suggested the predominance of additive gene action and indicated that these traits could be improved effectively through simple selection. On the other hand, traits such as days to first fruiting knot and pod weight per plant exhibited low heritability coupled with low GAM, indicating greater environmental influence and the possible involvement of non-additive gene action.

Correlation coefficient analysis

Genotypic and phenotypic correlation coefficients among the studied traits in the F_1 and F_2 generations are presented in Tables 3a and 3b. In general, genotypic and phenotypic correlations were similar in direction, with genotypic associations being slightly stronger for several trait combinations, suggesting a substantial genetic contribution to the observed relationships.

In the F_1 generation, number of pods per plant (NPP) exhibited strong positive associations with pod length (0.562), number of seeds per pod (0.484), pod weight per plant (0.568) and pod yield per hectare (0.610). Conversely, NPP was negatively associated with 100-seed weight (–0.611). Similar relationships were observed at the phenotypic level and were also maintained in the F_2 generation, emphasizing the importance of pod number

as a major yield-associated trait.

Pod length was positively associated with number of seeds per pod (0.695), NPP (0.562), total soluble solids (0.472), total protein content (0.478) and total sugar content (0.476), while negative associations were observed with pod width (–0.444) and 100-seed weight (–0.612). These associations were broadly consistent between genotypic and phenotypic estimates and persisted in F_2.

Pod weight-related traits showed particularly strong relationships with yield. Weight of 20 pods was strongly and positively correlated with single pod weight (0.933), pod weight per plant (0.726) and pod yield per hectare (0.667). Likewise, single pod weight was positively associated with pod weight per plant (0.532) and pod yield per hectare (0.504). These relationships were generally consistent at the phenotypic level and in F_2, indicating that pod weight components represent important yield-associated traits.

The maturity-related traits were strongly interrelated. Days to flowering showed significant positive associations with days to maturity (0.368) and days to first pod picking (0.493), whereas days to maturity was strongly correlated with days to first pod picking (0.717). Pod width exhibited significant negative associations with pod length, days to maturity and days to first pod picking.

A strong positive interrelationship was observed among the biochemical quality traits. Total soluble solids showed very strong positive correlations with total protein content (0.980) and total sugar content (0.984), while total protein and total sugar contents were almost perfectly correlated (0.999). Plant height was also positively associated with these quality attributes. Similar relationships were observed in the F_2 generation, indicating a stable association among biochemical quality traits.

In contrast, 100-seed weight exhibited strong negative associations with major yield components, including NPP (–0.611), number of seeds per pod (–0.680), pod length (–0.612), pod weight per plant (–0.566) and pod yield per hectare (–0.543). This inverse relationship was also evident at the phenotypic level and in F_2, suggesting a potential trade-off between seed size and pod-yield components. These results are in agreement with the observations of Prasad *et al*. (2019), Prajapati *et al*. (2022), Uhlarik *et al*. (2022), Panwar *et al*. (2023) and Kumar *et al*. (2023).

Most importantly, pod yield per hectare showed strong positive associations with pod weight per plant, weight of 20 pods, NPP, single pod weight and pod length, whereas 100-seed weight was negatively associated with yield. At the phenotypic level, pod weight per plant (0.865), weight of 20 pods (0.665) and NPP (0.606) were the strongest positive yield associations. These relationships were largely retained in F_2, identifying pod weight per plant, pod weight, pod number and single pod weight as promising indirect selection criteria for improving pod yield.

Path coefficient analysis

Path coefficient analysis was performed at both genotypic and phenotypic levels in the F_1 and F_2 generations to partition the correlation of component traits with pod yield per hectare (YPH) into direct and indirect effects. The analysis revealed considerable variation in the magnitude and direction of path coefficients, demonstrating complex interrelationships among yield components, maturity traits and quality attributes (Table 4a-b).

In the F_1 generation at the genotypic level, number of pods plant^{-1} (NPP) and pod weight plant^{-1} (PWP) exhibited the highest positive direct effects on YPH, with values of 1.0300 and 1.0150, respectively. These were followed by TSS (0.7056), pod length (PL; 0.5904), hundred-seed weight (HSW; 0.4509) and number of seeds pod^{-1} (NSP; 0.3716). Smaller positive effects were observed for SPW, TSC, TPC, W20P and DFPP. Negative direct effects were recorded for pod width (PW; –0.2168), W20S (–0.1755), days to maturity (DM; –0.1397), days to flowering (DF; –0.1015) and plant height (PH; –0.0537). At the phenotypic level, W20P (1.1325) and NPP (1.1019) showed the strongest positive direct effects, followed by TSS (0.7628), PL (0.6218) and TSC (0.5539), whereas TPC (–1.2291) and SPW (–0.7725) showed pronounced negative direct effects.

In the F_2 generation, TSC (1.6192) and TPC (1.6170) showed the largest positive genotypic direct effects, followed by NPP (0.8823) and SPW (0.5699). Positive effects were also observed for W20P, HSW, PWP and DM, while negative effects were recorded for TSS, PL, NSP, DFFK, W20S, DF, PW and DFPP. At the phenotypic level, NPP (0.7709) and W20P (0.6698) remained the major positive direct contributors, followed by TPC (0.3627) and TSC (0.3439). Conversely, HSW (–0.2544) and NSP (–0.2292) showed the strongest negative direct effects.

The indirect-effect analysis highlighted NPP as a key determinant of YPH. In F_1, NPP showed highly positive associations with YPH at both genotypic (0.610) and phenotypic (0.606) levels. Its genotypic association was mainly mediated through PL (1.0300), TSS (0.2450),

Table 3b : Genotypic and Phenotypic correlation coefficients analysis of F_{2s} for different Yield traits in garden pea.

Traits		DF	NPP	PL	PW	NSP	W20P	SPW	W20S	PH	DM	DFPP	DFFK	TSS	TPC	TSC	PWP	HSW	PYH
DF	P	1.000	0.399*	0.078	-0.055	0.165	-0.183	-0.240	-0.064	0.143	0.365*	0.490**	0.184	0.249	0.252	0.255	0.034	-0.235	0.146
	G	1.000	0.403*	0.079	-0.056	0.167	-0.184	-0.255	-0.065	0.144	0.368*	0.493**	0.187	0.250	0.253	0.256	0.039	-0.237	0.146
NPP	P	0.399*	1.000	0.558**	-0.160	0.479**	-0.183	-0.349	-0.178	-0.026	0.065	0.159	0.151	0.146	0.133	0.129	0.483**	-0.606***	0.606***
	G	0.403*	1.000	0.562**	-0.163	0.484**	-0.184	-0.372*	-0.179	-0.026	0.066	0.160	0.154	0.147	0.134	0.129	0.568**	-0.611***	0.610***
PL	P	0.078	0.558**	1.000	-0.436*	0.689***	-0.060	-0.143	0.000	0.404*	0.227	0.399*	-0.008	0.471**	0.477**	0.475**	0.320	-0.608***	0.360
	G	0.079	0.562**	1.000	-0.444*	0.695***	-0.061	-0.151	0.000	0.405*	0.227	0.401*	-0.008	0.472**	0.478**	0.476**	0.375*	-0.612***	0.361*
PW	P	-0.055	-0.160	-0.436*	1.000	-0.229	0.065	0.175	-0.017	-0.185	-0.440*	-0.590***	0.121	-0.147	-0.144	-0.143	-0.115	0.199	-0.035
	G	-0.056	-0.163	-0.444*	1.000	-0.234	0.066	0.189	-0.017	-0.188	-0.448*	-0.603***	0.125	-0.150	-0.146	-0.145	-0.137	0.203	-0.036
NSP	P	0.165	0.479**	0.689***	-0.229	1.000	0.008	-0.097	0.249	0.267	0.093	0.274	-0.055	0.250	0.234	0.236	0.305	-0.674***	0.350
	G	0.167	0.484**	0.695***	-0.234	1.000	0.008	-0.103	0.251	0.268	0.094	0.277	-0.056	0.251	0.235	0.237	0.360	-0.680***	0.353
W20P	P	-0.183	-0.183	-0.060	0.065	0.008	1.000	0.879***	-0.177	-0.052	0.023	-0.039	0.012	-0.115	-0.105	-0.113	0.619***	-0.117	0.665***
	G	-0.184	-0.184	-0.061	0.066	0.008	1.000	0.933***	-0.177	-0.052	0.023	-0.039	0.012	-0.115	-0.105	-0.113	0.726***	-0.118	0.667***
SPW	P	-0.240	-0.349	-0.143	0.175	-0.097	0.879***	1.000	-0.084	-0.007	-0.021	-0.091	0.027	-0.084	-0.070	-0.080	0.429*	0.043	0.475**
	G	-0.255	-0.372*	-0.151	0.189	-0.103	0.933***	1.000	-0.090	-0.008	-0.023	-0.097	0.029	-0.089	-0.074	-0.085	0.532**	0.046	0.504**
W20S	P	-0.064	-0.178	0.000	-0.017	0.249	-0.177	-0.084	1.000	0.388*	-0.094	-0.091	-0.376*	0.232	0.196	0.207	-0.256	0.537**	-0.279
	G	-0.065	-0.179	0.000	-0.017	0.251	-0.177	-0.090	1.000	0.389*	-0.094	-0.092	-0.381*	0.232	0.197	0.208	-0.301	0.541**	-0.280
PH	P	0.143	-0.026	0.404*	-0.185	0.267	-0.052	-0.007	0.388*	1.000	0.068	0.184	-0.085	0.635***	0.606***	0.610***	-0.232	0.057	-0.090
	G	0.144	-0.026	0.405*	-0.188	0.268	-0.052	-0.008	0.389*	1.000	0.068	0.184	-0.086	0.635***	0.606***	0.611***	-0.272	0.057	-0.090
DM	P	0.365*	0.065	0.227	-0.440*	0.093	0.023	-0.021	-0.094	0.068	1.000	0.713***	0.242	0.198	0.204	0.199	0.005	-0.178	0.049
	G	0.368*	0.066	0.227	-0.448*	0.094	0.023	-0.023	-0.094	0.068	1.000	0.717***	0.246	0.198	0.204	0.199	0.006	-0.179	0.049
DFPP	P	0.490**	0.159	0.399*	-0.590***	0.274	-0.039	-0.091	-0.091	0.184	0.713***	1.000	0.181	0.172	0.154	0.155	0.079	-0.322	0.068
	G	0.493**	0.160	0.401*	-0.603***	0.277	-0.039	-0.097	-0.092	0.184	0.717***	1.000	0.184	0.172	0.155	0.156	0.092	-0.325	0.068
DFFK	P	0.184	0.151	-0.008	0.121	-0.055	0.012	0.027	-0.376*	-0.085	0.242	0.181	1.000	-0.086	-0.073	-0.075	0.117	-0.256	0.117
	G	0.187	0.154	-0.008	0.125	-0.056	0.012	0.029	-0.381*	-0.086	0.246	0.184	1.000	-0.087	-0.074	-0.076	0.139	-0.260	0.119
TSS	P	0.249	0.146	0.471**	-0.147	0.250	-0.115	-0.084	0.232	0.635***	0.198	0.172	-0.086	1.000	0.980***	0.984***	-0.171	-0.023	0.002
	G	0.250	0.147	0.472**	-0.150	0.251	-0.115	-0.089	0.232	0.635***	0.198	0.172	-0.087	1.000	0.980***	0.984***	-0.200	-0.023	0.002
TPC	P	0.252	0.133	0.477**	-0.144	0.234	-0.105	-0.070	0.196	0.606***	0.204	0.154	-0.073	0.980***	1.000	0.999***	-0.122	-0.045	0.001
	G	0.253	0.134	0.478**	-0.146	0.235	-0.105	-0.074	0.197	0.606***	0.204	0.155	-0.074	0.980***	1.000	0.999***	-0.143	-0.045	0.001

Table 3b continued....

Table 3b continued....

TSC	P	0.255	0.129	0.475**	-0.143	0.236	-0.113	-0.080	0.207	0.610***	0.199	0.155	-0.075	0.984***	0.999***	1.000	-0.135	-0.036	-0.009
	G	0.256	0.129	0.476**	-0.145	0.237	-0.113	-0.085	0.208	0.611***	0.199	0.156	-0.076	0.984***	0.999***	1.000	-0.158	-0.037	-0.009
PWP	P	0.034	0.483**	0.320	-0.115	0.305	0.619***	0.429*	-0.256	-0.232	0.005	0.079	0.117	-0.171	-0.122	-0.135	1.000	-0.481**	0.865***
	G	0.039	0.568**	0.375*	-0.137	0.360	0.726***	0.532**	-0.301	-0.272	0.006	0.092	0.139	-0.200	-0.143	-0.158	1.000	-0.566**	1.015***
HSW	P	-0.235	-0.606***	-0.608***	0.199	-0.674***	-0.117	0.043	0.537**	0.057	-0.178	-0.322	-0.256	-0.023	-0.045	-0.036	-0.481**	1.000	-0.540**
	G	-0.237	-0.611***	-0.612***	0.203	-0.680***	-0.118	0.046	0.541**	0.057	-0.179	-0.325	-0.260	-0.023	-0.045	-0.037	-0.566**	1.000	-0.543**
PYH	P	0.146	0.606***	0.360	-0.035	0.350	0.665***	0.475**	-0.279	-0.090	0.049	0.068	0.117	0.002	0.001	-0.009	0.865***	-0.540**	1.000
	G	0.146	0.610***	0.361*	-0.036	0.353	0.667***	0.504**	-0.280	-0.090	0.049	0.068	0.119	0.002	0.001	-0.009	1.015***	-0.543**	1.000

W20P (0.2236) and TSC (0.0734), although negative contributions through TPC and HSW partially reduced the overall association. In F_2, NPP maintained a strong positive relationship with YPH, with PL (0.8823), PWP (0.5010) and TSC (0.2094) contributing positively at the genotypic level, while PL (0.7709) and PWP (0.3723) were important phenotypic pathways.

Pod length exhibited a positive association with YPH in both generations. In F_1, its genotypic association (0.361) was primarily mediated through NPP (0.5904), TSS (0.3264), W20P (0.1781) and TSC (0.0903). At the phenotypic level, NPP (0.6218), TSS (0.3496) and TSC (0.2400) were the principal positive pathways. NSP also showed a positive association with YPH, largely through NPP, whereas pod width showed a weak negative association (–0.036).

Among the pod-weight traits, W20P and SPW showed favourable associations with YPH. W20P exhibited highly significant positive correlations of 0.667 and 0.665 at genotypic and phenotypic levels, respectively, in F_1. Similarly, SPW showed positive associations of 0.504 and 0.475. Their favourable relationships were supported by contributions from other pod-weight and quality traits, although negative effects through TPC and HSW were also evident. In contrast, W20S showed a negative association (–0.280) with YPH, mainly because of negative pathways involving NPP, TPC and HSW.

Plant height showed a weak negative association with YPH (–0.090), despite positive indirect effects through NPP, TSS and TSC. Similarly, DM and DFPP exhibited only weak positive associations with yield (0.049 and 0.068, respectively), while DFFK showed a modest positive association (0.119). The relatively low net associations of these traits resulted from opposing indirect effects through yield components and quality attributes.

The quality traits TSS, TPC and TSC exhibited negligible overall associations with YPH, despite substantial direct and indirect effects. TSS showed an association of only 0.002, whereas TPC showed 0.001 and TSC –0.009. Their weak net relationships resulted from strong positive contributions through NPP and other quality traits being offset by substantial negative pathways, particularly through TPC.

Notably, PWP exhibited the strongest association with YPH, with genotypic and phenotypic values of approximately 1.015 and 0.865, respectively. In F_1, its association was supported mainly through NPP (0.8840), W20S (0.3073) and TPC (0.2795), while in F_2, NPP (0.5010), SPW (0.3032), TPC (0.2165) and W20P (0.1872) were important positive pathways.

Table 4a : Genotypic and Phenotypic path coefficient analysis of F_{1s} (Hybrids) for different Yield traits in garden pea.

Traits		DF	NPP	PL	PW	NSP	W20P	SPW	W20S	PH	DM	DFPP	DFFK	TSS	TPC	TSC	PWP	HSW	YPH
DF	P	-0.0097	0.3355	0.0013	0.0021	-0.0449	-0.1029	0.0683	0.0131	-0.0098	-0.0289	-0.0238	0.0048	0.1616	-0.2874	0.1282	0	0.013	0.146
	G	-0.1015	0.3173	0.001	0.0013	0.0894	-0.0184	-0.0188	-0.0135	-0.0075	-0.0419	0.0467	0.0057	0.1502	-0.1878	0.0481	-0.0001	-0.0448	0.146
NPP	P	-0.0029	1.1019	-0.0456	-0.0056	-0.112	0.0064	-0.0025	-0.0493	-0.0323	-0.0343	-0.0273	0.0044	0.2632	-0.4385	0.1955	-0.0008	0.0904	0.606***
	G	-0.0313	1.03	-0.0351	-0.0034	0.2236	0.0012	0.0007	0.0507	-0.0248	-0.0498	0.0537	0.0053	0.245	-0.2869	0.0734	-0.0093	-0.3107	0.610***
PL	P	0.0002	0.6218	-0.0808	-0.0083	-0.089	0.2211	-0.1408	0.0265	-0.0335	0.0026	-0.0066	-0.0017	0.3496	-0.5314	0.24	-0.0004	0.0499	0.360
	G	0.0017	0.5904	-0.0612	-0.0051	0.1781	0.0398	0.0389	-0.0273	-0.0258	0.0039	0.0129	-0.002	0.3264	-0.3486	0.0903	-0.0045	-0.172	0.361*
PW	P	-0.0007	-0.2275	0.0249	0.027	0.0624	-0.1114	0.0758	-0.003	0.015	-0.0144	-0.0128	-0.0035	-0.1433	0.1395	-0.0748	0.0002	-0.0346	-0.035
	G	-0.0079	-0.2168	0.0193	0.0162	-0.1253	-0.0201	-0.021	0.0031	0.0116	-0.021	0.0252	-0.0042	-0.1343	0.0918	-0.0282	0.0021	0.1198	-0.036
NSP	P	-0.0022	0.6207	-0.0361	-0.0085	-0.1989	0.0487	-0.0283	0.022	-0.0119	0.0044	0.0012	-0.004	0.1479	-0.2079	0.0951	0	0.1014	0.350
	G	-0.0244	0.6198	-0.0294	-0.0055	0.3716	0.0092	0.0082	-0.0239	-0.0096	0.0068	-0.0024	-0.005	0.1452	-0.1435	0.0376	-0.0002	-0.3677	0.353
W20P	P	0.0009	0.0063	-0.0158	-0.0027	-0.0086	1.1325	-0.7723	-0.0017	-0.0126	-0.0037	0.0078	-0.0014	0.0554	-0.1199	0.0495	-0.0005	0.0152	0.665***
	G	0.0093	0.0059	-0.0121	-0.0016	0.017	0.2013	0.2118	0.0017	-0.0097	-0.0053	-0.0154	-0.0017	0.0514	-0.0781	0.0185	-0.0062	-0.0519	0.667***
SPW	P	0.0009	0.0035	-0.0147	-0.0027	-0.0073	1.1322	-0.7725	-0.0032	-0.0125	-0.0037	0.0079	-0.0013	0.0507	-0.1138	0.0467	-0.0005	0.0149	0.475**
	G	0.009	0.0033	-0.0113	-0.0016	0.0145	0.2024	0.2106	0.0033	-0.0095	-0.0054	-0.0154	-0.0016	0.047	-0.0742	0.0175	-0.0062	-0.0512	0.504**
W20S	P	-0.0007	-0.3153	-0.0124	-0.0005	-0.0254	-0.0112	0.0142	0.1721	-0.0059	0.011	0.0132	0.004	0.1499	-0.2571	0.1146	0.0016	-0.0611	-0.279
	G	-0.0078	-0.2974	-0.0095	-0.0003	0.0506	-0.002	-0.0039	-0.1755	-0.0045	0.016	-0.0259	0.0048	0.139	-0.1676	0.0428	0.019	0.2092	-0.280
PH	P	-0.0014	0.5048	-0.0384	-0.0057	-0.0334	0.2031	-0.1364	0.0143	-0.0705	-0.0011	-0.0149	0.0125	0.4571	-0.7137	0.3208	-0.0004	0.0248	-0.090
	G	-0.0142	0.4755	-0.0294	-0.0035	0.0664	0.0362	0.0374	-0.0147	-0.0537	-0.0016	0.0291	0.0149	0.4234	-0.4645	0.1198	-0.0053	-0.0847	-0.090
DM	P	-0.0029	0.3891	0.0022	0.004	0.009	0.0429	-0.0298	-0.0196	-0.0008	-0.0971	-0.0349	0.0074	0.0091	-0.0662	0.0257	0.001	0.0086	0.049
	G	-0.0305	0.3671	0.0017	0.0024	-0.018	0.0077	0.0082	0.0201	-0.0006	-0.1397	0.0683	0.0088	0.0084	-0.0431	0.0096	0.0117	-0.0293	0.049
DFPP	P	-0.0043	0.5664	-0.01	0.0065	0.0044	-0.1672	0.1145	-0.0428	-0.0197	-0.0637	-0.0532	0.0096	0.0767	-0.1028	0.0426	-0.0005	0.0263	0.068
	G	-0.0459	0.5353	-0.0077	0.004	-0.0087	-0.0299	-0.0315	0.044	-0.0151	-0.0925	0.1032	0.0115	0.0713	-0.0671	0.0159	-0.0058	-0.0901	0.068
DFFK	P	-0.0017	0.1781	0.0049	-0.0034	0.0288	-0.0588	0.0379	0.0254	-0.0323	-0.0261	-0.0186	0.0274	0.1607	-0.2734	0.1261	0	-0.0312	0.117
	G	-0.2812	2.6412	0.0593	-0.0327	-0.9012	-0.1653	-0.1635	-0.4089	-0.3878	-0.5942	0.5733	0.0021	2.3439	-2.8018	0.7412	0.0025	1.6785	0.119
TSS	P	-0.0021	0.3802	-0.037	-0.0051	-0.0386	0.0823	-0.0513	0.0338	-0.0423	-0.0012	-0.0053	0.0058	0.7628	-1.2052	0.5452	0.0002	0.013	0.002
	G	-0.0216	0.3577	-0.0283	-0.0031	0.0765	0.0147	0.014	-0.0346	-0.0322	-0.0017	0.0104	0.0069	0.7056	-0.7835	0.2033	0.0029	-0.0443	0.002
TPC	P	-0.0023	0.3931	-0.0349	-0.0031	-0.0336	0.1104	-0.0715	0.036	-0.0409	-0.0052	-0.0044	0.0061	0.7479	-1.2291	0.5531	0.0003	0.0085	0.001
	G	-0.0238	0.3698	-0.0267	-0.0019	0.0667	0.0197	0.0196	-0.0368	-0.0312	-0.0075	0.0087	0.0073	0.6918	-0.7991	0.2063	0.0038	-0.0289	0.001

Table 4a continued....

Table 4a continued....

TSC	P	-0.0022	0.3889	-0.035	-0.0036	-0.0341	0.1013	-0.0651	0.0356	-0.0408	-0.0045	-0.0041	0.0062	0.7508	-1.2275	0.5539	0.0002	0.0084	-0.009
	G	-0.0236	0.3659	-0.0268	-0.0022	0.0677	0.018	0.0178	-0.0364	-0.0311	-0.0065	0.008	0.0074	0.6945	-0.798	0.2066	0.0029	-0.0287	-0.009
PWP	P	0	0.1451	-0.0052	-0.0008	-0.0004	0.0997	-0.0681	-0.0464	-0.0053	0.0161	-0.0044	-0.0001	-0.0319	0.0664	-0.0232	-0.0059	0.0248	0.865***
	G	-0.0013	0.884	-0.0256	-0.0032	0.0055	0.1151	0.1207	0.3073	-0.0264	0.1508	0.0553	-0.0005	-0.1913	0.2795	-0.0561	-0.0108	-0.5476	1.015***
HSW	P	0.001	-0.75	0.0304	0.007	0.1519	-0.1293	0.0869	0.0792	0.0132	0.0063	0.0105	0.0064	-0.0746	0.0783	-0.035	0.0011	-0.1328	-0.540**
	G	0.0101	-0.7096	0.0234	0.0043	-0.303	-0.0232	-0.0239	-0.0814	0.0101	0.0091	-0.0206	0.0077	-0.0694	0.0512	-0.0131	0.0131	0.4509	-0.543**

Phenotypic residual 0.17490514, Genotypic residual 0.09663987

Table 4b : Genotypic and Phenotypic path coefficient analysis of F_{2s} for different Yield traits in in garden pea.

Traits		DF	NPP	PL	PW	NSP	W20P	SPW	W20S	PH	DM	DFPP	DFFK	TSS	TPC	TSC	PWP	HSW	YPH
DF	P	-0.0023	0.308	0.0019	-0.0012	-0.0379	-0.1224	-0.0399	-0.012	-0.0065	-0.0043	0.0041	-0.0039	0.006	-0.0913	0.0877	-0.0002	0.0599	0.146
	G	-0.0316	0.3553	-0.0065	0.0012	-0.0163	-0.0473	-0.1454	-0.0035	0.0003	0.0118	-0.0007	-0.0118	-0.028	-0.3814	0.4143	0.0019	0.0344	0.146
NPP	P	-0.0009	0.7709	0.0134	-0.0034	-0.1099	-0.1226	-0.0581	-0.0332	0.0012	-0.0008	0.0013	-0.0032	0.0035	-0.0483	0.0443	-0.0027	0.1541	0.606***
	G	-0.0127	0.8823	-0.0466	0.0035	-0.0472	-0.0474	-0.2118	-0.0097	0.074	0.0021	-0.0002	-0.0097	-0.0165	-0.2018	0.2094	0.0275	0.0885	0.610***
PL	P	-0.0002	0.4301	0.024	-0.0092	-0.158	-0.0405	-0.0237	-0.076	-0.0184	-0.0027	0.0034	0.0002	0.0114	-0.1729	0.1633	-0.0018	0.1547	0.360
	G	-0.0025	0.4955	-0.083	0.0096	-0.0677	-0.0156	-0.0863	-0.028	0.0008	0.0073	-0.0006	0.0005	-0.0528	-0.7213	0.7706	0.0182	0.0887	0.361*
PW	P	0.0001	-0.1234	-0.0105	0.0211	0.0524	0.0435	0.0291	-0.0031	0.0084	0.0052	-0.005	-0.0026	-0.0036	0.0521	-0.049	0.0006	-0.0505	-0.035
	G	0.0018	-0.1442	0.0369	-0.0216	0.0228	0.017	0.1076	-0.0009	-0.0003	-0.0144	0.0009	-0.0079	0.0167	0.2208	-0.2347	-0.0066	-0.0294	-0.036
NSP	P	-0.0004	0.3696	0.0165	-0.0048	-0.2292	0.0056	-0.0161	0.0465	-0.0122	-0.0011	0.0023	0.0012	0.006	-0.0848	0.0812	-0.0017	0.1713	0.350
	G	-0.0053	0.4272	-0.0577	0.0051	-0.0975	0.0022	-0.0589	0.0136	0.0005	0.003	-0.0004	0.0035	-0.0281	-0.3549	0.3843	0.0174	0.0985	0.353
W20P	P	0.0004	-0.1411	-0.0015	0.0014	-0.0019	0.6698	0.1463	-0.033	0.0024	-0.0003	-0.0003	-0.0003	-0.0028	0.038	-0.0388	-0.0034	0.0298	0.665***
	G	0.0058	-0.1623	0.005	-0.0014	-0.0008	0.258	0.5316	-0.0096	-0.0001	0.0007	0.0001	-0.0008	0.0129	0.1583	-0.1829	0.0351	0.0171	0.667***
SPW	P	0.0005	-0.269	-0.0034	0.0037	0.0222	0.5886	0.1665	-0.0157	0.0003	0.0003	-0.0008	-0.0006	-0.002	0.0253	-0.0277	-0.0024	-0.011	0.475**
	G	0.0081	-0.328	0.0126	-0.0041	0.0101	0.2406	0.5699	-0.0049	0.0125	-0.0007	0.0001	-0.0018	0.01	0.1117	-0.1382	0.0258	-0.0067	0.504**
W20S	P	0.0001	-0.1371	-0.076	-0.0004	-0.0572	-0.1185	-0.014	0.1866	-0.0177	0.0011	-0.0008	0.008	0.0056	-0.0711	0.0712	0.0014	-0.1366	-0.279
	G	0.002	-0.158	-0.028	0.0004	-0.0245	-0.0458	-0.0511	0.0542	0.0007	-0.003	0.0001	0.0241	-0.026	-0.2968	0.336	-0.0146	-0.0783	-0.280
PH	P	-0.0003	-0.0197	0.0097	-0.0039	-0.0611	-0.0345	-0.0012	0.0723	-0.0457	-0.0008	0.0015	0.0018	0.0154	-0.2197	0.2097	0.0013	-0.0145	-0.090
	G	-0.0045	-0.0227	-0.0336	0.0041	-0.0262	-0.0133	-0.0045	0.0211	0.0019	0.0022	-0.0003	0.0054	-0.0712	-0.9155	0.9887	-0.0132	-0.0083	-0.090
DM	P	-0.0008	0.0502	0.0054	-0.0093	-0.0213	0.0155	-0.0036	-0.0175	-0.0031	-0.0117	0.006	-0.0052	0.0048	-0.0739	0.0683	0.074	0.0452	0.049
	G	-0.0116	0.0578	-0.0189	0.0097	-0.0091	0.006	-0.0129	-0.0051	0.0001	0.032	-0.0011	-0.0156	-0.0222	-0.3084	0.3222	0.0003	0.0259	0.049
DFPP	P	-0.0011	0.1223	0.0096	-0.0125	-0.0629	-0.026	-0.0152	-0.017	-0.0084	-0.0084	0.0084	-0.0039	0.0042	-0.0559	0.0533	-0.0004	0.0819	0.068
	G	-0.0156	0.1411	-0.0333	0.013	-0.027	-0.0101	-0.0555	-0.005	0.0003	0.023	-0.0015	-0.0117	-0.0193	-0.2337	0.2519	0.0045	0.047	0.068

Table 4b continued....

Table 4b continued....

DFFK	P	-0.0004	0.1164	-0.0002	0.0026	0.0125	0.0079	0.0045	-0.0701	0.0039	-0.0028	0.0015	-0.0214	-0.0021	0.0264	-0.0257	-0.0006	0.065	0.117
	G	-0.0059	0.1356	0.0007	-0.0027	0.0054	0.0031	0.0165	-0.0207	-0.0002	0.0079	-0.0003	-0.0632	0.0097	0.1113	-0.1225	0.0067	0.0377	0.119
TSS	P	-0.0006	0.1129	0.0113	-0.0031	-0.0572	-0.0769	-0.014	0.0433	-0.029	-0.0023	0.0014	0.0018	0.0242	-0.3556	0.3385	0.0009	0.0058	0.002
	G	-0.0079	0.1298	-0.0392	0.0032	-0.0245	-0.0296	-0.0508	0.0126	0.0012	0.0064	-0.0003	0.0055	-0.112	-1.4804	1.5938	-0.0097	0.0033	0.002
TPC	P	-0.0006	0.1026	0.0114	-0.003	-0.0536	-0.0702	-0.0116	0.0366	-0.0277	-0.0024	0.0013	0.0016	0.0237	-0.3627	0.3434	0.0007	0.0114	0.001
	G	-0.008	0.1179	-0.0397	0.0032	-0.0229	-0.027	-0.0422	0.0107	0.0011	0.0065	-0.0002	0.0047	-0.1098	-1.5099	1.617	-0.0069	0.0065	0.001
TSC	P	-0.0006	0.0992	0.0114	-0.003	-0.0541	-0.0756	-0.0134	0.0386	-0.0279	-0.0023	0.0013	0.0016	0.0238	-0.3622	0.3439	0.0007	0.0093	-0.009
	G	-0.0081	0.1141	-0.0395	0.0031	-0.0231	-0.0291	-0.0486	0.0113	0.0011	0.0064	-0.0002	0.0048	-0.1102	-1.5078	1.6192	-0.0077	0.0053	-0.009
PWP	P	-0.0001	0.3723	0.0077	-0.0024	-0.07	0.4147	0.0713	-0.0478	0.0106	-0.0001	0.0007	-0.0025	-0.0041	0.0444	-0.0464	-0.0055	0.1225	0.865***
	G	-0.0012	0.501	-0.0311	0.003	-0.0351	0.1872	0.3032	-0.0163	-0.0005	0.0002	-0.0001	-0.0088	0.0224	0.2165	-0.256	0.0484	0.082	1.015***
HSW	P	0.0005	-0.4671	-0.0146	0.0042	0.1544	-0.0785	0.0072	0.1002	-0.0026	0.0021	-0.0027	0.0055	-0.0006	0.0163	-0.0125	0.0026	-0.2544	-0.540**
	G	0.0075	-0.5394	0.0508	-0.0044	0.0663	-0.0304	0.0262	0.0293	0.0001	-0.0057	0.0005	0.0164	0.0026	0.0682	-0.0592	-0.0274	-0.1448	-0.543**

Phenotypic residual 0.05243011, Genotypic residual 0.13753713

Conversely, HSW consistently showed a negative association with YPH, with values of approximately –0.543 and –0.540 at genotypic and phenotypic levels, respectively. This negative relationship was mainly mediated through NPP, NSP and other yield-related traits. The present estimates are broadly in accordance with previous reports of Tofiq *et al*. (2015), Khan *et al*. (2017), Raj *et al*. (2020) and Prajapati *et al*. (2022).

Overall, the path analysis identified NPP, PWP, W20P, SPW and PL as the most important traits associated with pod yield. Among these, NPP showed the most consistent positive contribution across generations, while PWP and W20P demonstrated strong relationships with yield through multiple pathways. These results indicate that selection for increased pod number, pod weight and desirable pod length could be an effective strategy for improving pod yield, with simultaneous consideration of correlated traits to minimize undesirable indirect responses.

Conclusion

The present study demonstrated substantial genetic variability for yield, earliness and quality traits in garden pea, providing considerable scope for genetic improvement. The close estimates of GCV and PCV for most traits indicated relatively low environmental influence, while high heritability coupled with high genetic advance for several characters suggested good prospects for effective selection. Correlation and path analyses consistently identified number of pods per plant, pod weight per plant, weight of 20 pods, single pod weight and pod length as important traits associated with pod yield. In contrast, the negative association of 100-seed weight with major yield components indicated a potential trade-off between seed size and productivity. Overall, number of pods per plant and pod-weight-related traits emerged as the most useful selection criteria for improving pod yield, while the substantial variability observed for quality traits provides opportunities for simultaneous improvement of nutritional and processing attributes. These findings provide a useful basis for parental selection and development of high-yielding, quality-oriented garden pea genotypes.

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Author contributions

Archana Upadhyay: Data collection and original draft preparation; D.P. Singh: supervision, provision of resources, manuscript editing, and critical review; Rahul Kumar: manuscript editing and review; and Jaswant

Prajapati: statistical data analysis and interpretation of statistical results. All authors reviewed and approved the final version of the manuscript.

Declaration of AI use : This manuscript was prepared based on the intellectual contributions of the authors to the study design, data analysis, interpretation of results and scholarly content. Grammarly and ChatGPT were used solely for language refinement, grammatical correction, and reference formatting during manuscript revision. The authors take full responsibility for the accuracy, integrity, originality, and final content of the manuscript.

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