



Harnessing Genetic Variability, Correlation and Path Analysis among Garden Pea (*Pisum sativum* L.) Genotypes for Food Security and Sustainability

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ABSTRACT

Background: A field experiment was conducted at Lovely Professional University, Punjab (2022-23) to evaluate fourteen garden pea (*Pisum sativum* L.) genotypes for genetic variability, trait associations and direct and indirect effects of yield-related traits through path coefficient analysis. Understanding genetic variation and interrelationships among yield-contributing characters is essential for improving selection efficiency and enhancing productivity in garden pea breeding programs.

Methods: Genotypes were evaluated in a randomized complete block design (RCBD) with three replications. Observations were recorded on morphological and yield-related parameters including plant height, number of nodes to first flower, number of primary branches/plants, pod length, number of pods/plants, 100-seed weight and pod yield/plant. Data were statistically analysed for analysis of variance (ANOVA), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, genotypic and phenotypic correlations and path coefficient analysis to determine direct and indirect effects of various traits on pod yield.

Result: Analysis of variance revealed significant genetic variability among genotypes for all studied traits. PCV values exceeded GCV for most traits, indicating environmental influence, except for nodes/plant. High GCV, PCV and heritability were observed for traits like number of primary branches/plants, pod yield/plant, 100-seed weight and numbers of pods/plant. Pod yield showed strong positive correlations with number of pods, 100-seed weight and node to first pod appearance. Path analysis indicated that number of primary branches, pod length, plant height and nodes to first flower appearance had the strongest direct effects on yield, suggesting these as key selection criteria in breeding programs.

Key words: Garden pea, Genetic variability, Heritability, Path and correlation analysis, *Pisum sativum*.

INTRODUCTION

Garden pea (*Pisum sativum* L. sub sp. *hortense* Asch.; $2n=2x=14$) is a member of Leguminosae family and its primary center of origin are Central Asia, Abyssinia and Mediterranean region, while Near East is considered its secondary origin (Zohary and Hopf, 1973; Srivastava, 2025). Peas are cultivated for their immature pods, dry seeds, canned, frozen or dehydrated form (Singh *et al.*, 2022). It has a high nutritional content, particularly proteins and several other health-building components such as carbohydrates, minerals, vitamins and amino acids, like lysine (Ghobary, 2010; Singh *et al.*, 2019). Inclusion of pea in crop rotation is important agronomically due to its high nitrogen fixation efficiency and better potential to utilize minerals (Adgo and Schulze, 2002). A crop performance is the outcome of interactions between the crop's genetic makeup and environment (Bharti *et al.*, 2024; Neupane *et al.*, 2023). Germplasm screening is vital for identifying promising genotypes, while understanding genetic variability enables the discovery of key genes for crop improvement (Azmat *et al.*, 2011; Nwangburuka *et al.*, 2011). Path coefficient analysis further clarifies trait associations by partitioning correlation coefficients into direct and indirect effects, thereby highlighting the relative importance of each factor (Bhatt, 1973; Patil *et al.*, 2024). Such insights are essential for developing effective breeding programs.

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Thus, this study was designed to assess the extent of genetic variability and the relationships between traits that contribute to green pod yield/plant in peas.

MATERIALS AND METHODS

Experimental site

This particular experimental trial was conducted at the Research Farm of Lovely Professional University, Punjab, India, during *Rabi* season-2022-2023.

Experimental material and design

There were fourteen distinct genotypes of garden pea selected for this study including SATAYA-1010 (Kulak Seeds Company), Peas Vasundhara (Tycoon Seeds), Zanna + (Aggarwal Seeds), Imported Peas OS-10 (Omase Seeds), Samag (Samag Seeds), Sweet Ruby (Shriram Seeds), AP-3 (CSAUA and T, Kanpur), GS-10 (Advanta Golden Seeds), Niarli (Agro Seeds), Peas A-1 (Hara Seeds), Tako-10 (Takoyama Seeds), 11 Danno Wali (tiger) (Kalash Seed Pvt. Ltd.), BKS peas (Bundelkhand Seeds) and PB-89 (PAU, Ludhiana, Punjab used as a check variety) procured from PAU, Ludhiana, Punjab and other private companies. The selected genotypes were arranged in a randomized block design (RBD) with three replications.

Seed sowing

Seed sowing was done at 30 cm × 10 cm spacing and all essential cultural-practices were followed as suggested by PAU, Ludhiana, Punjab for raising a healthy crop.

Analysis of variance (ANOVA)

The collected data for the various studied parameters were analyzed using analysis of variance (ANOVA) to assess significance levels at $P = 0.01$ and 0.05 (Panse and Sukhatme, 1961).

Variability, heritability, path and correlation analysis

Variability coefficients, genetic advance (GA) and heritability in broad-sense (h^2b) were analyzed by following the methods of Johnson *et al.* (1955) and Burton and De Vane (1953). Subsequently, Correlation and path analyses at both phenotypic and genotypic levels were carried out as described by Wright (1934), Al-Jibouri *et al.* (1958) and Dewey and Lu (1959).

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The analysis of variance (ANOVA) results demonstrated a significant variation among genotypes for the considered traits in our study.

Variability analysis

The magnitude of PCV was greater than GCV for most parameters, with the exception of nodes/plant, which demonstrated an additive gene effect driven by the environment (Table 1). Characters like number of pods/plants, 100-seed weight, number of primary branches/plant and pod yield/plant exhibited the highest GCV and PCV values, both reaching 20%. These results suggest that certain traits exhibit higher variation genetically, that might be beneficial for crop improvement under selective breeding. However, environmental factors must also be considered when selecting traits with high variability. These results were in conformity with of Pal and Singh (2012); Katoch *et al.* (2016); Pandey *et al.* (2017); Kumar *et al.* (2019) and Gupta *et al.* (2020).

Moderate GCV and PCV values (ranging 10% to 20%) were recorded for traits like number of seeds/100 g of pods, number of seeds/pods, plant height, number of pods/100 g and TSS. These findings are consistent with those of Thakur

Table 1: Estimation of genetic variability and its components for various traits among garden pea genotypes.

Traits	Range		Mean	Variability			Heritability (H^2b) (%)	GA	GA % of mean
	Min.	Max.		PCV (%)	GCV (%)	ECV (%)			
Days to 50% flowering	62.00	82.66	73.95	8.44	7.84	5.41	86.33	14.22	19.23
Plant height (cm)	61.57	91.28	76.53	11.68	11.54	3.10	97.66	23.04	30.11
Number of nodes/plant	15.33	20.86	17.46	4.20	7.01	4.20	89.31	3.05	17.48
Number of primary branches/plant	1.60	4.60	3.68	23.80	23.01	10.54	93.46	2.16	58.72
Node to 1 st flower appears	9.13	11.33	10.33	6.43	5.37	6.12	69.78	1.22	11.84
Node to 1 st pod appears	10.40	13.63	11.33	6.86	5.70	6.63	68.90	1.42	12.48
Internodal length (cm)	3.86	5.52	4.57	9.81	8.31	9.03	71.77	0.85	18.59
Pod length (cm)	7.59	10.24	9.12	8.15	7.68	4.73	88.77	1.74	19.10
Number of seeds/pod	5.60	9.13	7.36	13.10	12.41	7.26	89.76	2.29	31.04
Number of pods/plant	10.66	26.06	17.08	26.74	26.09	10.10	95.25	11.48	67.23
Number of seeds/100 g pods	51.33	90.33	73.30	16.84	16.56	5.28	96.72	31.52	43.00
Number of pods/100 g	12.33	21.33	16.92	16.76	16.08	8.21	92.00	6.89	40.72
100-seed weight (g)	15.96	36.60	25.09	27.25	26.69	9.51	95.94	17.32	69.01
Pod yield/plant (g)	45.82	104.70	70.23	25.97	25.87	3.91	99.25	47.79	68.04
TSS (°Brix)	12.19	19.82	16.33	13.64	13.37	4.62	96.18	5.66	34.63

et al. (2016) and Barcchiya *et al.* (2018). The lowest values (less than 10%) of PCV and GCV were noticed for various characters including days to 50% flowering, node to 1st pod appears, internodal length (cm), node to 1st flower appears and nodes/plant. Similar results were presented by Katoch *et al.* (2016); Kumar *et al.* (2019) and Jaiswal *et al.* (2013).

Heritability in broad sense (%)

The heritability values were found to range from 68.90% for the trait node to 1st pod appear to a remarkably high 99.25% for the trait pod yield/plant (Table 1). Among traits, the highest heritability was observed in pod yield/plant (99.25%), followed closely by plant height (97.65%), number of seeds/100 g pods (96.72%), total soluble solids (96.18%), 100-seed weight (95.94%), number of pods/plant (95.25%), number of primary branches/plant (93.46%), number of pods/100 g (92.00%), number of seeds/pod (89.76%), number of nodes/plant (89.31%), pod length (88.77%), days to 50% flowering (86.33%), internodal length (71.77%), node to 1st flower appear (69.78%) and node to 1st pod appears (68.90%). These findings suggest that there is substantial genetic control over these traits in the plant species under study. These results were in confirmation with the findings of Pal and Singh (2012); Katoch *et al.* (2016); Kumar *et al.* (2019); Gupta *et al.* (2020); Thakur *et al.* (2016); Barcchiya *et al.* (2018); Jaiswal *et al.* (2013); Sharma and Bora, (2013); Georgieva *et al.* (2016); Gudadinni *et al.* (2017); Kumar *et al.* (2018); Singh *et al.* (2019) and Kumar *et al.* (2023).

Genetic advance (GA) as percentage of mean

Results presented in Table 1 revealed that higher heritability infused with high GA in percent of mean was observed for 100-seed weight, followed by number of pods/plants, number of primary branches/plants, number of seeds/100 g pods, number of pods/100 g, pod yield/plant and plant height. Lower genetic advance along with high heritability as % of

mean was observed for several characters viz., internodal length, days to 50% flowering, node to 1st pod appears, pod length, node to 1st flower appears and numbers of nodes/plant. These outcomes align with the conclusions of Pandey *et al.* (2017); Kumar *et al.* (2019); Thakur *et al.* (2016); Georgieva *et al.* (2016); Jagadeesh *et al.* (2023) and Aziz-ur-Rahman *et al.* (2021).

Correlation analysis

The results of correlation analysis among traits revealed a significant positive relationship between pod yield/plant (Table 2). Various traits such as node to 1st pod appearance, number of pods/plants and 100-seed weight may be considered as key influencers of pod yield in peas. Analogous outcome was recorded formerly by Mohanty *et al.* (2020) and Thapa *et al.* (2020). The trait plant height showed a high negative significant value with total soluble solids (TSS), while it was negatively significant with node to 1st pod appears and number of primary branches/plants. Based on the results, traits such as number of pods/plants, 100-seed weight and nodes to 1st pod appearance should be prioritized when selecting high-yielding genotypes for garden peas, as they show a strong correlation with pod yield.

Path analysis

Path analysis at genotypic and phenotypic both levels for various traits among genotypes is presented in Table 3. At genotypic level, the strongest direct positive effect on pod yield/plant was observed for the number of pods/plant (0.8576), followed by pod length (0.4974) and the number of pods/100 g (0.2559). Similar kind of findings were reported by Pal and Singh (2012) and Khan *et al.* (2017). The positive correlation of these traits with pod yield/plant can be attributed to the positive indirect effects of other related traits (Fig 1). Whereas, negative direct effect on pod yield/plant were found for traits like plant height (-0.4177), number of seeds/pod (-0.3873), number of

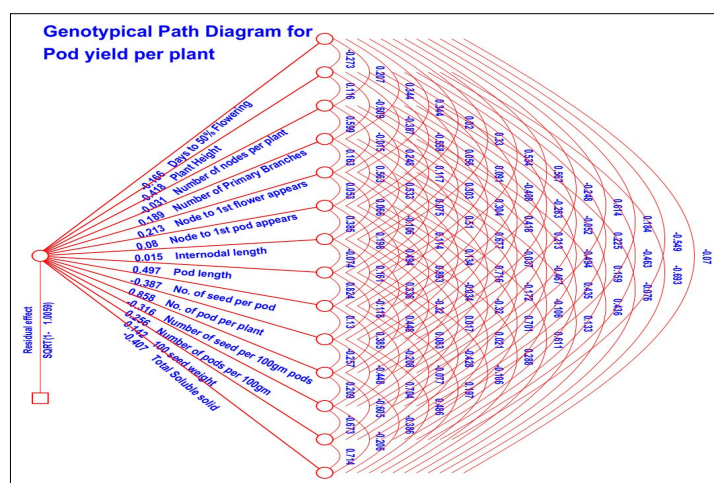


Fig 1: Genotypic path analysis illustrating the direct and indirect effects of yield-contributing traits on pod yield per plant in garden pea genotypes.

Table 2: Genotypic and phenotypic correlation coefficient for different traits among garden pea genotypes.

Traits	Level	Days to 50% flowering	Plant height (cm)	Number of nodes/branches	Node to 1 st flower appears plants	Node to 1 st pod appears plants	Internodal length (cm)	Pod length (cm)	Number of seeds/pod	Number of pods/plant	Number of seeds/100 g pods	Number of pods/100 g	100-seed weight (g)	Pod yield/plant (g)	TSS (°Brix)
Days to 50% flowering	P	1.000	-0.237	0.202	0.336	0.351	0.223	0.487	0.523	-0.231	0.581*	0.151	-0.507	-0.252	-0.083
	G	1.000	-0.273	0.207	0.344	0.345	0.330	0.534*	0.567*	-0.248	0.614*	0.184	-0.549*	-0.276	-0.070
Plant height (cm)	P	1.000	1.000	0.131	-0.588*	-0.274	0.048	0.0705	-0.396	-0.285	-0.050	0.206	-0.4471	-0.360	-0.671**
	G	1.000	1.000	0.116	-0.609*	-0.387	0.056	0.091	-0.408	-0.283	-0.052	0.225	-0.463	-0.367	-0.693**
Number of nodes/plant	P	1.000	1.000	1.000	0.550*	0.021	0.140	0.294	0.296	0.368	0.194	-0.447	0.156	0.256	-0.066
	G	1.000	1.000	0.599*	-0.015	-0.015	0.117	0.303	0.304	0.418	0.213	-0.495	0.159	0.269	-0.076
Number of primary branches/plant	P	1.000	0.076	1.000	1.000	0.076	0.376	0.081	0.486	0.636*	-0.030	-0.441	0.407	0.621*	0.402
	G	1.000	0.163	1.000	1.000	0.163	0.533	0.075	0.510	0.677**	-0.037	-0.467	0.435	0.652*	0.436
Node to 1 st flower appears	P	1.000	1.000	1.000	1.000	1.000	0.046	-0.139	0.077	0.064	0.591*	-0.135	-0.078	0.039	0.115
	G	1.000	1.000	1.000	1.000	1.000	0.066	-0.106	0.114	0.134	0.716**	-0.172	-0.106	0.032	0.133
Node to 1 st pod appears	P	1.000	1.000	1.000	1.000	1.000	0.195	0.113	0.365	0.706**	-0.041	-0.241	0.570*	0.717**	0.533*
	G	1.000	1.000	1.000	1.000	1.000	0.385	0.198	0.494	0.893**	-0.034	-0.320	0.701**	0.878**	0.6108*
Internodal length (cm)	P	1.000	-0.004	0.159	0.273	1.000	1.000	-0.074	0.161	0.336	-0.291	0.003	0.047	0.210	0.2280
	G	1.000	-0.074	0.161	0.273	1.000	1.000	-0.074	0.161	0.336	-0.320	0.017	0.021	0.259	0.288
Pod length (cm)	P	1.000	0.792**	0.409	-0.092	1.000	1.000	1.000	0.792**	-0.092	0.409	0.080	-0.376	-0.181	-0.108
	G	1.000	0.824**	0.448	-0.118	1.000	1.000	1.000	0.824**	-0.118	0.448	0.083	-0.428	-0.191	-0.106
Number of seeds/pod	P	1.000	0.127	0.361	1.000	1.000	1.000	1.000	1.000	0.127	0.361	-0.196	-0.084	0.092	0.166
	G	1.000	0.130	0.385	1.000	1.000	1.000	1.000	1.000	0.130	0.385	-0.208	-0.077	0.098	0.197
Number of pods/plant	P	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.241	-0.407	0.667**	0.969**	0.465
	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.257	-0.448	0.704**	0.997**	0.486
Number of seeds/100 g pods	P	1.000	0.2088	0.209	1.000	1.000	1.000	1.000	1.000	0.2088	1.000	0.2088	-0.578*	-0.282	-0.382
	G	1.000	0.209	1.000	1.000	1.000	1.000	1.000	1.000	0.209	1.000	0.209	-0.605*	-0.287	-0.386
Number of pods/100 g	P	1.000	-0.624*	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.624*	-0.322	-0.189
	G	1.000	-0.673**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.673**	-0.344	-0.206
100-seed weight	P	1.000	0.663**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.663**	0.663**	0.679**
	G	1.000	0.686**	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.686**	0.686**	0.714**
Pod yield/plant (g)	P	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
TSS (°Brix)	P	1.000	0.510	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.510	0.510	1.000
	G	1.000	0.518	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.518	0.518	1.000

Note: * and ** shows significance at 5 % and 1% probability level, respectively. G= Genotypic and P= Phenotypic.

Table 3: Direct and indirect effect of different studied traits on pod yield/plant (g) at phenotypic and genotypic level among garden pea genotypes.

Traits	Level	Days to 50% flowering	Plant height (cm)	Number of nodes/plant	Number of primary branches/plant	Node to 1 st flower appears	Node to 1 st pod appears	Internodal length (cm)	Pod length (cm)	Number of seeds/pod	Number of pods/100 g pods	100-seed weight 100 g	Pod yield/plant (g)	TSS (°Brix)
Days to 50% flowering	P	-1.323	0.314	-0.268	-0.445	-0.465	0.008	-0.295	-0.645	-0.692	0.305	0.6706	-0.2524	0.1102
	G	-0.166	0.045	-0.034	-0.057	-0.057	-0.003	-0.055	-0.089	-0.094	0.041	0.0910	-0.2762	0.0116
Plant height (cm)	P	-0.466	1.968	0.258	-1.157	-0.538	-0.884	0.094	0.139	-0.778	-0.561	-0.8799	-0.3603	-1.3198
	G	0.114	-0.418	-0.049	0.254	0.162	0.233	-0.023	-0.038	0.170	0.118	0.1932	-0.3669	0.2893
Number of nodes/plant	P	-0.285	-0.185	-1.410	-0.775	-0.029	-0.301	-0.120	-0.414	-0.417	-0.518	-0.2202	0.2559	0.0926
	G	-0.006	-0.004	-0.031	-0.018	0.001	-0.008	-0.004	-0.009	-0.009	-0.013	-0.0049	0.2688	0.0023
Number of primary branches/plant	P	1.482	-2.590	2.422	4.404	0.333	2.030	1.657	0.359	2.138	2.800	1.7940	0.6212	1.7716
	G	0.065	-0.115	0.113	0.189	0.031	0.106	0.100	0.014	0.096	0.128	0.0822	0.6522	0.0824
Node to 1 st flower appears	P	0.746	-0.581	0.044	0.160	2.122	0.154	0.098	-0.295	0.164	0.135	-0.1657	0.0387	0.2435
	G	0.073	-0.082	-0.003	0.035	0.213	0.011	0.014	-0.023	0.024	0.028	-0.0226	0.0322	0.0282
Node to 1 st pod appears	P	-0.009	-0.658	0.313	0.676	0.107	1.466	0.286	0.166	0.536	1.034	0.8362	0.717	0.7816
	G	0.002	-0.045	0.020	0.045	0.004	0.080	0.031	0.016	0.040	0.071	0.0561	0.8783	0.0488
Internodal length (cm)	P	-0.244	-0.052	-0.153	-0.412	-0.050	-0.214	-1.093	0.004	-0.174	-0.299	-0.0515	0.2103	-0.2493
	G	0.005	0.001	0.002	0.008	0.001	0.006	0.015	-0.001	0.002	0.005	0.0003	0.2591	0.0042
Pod length (cm)	P	0.973	0.141	0.586	0.163	-0.277	0.226	-0.008	1.997	1.581	-0.184	0.1591	-0.1806	-0.2147
	G	0.266	0.045	0.151	0.037	-0.053	0.099	-0.037	0.497	0.410	-0.059	-0.2130	-0.1908	-0.0527
Number of seeds/pod	P	-0.703	0.532	-0.398	-0.653	-0.104	-0.491	-0.214	-1.065	-1.344	-0.171	0.2639	0.0924	-0.2230
	G	-0.220	0.158	-0.118	-0.198	-0.044	-0.191	-0.062	-0.319	-0.387	-0.051	0.0806	0.098	-0.0761
Number of pods/plant	P	0.385	0.476	-0.614	-1.062	-0.106	-1.178	-0.456	0.154	-0.212	-1.670	0.6801	0.9692	-0.7768
	G	-0.213	-0.243	0.358	0.581	0.115	0.766	0.288	-0.101	0.112	0.858	-0.3840	0.9966	0.4165
Number of seeds/100 g pods	P	-0.778	0.066	-0.260	0.040	-0.791	0.055	0.390	-0.548	-0.483	0.323	-0.2795	-0.2815	0.5118
	G	-0.194	0.016	-0.067	0.012	-0.226	0.011	0.101	-0.142	-0.122	0.081	-0.0661	-0.2866	0.1219
Number of pods/100 g	P	0.114	0.155	-0.337	-0.332	-0.102	-0.181	0.003	0.060	-0.148	-0.307	0.1573	-0.3222	-0.1421
	G	0.047	0.058	-0.127	-0.120	-0.044	-0.082	0.004	0.021	-0.053	-0.115	0.0536	-0.1723	-0.0526
100-seed weight (g)	P	-0.168	-0.148	0.052	0.135	-0.026	0.189	0.016	-0.125	-0.028	0.221	-0.1919	0.6634	0.2254
	G	-0.078	-0.066	0.023	0.062	-0.015	0.010	0.003	-0.061	-0.011	0.100	-0.0860	0.6862	0.1016
TSS (°Brix)	P	0.025	0.202	0.020	-0.121	-0.035	-0.161	-0.069	0.032	-0.050	-0.140	0.1153	0.5096	-0.3015
	G	0.028	0.282	0.031	-0.177	-0.054	-0.249	-0.117	0.043	-0.080	-0.198	0.1570	0.5183	-0.4070

Note: P= Phenotypic and G= Genotypic.

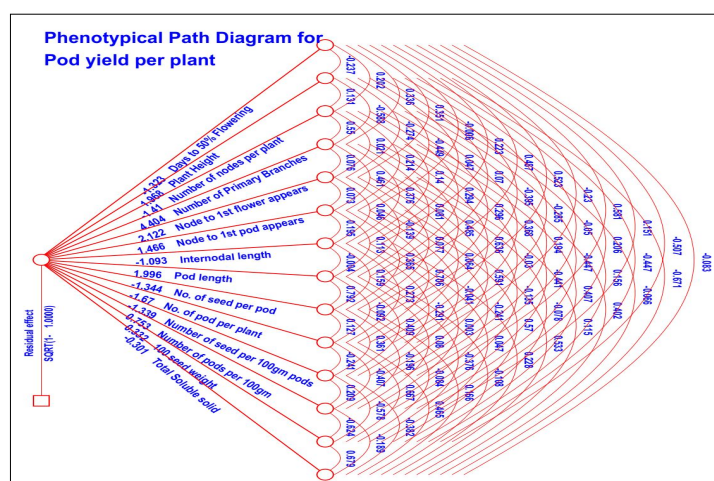


Fig 2: Phenotypic path analysis illustrating the direct and indirect effects of yield-contributing traits on pod yield per plant in garden pea genotypes.

seeds/100 g pods (-0.3159), days to 50% flowering (-0.1656), number of nodes/plant (-0.0307) and TSS (-0.4070).

Whereas, the direct highest positive effect on pod yield/plant was refereed number of primary branches/plant (4.4041), followed by node to 1st flower appears (2.1220), pod length (1.997 cm) and plant height (1.968 cm) at the phenotypic level (Fig 2). Similarly, findings were recorded by Saxena *et al.* (2014); Gupta *et al.* (2020) and Mehandi and Mishra, (2023) for pod length and plant height and by Mohanty *et al.* (2020) for plant height. Hence, these traits should be considered in the future selection procedures for getting higher pod yield/plant (Khan *et al.*, 2017). The negative direct effect on pod yield/plant were found by numerous traits such as number of nodes/plant (-1.410), internodal length (-1.093), number of pods/plant (-1.670), days to 50% flowering (-1.323), number of seeds/pod (-1.344) and number of seeds/100 g pods (-1.339) at phenotypic level. These outcomes align with the findings of Bijalwan *et al.* (2018). The maximum positive indirect effect was reported by number of primary branches/plants on characters like number of pods/plant (2.800), number of nodes/plant (2.422), number of seeds/pod (2.138) and node to 1st pod appears (2.030). In the present research, the residual effect was calculated to be 0.08, indicating that roughly 99.92% variation in pod yield may explained by the investigated traits. Nevertheless, it's evident that other factors, not accounted for in this analysis, must be included to comprehensively address the remaining variability in yield.

CONCLUSION

The character like number of primary branches/plants was found highly genetically variable and exhibits high heritability, indicating its potential for selective breeding to enhance yield and productivity. Similarly, the number of pods/plants showed the high genetic variability, moderate heritability and associated with high genetic advance (GA), making it a key determinant of pod yield/

plant. The trait pod yield/plant had higher GA and heritability thus, it emerges as a critical target for breeding programs aimed at improving overall yield and productivity. Correlation analysis revealed a strong positive relationship among pod yield/plant and variables such as number of pods/plants, 100-seed-weight and node to 1st pod appears. These findings suggested that these characteristics may play an important role in determining pod output in garden peas. Path analysis revealed that at the genotypic level, the trait number of pods/plants had the greatest direct beneficial effect on pod yield/plant, followed by pod length and number of pods/100 g. Similarly, at the phenotypic level, the number of primary branches/plants had the maximum favourable direct effect on pod yield/plant, followed by plant height, node to I flower appears and pod length. Thus, by identifying and harnessing genetic traits that enhance yield, resilience and nutritional value, we can contribute to the sustainable developmental goals (SDGs) by improving crop productivity, reducing environmental impact and ensuring a reliable food supply for growing populations. The obtained findings not only advance our scientific understanding but also support global efforts towards sustainable development and the well-being of communities worldwide.

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Authors' contribution

Vishal Tripathi designed the technical programme, edited and reviewed the work. Arkit Neupane conducted the research and collected the data. Suhel Mehendi did the statistical analysis. Yaman Kumar, Etalesh Goutam, Amrita Kumari, Rupinder Singh and Rajeev prepared the

manuscript. All the authors approved the final version of the manuscript.

Disclaimers

The views and conclusions expressed in this article are solely those of the authors and do not necessarily represent the views of their affiliated institutions. The authors are responsible for the accuracy and completeness of the information provided, but do not accept any liability for any direct or indirect losses resulting from the use of this content.

Informed consent

All animal procedures for experiments were approved by the Committee of Experimental Animal care and handling techniques were approved by the University of Animal Care Committee.

Conflict of interest

The authors declare that there are no conflicts of interest regarding the publication of this article. No funding or sponsorship influenced the design of the study, data collection, analysis, decision to publish, or preparation of the manuscript.

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