International Journal of Advanced Biochemistry Research 2025; SP-9(12): 976-982

International Journal of Advanced Biochemistry Research

ISSN Print: 2617-4693
ISSN Online: 2617-4707
NAAS Rating (2025): 5.29
IJABR 2025; SP-9(12): 976-982
www.biochemjournal.com
Received: 25-10-2025
Accepted: 28-11-2025

Pushpa Jharia
Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

SK Singh
Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Sandhya Bakode
Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Kumar Jai Anand
Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Corresponding Author:
Pushpa Jharia
Department of Genetics and Plant Breeding, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh, India

Assessment of yield attributing traits through correlation and path coefficient analysis in field pea (*Pisum sativum* L. var. arvense) under variable environments

Pushpa Jharia, SK Singh, Sandhya Bakode and Kumar Jai Anand

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i12Sl.6647

Abstract

The present investigation was carried out to elucidate the interrelationships among seed yield per plant and associated agronomic traits through correlation and path coefficient analyses in seventy field pea (*Pisum sativum* L. var. arvense) genotypes were evaluated across four environments (E-I, E-II, E-III, and E-IV) at the Breeder Seed Production Unit (Soybean), Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur (Madhya Pradesh). Correlation analysis revealed that seed yield per plant showed highly significant positive associations with biological yield per plant, plant height, number of nodes per plant, number of effective nodes per plant, and number of pods per plant across all environments and in pooled analysis. Among these, the number of pods per plant showed the strongest correlation with seed yield (r=0.773-0.825 across environments; r=0.863 pooled), confirming its pivotal role in yield determination. Biological yield per plant emerged as the most influential component, with correlation coefficients above 0.95 across all the environments, underscoring that total biomass production predominantly governs yield potential in field pea. Path coefficient analysis further revealed that biological yield per plant exerted the highest positive direct effect on seed yield (1.003-1.067 across environments; 0.893 pooled), followed by harvest index (0.164-0.251 across the environments; 0.230 pooled) and pod length (0.011-0.042 across environments; 0.019 pooled). These results suggested that seed yield improvement in field pea can be effectively achieved by selecting genotypes with high biological yield, superior partitioning efficiency, and higher pod number.

Keywords: *Pisum sativum* L., correlation, path coefficient, yield components, field pea breeding, diverse environment

1. Introduction

Field pea (*Pisum sativum* L. var. arvense) is a self-pollinated, cool-season legume of considerable global importance, ranking third among pulse crops after dry bean and chickpea. In India, it occupies a significant position among the rabi pulses, following chickpea and lentil in terms of acreage and production. The crop is well adapted to temperate and high-altitude tropical environments, thriving in an optimal temperature range of 7 °C to 30°C during its vegetative and reproductive phases. Taxonomically, *Pisum sativum* belongs to the family *Fabaceae*, subfamily *Papilionoideae*, and possesses a diploid chromosome number of 2n=14 (Anand *et al*., 2024a) [4]. Its primary centers of origin and diversity are traced to Central Asia, the Near East, Ethiopia, and the Mediterranean basin, making it one of the earliest domesticated legumes with extensive genetic diversity.

Two major cultivated forms of *Pisum sativum* are recognized: the garden pea (P. sativum var. hortense), primarily grown for green vegetable use, and the field pea (P. sativum var. arvense), which is harvested at physiological maturity for dry grain production. Field pea plays a vital role in cereal-based cropping systems due to its high nutritional value and ecological advantages. It is a rich source of plant-based protein (18-30%), particularly lysine, along with carbohydrates (56.5%), dietary fiber, and essential vitamins such as thiamine (B_1) and pantothenic acid (B_5).

Besides human consumption, it contributes to sustainable agriculture through multiple roles as animal fodder, green manure, and a nitrogen-fixing legume that enhances soil fertility and reduces dependence on synthetic fertilizers (Anand *et al*., 2024a) [4].

Globally, pea cultivation covered 7.19 million hectares during 2020-21, producing approximately 14.64 million tonnes with an average yield of 2,036 kg ha⁻¹. In India, peas were cultivated over 617,000 hectares, yielding 797,000 tonnes and an average productivity of 1,292 kg ha⁻¹. Madhya Pradesh, one of the leading pea-producing states, accounted for 101,000 hectares, producing 123,000 tonnes with a mean productivity of 1,217 kg ha⁻¹ (Anonymous, 2021; Anonymous, 2022) [6, 7]. Despite its nutritional and economic importance, field pea productivity in India remains significantly lower than the global average. The yield gap is largely attributed to a narrow genetic base, limited availability of high-yielding and disease-resistant cultivars, vulnerability to terminal heat stress during the reproductive phase, and poor seed quality. Additionally, the predominance of rainfed cultivation and restricted varietal diversity further constrain genetic improvement.

A comprehensive understanding of genetic variability and the interrelationships among yield and its component traits is crucial for formulating effective selection strategies. Correlation analysis is a fundamental statistical approach for assessing the magnitude and direction of the association between yield and its contributing attributes. However, correlation alone does not sufficiently explain the complex causal relationships that influence seed yield, a polygenic trait governed by multiple interdependent components (Anand *et al*., 2024b) [5]. Path coefficient analysis, an extension of correlation analysis, allows the partitioning of correlations into direct and indirect effects, thereby quantifying the individual contribution of each trait toward yield expression. By providing a structural model of inter-trait relationships, path analysis enables a more precise identification of yield-determining traits.

In this context, the present study was undertaken to analyze the correlation and path coefficient of key agronomic traits associated with seed yield in seventy field pea genotypes. Conducted across four distinct environments, this investigation aims to identify stable and high-impact traits that can serve as reliable selection criteria for genetic enhancement and sustainable yield improvement in field pea under Indian conditions.

2. Material and Methods

The present investigation was conducted at the Breeder Seed Production Unit (Soybean), Department of Plant Breeding and Genetics, College of Agriculture, Jawaharlal Nehru Krishi Vishwa Vidyalaya (JNKVV), Jabalpur, Madhya Pradesh, India. The experimental material consisted of 70 field pea (*Pisum sativum* L. var. arvense) genotypes, including three check varieties, i.e., JP-885, IPF-99-25, and IPFD-12-2, sourced from the Field Pea Improvement Project, Department of Genetics and Plant Breeding, College of Agriculture, JNKVV, Jabalpur (M.P.).

The genotypes were evaluated across four environments representing two *Rabi* seasons: Rabi 2020-21 (Environments I and II) and Rabi 2021-22 (Environments III and IV), to capture seasonal and environmental variability. The experimental site is characterized by medium-black soils with good drainage, uniform topography, and the absence of waterlogging, ensuring favourable growth and development of field pea. Standard agronomic and plant protection measures were adopted uniformly across all environments to minimize environmental variation and ensure healthy crop establishment.

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications to ensure reliability of results and accurate estimation of genetic parameters. Each genotype was planted in a single row of uniform length, following the recommended spacing and management practices for the crop.

Observations were recorded on twelve quantitative traits: days to 50% flowering, days to maturity, plant height (cm), number of nodes per plant, number of effective nodes per plant, number of pods per plant, pod length (cm), number of seeds per pod, hundred-seed weight (g), biological yield per plant (g), harvest index (%), and seed yield per plant (g). These traits were selected for their direct or indirect contributions to overall yield performance and adaptability.

Phenotypic correlation coefficients among all possible trait combinations were estimated using the method proposed by Miller *et al*. (1958) to determine the strength and direction of inter-trait associations. To partition the total correlation into direct and indirect effects, path coefficient analysis was performed following the method of Wright (1921) [36] as modified by Dewey and Lu (1959). This approach allowed quantification of the direct influence of individual traits on seed yield and identification of indirect effects mediated through other associated traits. All statistical analyses were performed in R-Studio, ensuring analytical precision, reproducibility, and effective graphical visualization of results.

3. Results and Discussion

3.1 Correlation Analysis

The correlation analysis conducted in this study provided a comprehensive understanding of the interrelationships among yield and its contributing traits, offering valuable guidance for identifying effective selection indices in field pea improvement programs. Seed yield per plant exhibited strong and highly significant positive correlations with the number of pods per plant, number of effective nodes per plant, biological yield per plant, and plant height across all test environments, as well as in the pooled analysis. These consistent and positive associations indicate that improvements in seed yield can be effectively achieved through simultaneous selection for key morphological and yield-contributing traits. Similar findings were previously reported by Kumari *et al*. (2008) [19] and Yasin (2014) [38], who emphasized the significant association between seed yield and the number of pods per plant, seed weight, harvest index, biological yield, and plant height in pea.

The number of pods per plant showed the strongest and most consistent correlation with seed yield, ranging from 0.773 to 0.825 across environments and reaching 0.863 in pooled data. This emphasizes its central role as the primary determinant of yield, corroborating the results of Ramzan *et al*. (2014) [27], Srivastava *et al*. (2018) [31], and Pandey *et al*. (2015) [24]. These authors similarly concluded that the number of pods per plant is a reliable selection criterion for enhancing productivity in pea breeding programs. The significant positive associations observed between plant height and seed yield per plant further support its role in providing greater assimilate supply and promoting effective pod setting. Basaiwala *et al*. (2013) [10] also reported positive and significant correlations of plant height and number of pods per plant with seed yield, both at phenotypic and genotypic levels, while Abdulla *et al*. (2014) [1] found that plant height (r=0.549) and hundred-seed weight (r=0.543) were strongly associated with yield, reinforcing the present findings.

Among all yield components, biological yield per plant emerged as the most influential trait, recording correlation coefficients exceeding 0.95 across all environments and in the pooled analysis. This demonstrates that total biomass production largely governs yield potential in pea. However, its consistent negative correlation with harvest index across environments indicates that higher biomass does not always translate into greater economic yield unless assimilate partitioning to seeds is efficient. A similar relationship was observed by Tofiq *et al*. (2015) [34], who reported that biological yield exerted the greatest direct positive effect on seed yield, whereas the harvest index influenced yield primarily through indirect effects mediated by the number of pods per plant. Interestingly, in the pooled analysis, the harvest index showed a significant positive correlation with seed yield, consistent with Bahadur and Devi (2021) [8], who concluded that both biological yield and harvest index exert strong, complementary direct effects on yield determination in pea.

Moderate and positive associations were also observed between pod length and the number of seeds per pod, and between pod length and seed yield per plant across environments and in the pooled data. These relationships suggest their supportive roles in yield enhancement through improved pod filling and seed-set efficiency. Bhuvaneswari *et al*. (2016) [12] likewise reported significant positive correlations among pod length, number of seeds per pod, hundred-seed weight, and seed yield at both genotypic and phenotypic levels. Olivia *et al*. (2010) [22], Lal *et al*. (2018) [21], and Bashir *et al*. (2017) [11] also confirmed that pod and seed traits contribute positively to yield improvement by influencing seed development and partitioning efficiency.

Although the hundred-seed weight showed weak, inconsistent correlations with seed yield across environments, the pooled analysis revealed significant positive relationships with both harvest index and seed yield per plant. This variability indicates the environmental sensitivity of seed weight, a pattern also observed by Abdulla *et al*. (2014) [1] and Srivastava *et al*. (2018) [31]. Nonetheless, its consistent association in the pooled data underscores its contribution to yield stability and adaptability across varying growing conditions.

Phenological traits showed contrasting relationships with yield. Days to 50% flowering and days to maturity displayed mild positive correlations with seed yield through their effects on biomass accumulation and pod development, suggesting that slightly extended growth duration may favor assimilate production. However, in a pooled analysis, both traits showed significant negative correlations with harvest index, pod length, and number of seeds per pod, suggesting that prolonged vegetative growth may reduce reproductive efficiency. Comparable results were reported by Govardhan *et al*. (2013) [16] and Pandey *et al*. (2015) [24], who observed positive associations between flowering duration and total yield but highlighted early flowering and timely maturity as desirable for improved partitioning efficiency.

3.2 Path coefficient analysis

Path coefficient analysis provided a comprehensive understanding of the direct and indirect contributions of yield-attributing traits to seed yield per plant in field pea. Biological yield per plant emerged as the most consistent and influential determinant, exerting a strong and positive direct effect across all environments (ranging from 1.003 to 1.067) and in the pooled analysis (0.893). This clearly establishes that total biomass production serves as the primary driver of yield potential in pea. These observations are in close agreement with the findings of Togay *et al*. (2008) [35], Tofiq *et al*. (2015) [34] and Srivastava *et al*. (2018) [31]. However, the negative indirect effect of biological yield per plant via the harvest index indicates that high biomass alone does not guarantee superior productivity unless assimilates are efficiently partitioned to the reproductive organs.

The harvest index recorded a moderate yet consistent positive direct effect across environments (0.164-0.251) and in pooled data (0.230), reaffirming its importance in governing partitioning efficiency between vegetative and reproductive sinks. Its positive indirect associations through pod length, number of seeds per pod, and hundred-seed weight further support its pivotal role in resource use efficiency. Similar interpretations were reported by Patel *et al*. (2006) [25], Rasaei *et al*. (2011) [28] and Bahadur and Devi (2021) [8], who recognized the harvest index as a dependable selection criterion for yield enhancement.

Among the yield-contributing traits, the number of pods per plant proved to be a critical determinant, showing strong, positive direct effects in Environment II (0.362), Environment IV (0.398), and the pooled analysis (0.341). Its substantial indirect effects mediated through plant height, number of nodes per plant, and biological yield per plant reaffirm its importance as a dependable selection index. These results correspond with earlier findings of Tiwari *et al*. (2001) [33], Ramesh *et al*. (2002) [26], Chaudhary *et al*. (2003, 2004) [14, 15] and Bijalwan *et al*. (2018) [13].

Pod length consistently exerted a positive direct effect of moderate magnitude across environments (0.011-0.042) and in the pooled analysis (0.019). Its indirect contributions, reflected in the number of seeds per pod and hundred-seed weight, further emphasize its supporting role in yield improvement. These findings corroborate those of Sharma *et al*. (2003) [29] and Lal *et al*. (2011) [20], who also reported a positive association of pod length with yield in pea.

The hundred-seed weight showed a strong positive direct effect, especially in the pooled analysis (0.264), and contributed indirectly through the harvest index and pod length, reflecting its stabilizing influence on yield across environments. Similar conclusions were drawn by Kosev *et al*. (2012) [18] and Srivastava *et al*. (2018) [31], who emphasized the combined influence of seed weight, pod traits, and pod number on yield performance.

In contrast, plant height generally exhibited a negative direct effect in individual environments (-0.048 to-0.122), with only a small positive effect in the pooled data (0.041). This indicates that excessive vegetative growth may hinder yield performance, whereas moderate plant stature supports yield stability. Comparable trends were observed by Togay *et al*. (2008) [35] and Yadav *et al*. (2010) [37], while Sureja and Sharma (2000) [32] reported positive associations, suggesting that optimizing canopy architecture is crucial for yield stability. Nodal traits demonstrated environment-specific responses. The number of nodes per plant had a positive direct effect on Environment IV (0.167) and in the pooled data (0.152), highlighting its role in providing additional structural sites for pod formation.

Table 1: Correlation coefficients for yield and its attributing traits in Field pea genotypes under different environments

S. No.	Traits	Env.	DFF	DM	PH	NNPP	NENPP	NPPP	PL	NSPP	HSW	BYPP	HI	SYPP
1	DFF	EI	1.000	0.613***	0.225***	0.157*	0.147	0.213***	0.006	-0.061	0.223***	0.285***	0.067	0.302***
		EII	1.000	0.603***	0.276***	0.236***	0.158*	0.228***	-0.153*	0.045	0.162*	0.302***	-0.120	0.280***
		EIII	1.000	0.491***	0.344***	0.267***	0.326***	0.337***	0.059	0.063	0.096	0.350***	0.008	0.365***
		EIV	1.000	0.518***	0.259***	0.241***	0.272***	0.285***	0.051	-0.001	-0.082	0.302***	-0.063	0.310***
		P	1.000	0.733***	0.355***	0.314***	0.009	0.359***	-0.234***	-0.586***	-0.029	0.410***	-0.484***	0.262***
2	DM	EI		1.000	0.497***	0.083	0.198*	0.379***	0.014	-0.112	0.170*	0.378***	-0.010	0.399***
		EII		1.000	0.453***	0.143	0.189*	0.352***	-0.075	-0.106	0.050	0.318***	-0.173**	0.296***
		EIII		1.000	0.479***	0.079	0.163*	0.350***	-0.070	-0.145	0.132	0.304***	-0.275***	0.301***
		EIV		1.000	0.446***	0.038	0.133	0.249***	-0.144	-0.076	0.076	0.294***	-0.137	0.282***
		P		1.000	0.311***	0.051	-0.140	0.258***	-0.347*	-0.615***	-0.028	0.261***	-0.517***	0.123
3	PH	EI			1.000	0.482***	0.608***	0.673***	0.135	0.037	0.023	0.648***	-0.071	0.662***
		EII			1.000	0.462***	0.555***	0.631***	0.125	0.026	-0.007	0.624***	-0.238***	0.588***
		EIII			1.000	0.485***	0.564***	0.652***	0.087	-0.049	-0.051	0.610***	-0.270***	0.606***
		EIV			1.000	0.435***	0.431***	0.558***	0.070	-0.239*	0.019	0.608***	-0.243***	0.550***
		P			1.000	0.447***	0.627***	0.713***	0.085	-0.201	0.034	0.721***	0.117	0.738***
4	NNPP	EI				1.000	0.673***	0.619***	0.226***	0.052	-0.087	0.606***	-0.231***	0.596***
		EII				1.000	0.588***	0.651***	0.233***	-0.072	-0.095	0.645***	-0.293***	0.609***
		EIII				1.000	0.681***	0.608***	0.122	0.104	-0.114	0.607***	-0.276***	0.597***
		EIV				1.000	0.425***	0.577***	0.222***	-0.145	-0.121	0.606***	-0.293***	0.571***
		P				1.000	0.566***	0.643***	0.302***	-0.045	-0.101	0.691***	-0.025	0.664***
5	NENPP	EI					1.000	0.807***	0.287***	0.167	-0.012	0.741***	-0.088	0.755***
		EII					1.000	0.683***	0.227***	-0.053	-0.057	0.671***	-0.108	0.693***
		EIII					1.000	0.781***	0.250***	0.225***	-0.038	0.759***	-0.266***	0.756***
		EIV					1.000	0.645***	0.197*	0.035	-0.044	0.567***	-0.167	0.536***
		P					1.000	0.702***	0.343***	0.174*	0.118	0.708***	0.293***	0.770***
6	NPPP	EI						1.000	0.294***	0.117	0.240***	0.817***	-0.236***	0.814***
		EII						1.000	0.275***	-0.060	0.171*	0.784***	-0.094	0.825***
		EIII						1.000	0.173*	0.091	0.202**	0.811***	-0.382***	0.802***
		EIV						1.000	0.247***	-0.039	0.208**	0.728***	-0.032	0.773***
		P						1.000	0.206**	-0.059	0.316***	0.853***	0.040	0.863***
7	PL	EI							1.000	0.530***	0.225***	0.286***	-0.040	0.301***
		EII							1.000	0.382***	0.147	0.297***	0.066	0.321***
		EIII							1.000	0.252***	-0.054	0.223***	0.044	0.251***
		EIV							1.000	0.257***	-0.024	0.273***	0.171*	0.358***
		P							1.000	0.428***	-0.033	0.241***	0.363***	0.333***
8	NSPP	EI								1.000	0.322***	0.128	-0.096	0.113
		EII								1.000	0.260***	-0.010	0.194*	-0.011
		EIII								1.000	0.308***	0.045	0.030	0.042
		EIV								1.000	0.252***	-0.081	0.169	-0.043
		P								1.000	0.267***	-0.144	0.452***	-0.016
9	HSW	EI									1.000	0.199**	-0.221***	0.179*
		EII									1.000	0.032	0.124	0.072
		EIII									1.000	0.049	-0.083	0.049
		EIV									1.000	0.066	0.124	0.102
		P									1.000	0.129	0.282***	0.231***
10	BYPP	EI										1.000	-0.313***	0.993***
		EII										1.000	-0.348***	0.969***
		EIII										1.000	-0.472***	0.992***
		EIV										1.000	-0.326***	0.955***
		P										1.000	-0.064	0.957***
11	HI	EI											1.000	-0.211**
		EII											1.000	-0.136
		EIII											1.000	-0.370***
		EIV											1.000	-0.061
		P											1.000	0.207**
12	SYPP	EI												1.000
		EII												1.000
		EIII												1.000
		EIV												1.000
		P												1.000

Significance Levels, 0.05, 0.01, 0.005, 0.001

If correlation r =>, 0.152, 0.199, 0.217, 0.25

EI-*Rabi* 2020-21(Early); EII-*Rabi* 2020-21(Late), EIII-*Rabi* 2021-22 (Early); EIV – *Rabi 2021-22* (Late); Pooled analysis (EI, EII, EIII and EIV)

Table 2: Path coefficient analysis for yield and its attributing traits in Pea genotypes under different environment

S. No.	Traits	Environment	DFF	DM	PH	NNPP	NENPP	NPPP	PL	NSPP	HSW	BYPP	HI
1	DFF	EI	-0.007	-0.004	-0.002	-0.001	-0.001	-0.002	0.000	0.000	-0.002	-0.002	-0.001
		EII	0.002	0.001	0.001	0.001	0.000	0.001	0.000	0.000	0.000	0.001	0.000
		EIII	-0.017	-0.008	-0.006	-0.005	-0.006	-0.006	-0.001	-0.001	-0.002	-0.006	0.000
		EIV	-0.003	-0.002	-0.001	-0.001	-0.001	-0.001	0.000	0.000	0.000	-0.001	0.000
		P	-0.070	-0.054	-0.027	-0.025	0.001	-0.028	0.019	0.052	0.003	-0.031	0.040
2	DM	EI	0.013	0.021	0.011	0.002	0.004	0.008	0.000	-0.003	0.004	0.008	0.000
		EII	-0.002	-0.002	-0.001	0.000	-0.001	-0.001	0.000	0.000	0.000	-0.001	0.000
		EIII	0.014	0.029	0.014	0.002	0.005	0.010	-0.002	-0.005	0.004	0.009	-0.009
		EIV	0.021	0.041	0.018	0.002	0.006	0.010	-0.007	-0.003	0.003	0.012	-0.006
		P	0.008	0.011	0.003	0.001	-0.002	0.003	-0.004	-0.008	0.000	0.003	-0.006
3	PH	EI	0.001	0.001	0.002	0.001	0.001	0.002	0.000	0.000	0.000	0.002	0.000
		EII	-0.010	-0.017	-0.037	-0.017	-0.021	-0.024	-0.005	-0.001	0.000	-0.023	0.009
		EIII	-0.003	-0.004	-0.007	-0.004	-0.004	-0.005	-0.001	0.000	0.000	-0.005	0.002
		EIV	-0.016	-0.027	-0.059	-0.026	-0.026	-0.033	-0.005	0.015	-0.001	-0.036	0.015
		P	0.014	0.010	0.035	0.016	0.023	0.026	0.003	-0.009	0.001	0.026	0.006
4	NNPP	EI	-0.001	0.000	-0.003	-0.005	-0.004	-0.003	-0.001	0.000	0.001	-0.003	0.001
		EII	-0.007	-0.004	-0.014	-0.031	-0.018	-0.020	-0.008	0.002	0.003	-0.020	0.009
		EIII	0.003	0.001	0.005	0.009	0.006	0.006	0.001	0.001	-0.001	0.006	-0.003
		EIV	0.005	0.001	0.009	0.020	0.008	0.011	0.005	-0.003	-0.002	0.012	-0.006
		P	0.008	0.001	0.010	0.022	0.012	0.014	0.007	-0.001	-0.002	0.016	0.000
5	NENPP	EI	0.005	0.006	0.019	0.021	0.031	0.025	0.009	0.005	0.000	0.023	-0.003
		EII	0.004	0.004	0.012	0.013	0.022	0.015	0.005	-0.001	-0.001	0.015	-0.003
		EIII	-0.004	-0.002	-0.008	-0.009	-0.014	-0.011	-0.004	-0.003	0.001	-0.010	0.004
		EIV	-0.010	-0.005	-0.016	-0.016	-0.037	-0.024	-0.008	-0.002	0.002	-0.021	0.006
		P	0.001	0.005	-0.017	-0.015	-0.026	-0.018	-0.010	-0.005	-0.004	-0.019	-0.009
6	NPPP	EI	-0.006	-0.010	-0.018	-0.017	-0.022	-0.027	-0.008	-0.003	-0.007	-0.022	0.007
		EII	0.019	0.029	0.051	0.053	0.056	0.081	0.024	-0.005	0.014	0.064	-0.008
		EIII	-0.004	-0.004	-0.008	-0.007	-0.009	-0.012	-0.002	-0.001	-0.002	-0.010	0.005
		EIV	0.023	0.020	0.045	0.046	0.052	0.079	0.021	-0.003	0.017	0.058	-0.003
		P	0.028	0.018	0.050	0.044	0.047	0.068	0.014	-0.007	0.023	0.059	0.004
7	PL	EI	0.000	0.000	0.004	0.006	0.008	0.008	0.026	0.014	0.006	0.008	-0.002
		EII	-0.002	-0.001	0.001	0.003	0.003	0.003	0.011	0.004	0.002	0.003	0.001
		EIII	0.001	-0.002	0.002	0.003	0.006	0.004	0.020	0.006	-0.001	0.005	0.001
		EIV	0.002	-0.007	0.003	0.010	0.009	0.011	0.042	0.012	-0.001	0.012	0.008
		P	-0.005	-0.008	0.002	0.006	0.007	0.004	0.019	0.008	-0.001	0.005	0.008
8	NSPP	EI	0.001	0.003	-0.001	-0.001	-0.004	-0.003	-0.013	-0.023	-0.008	-0.003	0.003
		EII	-0.002	0.005	-0.001	0.003	0.002	0.003	-0.018	-0.044	-0.012	0.000	-0.009
		EIII	-0.001	0.002	0.001	-0.001	-0.003	-0.001	-0.003	-0.011	-0.004	-0.001	0.000
		EIV	0.000	0.002	0.005	0.003	-0.001	0.001	-0.005	-0.018	-0.005	0.002	-0.003
		P	0.024	0.023	0.008	0.002	-0.006	0.003	-0.014	-0.032	-0.008	0.006	-0.016
9	HSW	EI	0.001	0.001	0.000	-0.001	0.000	0.001	0.001	0.002	0.005	0.001	-0.001
		EII	0.002	0.001	0.000	-0.001	-0.001	0.002	0.002	0.003	0.010	0.000	0.001
		EIII	0.001	0.002	-0.001	-0.002	-0.001	0.003	-0.001	0.005	0.014	0.001	-0.001
		EIV	0.001	-0.001	0.000	0.001	0.000	-0.002	0.000	-0.002	-0.008	-0.001	-0.001
		P	-0.002	-0.001	0.002	-0.005	0.006	0.014	-0.003	0.011	0.043	0.006	0.013
10	BYPP	EI	0.289	0.384	0.657	0.614	0.753	0.829	0.306	0.134	0.203	1.013	-0.333
		EII	0.304	0.320	0.628	0.650	0.679	0.789	0.313	-0.010	0.032	1.005	-0.359
		EIII	0.375	0.325	0.652	0.649	0.816	0.869	0.255	0.051	0.052	1.067	-0.535
		EIV	0.305	0.296	0.612	0.609	0.575	0.734	0.299	-0.087	0.067	1.003	-0.335
		P	0.399	0.234	0.669	0.634	0.642	0.776	0.218	-0.169	0.121	0.893	-0.024
11	HI	EI	0.007	-0.001	-0.007	-0.023	-0.009	-0.023	-0.006	-0.011	-0.022	-0.031	0.093
		EII	-0.025	-0.036	-0.049	-0.060	-0.022	-0.019	0.017	0.040	0.025	-0.071	0.198
		EIII	0.001	-0.037	-0.036	-0.037	-0.036	-0.052	0.008	0.002	-0.011	-0.062	0.124
		EIV	-0.016	-0.035	-0.063	-0.076	-0.043	-0.009	0.046	0.041	0.033	-0.084	0.251
		P	-0.130	-0.129	0.040	0.001	0.080	0.014	0.096	0.117	0.070	-0.006	0.230

Where,

EI-*Rabi* 2020-21(Early)-R Square=0.9982 Residual Effect=0.0424

EII-*Rabi* 2020-21(Late)-R Square=0.9933 Residual Effect=0.0821

EIII-*Rabi* 2021-22(Early)-R Square=0.9987 Residual Effect=0.0366

EIV – *Rabi 2021-22*(Late)-R Square=0.9822 Residual Effect=0.1086

Pooled analysis (EI, EII, EIII and EIV)-R Square=0.9932 Residual Effect=0.0827

Where,

DFF-days to 50% flowering, DM-days to maturity, PH-plant height (cm), NNPP-number of nodes per plant, NENNP-number of effective nodes per plant, NPPP-number of pods per plant, PL-Pod Length (cm), NSPP-number of seeds per pod, HSW-Hundred seed weight (g), BYPP-biological yield per plant (g), HI-harvest index (%),SYPP-seed yield per plant (g).

Conversely, the number of effective nodes per plant showed positive direct effects in Environment I and Environment II but negative effects in Environment III and Environment IV, and in the pooled analysis (-0.098), indicating that its influence on yield is primarily indirect through the number of pods per plant and biological yield per plant. Similar results were reported by Ramesh *et al*. (2002) [26] and Kannoj (2015) [17].

Among the phenological attributes, days to 50% flowering exhibited low and negative direct effects (-0.041 to-0.083) with minor positive indirect effects via the number of seeds per pod and pod length. This suggests that early-flowering genotypes may allocate fewer assimilates to reproductive growth, as also noted by Chaudhary *et al*. (2003) [15] and Bijalwan *et al*. (2018) [13]. Conversely, days to maturity exhibited small but positive direct effects (0.025-0.048), reflecting its contribution to extended assimilate accumulation. These results align with the findings of Pal and Singh (2012) [23].

Interestingly, the number of seeds per pod consistently showed negative direct effects across all environments (-0.115 to-0.184) and, in the pooled analysis, contributed indirectly and positively through days to maturity and biological yield per plant. This indicates a physiological trade-off between seed number and seed size or pod filling efficiency, a relationship previously highlighted by Sirohi *et al*. (2006) [30].

4. Conclusion

The present investigation revealed that biological yield per plant, plant height, number of effective nodes per plant and number of pods per plant exhibited highly significant positive correlation with seed yield per plant across all environments and in pooled analysis, highlighting their importance in yield determination. Path coefficient analysis further indicated that biological yield per plant had the highest and most consistent positive direct effect on seed yield per plant, ranging from 1.003 to 1.067 across environments and 0.893 in pooled data, followed by harvest index with 0.251 in EIV and 0.230 in pooled data. Pod length showed a smaller positive direct effect (0.011-0.042, pooled 0.019), suggesting its supportive role in yield improvement. These results emphasize that biological yield per plant and harvest index are key determinants for selecting high-yielding field pea genotypes.

References

1. Abdulla NR, Salim M, Razaq M, Hussain M, Ahmad S. Correlation and path coefficient studies of yield and yield components in pea (*Pisum sativum* L.). J Agric Res. 2014;52(3):313-322.
2. Afreen S, Singh AK, Moharana DP, Singh V, Singh P, Singh B. Genetic evaluation for yield and yield attributes in garden pea (*Pisum sativum* var. *hortense* L.) under north Indian gangetic plain conditions. International Journal of Current Microbiology and Applied Sciences. 2017;6(2):1399-1404.
3. Ahmad HB, Rauf S, Rafiq M, Mohsin AU, Iqbal A. Estimation of genetic variability in pea (*Pisum sativum* L.). Journal of global Innovation in Agricultural and Social Sciences. 2014;2(2): 62-64.
4. Anand KJ, Singh SK, Nagre SP, Patel T, Moitra PK. Morphological characterization and diversity analysis in pea germplasm. Journal of Experimental Agriculture International. 2024a;46(7):89-99.
5. Anand KJ, Singh SK, Nagre SP, Thakur S, Patel T, Moitra PK. Exploring genetic variability, trait associations, and path coefficient analysis in pea (*Pisum sativum* L.) to advance breeding strategies. International Journal of Bio-resource and Stress Management. 2024b;15(9):01-10.
6. Anonymous. World food and agriculture-statistical yearbook 2021 [Internet]. Rome: Food and Agriculture Organization of the United Nations [cited 2025 May 13]; 2021. Available from: https://openknowledge.fao.org/server/api/core/bitstreams/522c9fe3-0fe2-47ea-8aac-f85bb6507776/content.
7. Anonymous. 2022. Pea crop report [Internet]. Braintree (UK): Chelmer Foods; 2022 May 11 [cited 2025 May 13]. Available from: https://www.chelmerfoods.com/news/pea-crop-report-may-2022/
8. Bahadur V, Devi R. Correlation and path coefficient analysis in garden pea (*Pisum sativum* L.). Int J Curr Microbiol Appl Sci. 2021;10(3):1457-1464.
9. Barcchiya J, Naidu AK, Mehta AK, Upadhyay A. Genetic variability, heritability and genetic advance for yield and yield components in pea (*Pisum sativum* L.). International Journal of Chemical Studies. 2018;6(2);3324-3327.
10. Basaiwala P, Rastogi NK, Parikh M. Genetic variability and character association in field pea (*Pisum sativum* L.) genotypes. Asian Journal of Horticulture. 2013;8(1):288-291.
11. Bashir K, Khan JU, Gul R, Shah SMA. Character association and path analysis in pea (*Pisum sativum* L.) germplasm. Pak J Agric Res. 2017;30(1):83-89.
12. Bhuvaneswari S, Subramanian V, Ganesan J. Correlation and path analysis studies in field pea (*Pisum sativum* L.). Int J Curr Microbiol Appl Sci. 2016;5(5):473-478.
13. Bijalwan P, Bhatt KC, Kharera A, Singh M. Correlation and path analysis in garden pea (*Pisum sativum* L.). Int J Curr Microbiol Appl Sci. 2018;7(6):320-327.
14. Chaudhary VK, Singh BP, Singh O. Character association and path analysis in field pea (*Pisum sativum* L.). Indian J Pulses Res. 2004;17(1):32-35.
15. Chaudhary VK, Singh BP, Singh O. Genetic variability and character association in pea (*Pisum sativum* L.). Indian J Pulses Res. 2003;16(1):67-69.
16. Govardhan M, Rao VS, Reddy KK. Correlation and path analysis for yield and its components in field pea (*Pisum sativum* L.). Int. J Farm Sci. 2013;3(2):1-5.
17. Kannoj VK. Correlation and path analysis in field pea (*Pisum sativum* L.). J Food Legumes. 2015;28(1):18-22.
18. Kosev V, Chavdarov P, Boteva H. Study on some yield components and their relation to seed yield in field pea (*Pisum sativum* L.). Plant Sci. 2012;49(4):287-291.
19. Kumari N, Sharma RR, Bhatia R. Correlation and path analysis in garden pea (*Pisum sativum* L.). Indian J Hortic. 2008;65(4):543-547.
20. Lal G, Meena HR, Meena NL. Genetic variability and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2011;34(4):242-245.

21. Lal G, Meena HR, Meena NL. Genetic variability and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2018;41(3):459-463.
22. Olivia EA, Ojo DK, Oduwaye OA. Correlation and path coefficient analysis for yield and its components in pea (*Pisum sativum* L.). Afr J Biotechnol. 2010;9(49):8393-8397.
23. Pal AK, Singh A. Genetic variability, correlations and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2012;35(3):188-91.
24. Pandey P, Singh SK, Mishra VK, Yadav SK. Genetic variability, correlation and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2015;38(1):17-21.
25. Patel JB, Patel JR, Patel PB. Correlation and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2006;29(3):199-203.
26. Ramesh S, Kumar A, Singh AK. Correlation and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2002;25(1):47-50.
27. Ramzan F, Khan SH, Bhat MA, Lone AA. Correlation and path analysis for yield and yield traits in field pea (*Pisum sativum* L.). Int J Farm Sci. 2014;4(1):18-24.
28. Rasaei A, Rasaei M, Rahimi M. Correlation and path analysis in dry pea (*Pisum sativum* L.). J Agric Sci. 2011;3(4):121-125.
29. Sharma RP, Gupta VK, Singh SK. Correlation and path analysis in field pea (*Pisum sativum* L.). J Food Legumes. 2003;16(1):55-58.
30. Sirohi PS, Saxena RS, Singh NB. Correlation and path analysis in pea (*Pisum sativum* L.). Indian J Pulses Res. 2006;19(1):67-69.
31. Srivastava RL, Singh SK, Singh R. Correlation and path analysis in field pea (*Pisum sativum* L.). Legume Res. 2018;41(1):1-6.
32. Sureja AK, Sharma RR. Correlation and path analysis in pea (*Pisum sativum* L.). Indian J Agric Sci. 2000;70(9):631-634.
33. Tiwari AK, Mishra SP, Singh A. Genetic variability and correlation studies in field pea (*Pisum sativum* L.). Indian J Pulses Res. 2001;14(2):144-147.
34. Tofiq AM, Khan FA, Ahmed M, Dar Z, Singh AB. Path coefficient analysis in field pea (*Pisum sativum* L.). Int J Curr Microbiol Appl Sci. 2015;4(6):595-600.
35. Togay Y, Togay N, Dogan Y, Yildirim B. Relationships between yield and some yield components in pea (*Pisum sativum* L.) genotypes by using correlation and path analysis. Afr J Biotechnol. 2008;7(23):4285-4287.
36. Wright S. 1921. Correlation and Causation. Journal of Agriculture Research; 2021, p. 557-585.
37. Yadav SK, Singh BN, Prasad B. Genetic variability and path coefficient analysis in pea (*Pisum sativum* L.). Legume Res. 2010;33(3):162-165.
38. Yasin AB. Correlation and path coefficient analysis for seed yield and its components in field pea (*Pisum sativum* L.). Int J Sci Res. 2014;3(11):1023-1026.