PLANT SCIENCE TODAY
Vol XX(1): 1-XX
https://doi.org/10.14719/pst.14682

eISSN 2348-1900
OPEN ACCESS

Research Article | Agriculture
2026, Volume XX, Issue X, pp. 1-XX

Stability analysis of field pea (*Pisum sativum* L.) genotypes across sowing windows and locations using the Eberhart and Russell model

Vinay Kumar[1], Shivam Kushwaha[1], Banshidhar[1], Baudh Bharti[1], Shivi Yadav[2], Pankaj Saroj[1], Deepak Kumar Prajapati[1], Rajendra Prasad Meena[1], Laxmidas Verma[1], Jyanendra Pratap[1] & Shiva Nath[1*]

[1]Department of Genetics and Plant Breeding, Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya 224 229, Uttar Pradesh, India

[2]Department of Genetics and Plant Breeding, Chaudhary Charan Singh University, Meerut 250 004, Uttar Pradesh, India

***Correspondence:** Shiva Nath, shivanduat@yahoo.com

Abstract

The field pea (*Pisum sativum* L.) is an important pulse crop worldwide and one of the major pulses grown in India, cultivated over an area of 0.64 million hectares with an annual production of 0.896 million tonnes. To evaluate environmental adaptability, this study was conducted at Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya during two consecutive years 2023–24 and 2024–25 with two growing seasons i.e., early and late using a randomised complete block design. The stability analysis of 8 genotypes was performed across four different environments to assess yield and yield related traits by utilising the Eberhart and Russell model of additive main effects and multiplicative interaction (AMMI) stability models. The pooled analysis of variance and stability parameters revealed significant genetic diversity among the studied genotypes, with strong genotype × environment interactions influencing trait expression. The linear component was high for most of the variability, while the non-significant deviation from regression indicated predictable and stable performance across environments. Stability parameters identified IPF 14-13, Pant P-243, Pant P-200 and Pant P-347 as superior performers, combining high-yield potential with broad adaptability. An AMMI biplot analyses further distinguished genotypes with broad stability, such as VL-42 and HUDP-15, from those with specific environmental responsiveness, such as Pant P-347 and IPF-14-13. These findings highlight the importance of multi-environment trials in breeding programs and suggest that the identified genotypes are promising candidates for enhancing productivity and resilience in crop improvement initiatives.

Keywords: AMMI; biplot; Eberhart and Russell model; field pea; genotype × environment interaction; stability

Received: 24 March 2025. **Accepted:** 06 October 2026. **Available online:** Version 1.0: 20 November 2026.

Cite this article: Vinay K, Shivam K, Banshidhar, Baudh B, Shivi Y, Pankaj S, Deepak KP, Rajendra PM, Laxmidas V, Jyanendra P, Shiva N. Stability analysis of field pea (*Pisum sativum* L.) genotypes across sowing windows and locations using the Eberhart and Russell model. Plant Science Today. 2026;XX(X):1-XX. https://doi.org/10.14719/pst.14682

Introduction

The pea (*Pisum sativum* L.) is a diploid (2n = 2x = 14) legume with a genome size of approximately 4500 Mb that is a member of the tribe Vicieae, subfamily Papilionaceae and species of Fabaceae (1). With temperatures ranging from 7° to 30 °C, it is produced in various climates across the globe, from semi-arid to temperate (2). The seeds of field pea are a rich source of protein complexes, carbohydrates, vitamins, minerals and phytochemicals and are therefore regarded as a nutritional powerhouse (3). According to previous studies, pea seeds are high in protein (23–25 %), slowly digested starch (50 %), soluble sugars (5 %), fibre, minerals and vitamins (4). Another researchers has also suggested that a portion of the starch fraction, resistant starch, is not broken down by the small intestine and functions similarly to dietary fibres, which accounts for its numerous health benefits, the low digestibility of starch from pulses is one of the primary reasons they can offer high nutritional value to humans (5). By fixing atmospheric nitrogen through *Rhizobium* in its root nodules, field pea improves soil fertility and lowers environmental pollution (6).

With a productivity of 888 kg/ha, India produced 27.30 million tonnes of pulses in 2021–22 over an area of about 30.73 million hectares (7). In 2020–21, India produced about 0.64 million hectares and 0.88 million tonnes of peas, with an annual productivity of 1375 kg/ha (8). The primary states in India where peas are grown include Uttar Pradesh, Madhya Pradesh, Jharkhand, Punjab, Haryana, Assam, Odisha, Manipur, West Bengal and Bihar. Approximately 92 % of India's total acreage and pea production are found in 8 states: Uttar Pradesh, Madhya Pradesh, Jharkhand, Assam, Odisha, Manipur, West Bengal and Bihar. Among these, Uttar Pradesh produced the most peas, with 5.03 lakh tonnes and 3.43 lakh hectares under cultivation. This state accounts for over 46 % of India's total cultivated land and 55 % of its total production, with a yield of roughly 1467 kg/ha (8).

Among the districts of Uttar Pradesh, Jalaun contributes the most to the state's field pea cultivation, accounting for 21 % of the total acreage and 29 % of the total production. This is followed, in order of area and production share, by Lalitpur (18 % area, 19 % production), Jhansi (14 % area, 14 % production), Mahoba (8 % area, 5 % production), Hamirpur (3 % area, 3 % production) and Azamgarh (2 % area, 2 % production) (9). The final seed production and quality are the most important factors when choosing potential genotypes in breeding operations. Effective selection also requires an understanding of the relationship between yield and its contributing elements (10, 11).

Pea yield is significantly impacted by environmental conditions such as drought, cold and resource-limited soil. Rising temperatures are a serious threat to cold-season legumes like field peas and global warming is currently having an increasing effect on crop productivity and yield. High-temperature stress has become a serious problem especially during flowering and seed development causing loss in production (12–14). Heat stress in field peas can cause reduction in seed size and blossom, fruit and seed drops (15, 16). In areas where high temperatures occur especially during the reproductive period, the development of heat-tolerant cultivars is essential to reducing yield loss and improving adaptation. A comprehensive understanding of the genetic diversity and correlations among many traits of field pea germplasm is crucial for improvement and selection of appropriate parents in breeding programmes (17).

Genotype by environment (G × E) interaction refers to the differential response of genotypes when grown across varying environmental conditions and it directly affects the consistency of genotype performance across locations and seasons. Because of this interaction, the stability of genotypes is typically tested using a single characteristic, whereas combination breeding requires the selection of a stable superior genotype based on a greater number of attributing traits, such as yield, its contributing components and stress tolerance parameters. The multi trait stability index (MTSI) detects stable genotypes by taking all such attributing traits into account (18). This index score is extremely valuable to breeders in the selection of genotypes that are superior in numerous aspects. This index is ideal for ideotype breeding since it represents the distance between a genotype and an ideotype.

To create new cultivars and conserve without compromising genetic integrity and variability, plant breeding depends on choosing a variety of germplasm with desirable features (19). However, information on the multi-trait stability of field pea genotypes under heat stress conditions in the sub-tropical humid climate of eastern Uttar Pradesh remains limited, which restricts the reliable identification of genotypes suited to this agro-climatic zone. Therefore, the present study was undertaken to evaluate the phenotypic stability of field pea genotypes and to select stable superior genotypes based on multiple traits under heat stress conditions in the sub-tropical humid climate of Ayodhya, India.

Materials and Methods

Experimental site

The experiment was conducted at two different locations, viz., the Genetics and Plant Breeding farm and the Main Experimental Site farm of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya, Uttar Pradesh, India, during two consecutive years, 2023–24 and 2024–25. By combining the two sowing conditions (early and late) with the two years, a total of 4 environments was established: early sowing in 2023–24, denoted as E1; late sowing in 2023–24, denoted as E2; early sowing in 2024–25, denoted as E3; and late sowing in 2024–25, denoted as E4.

Weather and soil characteristics

The mean weekly maximum and minimum temperatures during the crop growing period ranged from approximately 24–32 °C and 6–15 °C, respectively, across the four environments, with the E1 and E3 experiencing comparatively cooler temperatures during the flowering and pod-filling stages than the E2 and E4, which were exposed to a rise of about 4–6 °C in maximum temperature during these critical stages and thereby represented the heat-stress environments. Relative humidity during the crop season ranged between 45 % and 85 % and total rainfall received during the crop growing period was low and largely confined to a few showers in each year, so the crop was predominantly grown under assured irrigation. Weather data were recorded at the meteorological observatory of Acharya Narendra Deva University of Agriculture and Technology, Kumarganj, Ayodhya. The soil of the experimental site was sandy loam in texture, with a nearly neutral soil reaction (pH about 7.2–7.6), medium in organic carbon and available nitrogen and medium to high in available phosphorus and potassium, at both the Genetics and Plant Breeding farm and the Main Experimental Site farm.

Experimental materials

The experimental material comprised 8 genotypes of field pea (*P. sativum*), which were procured from different research institutes and organisations working on pulse crops in India; their pedigree and source are given in Table 1.

Experimental design

The trials were sown in a randomised block design (RBD) with 3 replications during both the years. The plot size was 4.0 m × 1.5 m and the row to row and plant to plant distance was kept at 40 cm and 10 cm, respectively. The experiment was conducted under four environments (E1–E4), with early sowing on 10 November 2023 (E1), late sowing on 15 December 2023 (E2), early sowing on 15 November 2024 (E3) and late sowing on 10 December 2024 (E4).

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.14682

Table 1. List of genotypes and their pedigree used in the experiment

Sl. NO.	Genotype	Pedigree	Source
1.	SKNP 04-09	Sel. From DDR 49	SDAU, S. K. Nagar
2.	VL 42	VL Matar 1 × P 388	VPKAS, Almora
3.	HUDP - 15	PG 3 (PG 3 × S-143) FC 1	BHU Varanasi
4.	HFP - 4	T 163 × Ec190196	Hisar
5.	Pant P 243	Pant P 14 × Pant P 41	GBPUAT Pantnagar
6.	Pant P 200	-	GBPUAT Pantnagar
7.	IPF 14-13	-	IIPR, Kanpur
8	Pant P 347	Pant P 13 × IPFD 08-3	GBPUAT Pantnagar

Observations recorded

The data were recorded on 10 characters, viz., days to 50 % flowering (DF), days to maturity (DM), plant height (PH, cm), number of primary branches per plant (NPPP), number of pods per plant (PPP), number of seeds per pod (SPP), 100-seed weight, harvesting index (HI, %), biological yield per plant (BYPP, g) and seed yield per plant (SYPP, g). For DF and DM, data were recorded on plot basis, while data for rest of the morphological traits was recorded on randomly selected 5 competitive plants in the middle 3 rows of each plot in all three replications. The recommended package of practices was followed to raise a good crop.

Statistical analysis

The data recorded for each of the 10 characters were subjected to analysis of variance (ANOVA) for each environment separately and pooled over environments, following a RBD, to test for the significance of differences among genotypes. All statistical analyses, including ANOVA and the stability analysis described below, were performed using Indostat, version 9.3.

The stability of yield performance for each genotype was calculated by regressing the mean yield of individual genotypes on environmental index and calculating the deviations from regression as suggested by Eberhart and Russell (20). Regression coefficient (βi) was considered as an indication of the response of the genotype to varying environment while the environment and genotype × environment (G × E) interactions were partitioned into three components viz., environment (linear), G × E (linear) and deviation from regression (pooled deviation over the genotypes). The stability analysis was done using the linear regression model suggested by Eberhart and Russell (20).

The model is defined as follows:

$$Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$$

Where,

Y_{ij} = Mean performance of i^{th} genotype in j^{th} environment

μ_i = Mean performance of i^{th} genotype over all environments.

β_i = Regression coefficient that measures the response of i^{th} genotype to varying environments.

Ij = Environment index, as the deviation of the mean of all genotypes in the j^{th} environment from grand mean.

δij = The deviation from regression of the i^{th} genotype in j^{th} environment.

i = Number of genotypes (1, 2…i)

j = Number of environments (1, 2…j)

Results and Discussion

Analysis of variance

The pooled analysis of variance for stability showed highly significant differences among varieties for all the traits under study ($p < 0.01$), with genotype mean squares several-fold larger than the corresponding error mean squares for most traits (Table 2). The occurrence of such heterogeneity between genotypes indicated the presence of adequate genetic variability in the material, which allows for efficient selection and development through breeding programs.

The environment and G × E interaction [Env. + (Var. × Env.)] had a significant effect on almost all traits, together accounting for a substantially larger share of the total treatment sum of squares than the genotype main effect alone, which indicated that environment, rather than genotype identity, was the dominant source of variation across the four environments tested in this study. Previous researchers found similar results, showing that strong G × E interaction means genotype performance changes depending on the environment (21). When genotypes respond differently in various environments, it shows a G × E interaction, which is common in multi-environment trials and can affect how consistently genotypes perform (22). Breaking down the interaction showed that both environmental (linear) and G × E (linear) components were significant, meaning genotypes react differently as environmental factors change. The linear part of the environment and E × G interaction suggests that predictable environmental factors can explain much of the G × E interaction (23). In the ANOVA, the pooled deviation was not significant (Table 2), which means there was little non-linear G × E interaction was also reported (24). This means the genotypes tested were stable across environments, making them good choices for selection in different environmental conditions (25). In the context of the

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.14682

present study, this predominantly linear pattern of G × E interaction suggests that the heat stress imposed by late sowing in E2 and E4 acted in a largely predictable manner across genotypes, which is encouraging from a breeding standpoint because it means that genotype performance under such conditions can be reasonably anticipated from their regression response rather than requiring separate selection in every environment.

Stability analysis

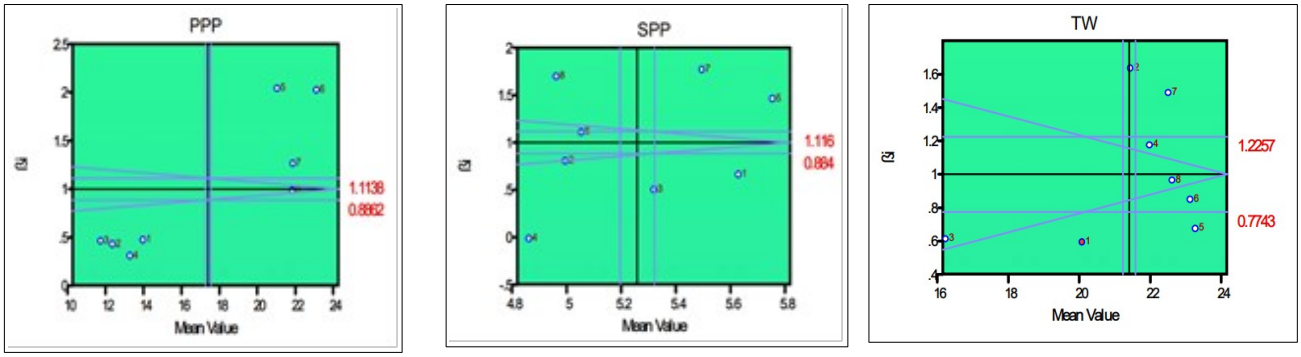
The stability parameters for various traits and genotypes are shown in Table 3. As suggested by earlier researchers, to measure stability performance of genotypes, three parameters were used i.e. mean performance (μ), regression coefficient (β_i) and deviation from regression (σ^2di) (26). A genotype with a higher mean value, a regression coefficient close to unity ($\beta_i = 1$) and non-significant deviation from regression ($\sigma^2di \approx 0$) is classified as stable in various environments.

Stability analysis using the Eberhart and Russell model showed that genotypes varied significantly in the traits tested, which means they responded differently to different environments (Fig. 1, Table 3). For example, genotype IPF 14-13 had higher average values for days to flowering (60.92) and DM (118.00). Its regression coefficients were close to one (1.18 and 1.2) and the deviations from regression were not significant (-0.96 and -1.45), suggesting stable performance and adaptability across environments (27). Pant P-243 also had a high average for days to flowering (60.75) and performed well in other important traits, such as PPP (20.76), SPP (5.73) and test weight (23.10 g), which points to better yield. Pant P-200 had more PPP (22.83) than IPF 14-13, as well as more SPP (5.48) and a test weight of 22.35 g. On the other hand, VL-42 had lower averages for days to flowering (49.25) and DM (109.5) and its regression coefficient was less than one, which showed that it was less adapted to changes in the environment (28). HFP-4 had a regression coefficient close to one for the harvest index (HI, 0.97), showing that it performed consistently across environments. Previous study noted that stability measures like mean performance, regression coefficient and deviation from regression are important for finding stable genotypes that produce well and perform reliably in different environments (29).

Table 2. Analysis of variance for different traits used in stability analysis

	d.f.	DF	DM	PH	NPPP	PPP	SPP	TW	HI	BYPP	SYPP
Rep within Env.	8	2.101*	2.986**	14.050**	0.042***	0.471**	0.036*	0.035	0.155	3.423***	0.348**
Varieties	7	65.079***	87.022***	2084.923***	0.264***	97.935***	0.456***	21.645***	12.530***	2198.065***	272.776***
Env.+ (Var.* Env.)	24	18.193***	51.428***	28.993***	0.108***	2.911***	0.396***	0.729***	12.515***	122.669***	30.190***
Environments	3	128.911***	381.495***	157.555***	0.611***	15.825***	2.313***	4.696***	81.074***	729.839***	215.515***
Var.* Env.	21	2.376**	4.276***	10.626**	0.036***	1.066***	0.122***	0.162	2.721***	35.930***	3.715***
Environments (Lin.)	1	386.733***	1144.486***	472.666***	1.832***	47.476***	6.939***	14.088***	243.223***	2189.517***	646.544***
Var.* Env.(Lin.)	7	5.875***	11.464***	26.464***	0.096***	3.023***	0.339***	0.281*	7.805***	107.409***	10.947***
Pooled Deviation	16	0.549	0.597	2.369	0.006	0.077	0.012	0.090	0.157	0.167	0.086
Pooled Error	56	1.882	3.188	4.252	0.025	0.261	0.039	0.094	0.249	1.034	0.131
Total	31	28.780	59.466	493.235	0.143	24.368	0.409	5.452	12.519	591.307	84.967

DF: days to 50 % flowering; DM: days to maturity; PH: plant height; NPPP: number of primary branches per plant; PPP: number of pods per plant; SPP: number of seeds per pod; TW: test weight; HI: harvest index; BYPP: biological yield per plant; SYPP: seed yield per plant. *Significant at $p \leq 0.05$; **significant at $p \leq 0.01$; ***significant at $p \leq 0.001$; ns: non-significant. Rep. within Env.: replications within environments; Var.: varieties; Env.: environments; Lin.: linear component.



(a) (b) (c)

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.14682

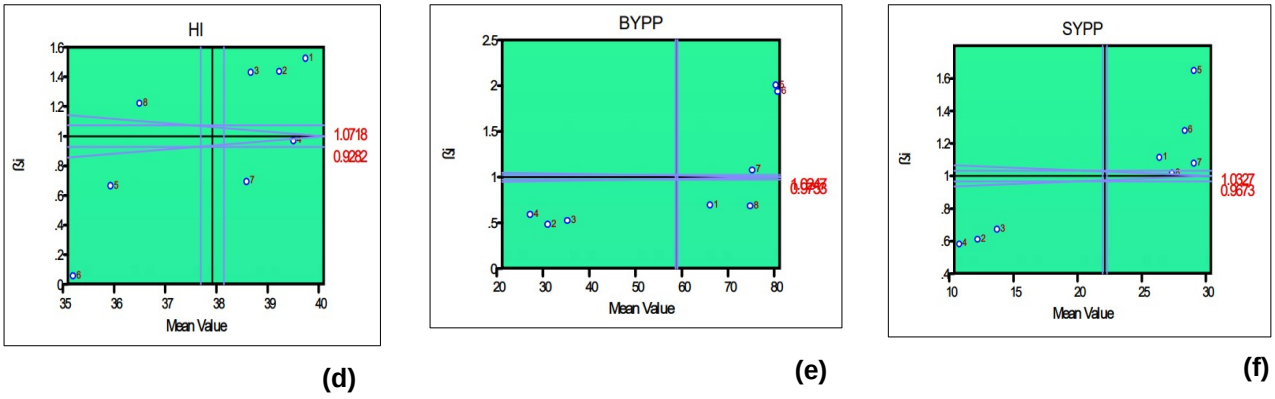


Fig. 1. Stability performance across environments. a: number of pods per plant; b: number of seeds per pod; c: test weight (g); d: harvest index; e: biological yield per plant (g); f: seed yield per plant (g).

Table 3. Performance of different genotypes under stability analysis for different traits

Genotypes	DF			DM			PH			NPPP			PPP		
	Mean	βi	σ²di	Mean	βi	σ²di	Mean	βi	σ²di	Mean	βi	σ²di	Mean	βi	σ²di
SKNP 04-09	55.917	0.5	-1.24	115.333	0.81	-2.85	69.851	0.85	-3.3	2.318	0.63	-0.02	13.697	0.47*	-0.27
VL 42	49.25	0.7	-1.59	109.5	0.56**	-2.98	110.138	1.57	2.42	2.451	0.77	-0.03	12.083	0.43*	-0.27
HUDP 15	57.5	1.35**	-1.9	115.75	0.79*	-3.07	55.6	0.88*	-5.46	2.526	0.68	-0.02	11.466	0.47	-0.06
HFP 4	60	0.86	-1.64	122.667	0.89	-2.93	56.954	0.77	-4.65	2.345	0.79	-0.02	13.014	0.31*	-0.22
Pant P 243	60.75	1.51	-0.42	108	1.42	-1.71	111.084	0.13	-2.8	2.713	2.47*	-0.02	20.76	2.04*	-0.2
Pant P 200	61.25	0.75	-1.37	113.333	1.12	-2.85	74.738	0.58	-1.13	3.118	1.33*	-0.03	22.832	2.02*	-0.25
IPF 14-13	60.917	1.18	-0.96	118	1.2	-1.45	102.815	2.33**	-4.53	2.558	0.89	-0.02	21.587	1.27	-0.17
Pant P 347	59.5	1.16	-1.77	112.917	1.21	-2.69	74.709	0.89	-5.42	2.459	0.44	-0.02	21.553	0.99	-0.24
Population Mean	**58.135**			**114.438**			**81.986**			**2.561**			**17.124**		

Genotypes	SPP			TW			HI			BYPP			SYPP		
	Mean	βi	σ²di	Mean	βi	σ²di	Mean	βi	σ²di	Mean	βi	σ²di	Mean	βi	σ²di
SKNP 04-09	5.608	0.66*	-0.04	19.915	0.59	0.28*	39.638	1.53*	-0.03	64.898	0.7*	-0.83	25.971	1.11	0.23
VL 42	4.975	0.81	-0.04	21.274	1.64*	-0.05	39.126	1.44*	-0.07	29.8	0.48**	-1.33	11.818	0.61**	-0.15
HUDP 15	5.3	0.5*	-0.03	16.074	0.61	-0.03	38.572	1.43*	0.01	34.077	0.53**	-1.26	13.318	0.67**	-0.1
HFP 4	4.842	-0.01*	-0.01	21.815	1.18	-0.03	39.403	0.97	-0.09	26.017	0.59**	-1.3	10.382	0.58**	-0.16
Pant P 243	5.733	1.46	0	23.103	0.68	-0.07	35.829	0.66*	-0.08	79.114	2.01**	-1.04	28.65	1.65**	-0.13
Pant P 200	5.033	1.11*	-0.04	22.957	0.85	0.01	35.098	0.06**	-0.15	79.538	1.94**	-1.23	27.942	1.28*	-0.06
IPF 14-13	5.475	1.77*	-0.03	22.346	1.49	0	38.489	0.69	-0.04	74.018	1.08	-1.22	28.653	1.08	-0.07
Pant P 347	4.942	1.7**	-0.04	22.45	0.97	-0.08	36.397	1.22*	-0.2	73.601	0.69**	-1.12	26.944	1.02	-0.13
Population Mean	**5.239**			**21.242**			**37.819**			**57.633**			**21.71**		

DF: days to 50 % flowering; DM: days to maturity; PH: plant height; NPPP: number of primary branches per plant; PPP: number of pods per plant; SPP: number of seeds per pod; TW: test weight; HI: harvest index; BYPP: biological yield per plant; SYPP: seed yield per plant. Mean: overall mean performance of the genotype across environments; b_i: regression coefficient, indicating the response of a genotype to environmental variation; S^2d_i: deviation from regression, indicating the stability of genotype performance across environments. Genotypes with high mean performance, a regression coefficient close to unity ($b_i \approx 1$) and a non-significant deviation from regression ($S^2d_i \approx 0$) were considered stable across environments. * and ** indicate significance at $p \leq 0.05$ and $p \leq 0.01$, respectively.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.14682

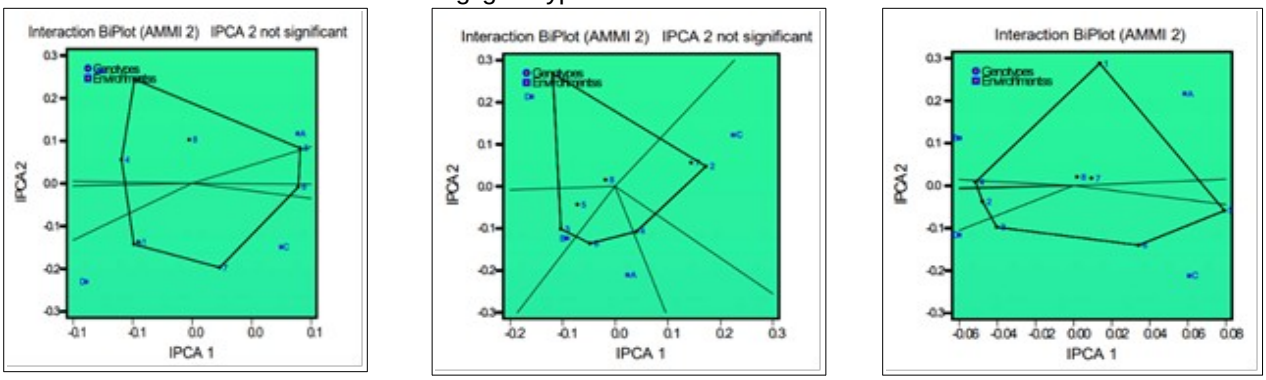
For the key productivity traits, the average BYPP (57.63 g) and SYPP (21.71 g) varied widely among genotypes. Genotypes like Pant P-200, Pant P-243, IPF 14-13 and Pant P-347 had higher averages than the population means, suggesting stable yield performance. IPF 14-13 (1.08) and Pant P-347 (1.02) had regression coefficients near one and little deviation, showing steady and adaptable performance in different environments. Their higher yields and stability mean these genotypes may give consistently good results regardless of conditions, similar patterns were observed in earlier reports (30). Thus, these genotypes can be considered good choices for cultivation and breeding programmes focused on reliable yield. These findings are broadly consistent with the recent work (31), which evaluated the yield adaptability and stability of field pea genotypes using additive main effects and multiplicative interaction (AMMI); genotype plus genotype × environment (GGE); genotype × yield × trait (GYT) biplot analyses and similarly identified a small subset of genotypes combining high mean yield with regression coefficients close to unity as the most desirable for cultivation across variable environments; however, unlike the present study, previous researchers relied primarily on multiplicative (AMMI/GGE) stability statistics rather than the Eberhart and Russell regression approach, so the present results extend this line of evidence by showing that a regression-based stability framework identifies a largely overlapping set of stable, high-yielding field pea genotypes, which strengthens confidence in the practical usefulness of both approaches for field pea improvement (31). The results also agree with the more recent field pea stability work previous researchers, which reported that genotype performance for yield-contributing traits under timely and late sown conditions was strongly influenced by genotype × environment interaction, reinforcing the present observation that late-sown, heat-stressed environments (E2 and E4) discriminated more strongly among genotypes than the timely-sown environments (14).

Interaction biplot

An interaction biplot based on principal component analysis was employed to analyse the G × E interaction. The first two principal components (PC1 and PC2) accounted for most of the variation among genotypes and environments (Fig. 2). Genotypes positioned near the origin exhibited consistent performance, while those located farther from the origin demonstrated stronger interactions with their respective environments. Genotypes with positive values on PC1 and higher mean trait values indicated improved performance. Genotypes situated close to the average environment axis are likely to be more stable and adaptable across diverse environments.

The AMMI-2 biplot for the PPP revealed pronounced G × E interactions, indicating that genotype performance is environment-dependent. The genotypes SKNP-04-09, HFP-4, IPF-14-13 and Pant P-347 exhibited variable responses across all environments. HFP-4 and Pant P-347 were positioned away from the origin, reflecting strong specific interactions with certain environments and suggesting adaptation to particular environmental conditions (32). Conversely, SKNP-04-09 was located closer to the origin, signifying more consistent performance across environments. The polygon connecting the outermost genotypes facilitates identification of superior genotypes for specific traits in different environments. Pant P-347 was most suited to environments E1 and E4, whereas IPF-14-13 demonstrated a stronger association with environment E3. This graphical analysis of the AMMI biplot enables identification of genotypes with either broad or specific adaptability, thereby supporting selection for enhanced pod yield under diverse environmental conditions (31).

The AMMI-2 interaction biplot for test weight (g), where IPCA 2 was shown to be non-significant for the genotype-environment interaction primarily through the IPCA 1 axis. The biplot shows all genotypes in environments E1 and E3, with genotypes represented by circles and environments by squares. Genotypes close to the origin, such as VL-42 and HUDP-15, demonstrated relatively stable performance across environments, whereas genotypes away from the origin, such as Pant P-347, exhibited stronger interaction with specific environments, indicating their specific adaptation to environmental conditions. The biplot's relatively narrow distribution of environments revealed that the environments had a modest discriminating capacity, consistent with the previous findings (33).



(a) (b) (c)

Fig. 2. Genotype × environment interaction biplots. a: number of pods per plant; b: test weight (g); c: seed yield per plant.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.14682

The AMMI-2 interaction biplot for seed yield per plant shows how genotypes respond differently across environments using the IPCA 1 and IPCA 2 axes. All genotypes and environments (E1, E2 and E3) were dispersed across the biplot, indicating G × E interaction. Genotypes close to the origin, such as VL-42 and HUDP-15, showed increased stability and adaptation to different conditions. In contrast, genotypes located away from the origin, particularly Pant P-347, exhibited more interaction with certain environments, indicating greater responsiveness but lower stability (25). The polygon generated by linking the outermost genotypes aids in determining the stable genotypes for various traits. Genotype Pant P-347 appeared to be more suited to environment E2, whereas genotype SKNP-04-09 was more closely associated with environment E1.

Conclusion

The pooled analysis of variance and stability parameters revealed considerable genetic diversity among the studied genotypes ($p < 0.01$), with strong genotype × environment (G × E) interactions that showed better trait expression in the late-sown, heat-stressed environments (E2 and E4) than in the timely-sown environments (E1 and E3). The predominance of the linear component over the non-significant deviation from regression (σ^2di approximately 0) indicated that most of this variability was predictable and genotypes such as IPF 14-13, Pant P-243, Pant P-200 and Pant P-347 combined stable population means with regression coefficients close to unity, confirming their potential for consistent production across environments. Additive main effects and multiplicative interaction (AMMI) biplot analysis supported these regression-based results, showing VL-42 and HUDP-15 as broadly stable and Pant P-347 and IPF 14-13 as specifically adapted to E1 and E3, respectively. Together, the two approaches provide a complementary framework for identifying genotypes combining high yield with stability, reinforcing the value of multi-environment trials for improving productivity and heat stress resilience in future field pea breeding.

As this study was limited to two locations and two years and stability was assessed on phenotypic data alone, future work should validate these genotypes across a wider range of environments and integrate molecular or physiological markers of heat tolerance to strengthen selection.

Acknowledgements

The authors express their sincere gratitude to the University for providing the necessary facilities and support to conduct this research. The authors are also grateful to the Head of the Department for their guidance, encouragement and administrative support throughout the study. They also extend their appreciation to the members of the Advisory Committee for their valuable suggestions and constructive guidance during the research.

Authors' contributions

SN, B and BB contributed to the conceptualisation and design of the study and development of the initial manuscript. SK contributed to data analysis and manuscript preparation. DKP, RPM and SY contributed to manuscript formatting. LV, PS and JP contributed to field layout preparation and data handling. All authors have read and approved the final manuscript.

Compliance with ethical standards

Conflict of interest

Authors do not have any conflict of interests to declare.

Ethical issues

None

References

1. Rispail N, Wohor OZ, Osuna-Caballero S, Barilli E, Rubiales D. Genetic diversity and population structure of a wide *Pisum* spp. core collection. Int J Mol Sci. 2023;24(3):2470. https://doi.org/10.3390/ijms24032470
2. Olle M, Williams IH, Rosa E, Tamm S. Finding best field pea (*Pisum sativum* L.) cultivars for breeding in Northern climatic conditions. Acta Agric Scand B Soil Plant Sci. 2020;70(1):1–7. https://doi.org/10.1080/09064710.2019.1660400
3. Burstin J, Gallardo K, Mir RR, Varshney RK, Duc G. Improving protein content and nutrition quality. In: Biology and breeding of food legumes. Wallingford, UK: CABI; 2011. p. 314–28. https://doi.org/10.1079/9781845937669.0314
4. Bastianelli D, Grosjean F, Peyronnet C, Duparque M, Regnier JM. Feeding value of pea (*Pisum sativum* L.) 1. Chemical composition of different categories of pea. Anim Sci.1998;67(3):609–19. https://doi.org/10.1017/S1357729800033051
5. Singh B, Singh JP, Shevkani K, Singh N, Kaur A. Bioactive constituents in pulses and their health benefits. J Food Sci Technol.2017;54(4):858–70. https://doi.org/10.1007/s13197-016-2391-9
6. Dahl WJ, Foster LM, Tyler RT. Review of the health benefits of peas (*Pisum sativum* L.). Br J Nutr. 2012;108(S1)–10. https://doi.org/10.1017/S0007114512000852
7. Directorate of Economics and Statistics (DES). Agriculture statistics at a glance 2020. New Delhi: Department of Agriculture, Cooperation and Farmers' Welfare, Government of India; 2021.
8. Indian Council of Agricultural Research, Indian Institute of Pulses Research. All India Coordinated Research Project on MULLaRP crops: project coordinators report (2021-22). Kanpur: Indian Institute of Pulses Research; 2022.
9. Indian Council of Agricultural Research, Indian Institute of Pulses Research. All India Coordinated Research Project on MULLaRP crops: project coordinators report (2015-16). Kanpur: Indian Institute of Pulses Research; 2016.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.
https://doi.org/10.14719/pst.14682

10. Afify RR, El-Nwehy SS, Bakry AB, Abd El-Aziz ME. Response of peanut (*Arachis hypogaea* L.) crop grown on newly reclaimed sandy soil to foliar application of potassium nano fertilizer. Middle East J Appl Sci. 2019;9(1):78–85.
11. Rabiei B, Valizadeh M, Ghareyazie B, Moghaddam M. Evaluation of selection indices for improving rice grain shape. Field Crops Res. 2004;89(2-3):359–67.
12. Jiang Y, Lindsay DL, Davis AR, Wang Z, MacLean DE, Warkentin TD, et al. Impact of heat stress on pod-based yield components in field pea (*Pisum sativum* L.). J Agron Crop Sci. 2020;206(1):76–89. https://doi.org/10.1111/jac.12365
13. Sharma V, Dubey RB, Khan R. Genotype-environment interaction on stability of grain yield and physio-biochemical traits in bread wheat (*Triticum aestivum* L.). Bangladesh J Bot.2019;48(4):1143–51. https://doi.org/10.3329/bjb.v48i4.49070
14. Seepal YS, Sharma V, Mishra A, Singh SK, Gangwar V. Trait association and genetic diversity analysis in field pea (*Pisum sativum* var. *arvense* L.) under timely and late sown conditions. Electron J Plant Breed. 2025;16(2):249–57. https://doi.org/10.37992/2025.1602.024
15. Bueckert RA, Wagenhoffer S, Hnatowich G, Warkentin TD. Effect of heat and precipitation on pea yield and reproductive performance in the field. Can J Plant Sci. 2015;95(4):629–39. https://doi.org/10.4141/cjps-2014-342
16. Sharma V, Singh CM, Chugh V, Prajapati PK, Mishra A, Kaushik P, et al. Morpho-physiological and biochemical responses of field pea genotypes under terminal heat stress. Plants. 2023;12(2):256. https://doi.org/10.3390/plants12020256
17. Stavridou E, Lagiotis G, Karapetsi L, Osathanunkul M, Madesis P. DNA fingerprinting and species identification uncovers the genetic diversity of katsouni pea in the Greek islands Amorgos and Schinoussa. Plants. 2020;9(4):479. https://doi.org/10.3390/plants9040479
18. Olivoto T, Lúcio AD, da Silva JA, Sari BG, Diel MI. Mean performance and stability in multi-environment trials II: Selection based on multiple traits. Agron J. 2019;111(6):2961–9. https://doi.org/10.2134/agronj2019.03.0221
19. Crossa J. Methodologies for estimating the sample size required for genetic conservation of outbreeding crops. Theor Appl Genet. 1989;77(2):153–61. https://doi.org/10.1007/BF00266180
20. Eberhart ST, Russell W. Stability parameters for comparing varieties 1. Crop Sci. 1966;6(1):36–40. https://doi.org/10.2135/cropsci1966.0011183X00060001001 1x
21. Ghazy MI, Abdelrahman M, El-Agoury RY, El-Hefnawy TM, El-Naem SA, Daher EM, et al. Exploring genetics by environment interactions in some rice genotypes across varied environmental conditions. Plants. 2023;13(1):74. https://doi.org/10.3390/plants13010074
22. Perkins JM, Jinks JL. Environmental and genotype-environmental components of variability. Heredity. 1968;23(3):339–56. https://doi.org/10.1038/hdy.1968.48
23. Crossa J. From genotype × environment interaction to gene × environment interaction. Curr Genomics. 2012;13(3):225–44. https://doi.org/10.2174/138920212800543066
24. Gupta V, Kumar M, Singh V, Chaudhary L, Yashveer S, Sheoran R, et al. Genotype by environment interaction analysis for grain yield of wheat (*Triticum aestivum* (L.) em. Thell) genotypes. Agriculture. 2022;12(7):1002. https://doi.org/10.3390/agriculture12071002
25. Ceccarelli S, Acevedo E, Grando S. Breeding for yield stability in unpredictable environments: single traits, interaction between traits, and architecture of genotypes. Euphytica.1991;56(2):169–85. https://doi.org/10.1007/BF00042061
26. Balcha A. Genotype by environment interaction for grain yield and association among stability parameters in bread wheat (*Triticum aestivum* L.). Am J Plant Sci. 2020;11(1):1–10. https://doi.org/10.4236/ajps.2020.111001
27. Viana JM, Cruz CD. Analysis of stability and adaptability through different models of linear regression. Cienc Agrotec Lavras. 2002;26:455–62.
28. de Souza MH, Pereira Júnior JD, Steckling SD, Mencalha J, Dias FD, Rocha JR, et al. Adaptability and stability analyses of plants using random regression models. PLoS One. 2020;15(12). https://doi.org/10.1371/journal.pone.0233200
29. Pour-Aboughadareh A, Barati A, Gholipoor A, Zali H, Marzooghian A, Koohkan SA, et al. Deciphering genotype-by-environment interaction in barley genotypes using different adaptability and stability methods. J Crop Sci Biotechnol.2023;26(5):547–62. https://doi.org/10.1007/s12892-023-00199-z
30. Mohammadi R, Amri A. Genotype × environment interaction and genetic improvement for yield and yield stability of rainfed durum wheat in Iran. Euphytica. 2013;192(2):227–49. https://doi.org/10.1007/s10681-012-0839-1
31. Yang X, Soliman AA, Hu C, Yang F, Lv M, Yu H, et al. Yield adaptability and stability in field pea genotypes using AMMI, GGE, and GYT biplot analyses. Agriculture. 2023;13(10):1962. https://doi.org/10.3390/agriculture13101962
32. Singh V, Sharma A, Kumar N, Rana N. Stability models regulate the adaptation of male sterility-based chilli hybrids for agro-ecologically diverse regions. 2024. https://doi.org/10.21203/rs.3.rs-5781022/v1
33. Yan W, Tinker NA. An integrated biplot analysis system for displaying, interpreting, and exploring genotype × environment interaction. Crop Sci. 2005;45(3):1004–16. https://doi.org/10.2135/cropsci2004.0076

Additional information

Peer review: Publisher thanks the Sectional Editor and anonymous reviewers for their contribution to the peer review of this work.

Reprints & permissions information: Available at https://horizonepublishing.com/journals/index.php/PST/open_access_policy.

Publisher's Note: Horizon e-Publishing Group remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Indexing: See https://horizonepublishing.com/journals/index.php/PST/indexing_abstracting.

Copyright: © The Author(s). This is an open-access article distributed under the Creative Commons Attribution License CC BY 4.0.

Publisher information: Plant Science Today is published by Horizon e-Publishing Group with support from Empirion Publishers Private Limited, Thiruvananthapuram, India.

© The Author(s) 2026. Creative Commons CC BY 4.0. Published by Horizon e-Publishing Group.

https://doi.org/10.14719/pst.14682