Received: 10 Nov 2024 | Revised: 26 May 2025 | Accepted: 29 May 2025

Electronic Journal of Plant Breeding

Research Note

Trait association and genetic diversity analysis in field pea (*Pisum sativum* var. *arvense* L.) under timely and late sown conditions

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Abstract
One hundred and forty three genotypes of field pea including three check varieties were evaluated for morpho-physiological characters under timely and late sown conditions for the study of trait association and genetic diversity. Correlation analysis revealed that for timely and late sown conditions, seed yield per plant showed a strong positive correlation with effective pods per plant, biological yield per plant and plant height. In addition to the above traits, 100-seed weight and pollen viability also exhibited a significant and positive interrelationship with seed yield in late sown conditions. This relationship suggests that selection of more effective pods per plant, biological yield, plant height, 100-seed weight and pollen viability are desirable under late sown conditions to enhance the yield. These traits were also commonly correlated with each other in both environmental conditions. Path coefficient analysis revealed that in timely sown environment, effective pods per plant and biological yield per plant; and in late sown environment, effective pods per plant, biological yield per plant, 100-seed weight, plant height and pollen viability contributed to seed yield directly as well as indirectly. Consequently, it is essential to prioritize these traits when designing a selection strategy for developing high-yielding field pea cultivars. The D^2 cluster analysis grouped 143 genotypes into 05 multi-genotypic clusters in both sowing conditions. Genotype distribution was different in different environments, suggesting that the environment has an influence on genotype performance.

Keywords: Field Pea, Correlation, Path coefficient, Cluster, Genetic diversity.

Field pea (*Pisum sativum* var. *arvense* L.) is an annual, self-pollinating crop with cold tolerance, belonging to *Fabaceae* family. It thrives in a diverse range of climates, from semi-arid to temperate regions globally (Olle *et al.,* 2020). As the second most productive legume worldwide, trailing only the common bean (Mohapatra *et al*., 2019), it serves as a significant protein source (21-25%) and is notably rich in the amino acids lysine and tryptophan (Gregory *et al.,* 2016), though it is relatively low in cysteine and methionine (Ceyhan and Avci, 2005). Field pea contribute to soil fertility by fixing atmospheric nitrogen through Rhizobia in its root nodules, thus reducing environmental pollution (Wendy *et al*., 2012). In India, pulses were cultivated on approximately 29.03 million hectares in 2018-2019, yielding nearly 23.39 million tonnes at an average of 806 kg/ha (DES, 2019). Field pea occupied around 8.2 lakh hectares of this area, producing 9.87 lakh tonnes annually, with a productivity of 1204 kg/ha in 2017-18 (AICRP MULLaRP, 2019). The principal producers in India are Uttar Pradesh and Madhya Pradesh, with Uttar Pradesh alone covering 2.94 lakh hectares, yielding 4.32 lakh tonnes, and achieving a productivity of 1469.3 kg/ha (AICRP MULLaRP, 2019). Nowadays, global warming is increasingly impacting crop production and yield, with rising temperatures posing a significant threat to cold-season legumes like field peas. High-temperature stress, particularly during flowering and seed development, has become a major concern, leading to considerable yield losses (Jiang *et al*., 2019; Sharma *et al*., 2019; Seepal *et al*., 2025). In India, this issue is exacerbated by late sowing due to delayed rice harvests in the rice-pea/mungbean/vegetable cropping system, which shortens the cool winter period and causes temperatures to spike during flowering and fruit formation between late February and April (Mohapatra *et al.,* 2019). Heat stress in peas can result in flower, fruit, and seed drops, as well as reduced seed size (Bueckert *et al*., 2015; Sharma *et al*., 2023). Developing heat-tolerant varieties is crucial to minimizing yield loss and enhancing adaptability in regions where high temperatures occur during the reproductive stage.

A thorough knowledge of genetic diversity and relationships of various traits among field pea germplasm is essential for pea improvement program and the choice of suitable parents in breeding programs (Stavridou *et al*., 2020). Genetic reconstruction helps to create varieties with higher yields by recombining and improving the desired traits. Correlation studies offer information about the interaction between characters. Since, simple correlation analysis cannot provide detailed and realistic information on relationships between dependent variables and predictor variables, path analysis was employed in most causation relationships (Bharti *et al*., 2013; Sharma *et al*., 2014). The path coefficient analysis classifies the correlation coefficients into direct and indirect effect results that provide equal value for each causal factor (Kamaluddin *et al*., 2020; Kishor *et al.,* 2020). Therefore, studying the relationship between different traits is very important for developing an effective selection process. Successful selection of heat-tolerance requires a simple, rapid, and efficient breeding plan to consistently detect heat tolerance differences among many genotypes, as well as identification of the cause of heat tolerance (Adams, 1967). The D^2 statistic is a very useful method for identifying and selecting diverse parental lines (Sanwal *et al.,* 2015).

With the above points in mind, this study was conducted under two planting conditions, namely timely sown and late sown, in order to evaluate the field pea genotypes for diversity and association of different traits to evolve/ suggest suitable breeding strategies for developing high-yielding pea cultivars under heat stress.

The current study was conducted toevaluate140 pea germplasm with three checks in augmented block design under two environmental conditions during *Rabi* 2020-21. Conditions were created by two sowing dates: timely sown (November 10, 2020) and late sown (December 10, 2020). The experimental field was divided into 7 blocks and each block contained 23 entries. Each block contained 20 test genotypes and 3 checks. Each row was 4m long, with a row spacing of 30cm and a plant spacing of 15cm.

The results were noted on five competitive plants randomly sampled from each genotype on eight morphological traits, *viz.,* days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of effective pods per plant (EPP), number of seeds per pod (SPP), 100-seed weight (TSW), biological yield per plant (BYP), seed yield per plant (SYP), with the exception of DF and DM which recorded single time from each genotype as recorded by Yadav *et al.,* 2023 and Parihar *et al*., 2024.

Observations on three physiological traits were measured during the pod-filling stage in field pea. Several physiological traits, namely canopy temperature depression, pollen viability and relative water content were studied.

***Canopy temperature** depression* (CTD): It was recorded from leaves of field pea plants by an infrared thermometer at the pod formation stage in the daytime of minimum humidity, high temperature, full sunshine and least wind velocity, *i.e.,* at 12.00 to 2.00 pm using the formula given below:

CTD = (Tc – Ta)
Where, Tc = Temperature of Canopy;
Ta = Temperature of Atmosphere

***Pollen viability* (PV):** Pollen grains from the anthers of pea plants were excised and stained on glass slides with a drop of 1% acetocamine. 100 pollen grains/slide were counted to determine pollen viability. The percentage of pollen viability was estimated based on the percentage of colored pollen grains (viable) and colourless pollen grains (non-viable).

***Relative water content* (RWC):** It represents the water content of the original sample as a percentage of the water content of the fully hydrated tissue. It was measured on leaf samples at anthesis stage. It was evaluated according to a method of Barr and Weatherly (1962).

RWC = [(Fresh weight-Dry weight)/
(Turgid weight- Dry weight)]× 100

Statistical Analysis: For statistical analysis, the mean data from each sampled plant across different traits was calculated and analyzed using XLSTAT, R 4.0, and online tools developed by IASRI, New Delhi.

The observations were recorded on eleven morpho-physiological characters of field pea including SYP and subjected to various statistical analyses. A critical analysis of the performance of genotypes under timely and late sown conditions suggested the presence of a wide spectrum of genetic variations in evaluated germplasm of field pea.

Correlation Analysis: Knowledge of the correlation between seed yields, their components and the various physiological traits is especially important when a farmer is faced with the challenge of combining high yield strength with heat tolerance parameters.

The simple correlation coefficients among various traits of field pea were calculated for both timely (E_1) and late sown (E_2) experiments, with results summarized in **Table 1**. **Fig. 1a and 1b** present heat maps of these correlations under E_1 and E_2 conditions, respectively. The colour of each grid point on the heat map reflects the strength of correlation, with red indicating positive correlations and blue indicating negative correlations, as shown in the colour key.

The SYP in a timely and late sown environment was very significant and was closely correlated with EPP, BYP and PH. In addition to the above factors, the weight of 100 seeds and the pollen viability also showed strong positive correlation with seed yield in stress conditions. The EPP plant had a significant association with SYP, PH and BYP under timely condition but in late sown condition, showing a significant positive correlation of SYP, BYP, CTD, PV and RWC.

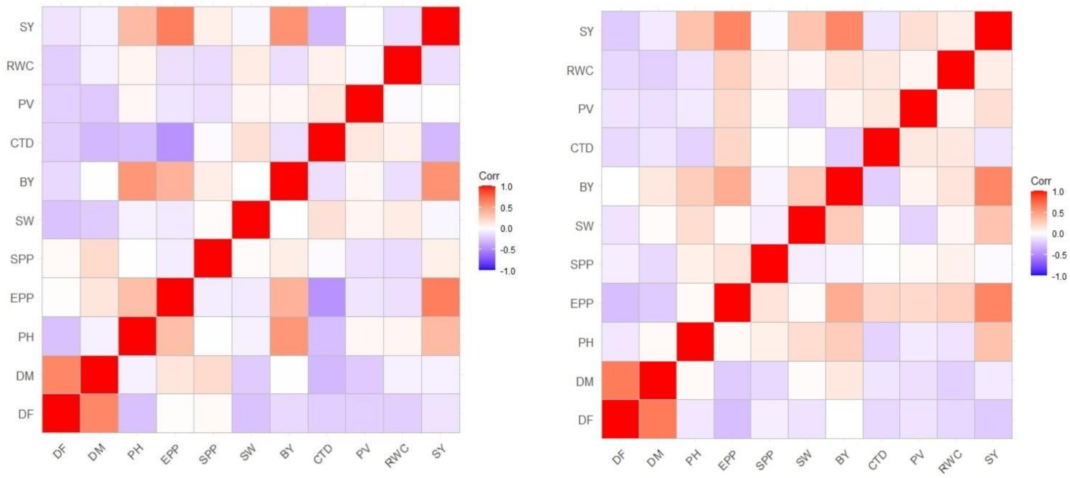
The BYP in a timely environment was very significant and was positively correlated to the SYP, PH and EPP. In addition to the above factors, the weight of 100 seeds also had a strong association with seed yield in the stress conditions. PH showed a positive correlation with the EPP, BYP and SYP in a non-stress environment, whereas it was positively correlated with the BYP, SYP and TSW in stress conditions. Under conditions of heat stress, in addition to seed yield, the weight of 100 seeds was positively correlated with BYP and PH; and PV has shown a significant and positive correlation with EPP. These correlations suggest that selecting highly effective pods that work best for each plant, BYP, PH, TSW and PV are desirable under conditions of heat stress to increase yields.

Table 1. Simple correlation coefficients between different traits in field pea under timely (E_1) and late sown (E_2) conditions.

Characters	Environment	DF	DM	PH	EPP	SPP	TSW	BYP	CTD	PV	RWC	SYP
DF	E_1		0.61**	-0.27**	0.01	0.03	-0.26**	-0.16*	-0.21*	-0.20*	-0.21*	-0.12
	E_2		0.66**	-0.10	-0.28**	-0.07	-0.12	0.00	-0.16	-0.12	-0.17*	-0.22**
DM	E_1			-0.06	0.13	0.19*	-0.22**	-0.01	-0.31**	-0.23**	-0.06	-0.06
	E_2			0.03	-0.22**	-0.16	0.02	0.12	-0.11	-0.13	-0.20*	-0.09
PH	E_1				0.34**	-0.01	-0.06	0.54**	-0.28**	0.04	0.05	0.36**
	E_2				0.03	0.08	0.18*	0.26**	-0.19*	-0.09	-0.12	0.32**
EPP	E_1					-0.08	-0.09	0.40**	-0.47**	-0.11	-0.13	0.65**
	E_2					0.14	0.02	0.43**	0.21*	0.20*	0.25**	0.62**
SPP	E_1						0.02	0.09	-0.02	-0.13	-0.15	0.08
	E_2						-0.07	-0.05	-0.01	0.03	0.07	-0.02
TSW	E_1							0.00	0.16	0.05	0.10	-0.04
	E_2							0.27**	0.01	-0.19*	0.04	0.31**
BYP	E_1								-0.13	0.04	-0.14	0.56**
	E_2								-0.21*	0.06	0.14	0.61**
CTD	E_1									0.12	0.07	-0.31**
	E_2									0.12	0.12	-0.11
PV	E_1										-0.02	-0.01
	E_2										0.05	0.17*
RWC	E_1											-0.14
	E_2											0.09

, * Significant at 5% and 1% probability level, respectively. E_1 and E_2 denotes timely sown and late sown conditions.

DF : Days to 50% flowering
DM : Days to maturity
PH : Plant height
EPP : Effective pods per plant
SPP :Seeds per pod
TSW :100-seed weight
BYP :Biological yield per plant
CTD :Canopy Temperature Depression
PV : Pollen viability
RWC : Relative water content
SYP : Seed yield per plant



(a) (b)

Fig. 1. Heat map of simple correlation between different characters of field pea under timely (a) and late (b) sown conditions.

These traits can be effectively used as additional conditions to increase yield under heat stress conditions. Therefore, EPP, BYP, PH, TSW, and PV were found to be closely related yield traits under stress, showing the potential to increase seed yield through simultaneous selection. The parallel conclusions of seed yields with one or more of the above characteristics were also noted by previous breeders (Bhuvaneswari *et al.,* 2017; Pratap *et al*., 2024a; Sharma *et al*., 2023; Satyendra *et al*., 2025).

Path Coefficient Analysis: Path coefficient analysis evaluates the causal influence of one variable on another, enabling the decomposition of correlation coefficients into direct and indirect effects (Wright, 1921; Dewey and Lu, 1959). This method is crucial for selecting traits that contribute to yield improvement by providing accurate information about each trait's impact. **Table 2** presents the direct and indirect effects of various traits on seed yield per plant under two different environmental conditions (E_1 and E_2).

Under timely conditions, the trait EPP exhibited the highest positive direct effect on seed yield, followed by BYP, SPP, PV, and DF. Both EPP and BYP showed a positive correlation with seed yield, indicating a strong relationship with this trait. Additionally, BYP, PH, DM, and DF had the highest indirect effects on SYP through EPP, while PH, EPP, SPP, and PV showed positive indirect effects on SYP via BYP. These findings are consistent with previous studies on field pea by Srivastava *et al*. (2018), Ton *et al*. (2018), and Singh *et al*. (2019).

Although in the case of late sown conditions, EPP followed by BYP, TSW, PH and PV had shown a significant direct effect on SYP; and all these characters also showed a positive strong relationship with the seed yield. This clearly indicates that the improvement of any of the above characters may contribute to seed yield. In late sown conditions, the highest positive indirect effect on SYP were shown by BYP followed by RWC, CTD, PV, SPP and PH via EPP. Other factors such as EPP, TSW, PH, RWC, DM and PV also showed a positive indirect effect on SYP via BYP. This indicates that these traits significantly contributed to seed yield by influencing the effective pods per plant and the overall biological yield. These findings are consistent with earlier report (Srivastava *et al*., 2018; Prasad *et al.,* 2019).

Thus, the current study has shown that EPP, BYP, TSW, PH and PV have emerged as factors that have a significant impact on seed yield under late sown conditions. Therefore, in order to improve yield under late sown conditions, the breeder should aim to select genotype with more effective pods, higher biological yield, bold seeds, higher plant stature and pollen viability. In formulating a selection strategy for the development of highly productive varieties of field peas that have improved heat tolerance, the above-mentioned characteristics as major direct and indirect participants in seed yield are useful for consideration.

Genetic Divergence Analysis:The Mahalanobis D^2 statistical procedure was performed to analyze the genetic divergence of 143 genotypes. Analysis of genetic divergence will help breeders to establish an efficient breeding program by reducing the use of similar genotypes in crop improvement systems. The 143 genotypes were grouped into five multi-genotype groups in each of the timely (E_1) and late (E_2) seeding experiments and are presented in **Tables 3 and 4**, respectively.

Table 2. Direct and indirect effects of different traits on seed yield per plant in field pea under timely (E_1) and late sown (E_2) condition.

Characters	Environment	Direct effect	Indirect effect									
			DF	DM	PH	EPP	SPP	TSW	BYP	CTD	PV	RWC
DF	E_1	0.0053		-0.1068	0.0067	0.0054	0.0033	0.0050	-0.0560	0.0160	-0.0034	0.0007
	E_2	-0.0625		-0.0007	-0.0180	-0.1420	0.0061	-0.0252	0.0011	0.0236	-0.0151	0.0099
DM	E_1	-0.1763	0.0032		0.0016	0.0683	0.0227	0.0041	-0.0048	0.0241	-0.0039	0.0002
	E_2	-0.0011	-0.0412		0.0045	-0.1111	0.0141	0.0047	0.0298	0.0166	-0.0167	0.0119
PH	E_1	-0.0247	-0.0014	0.0112		0.1740	-0.0011	0.0011	0.1821	0.0217	0.0006	-0.0002
	E_2	0.1769	0.0064	0.0000		0.0154	-0.0067	0.0376	0.0676	0.0287	-0.0123	0.0072
EPP	E_1	0.5159	0.0001	-0.0233	-0.0083		-0.0095	0.0017	0.1376	0.0360	-0.0018	0.0005
	E_2	0.5155	0.0172	0.0002	0.0053		-0.0118	0.0038	0.1092	-0.0308	0.0254	-0.0151
SPP	E_1	0.1227	0.0001	-0.0327	0.0002	-0.0399		-0.0003	0.0304	0.0015	-0.0021	0.0005
	E_2	-0.0860	0.0044	0.0002	0.0138	0.0710		-0.0153	-0.0135	0.0022	0.0042	-0.0044
TSW	E_1	-0.0189	-0.0014	0.0381	0.0015	-0.0468	0.0021		0.0000	-0.0122	0.0009	-0.0004
	E_2	0.2140	0.0073	0.0000	0.0310	0.0092	0.0062		0.0697	-0.0020	-0.0248	-0.0022
BYP	E_1	0.3402	-0.0009	0.0025	-0.0132	0.2087	0.0110	0.0000		0.0100	0.0007	0.0005
	E_2	0.2561	-0.0003	-0.0001	0.0467	0.2198	0.0045	0.0582		0.0307	0.0072	-0.0086
CTD	E_1	-0.0768	-0.0011	0.0553	0.0070	-0.2418	-0.0024	-0.0030	-0.0441		0.0020	-0.0003
	E_2	-0.1486	0.0099	0.0001	-0.0341	0.1067	0.0013	0.0029	-0.0529		0.0154	-0.0069
PV	E_1	0.0169	-0.0011	0.0408	-0.0009	-0.0558	-0.0155	-0.0010	0.0136	-0.0092		0.0001
	E_2	0.1293	0.0073	0.0001	-0.0168	0.1011	-0.0028	-0.0410	0.0143	-0.0177		-0.0028
RWC	E_1	-0.0035	-0.0011	0.0102	-0.0012	-0.0665	-0.0179	-0.0019	-0.0479	-0.0057	-0.0003	
	E_2	-0.0595	0.0104	0.0002	-0.0213	0.1306	-0.0063	0.0081	0.0370	-0.0173	0.0061	

Residual factor in E_1 = 0.440; Residual factor in E_2 = 0.352

Table 3. Clustering pattern of 143 field pea genotypes for morpho-physiological characters under timely sown condition

Cluster Number	Number of Genotypes	Genotypes
I	21	HFP 802, KPMR 522, LFP 431, HUDP 954, RFP 2000-3, KPMR 928, VL 202, HFP 1036, HFP 1307, IPFD 2014-11, IPF 15-8, KPMR 945, KPMR 400, P-1297-84, P-1297-96, P-1297-97, P-1531, P-1613, P-1697, P-1591, IPFD 10-12
II	57	JP-885, KPMR 935, 02/1071, 02/1084, 02/1118, 02/1121, EC 564816, EC 564806, EC 564812, EC 564815, EC 564805, KFPG 79, KPMR 940, HF 13-14, KPMR 923, P-867, P-782, P-864, P-DMR-11, P-1434-1, P-1440-19, P-1535-2, P-781, P-201, P-1300-2-2, P-600, P-1438-1, P-729, P-1301, P-7-674-4, P-108-2, EC-341792, EC-341987, EC-322748, P-1545-1, P-1597-11, P-1440-21, P-1384-3, P-814, P-1400, P-992, P-1378, P-1446-6, P-1777, P-1516,P-1425,P-1429, P-107-2-2, P-1589, P-1679, P-1673, P-1673, P-1691, EC 564813, JM-6, Shikha (KFP103), IPF4-9, Adarsh, EC-341792
III	19	IPFD 13-14, HFP 916, NDP 2014-4, Pant P 273, KPMR 913, EC 564817, EC 564808, EC 564803, VRP-3, KPMR 225, KPMR 874, P-1297-7-1, P-1497, P-1541-6, P-1541-19, P-1440-2, P-1440-17, P-1534, EC 389377
IV	30	02/1088, 02/1090, 02/1119, 02/1120, 02/1129, 02/1132, NGSN-3, KPMR 839, HF-2, P-1450, P-725, P-1436-9, P-1384-1, P-1558, P-1297-11, P-1456A-3, P-647, EC-324133, EC-328743, P-122-9, P-122-19, EC-324576, EC-329761, P-4-1479-4, P-1451, P-1448-2, P-1089, P-1468, P-263
V	16	P-1297-39 (JP 2), P-1075, P-1300, P-1440-10, P-133-2-1, P-1541-16, P-1532, P-107, T-163, P-91-3, P-1457-1,P-1658, EC-324131, EC-329554, P-179, EC-341743

Table 4. Clustering pattern of 143 field pea genotypes for morpho-physiological characters under late sown condition.

Cluster Number	Number of Genotypes	Genotypes
I	27	HFP 802, KPMR 522, RFP 2000-3, KPMR 928, IPFD 13-14, VL 202, Pant P 273, KPMR 913, HFP 1036,HFP 1307, IPFD 2014-11, IPF 15-8, NDP 2014-4, 02/1084, NGSN-3, EC 564816, EC 564803, VRP-3, KPMR945,P-1297-84, P-1297-97, P-1531, P-1613, P-1541-19,P-1589, IPFD 10-12
II	39	JP-885, HUDP 954, HFP 916, KPMR 935, 02/1088, 02/1090, 02/1118, 02/1119, 02/1121, 02/1129, 02/1132, EC564806, EC 564817, EC 564812, EC 564808, EC 564805, KPMR 839, KPMR 225, KPMR 400, KPMR 874,KPMR 923, P-1297-7-1, P-1297-39 (JP 2), P-1440-19, P-1535-2, P-1297-96, P-1558, EC-324133, P-122-9, P-814, P-1378, P-1440-2, P-1446-6, P-1777, P-1516, P-1425, P-1429, P-1591, Adarsh
III	36	LFP 431, 02/1071, 02/1120, EC 564815, HF-2, P-20, P-600, P-1300, P-1384-1, P-1440-10, P-133-2-1, P-1541-16, P-1456 A-3, EC-341743, P-91-3, P-1457-1, P-1658, P-647, EC-328743, P-1440-21, P-992, P-1541-6, P-440-17, P-1534, P-1451, P-1448-2, P-1089, P-1468, P-1679, Shikha (KFP103), IPF4-9, EC-341792
IV	17	P-122-19, P-1301, P-1297-11, EC564811, P-864, P-729, P-1532, P-107, T-163, EC-324131, EC-324576, EC-329761, P-1597-11, P-1384-3, P-1400, EC 389377
V	24	KFPG 79, KPMR 940, HF 13-14, P-867, P-782, P-DMR-11, P-1434-1, P-1497, P-781, P-1300-2-2, P-1438-1, P-1450,P-1075, P-725, P-1436-9, P-263, P-179, P-1673, P-1691, EC 564813, JM-6, P-107-2-2

In E_1, the maximum number of was genotypes grouped into cluster II (57 genotypes) followed by cluster IV (30 genotype) and a minimum of 16 genotypes were included in cluster V, while in E_2, cluster II included the highest 39 genotypes, followed by cluster III (36 genotypes) and a minimum of 17 genotype were included in cluster IV. The study of genotype in different environment suggesting that change of environment play significant role in affecting mean performance of genotypes. The discrimination of germplasm into diverse clusters reflects the presence of adequate diversity in experimental material. These findings are consistent with earlier reports (Pratap *et al*., 2024b; Khan *et al*., 2016; Rahul *et al*., 2017; Lal *et al*., 2018). Some genotypes came together in the same group in both environments. Such genotypic variation has suggested that these genotype species are very similar to the group. However, they are genetically different compared to other groups.

The estimates of intra- and inter-cluster distances for five diverse clusters are provided in **Table 5**. Under timely conditions, cluster IV had the largest intra-cluster distance, followed by cluster V, while in late sown condition, cluster V exhibited the highest intra-cluster distance, followed by cluster I, indicating significant genetic variation within these clusters. The greatest inter-cluster distance was found between clusters I and V, followed by clusters I and IV, III and V, and I and II in timely sown conditions, whereas, in late conditions, the highest inter-cluster distance occurred between clusters I and V, followed by clusters I and IV, I and III, and II and V, reflecting the greatest diversity among genotypes in these clusters under late sown conditions. The minimum inter-cluster distance was found between clusters II and III under timely conditions, but under late seeding conditions it was lowest for the clusters III and IV, suggesting that the genotypes of these clusters were genetically less diverse and had almost the same genetic architecture (Singh *et al*., 2002). Intra-cluster distance was lower than inter-cluster distance in both environments, suggesting that genotypes within the group tended to be slightly different from each other. To find useful recombinants for segregating generations, hybridization genotypes can be selected based on their broad inter-cluster distance, *i.e*., from clusters I and IV in the case of non-stress and clusters I and V in the case of heat stress.

The diversity was further evidenced by the substantial variability in cluster means across different traits in both timely and late sown conditions. The calculated cluster mean values of all the eleven characters under E_1 and E_2 are presented in **Table 6**.As revealed by **Table 6**, in the case of timely sown conditions, cluster I showed the maximum estimate of mean for TSW, CTD as well as least mean values for PH, EPP, BYP and SYP. The minimum mean value for DM, RWC and PV found in cluster II. Cluster III had maximum mean for DF and PV as well as least mean value for SPP and TSW. Cluster III had maximum mean value for RWC only. The highest mean value for DM, PH, EPP, BYP, SYP found in cluster V and this cluster also had the least mean value for DF and CTD. In the case of late sown condition, the cluster I showed a very high mean value for CTD and as well as least mean values for PH. Very low mean value for EPP, TSW, BYP, RWC and SYP found from cluster II. The highest mean value of DF, DM and PV found in cluster III. Cluster IV had a very high mean value for EPP, RWC and SYP and low mean value for DF, SPP and CTD. Cluster V showed a very high average value for PH, SPP and

Table 5. Estimates of average intra- and inter-cluster distances for five clusters in field pea germplasm under timely (E_1) and late (E_2) sown conditions

Cluster number	Environment	Intra-cluster distance	II	III	IV	V
I	E_1	26.79	71.03	44.28	102.10	131.15
	E_2	26.32	38.88	48.80	66.95	73.50
II	E_1	28.18		41.41	43.85	67.69
	E_2	25.18		31.16	44.73	47.47
III	E_1	28.49			69.58	97.13
	E_2	23.50			30.22	39.06
IV	E_1	34.09				43.78
	E_2	22.04				31.28
V	E_1	29.05				
	E_2	28.01				

Table 6. Cluster mean for different characters in field pea under timely (E_1) and late (E_2) sown conditions

Cluster number	Environment	DF	DM	PH	EPP	SPP	TSW	BYP	SYP	CTD	PV	RWC
I	E_1	69.50	116.80	66.81*	25.40*	4.57**	14.65**	34.21*	9.39*	16.49**	94.25	87.73
	E_2	64.72	99.75	44.76*	10.85	3.43	10.62	23.91	3.43	10.37**	74.93	74.75
II	E_1	69.84	115.92*	132.00	30.13	4.38	12.50	44.50	14.42	14.42	93.74*	86.98*
	E_2	64.07	99.55	73.84	8.96*	3.51	9.85*	18.62*	2.61*	9.77	75.52	66.42*
III	E_1	71.75**	117.55	101.29	26.91	4.21*	12.24*	42.20	10.43	14.84	95.26**	87.63
	E_2	66.16**	101.76**	86.82	10.36	3.48	10.31	32.90	4.89	7.96	77.13**	71.27
IV	E_1	67.29	116.20	161.02	34.26	4.46	12.94	57.50	15.39	14.41	94.53	89.04**
	E_2	62.92*	100.26	106.73	11.99**	3.33*	10.79	37.53**	5.82**	7.68*	75.60	75.86**
V	E_1	66.54*	117.56**	191.84**	37.18**	4.45	13.84	61.54**	16.03**	12.30*	95.16	88.25
	E_2	63.30	98.99*	113.45**	9.12	3.73**	12.06**	23.33	4.31	9.65	67.27*	68.80

*Lowest value, **Highest value

TSW and low mean value for DM and PV. These findings indicate that different clusters excelled in various traits across both environmental conditions.

In the current study, correlation analysis revealed that SYP in timely and late sown condition was strong and positively correlated with EPP, BYP and PH. It also suggested that selection for high EPP, BYP, PH, TSW and PV are desirable under heat stress condition to increase the yield. Under timely conditions, EPP and BYP, and under late seeding conditions, EPP, BYP, TSW, PH, and PV contributed both directly and indirectly to seed yield. Consideration of the cluster pattern indicates that the distribution of genotypes differed in the different environments, suggesting that environmental changes were effective in influencing genotype performance. The different clusters in both environments displayed significant variations in cluster mean for all eleven characters. Consequently, crosses between cluster members with high mean values for key traits, combined with significant inter-cluster distances, are likely to yield more favorable results.

ACKNOWLEDGEMENT

The authors acknowledge IIPR, Kanpur, CSAUAT, Kanpur and CCSHAU, Hisar for providing field pea germplasm. The research support extended by Centre of Excellence on Dryland Agriculture Project funded by Government of Uttar Pradesh, India is also gratefully acknowledged.

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