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Genetic Divergence, Variability and Association Analysis for Seed Yield and its Contributing Traits in Selected Germplasm of Field Pea (*Pisum sativum* L.)

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ABSTRACT

Background: Pea seeds are considered as a nutritional powerhouse because they are rich in protein, complex carbohydrates, vitamins, minerals and phytochemicals.

Methods: The material of this study consisted of 28 genotypes. Experiment was conducted during *Rabi* season (2021-2022) at 24.47° to 26.56°N latitude and 82.12° to 83.98°E longitude at an altitude of 113 m above from sea level.

Result: An increasing H2b and genetic advance mean percent (GAM) were observed in primary branches per plant (PBP), plant height (PH), pods per plant (PP), seed per pod (SP), 100-seed weight (SW), biological yield per plant (BYP), harvest index (HI) and seed per plant. This indicates these traits are governed by additive gene action. Seed yield per plant SYP has positive and significant correlation with PBP, PH, PP, SP, SW, BYP and HI at both genotypic and phenotypic level. Positive direct effect on SYP was exhibited by BYP, HI, PBP and DFF (day to 50% flowering) at both genotypic and phenotypic level of path. The 28 genotypes were grouped into six different clusters. The highest number of genotypes appeared in cluster II and III. The highest intra-cluster distance was found for cluster I (277.296) followed by cluster II and III and the lowest intra-cluster distance was found for cluster IV. The genotype of cluster II was early flowering followed by cluster I. Cluster I recorded highest cluster mean for SYP, while the lowest cluster mean was recorded in cluster VI Diverse clusters could be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

Key words: Correlation, D^2 analysis, Heritability, Path analysis, Seed yield.

INTRODUCTION

Pea (*P. sativum* L.) is a diploid (2n = 2x = 14) legume that belongs to species of Fabaceae, subfamily Papillionaceae and the tribe Vicieae with a genome size of about 4,500 Mb (Rispail *et al.,* 2023).Pea seeds are considered as a nutritional powerhouse because they are rich in protein complex carbohydrates, vitamins, minerals and phytochemicals (Burstin *et al.,* 2011). The low digestibility of starch from pulses is one of the main reasons why they can provide high nutritional value to humans, given that part of the starch fraction-resistant starch is not digested by the small intestine and functions similarly to dietary fibres, accounting for its several health benefits (Singh *et al.*, 2017). Additionally, the lack of gluten proteins in pulse seeds is very important in helping to meet the demands of gluten-free diets for people who suffer from celiac disease (Singh *et al.,* 2017). The use of diverse genetic resources is important for breeding crop varieties (Glaszmann *et al.*, 2010). Genetic diversity is critical for enhancing breeding programs. It provides the essential genetic resources needed for developing improved cultivars, ensuring resilience, high yield and nutritional value and adapting to changing environmental conditions and global food demands. Landraces and crop wild relatives play a crucial role in preserving genetic diversity in crops, harboring a wide array of unique traits and alleles that can be vital for future breeding programs (Marone *et al.,* 2021). Plant breeding relies on selecting diverse germplasm with desirable traits and optimum seed sample size to develop new cultivars and conserve without disturbing the genetic integrity and variability (Crossa, 1989). This selection process involves understanding the genetic variations among the germplasm used in crop improvement program. The objectives of this study were to identified divergent germplasm among the existing genetic stock and strong association between seed yield and its contributing traits. This study provides genetic resources and knowledge of

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the available germplasm as a contribution to the development of improved pea cultivars.

MATERIALS AND METHODS

Plant material

The material of this study consisted of 28 genotypes namely IPF 2116,Pant P 517, SKNP 04-09, KPMR 907, RFP 2010-21, HFP 1811, SKAU-P-17, RFP 2011-1, Pant P 523, Pant P 514, KPMR 954, Pant P 479, IPFD 21-5, Pant P 508, HUDP1802, Pant P 480, Pant P 509, NDP-2014-1, IPFD 21-4, Pant P 484, IPFD 18-3, IPFD20-2, HFP 1709, IPFD 21-7, HFP 1817, HFP 4, HUDP 15 and VL 42. The study was carried out during 2021-22 (*Rabi season*) at the Faculty of Agriculture Experimental Field (Genetics and Plant Breeding), Acharya Narendra Deva University of Agriculture and Technology, Ayodhya (U.P.) India. The experiment was designed with three replicates under randomized block design.

Experiential site

Experiment was conducted at 24.47° to 26.56°N latitude and 82.12° to 83.98°E longitude at an altitude of 113 m above from sea level in the Gangetic Alluvial Plains of Eastern Uttar Pradesh. The climate of experimental site is semi-arid with cold winter and hot summer.

Crop geometry

Each genotype was sown in four rows of 4 meter length with a spacing of 30 cm between the rows and 10 cm between the plants within rows. The crop was well managed for optimum growth and yield.

Data collection

Observations were recorded on five randomly selected plant for each genotypes for following parameters *viz.*, primary branches per plant, plant height (cm), pods per plant, seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g) except days to 50% flowering and days to maturity which were recorded on plot basis.

Statistical analysis

All results were displayed as mean standard error kurtosis and skewness three replicates for phenotypic analysis, in the experiments. Data were analysed by one-way ANOVA (Panse and Sukhatme, 1967) using the statistical software IBM SPSS. The correlation (Al-ji-bouri *et al.*,1958), path coefficient analysis (Dewey and Lu,1959), heritability (Robinson *et al.,* 1949), GCV and PCV (Johnson *et al.* (1955) genetic advance (Allard, 1960) and D^2 analysis (Mahalanobis,1928) analysis of various genotypes were performed with Windostat Version 9.2.

RESULTS AND DISCUSSION

Analysis of variance (ANOVA) results offield pea germplasm under the field condition is given in Table 1. Mean square

Table 1: Analysis of variance for ten characters of field pea germplasms.

Source	DF	Mean square									
		DFF	DM	PBP	PH (cm)	PP	SP	SW(g)	BYP (g)	HI (%)	SYP (g)
Replications	2	2.28	11.44**	0.014	35.32**	0.31	0.37	0.082	12.14	4.98	1.41
Treatments	27	59.038**	43.52**	0.569**	3782.61**	61.053**	2.94**	23.59**	829.76**	78.23**	124.03**
Error	54	1.32	1.71	0.05	3.03	0.72	0.16	0.62	5.18	3.32	1.40
Mean ± SE		57.89±0.66	120.92±0.76	2.27±0.13	85.75±1.01	10.58±0.49	5.74±0.23	20.19±0.45	34.47±1.31	36.40±1.05	12.71±0.68
CV (%)		1.99	1.08	10.02	2.03	8.03	7.01	3.90	6.61	5.00	9.30
LSD at 5%		1.88	2.14	0.37	2.85	1.39	0.66	1.29	3.73	2.98	1.94
Min		48.33	114	1.47	49.70	4.40	3.63	14.05	9.39	22.37	3.06
Max		63.00	126.33	3.43	150.27	22.5	7.37	25.19	73.07	44.53	26.48
Kurtosis		-0.84	-0.40	0.64	0.64	0.75	-0.32	-0.67	0.47	-1.14	0.31
Skewness		-0.59	-0.91	0.84	-1.40	0.27	-0.27	0.07	-0.41	1.39	-0.78

*and** Significant at 5% and 1% probability level respectively DFF: Days to 50% flowering, DM: Days to maturity, PBP: Primary branches per plant, PH: Plant height cm, PP: Pods per plant, SP: Seed per pod, SW: 100-seed weight, BYP: Biological yield per Plant g, HI: Harvest Index %, SYP: Seed yield per plant g.

Table 2: Genetic components of variability, genotypic coefficient of variation (GCV), coefficient of variation (PCV), genetic advance mean percent (GAM) and heritability (broad sense) estimate for ten characters of field pea germplasms.

Traits	GCV	GCV category	PCV	PCV category	hBS	Hbs category	GAM	GAM category
DFF	7.57	Low	7.83	Low	93.60	High	15.09	Medium
DM	3.08	Low	3.27	Low	89.10	High	6.00	Low
PBP	18.28	Medium	20.84	High	76.90	High	33.03	High
PH (cm)	41.39	High	41.44	High	99.80	High	85.17	High
PP	42.39	High	43.15	High	96.50	High	85.81	High
SP	16.76	Medium	18.17	Medium	85.10	High	31.86	High
SW (g)	13.70	Medium	14.25	Medium	92.50	High	27.16	High
BYP (g)	48.09	High	48.54	High	98.10	High	98.16	High
HI (%)	13.72	Medium	14.61	Medium	83.30	High	26.57	High
SYP (g)	50.29	High	51.15	High	96.70	High	101.89	High

Table 3: Correlation matrix of the yield and its contributing traits of 28 field pea germplasms.

Traits	DFF	DM	PBP	PH (cm)	PP	SP	SW(g)	BYP (g)	HI (%)
DFF	0.740**	-0.273*	-0.382**	-0.097	0.052	-0.400**	-0.13	-0.194	-0.142
DM	0.694**	-0.354**	-0.717**	-0.254*	-0.254*	-0.331**	-0.337**	-0.327**	-0.364**
PBP	-0.204	-0.287**	0.575**	0.557**	0.242*	0.032	0.460**	0.211	0.504**
PH (cm)	-0.369**	-0.677**	0.505**	0.395**	0.183	0.136	0.404**	0.124	0.384**
PP	-0.082	-0.240*	0.492**	0.388**	0.420**	0.117	0.826**	0.450**	0.891**
SP	0.061	-0.226*	0.230*	0.170	0.363**	0.261*	0.642**	0.344**	0.651**
SW(g)	-0.367**	-0.278*	0.020	0.127	0.105	0.227*	0.442**	0.219*	0.430**
BYP (g)	-0.117	-0.313**	0.406**	0.401**	0.818**	0.608**	0.430**	0.191	0.954**
HI(%)	-0.149	-0.287**	0.200	0.115	0.441**	0.343**	0.216*	0.190	0.452**
SYP (g)	-0.121	-0.336**	0.451**	0.377**	0.881**	0.627**	0.419**	0.951**	0.459**

* and** Significnat at 5% and 1% probability level above diagonal show genotypic and below diagonal represent phenotypic correlation coefficient.

due to genotypes were significant for all traits under the study, its means exist the ample amount genetic variability among the genotypes. Similar findings reported by Bhardwaj *et al.* (2020); Bishnoi *et al.* (2021) and Ertiro (2022).

Considering coefficient of variation for the parameters analysed the variation improves in agricultural production enhancement by combining beneficial genes from genetically dissimilar genotypes. coefficient of variation is also useful in displaying the precision of the experiment performed. The top five significant genotypes from the 28 genotypes for higher seed yield per plant comprising were IPF 21-16 (26.48 g), KPMR 907 (22.50 g), HFP 1817 (21.23 g), HFP 1811 (20.78 g) and Pant P 480 (20.68 g) and general mean was 12.71 g. This result confirmed with Yadav *et al*. (2021) Kurtosis is a statistical measure used to describe a characteristic of a dataset. When normally distributed data is plotted on a graph, it generally takes the form of a bell. Kurtosis indicates how much data resides in the tails. Positive Kurtosis show primary branches, plant height, pods per plant, biological yield per plant and seed yield per plant. Skewness means lack of symmetry.

Measures of skewness help us to know to what degree and in which direction (positive or negative) the frequency distribution has a departure from symmetry. 100 seed weight show the symmetry because this skewness value near zero. Genetic variability analysis Genetic variability analysis of 28 germplasm displayed in Table 2.

The genotypic coefficient of variation (GCV) was observed to be slightly lower than the phenotypic coefficient of variation (PCV) for all the studied traits indicating that the environment was the least influential on these traits. An increasing H2b and genetic advance mean percent (GAM) were observed in PBP, PH, PP, SP, SW, BY, HI and SYP. This indicates these traits are governed by additive gene action Genetic advance mean per per cent (GAM); determined to be low for DM. Azam *et al*. (2020) reported that High GCV as well as PCV were observed for the number of pods per plant, 100 seed weight, powdery mildew severity and pod yield, indicating the existence of a broad genetic basis. Bhardwaj *et al*. (2020) significant genetic variations were observed for pod yield and related traits. PCV and GCV were high for pods per plant and pod yield per plant. High heritability coupled with high genetic advance was observed for pods per plant and pod yield per plant. Bahadur *et al*. (2021); Pratap *et al*. (2024) reported that variability and determine the relative importance of primary and secondary traits as selection criteria to improve productivity.

Higher estimate of GCV was recorded for plant height followed by number of secondary branches per plant. Bishnoi *et al*. (2021) studied that high heritability coupled with high genetic advance as per cent of mean, was observed in characters *viz*., yield/plant, 100-seed weight, number of pods/plant, harvest index, plant height, number of effective nodes, number of seeds/podand width of pods. Genetic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) are crucial parameters in plant breeding and genetic studies, particularly in enhancing crop yields and understanding. Those traits exhibiting high GCV and PCV with low adverse environmental effects are advantageous for selection. Correlation and path analysis through correlation and path analysis, the nature and extent of association between different characters influencing yield and causes of association can be better understood which helps in formulation of selection criteria for improvement of yield. Estimates of genotypic correlations in general were higher than phenotypic correlations (Table 3).

In general directions of phenotypic and genotypic correlations were almost same for the most of the character combinations. In the present study seed yield per plant was found to have highly significant and significant positive correlation with primary branches per plant (0.504 and 0.451), plant height (0.348 and 0.377), pods per plant (0.891 and 0.881), seeds per pod (0.651 and 0.627), seed weight (0.430 and 0.419), biological yield per plant (0.954 and 0.951) and harvest index (0.452 and 0.459) at both genotypic and phenotypic level respectively.

However, it was noticed that significant and negative association with days to maturity (-0.364 and -0.336). Days to 50% flowering had negative and non significant correlation with seed yield per plant at both genotypic and phenotypic level. It indicated that earliness of genotypes, seed yield has increased and vice versa. These finding confirm with Tasnim *et al*. (2022). Whereas, Uhlanik *et al*. (2022) found that highest positive correlation was between number of seeds per plant and number of pods per plant. Tasnim *et al*. (2022) found that pods per plant, pod width and seeds per pod showed a highly positive correlation with seed yield per plant. Similar finding reported by Aziz *et al. (*2019) Veram *et al*. (2021). The expression of yield depends upon a number of yield contributing traits. It is not always independent in their action but may be interlinked. The selection practiced for one character may simultaneously bring change in the other related character. Path analysis with direct and indirect effects is shown in Table 4. Positive direct effect on seed yield per plant was exhibited by BYP, HI, PBP and DFF at both genotypic and phenotypic level of path. Pods per plant (PP) exhibited highest positive indirect effects followed by SP, PBP, SW and PH *via* BY on seed yield per plant at both genotypic and phenotypic level path These traits shows that while selecting for high yield, emphasis should be given on those characters which shows high direct positive effect with positive correlation with seed yield. Similar results were also reported by Gupta *et al*. (2020) on highest positive direct effect on seed yield per plant was exhibited by several pods per plant, several seeds per pod and days to 50% flowering at both genotypic and phenotypic level. Verma *et al*. (2021) and Sharma *et al.* (2025) revealed that maximum positive direct effect on seed yield per plant was exhibited by biological yield per plant and harvest index followed by number of seed per plant at both genotypic and phenotypic level. Tasnim *et al*. (2022)

Table 4: Path analysis for ten characters of field pea germplasms.

Traits	Path	DFF	DM	PBP	PH (cm)	PP	SP	SW (g)	BYP (g)	HI (%)	SYP (g)
DFF	G	0.048	-0.018	-0.017	0.020	0.000	-0.003	0.007	-0.122	-0.057	-0.142
	P	0.029	-0.007	-0.010	0.014	-0.001	-0.002	0.006	-0.107	-0.044	-0.121
DM	G	0.035	-0.025	-0.022	0.038	0.001	0.015	0.005	-0.316	-0.096	-0.364**
	P	0.020	-0.010	-0.014	0.026	-0.003	0.008	0.005	-0.285	-0.084	-0.336**
PBP	G	-0.013	0.009	0.062	-0.030	-0.002	-0.015	-0.001	0.431	0.062	0.504**
	P	-0.006	0.003	0.048	-0.019	0.006	-0.009	0.000	0.370	0.059	0.451**
PH (cm)	G	-0.018	0.018	0.036	-0.052	-0.001	-0.011	-0.002	0.379	0.037	0.384**
	P	-0.011	0.007	0.024	-0.038	0.004	-0.006	-0.002	0.366	0.034	0.377**
PP	G	-0.005	0.006	0.035	-0.021	-0.004	-0.026	-0.002	0.775	0.132	0.891**
	P	-0.002	0.002	0.023	-0.015	0.011	-0.014	-0.002	0.746	0.130	0.881**
SP	G	0.003	0.006	0.015	-0.010	-0.002	-0.061	-0.004	0.602	0.101	0.651**
	P	0.002	0.002	0.011	-0.007	0.004	-0.037	-0.004	0.555	0.101	0.627**
SW(g)	G	-0.019	0.008	0.002	-0.007	0.000	-0.016	-0.016	0.415	0.064	0.430**
	P	-0.011	0.003	0.001	-0.005	0.001	-0.008	-0.017	0.392	0.063	0.419**
BYP (g)	G	-0.006	0.008	0.029	-0.021	-0.003	-0.039	-0.007	0.938	0.056	0.954**
	P	-0.003	0.003	0.019	-0.015	0.009	-0.023	-0.008	0.912	0.056	0.951**
HI (%)	G	-0.009	0.008	0.013	-0.007	-0.002	-0.021	-0.004	0.179	0.294	0.452**
	P	-0.004	0.003	0.010	-0.004	0.005	-0.013	-0.004	0.173	0.294	0.459**

Residual effect (G)=0.0950 and (P) =0.1095 Diagonal value represent direct and diagonal off show the indirect effects.

revealed that plant height, pod per plant, and seeds per pod had a highly positive effect on yield per plant DM had showed maximum negative indirect effects followed by DFF on seed yield per plant *via* biological yield per plant at both genotypic and phenotypic level path. Singh *et al*. (2017) direct negative effect on pod yield per plant was exhibited by days to 50% flowering.

Association of primary branches per plant, plant height, pods per plant, seeds per pod, seed weight, biological yield per plant and harvest index showed positive and highly significant due to the positive direct effects. This shows that a greater yield response can be obtained if indirect selection is practiced. Genetic diversity analysis statistics is a very useful tool to assess the genetic diversity in crop plants. By the application of clustering technique, the 28 types were grouped into six different clusters (Fig 1). The highest number of genotypes appeared in cluster II and III contained 8 genotypes each followed by cluster V (6) and VI (3). However, cluster IV had minimum number of genotype followed by cluster I among all clusters. The estimates of intra and inter-cluster distance for six clusters are presented in Table 5. The highest intra-cluster distance was found for cluster I (277.296) followed by cluster II (210.862) and cluster III (193.424) and the lowest intra-cluster distance was found for cluster IV (0.000). Between cluster I and V (3042.988) the maximum inter-cluster distance was measured followed by cluster I and VI (2971.915), cluster II and V (2509.177), cluster II and VI (2369.287), cluster I and III (2256.286). cluster V and VI (241.182) were found to have the shortest inter-cluster distance. Similar results were reported by Jaiswal *et al.* (2021), Priyanka *et al*. (2021), Singh *et al*. (2021) and Kumar *et al*. (2022).

The mean performance of clusters for 10 characters is presented in Table 6. The genotype of cluster II was earlier flowering 55.29 days followed by cluster I (57.00 days). The highest cluster mean for harvest index was showed by cluster IV (39.14) followed by cluster III (38.87). The lowest cluster mean for this trait was showed b y cluster VI (29.38) followed by cluster I (31.96) and remaining clusters had moderate cluster mean for harvest index. Cluster I recorded highest cluster mean for seed yield per plant (22.08), while the lowest cluster mean was recorded in cluster VI (3.54). The remaining clusters showed moderate performance. Singh *et al*. (2021) and Kumar *et al*. (2022) these scientists revealed that similar findings.

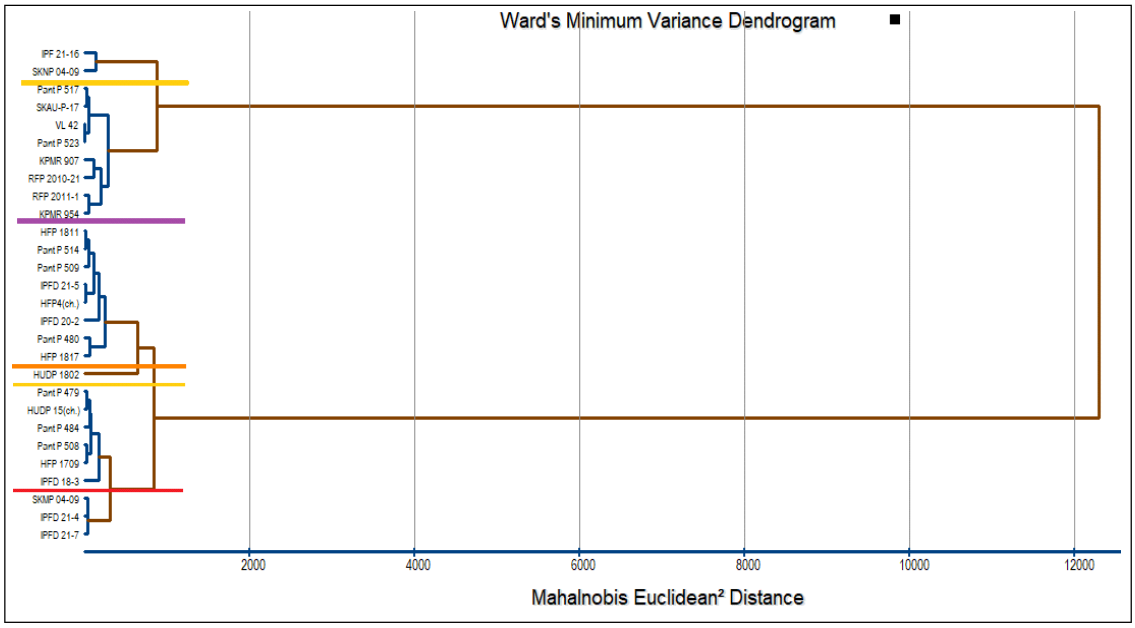


Fig 1: Dendrogram for 28 genotype of germplasm of field pea.

Table 5: Inter and intra cluster distance among the germplasms.

Cluster number	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Cluster-I	277.30	712.64	2256.29	2007.55	3042.99	2971.92
Cluster-II		210.86	1913.17	1362.11	2509.18	2369.29
Cluster-III			193.42	805.96	280.23	425.57
Cluster-IV				0.00	1061.65	1241.33
Cluster-V					143.29	241.18
Cluster-VI						75.55

Table 6: Cluster Mean for ten characters of field pea germplasms.

Cluster/ Traits	DFF	DM	PBP	PH (cm)	PP	SP	SW (g)	BYP (g)	HI (%)	SYP (g)
I	57.00	116.17	2.33	138.88	15.35	6.53	21.83	68.47	31.97	22.08
II	55.29	117.50	2.58	128.74	11.13	5.83	20.58	33.93	38.54	13.33
III	57.08	121.54	2.17	63.43	11.95	5.75	22.45	40.23	38.87	15.67
IV	62.00	124.67	3.00	90.19	22.50	6.43	14.05	51.93	39.15	20.33
V	60.00	124.06	1.97	53.64	7.04	6.00	19.41	24.43	34.80	8.14
VI	62.00	124.00	2.08	57.96	5.37	4.23	15.63	12.16	29.39	3.54

CONCLUSION

On the basis of result and discussion we concluded that an increasing H2b and genetic advance mean percent (GAM) were observed in PBP, PH, PP, SP, SW BYP, HI and SYP. This indicates these traits are governed by additive gene action. Association of primary branches per plant, plant height, pods per plant, seeds per pod, seed weight , biological yield per plant and harvest index were positive and highly significant due to the positive direct effects. This shows that a greater yield response can be obtained if indirect selection is practice. The highest number of genotypes appeared in cluster II and III. The highest intra-cluster distance was found for cluster I followed by cluster II and III and the lowest intra-cluster distance was found for cluster IV. The genotype of cluster II was earlier flowering followed by cluster I. Cluster I recorded highest cluster mean for seed yield per plant, while the lowest cluster mean was recorded in cluster VI diverse clusters could be used for further improvement in heterosis in yield targeted traits with creation of wider variability.

Conflict of interest

All the authors have no conflict of interest.

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