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COMPARATIVE STUDY OF DIALLEL, PARTIAL DIALLEL AND LINE X TESTER MATING DESIGNS FOR YIELD AND QUALITY TRAITS IN FIELD PEA (*PISUM SATIVUM* L.)

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ABSTRACT

An experiment was carried out at research area of Pulses Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *Rabi* season of 2022-23 to assess the efficiency of diallel, partial diallel and Line x Tester (two sets, A and B) designs for selection of parents and crosses in field pea. Significant variability was observed among breeding materials used in each mating design. Among all the mating designs studied, diallel identified maximum number of good and poor combiners followed by Line x Tester which in turn was followed by partial diallel. Based on Spearman's rank correlation between diallel and other designs on the basis of estimates of *gca* and *sca* effects, partial diallel was found to be effectively capturing *gca* and *sca* effects and thus can be treated in closer approximation of diallel followed by L x T (A) and the least alignment with L x T (B). With regard to mean degree of dominance, Line x Tester (A) was more aligned with diallel whereas, partial diallel and L x T (A) were observed with low and non-significant monotonic relationships with diallel. All the mating designs studied were equally efficient in estimation of σ^2*sca* and σ^2*gca*. Predominance of non-additive gene action for most of the traits under study was disclosed by all the mating designs. These findings can be further utilized to develop and enhance the yield potential of field pea cultivars.

***Keywords*: Diallel, Partial diallel, line x tester mating designs, yield and quality traits, field pea (*Pisum sativum* L.)

Introduction

It is also not feasible to meet out the dietary protein requirement of ever-growing population only through animal sources which is also not economical and environment friendly. Thus, interest in pulses for their high protein content is rising. Pulses also aid in improving the soil health though its contribution in organic matter, nitrogen fixation, phosphorus solubilization, *etc* (Sharma *et al.,* 2025; Kumar *et al.*, 2023). Although India is the largest grower and producer of pulses and is close to self-sufficiency yet the production is still low and will be deficient for the growing population in the coming years (Anonymous, 2024). Fieldpea, one of the oldest pulse crop to be domesticated and grown over since its appearance in Mediterranean between 7000 – 6000 BC and is now well adapted to the tropical and subtropical conditions of the India (Parihar *et al.*, 2022; Sharma *et al.,* 2023). For diversification of cereal-based cropping systems, presently it is competing crop with other crops in irrigated areas (Kumar *et al.*, 2018). As fieldpea is rich in iron and zinc, it could help in resolving two most common mineral deficiencies of human population in the world (Amarakoon *et al.*, 2012), which can help in alleviating hidden hunger. Therefore, it can be a very good option for shrinking the gap between demand and supply of pulses. Despite all these benefits, as per FAOSTAT (2022), its cultivation has been lagging far behind the cereals and in India its productivity is 1.38 t ha^{-1}, *i.e.*, much less than the global average (1.97 t ha^{-1}). To overcome this yield gap, substantial concentration is required in research to increase its productivity potential through systematic breeding programs.

Choosing a suitable breeding strategy largely depends on the nature of gene action of economically important characters. In general, the objectives of mating designs are to provide information for evaluating parents (*gca* and *sca*), estimates of genetic parameters, estimates of genetic gains and a base population for selection (Klein *et al*., 1973). Diallel and Line x Tester mating designs have been widely used to understand the gene effects in different crops. However, a diallel set becomes unmanageable with large number of parents while with the smaller it gives poor estimate due to large sampling errors. Partial diallel analysis provides better estimates of general combining ability than that of specific combining ability while in case of Line x Tester analysis the choice and number of tester parents continued to be unsolved. As negligible information is available on the comparative performance of mating designs for selection of parental lines in fieldpea, therefore, this investigation tried to compare the efficacy of three major mating designs – diallel, partial diallel and Line x Tester, working on the same breeding material, although sampled for the respective requirements of the mating design.

Materials and Methods

The present investigation was carried out at Pulses Section, Department of Genetics and Plant Breeding, CCS Haryana Agricultural University, Hisar during *rabi* season of 2022-23. The experimental material consisted of six parents (HFP 8909, HFP 9426, HFP 9907B, HFP 529, HFP 715, HFP 1428) and their 30 crosses in all possible combinations. The six parents used to produce hybrids involved both dwarf and tall plant types. As far as the genetic base is concerned proper care was taken to utilize parents with broad genetic base (Sharma and Mani, 2007). Among these two parents *i.e.* HFP 9907B and HFP 9426 were tall types and other four *viz*., HFP 8909, HFP 529, HFP 715 and HFP 1428 were dwarf types and among these dwarf types, two parents *i.e*., HFP 8909 and HFP 715 were *afila* types. The crossing programme (carried out in *Rabi* 2021-22) consisted of two parents *i.e*., HFP 8909 (EC 109185 x HFP 4) and HFP 9426 (KPMR 84-2 x EC 109195) which involved exotic types, while two others *i.e*., HFP 9907B (Rachna x Bonneville) and HFP 529 [(HUDP-9 x Arkel) x (HUDP 12 x Arkel) involved vegetable peas in their pedigree. The parents and crosses were grown in Randomized Block Design (RBD) with three replications. Each plot consisted of a single row of 4m length with 45 x 15cm spacing. The recommended package of practices was adopted to raise a good and healthy crop.

The observations were recorded on eleven morphological (*viz*., days to flowering, days to maturity, number of primary branches per plant, number of nodes per plant, number of pods per plant, plant height, biological yield per plant, seed yield per plant, harvest index, number of seeds per pod and 100-seed weight) and six quality (*viz*., protein, starch, ash, ADF, NDF and crude fat contents) traits. The breeding material was sampled for diallel (Griffing 1956, Method 1, Model I), partial diallel with sample size ‘s’ = 5 (Kempthorne and Curnow, 1961) and Line x Tester (Kempthorne, 1957). For diallel all the 30 crosses were analysed and for partial diallel 15 crosses were selected (s = 5, k = 1) for analysis. The Line x Tester (L x T) analysis was done in two sets with nine crosses each. The six parents were divided in two groups *i.e*., Group A (HFP 8909, HFP 9426, HFP 9907B) and Group B (HFP 529, HFP 715, HFP 1428). In L x T (A), Group A parents were considered as lines (female) and Group B parents as testers (male), *vice versa* in case of L x T (B).

Results and Discussion

Mating design is a procedure for arranging controlled crossings between plant groups or strains in plant breeding (Klein *et al*., 1973) or in simple words it is defined as schematic crossing between two groups or strains or plants made to produce progenies in plant breeding that is concerned in agriculture and biosciences. The choice of mating design is critical for a efficient and successful plant breeding program. The mating designs should be capable enough to provide information on the genetic control of the character under investigation, to generate a breeding population to be used as a basis for the selection and development of potential varieties, to provide estimates of genetic gain and to provide information for evaluating the parents used in the breeding program (Acquaah, 2012). Hence, the plant breeders have many options available among which they can select one of the most suitable designs which fulfil the objectives and fall under available resources. Among these diallel design is the most comprehensive design which require much resources when more number of parents are used whereas, partial diallel balances comprehensiveness with resource efficiency and Line x Tester conversely focuses on specific hybrid combinations.

The present study revealed that the mean squares due to treatments or crosses were significant across all the mating designs for most traits under investigation. This finding underscores the presence of considerable magnitude of genetic variability in the breeding material utilized in each design, affirming its suitability for combining ability analysis. However, there were exceptions where mean squares for specific traits were not significant, indicating a lack of substantial variation for those traits. For instance, in the diallel design, mean squares due to the number of seeds per pod were not significant. Similarly, in the partial diallel design, the mean squares due to number of primary branches per plant and number of seeds per pod, in the Line × Tester (A) for days to flowering, number of primary branches per plant and number of seeds per pod and in L x T (B) for days to maturity, number of primary branches per plant, number of seeds per pod and 100-seed weight, were found non-significant. The significance of the mean squares for treatments indicated that the breeding material holds promise for identifying parents and hybrids with high general and specific combining ability, respectively. The results of this study align with previous studies in fieldpea done by Georgieva *et al.* (2016), Dar *et al.* (2017), Kumar *et al.* (2018), Pathak *et al.* (2019), Hama-Amim (2020), Jaiswal *et al.* (2021), Meena *et al.* (2022), Jagadeesh *et al.* (2023) and Mohammad and Ahmad (2024) who also reported significant variability among breeding materials for various traits, emphasizing the importance of genetic diversity in fieldpea improvement programmes.

Diallel design identified most number of parents as good and poor combiners followed by Line x Tester sets (Table 1). Partial diallel identified the least number of good and poor combiners. Good combiners (positive and significant *gca* effect) are denoted by (+) and poor combiners (negative and significant *gca* effect) are denoted by (-). For each character the numbers of good and poor combiners were counted across the designs. The total for each design was thus computed and used for comparison. Diallel design identified the highest number of total significant general combiners (total 61, 25 good and 36 poor), followed by L x T (A) (total 44, 23 good, 21 poor) and L x T (B) (total 41, 20 good, 21 poor) and lastly partial diallel (total 32, 15 good and 17 poor). The results of present study are in perfect harmony with the findings of Malik (1980) in wheat who reported that diallel analysis identified large number of parents with significant *gca* in comparison to L x T analysis. This was also in agreement with the study done by Sharma and Mani (2007) in rice.

Table 1: Comparative performance of Diallel, Partial diallel and Line x Tester analyses for the identification of good and poor combiners

Character	**Diallel**		**Partial Diallel**		**LxT (A)**		**LxT (B)**	
	(+)	(-)	(+)	(-)	(+)	(-)	(+)	(-)
Days to flowering	1	2	1	0	0	1	1	2
Days to maturity	2	3	0	0	2	1	0	0
Number of primary branches/plants	1	1	0	0	0	0	0	0
number of nodes per plant	2	3	1	1	1	1	2	2
Number of pods per plant	2	3	3	3	1	2	2	2
Plant height	2	4	2	3	3	2	2	1
Biological yield	2	4	1	1	1	1	2	1
Seed yield per plant	1	3	1	2	2	1	2	2
Harvest Index	1	2	1	0	3	2	2	2
Number of seeds per pod	0	0	0	0	0	0	0	1
100-seed weight	0	1	0	0	0	0	0	0
Protein	3	3	3	2	2	3	2	3
Starch	2	1	1	2	1	1	1	0
Ash	2	3	0	1	3	2	2	3
Acid detergent fiber	1	0	0	1	0	1	1	1
Neutral detergent fiber	1	2	1	1	2	2	0	0
Crude Fat	2	1	0	0	2	1	1	1
TOTAL	**25**	**36**	**15**	**17**	**23**	**21**	**20**	**21**

+, - sign in parenthesis indicated positively and negatively significant *gca* effects respectively.

The diallel mating design is most comprehensive and it estimates were close to true values for that particular population (Bray, 1971). Therefore, estimates of *gca* and *sca* effects and their variances obtained in diallel were compared against other mating designs *viz.*, partial diallel and two sets of Line x Tester. All the parents revealed significant correlation between diallel and partial diallel designs with respect to Spearman's rank correlation for *gca* effects (Table 2). The parents HFP 8909, HFP 9426, and HFP 9907B showed high and significant correlations across all designs, indicating that their *gca* effects are consistent and stable regardless of the mating design. This suggests a strong additive genetic contribution for these parents. The parents HFP 529, HFP 715 and HFP 1428 exhibited non-significant correlations between diallel and L x T (A), and between diallel and L x T (B), highlighting variability in their *gca* effects across these designs. Thus, partial diallel was found most similar to diallel design when parents were compared against their combined trait values across designs. Group A parents (HFP8909, HFP9426 and HFP9907B) had significant correlation across all designs. No such significant similarity was noticed in case of Group B parents (HFP529, HFP715 and HFP1428). This might be because of broader genetic base of Group A parents which involved exotic and vegetable type peas in their parentage.

Table 2: Spearman's rank correlation for *gca* effects across different mating designs

Parents	DL & PD	DL & L x T (A)	DL & L x T (B)
HFP 8909	0.740 (0.001)	0.671 (0.004)	0.558 (0.0216)
HFP 9426	0.720 (0.001)	0.786 (0.0001)	0.773 (0.0002)
HFP 9907B	0.703 (0.002)	0.759 (0.0006)	0.816 (< 0.001)
HFP 529	0.708 (0.002)	0.399 (0.1119)	0.460 (0.0645)
HFP 715	0.678 (0.003)	0.192 (0.4591)	0.350 (0.168)
HFP 1428	0.487 (0.040)	-0.192 (0.4591)	0.154 (0.553)

p-values are provided in parenthesis with the correlation coefficient value; DL = Diallel, PD = Partial Diallel, L x T (A) = Line by tester set A, L x T (B) = Line by tester set B

Similarly, Table 3 depicts Spearman's rank correlation based on *gca* effects between traits across designs. Partial diallel showed a stronger and more consistent correlation with diallel in comparison to both sets of Line x Tester design. Significant correlations with diallel were observed for number of pods per plant, plant height, biological yield per plant, protein content and NDF content for partial diallel design. For several characters like number of seeds per pod, harvest index and crude fat, the correlations were moderate to weak but still better than both sets of line by tester design. This suggested that partial diallel captured *gca* effects more reliably and aligned closely with diallel. L x T (A) exhibited moderate to weak correlations with diallel for most of the characters. Notable higher correlations with diallel were seen for plant height, biological yield and ash content. This assured its some but poorer alignment with diallel than partial diallel. Lastly, L x T (B) exhibited weak or negative correlations with most of the characters thus aligned least with diallel. Therefore, partial diallel can effectively be said to have captured *gca* effects and thus can be treated in a closer approximation of diallel.

Table 3: Spearman's rank correlation based on *gca* between traits across designs

Characters	DL & PD		DL & L x T (A)		DL & L x T (B)	
	ρ	p-value	ρ	p-value	ρ	p-value
Days to flowering	0.771	0.103	0.638	0.173	-0.086	0.919
Days to maturity	0.441	0.381	0.441	0.381	0.088	0.868
Number of primary branches / plants	0.132	0.802	-0.117	0.824	-0.441	0.381
Number of nodes per plant	0.771	0.103	0.371	0.497	-0.314	0.564
Number of pods per plant	0.886	0.033	0.428	0.419	-0.257	0.658
Plant height	0.943	0.017	0.943	0.017	-0.371	0.497
Biological yield	0.943	0.017	0.828	0.058	0.371	0.497
Seed yield per plant	0.714	0.136	0.771	0.103	-0.314	0.564
Harvest Index	0.428	0.419	0.771	0.103	-0.485	0.355
Number of seeds per pod	0.586	0.221	0.600	0.241	0.377	0.461
100-seed weight	0.428	0.419	-0.257	0.658	0.753	0.083
Protein	0.943	0.017	0.257	0.658	-0.428	0.419
Starch	0.028	1.000	0.143	0.803	-0.371	0.497
Ash	0.828	0.058	0.828	0.058	-0.257	0.658
Acid detergent fibre	-0.143	0.803	-0.714	0.136	0.028	1.000
Neutral detergent fiber	0.885	0.033	0.371	0.497	0.828	0.058
Crude Fat	0.543	0.297	0.522	0.288	-0.371	0.497

DL = Diallel, PD = Partial diallel, LT = Line by Tester, **ρ =** Spearman's rank correlation coefficient

Spearman's rank correlation based on *sca* effects between diallel and other designs for each trait under study was calculated using *sca* effects among the various traits to compare different designs (Table 4). As far as correlation between diallel and partial diallel is concerned, moderate to strong (ρ>0.5) significant correlations were observed for most of the traits except for days to flowering, 100-seed weight, protein, starch and crude fat content. This indicated that partial diallel was closely aligned with diallel in its efficiency in estimating *sca* effects for most traits under study. When diallel and Line x Tester (A) were compared, eight out of seventeen traits demonstrated strong and significant rank correlation (ρ>0.7). These were number of primary branches per plant, biological yield per plant, seed yield per plant, number of seeds per pod, 100-seed weight, protein, ash and ADF content. Thus L x T (A) exhibited some alignment with diallel in estimating *sca* effects but not as good as partial diallel. The correlation between diallel and Line x Tester (B) depicted significantly high correlation for only two traits (plant height and starch content) out of total seventeen traits under study. Thus, making L x T (B) the one with the least alignment with diallel for its estimation of *sca* effects.

Table 4: Spearman's rank correlation based on *sca* between traits across designs

Characters	**DL & PD**		**DL & L x T (A)**		**DL & L x T (B)**	
	ρ	**p-value**	**ρ**	**p-value**	**ρ**	**p-value**
Days to flowering	0.122	0.666	-0.359	0.343	0.538	0.135
Days to maturity	0.785	0.001	0.162	0.678	0.513	0.158
Number of primary branches / plants	0.870	0.000	0.850	0.006	0.353	0.351
Number of nodes per plant	0.841	0.000	0.383	0.313	0.262	0.536
Number of pods per plant	0.696	0.005	0.350	0.359	0.285	0.458
Plant height	0.771	0.001	0.194	0.617	0.817	0.011
Biological yield	0.882	0.000	0.750	0.025	0.500	0.178
Seed yield per plant	0.829	0.000	0.883	0.003	0.350	0.359
Harvest Index	0.671	0.008	0.517	0.162	-0.200	0.613
Number of seeds per pod	0.952	0.000	0.933	0.001	-0.813	0.008
100-seed weight	0.183	0.514	0.790	0.011	0.346	0.362
Protein	0.289	0.295	0.833	0.008	0.033	0.948
Starch	-0.318	0.248	0.367	0.336	0.800	0.014
Ash	0.561	0.032	0.733	0.031	0.283	0.463
Acid detergent fibre	0.512	0.050	0.845	0.004	0.351	0.354
Neutral detergent fiber	0.621	0.016	0.650	0.067	0.467	0.213
Crude Fat	-0.189	0.498	0.625	0.072	-0.250	0.521

DL = Diallel, PD = Partial diallel, LT = Line by Tester, **ρ =** Spearman's rank correlation coefficient

As an alternative approach for comparing the efficiency of each of the mating designs the one more criterion was used. The parents were ranked based on their parental means which were evaluated under full diallel and the pooled ranks over all the characters were compared with the pooled ranking of the individual parent on the basis of *gca* effects obtained under different mating designs using Spearman's rank correlation. Further, the respective subset of crosses was ranked based on their + -*per se* performance and the pooled ranks over all the characters were compared with the pooled rankings of the individual cross based on their *sca* effect values and then Spearman's rank correlation was computed.

Table 5 summarizes Spearman's rank correlation coefficients and their p-values, reflecting the consistency of *gca* effects for parents and *sca* effects for crosses across three different mating designs *i.e.*, diallel and partial diallel, diallel and Line x Tester (A) and diallel and Line x Tester (B). It can be inferred from the table that only diallel demonstrated marginally significant correlation, thus making it the most efficient design such that the estimates of *gca* effects were closely reflected by parental means. Partial diallel estimated high correlation though non-significant making this design a strong alternative to diallel for its efficiency in estimating *gca* effects. Both the sets of Line x Tester design depicted weak and non-significant correlations meaning thereby that the ranking pattern of the parents was not similar to that of a full diallel. Line x tester (B) depicted the weakest correlation with highest p-value. Moderate and significant correlation was observed between *sca* effects and *per se* performance of crosses in diallel; strong and significant correlation was observed in case of partial diallel and L x T (A) and weak and non-significant correlation was recorded for L x T (B). This indicated that the pattern of *sca* effects in all designs was similar to the pattern of *per se* performance of crosses except for L x T (B). Partial diallel was found to be the best followed by L x T (A) which in turn was followed by diallel L x T (B).

Table 5: Spearman's rank correlations to check efficiency of mating designs

Correlation between cross *per se* Performance and *sca* effects of:	**Spearman's correlation Coefficient**	**p-value**
Diallel	0.547	0.001
Partial diallel	0.847	0.000
Line x tester (A)	0.733	0.031
Line x tester (B)	0.083	0.843
Correlation between Parental Means and *gca* effects of:	**Spearman's correlation Coefficient**	**p-value**
Diallel	0.828	0.058
Partial diallel	0.714	0.136
Line x tester (A)	0.314	0.563
Line x tester (B)	0.085	0.919

In the present investigation, the efficiency at which mating designs captured *per se* performances of parents (parental means) and their crosses into their estimation of *gca* and *sca* effects revealed that diallel was the most efficient design followed by partial diallel for both *gca* and *sca* effects estimation. It was evident that the efficiency of estimation of *gca* and *sca* effects when compared to diallel decreases in the order of Partial diallel > Line x Tester (A) > Line x Tester (B). Thus, it can be inferred that partial diallel can be considered as an alternative to diallel for estimation of both *gca* and *sca* effects. Similar conclusion was drawn between diallel and partial diallel designs in study conducted by Chaudhary *et al.* (1977) in barley. In our study, both Line × Tester sets (A and B) showed a weak correlation with *per se* performances of both parents and crosses, indicating a limited ability to predict *gca* and *sca* effects accurately. This limitation would have arisen due to the restricted number of testers and the specific pairing strategy used in the Line x Tester design, which may not have adequately captured the complete genetic potential of the parents and their combinations. Singh and Singh (1991) also suggested that Line x Tester is more preferred and reliable when number of lines to be tested are large. Present investigation too agreed with Dubey and Lal, (1983) and Sarawat *et al.* (1994) that *per se* performances should not be taken as rough estimates of *gca* effects because for some traits the *gca* effects could be weakly correlated with the *per se* performances of parents.

Comparison among diallel, partial diallel, L x T(A) and L x T(B) designs based on *gca* variance, *sca* variance, *gca*/*sca* and mean degree of dominance for each character on the basis Spearman's rank correlation was also done (Table 6). Perusal of the table revealed moderate and significant Spearman's correlation with diallel, indicating a close match in the mean degree of dominance between these designs. L x T (A) exhibited correlation coefficient which was neither too high nor too low with diallel. Weak and non-significant correlation coefficients were observed between diallel and partial diallel and between diallel and L x T (B). In case of *gca* variance, partial diallel, L x T (A) and L x T (B) recorded strong and significant rank correlation with diallel indicating the close similarity between their pattern of *gca* variance estimates and diallel. Similarly, in case of *sca* variance partial diallel and Line x Tester both sets observed strong and highly significant correlation with diallel indicating high similarity in pattern of *sca* variance estimates among these designs. Line x Tester (A) observed moderate and significant correlation.

Table 6: Spearman's correlation coefficients based on mean degree of dominance, *gca* variance (σ^2_{gca}) and *sca* variance (σ^2_{sca}) between diallel, partial diallel and Line x Tester (A & B)

	Spearman's rank correlation Coefficient		
	σ^2_{gca}	σ^2_{sca}	**DoD**
DL&PD	0.517 (0.0355)	0.949 (0.000)	0.306 (0.231)
DL&L x T (A)	0.863 (0.000)	0.566 (0.019)	0.600 (0.012)
DL&L x T (B)	0.836 (0.000)	0.877 (0.000)	0.267 (0.298)

p-values in parenthesis; DL = Diallel, PD = Partial diallel, L x T (A) = line by tester set A, L x T (B) = line by tester set B, DoD = degree of dominance

Table 7: Gene effects for different characters as revealed by partial diallel, diallel and Line x Tester analyses

Characters	**Diallel**	**Partial Diallel**	**L x T (A)**	**L x T (B)**
Days to flowering	NA	NA	A/NA	NA
Days to maturity	NA	NA	A	NA
Number of primary branches / plants	NA	NA	NA	NA
Number of nodes per plant	NA	NA	NA	NA
Number of pods per plant	NA	NA	NA	NA
Plant height	A	A	A	A
Biological yield	NA	NA	NA	NA
Seed yield per plant	NA	NA	NA	NA
Harvest Index	NA	NA	NA	NA
Number of seeds per pod	NA	NA	NA	NA
100-seed weight	NA	NA	NA	NA
Protein	NA	NA	NA	NA
Starch	NA	NA	NA	NA
Ash	NA	NA	NA	NA
Acid detergent fibre	NA	NA	NA	NA
Neutral detergent fiber	NA	NA	NA	NA
Crude Fat	NA	A	A	A

A = Additive, NA = Non-additive

The measure of mean degree of dominance revealed a different picture. The rank correlation based on mean degree of dominance between diallel and L x T (A) was found to be significant whereas it was found non-significant between diallel and other designs. The study done by Chaudhary *et al.* (1977) also revealed such relationship between diallel and partial diallel based on mean degree of dominance. The present investigation also revealed that all the designs exhibited predominance of non-additive gene action for all the traits under study (Table 7). The overall picture of gene action was found to be not that different among the designs except for characters like plant height and crude fat content. It was also revealed by our study that the diallel design was most comprehensive among all designs. In case of partial diallel the sample size chosen in present investigation was greater than p/2 (where p is number of parents) which corresponds to its alignment in estimation of gene effects and genetic components which was in agreement with Sharma and Mani (2007), Kumar *et al.* (2008) and Singh and Singh (1991).

Hence, the present investigation proved to be successful in recognizing the choice and usefulness of different mating designs and quantifying *gca* and *sca* variances along with gene action for different characters across the three mating designs in fieldpea. The results of the present study can be used as a springboard for developing specific objectives based well defined approach in various fieldpea breeding programmes for improvement of yield and quality traits.

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