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Genetic Analysis of Yield and Its Component Traits in Field Pea (*Pisum sativum* L.) Using Half-Diallel Crosses Under Timely Sown Conditions

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ABSTRACT

The present investigation assessed genetic variability, heritability, and genetic advance in field pea (*Pisum sativum* L.) through a half-diallel mating design involving ten diverse parental genotypes. Fifty-five F_1 hybrids and 11 parents were evaluated under timely sown conditions at Acharya Narendra Deva University of Agriculture and Technology, Ayodhya, U.P., using a randomized block design. Significant genotypic differences were found for all eleven traits studied, including phenological, morphological, and yield components. High heritability (>80%) coupled with moderate to high genetic advance for traits like days to 50% flowering, plant height, pods per plant, 100-seed weight, and seed yield per plant indicates the predominance of additive gene action and suggests the efficacy of direct selection. Traits such as seeds per pod and first flowering node showed moderate heritability and were more environmentally influenced, suggesting the need for refined breeding strategies. The narrow gap between GCV and PCV for most traits indicated limited environmental influence. Overall, the findings highlight the potential for genetic improvement through selection and provide a valuable base for field pea breeding.

INTRODUCTION

Field pea (*Pisum sativum* L.) is one of the oldest cultivated legume crops, believed to have originated in the region spanning the Mediterranean to the Near East. Domesticated alongside cereals around 7000 years ago, it has since become an important food and forage crop worldwide (McPhee, 2003). Belonging to the family **Leguminosae** and possessing a diploid genome (2n = 14), field pea plays a significant role in sustainable agriculture due to its nitrogen-fixing capability, which enriches soil fertility and reduces dependence on synthetic fertilizers (Jamil et al., 2019; Thavarajah and Thavarajah, 2017). Nutritionally, field pea is valued for its high protein, carbohydrate, and dietary fiber content, while being low in fat. It is also rich in essential vitamins such as vitamin A, C, thiamine (B_1), folate, and important minerals including iron and phosphorus (Bastian Elli, 1998). Carbohydrates constitute the major component (approximately 42.65% of seed weight), with amylose making up around 34% (Bressani and Elias, 1988). According to Hulse (1994), dried peas contain 10.9% water, 22.9% protein, 1.4% fat, 60.7% carbohydrates, 1.4% crude fiber, and 2.7% ash, highlighting their importance as a nutrient-dense food source. Globally, field pea is cultivated mainly in temperate regions, with major producers being Canada, Russia, Australia, and the United States. As per FAO estimates (2024), global production of field pea during the 2023-24 season was approximately 16 million metric tonnes from about 2.1 million hectares. In India, field pea is a vital pulse crop, predominantly grown in the states of Uttar Pradesh, Bihar, and Madhya Pradesh. The country produced around 1.5 million metric tonnes from 0.65 million hectares, with an average productivity of 2.3 tonnes/ha during the same season (Ministry of Agriculture & Farmers Welfare, 2024).

Genetic variability forms the foundation for any crop improvement program. A diverse gene pool enables breeders to exploit traits through selection and hybridization. Among various genetic parameters, heritability and genetic advance offer insights into the inheritance pattern and the efficiency of selection. High heritability coupled with high genetic advance suggests additive gene action, making selection more effective. Understanding these parameters helps in formulating appropriate breeding strategies. Hence, the present investigation was undertaken to evaluate genetic variability, heritability, and genetic advance for yield and its related traits in field pea using a half-diallel set of ten diverse parental genotypes.

2. Materials and Methods

A diallel crossing design was used to cross ten genetically different chickpea lines, omitting reciprocals. The formula for crosses was:

$$p(p-1)/2$$

Where ‘p’ = Number of parents.

At the Genetics and Plant Breeding Farm of Acharya Narendra Deva University of Agriculture and Technology in Ayodhya, Uttar Pradesh, India, 55 F_1s and 11 parental lines (HUDP 15, RFP 1904, KPMR 954, HFP 18-19, IPFD 22-6, Pant P-34, IPFD 22-9, Pant P-536, VL-42, HFP-4, HUDP-15) were grown in timely-sown conditions using a randomised block design (RBD for optimal crop growth, prescribed agricultural methods were followed. Each genotype was planted in a four-meter row with 30 cm row spacing and 10 cm plant spacing. Eleven traits were monitored, including days to 50% flowering, days to maturity, plant height (cm), primary branches plant-^{1}, secondary branches plant-^{1}, pods plant-^{1,} seeds pod-1, 100-seed weight (g), biological yield plant-1 (g), seed yield plant-1 (g) and harvest index (%). Data were collected from five randomly selected competitive plants per plot. Statistical and biometrical methods, including ANOVA (Panse and Shukhatme, 1985), PCV and GCV (Burton and Devane, 1953), heritability in the broad sense (h^2b) (Allard, 1960), genetic advance as a percentage of the mean (Johnson et al., 1955).

2.6 Statistical Analysis

The collected data were subjected to **analysis of variance (ANOVA)** as outlined by **Panse and Sukhatme (1985)** to determine the presence of significant differences among genotypes for the traits under study. To assess the extent of variability, **genotypic coefficient of variation (GCV)** and **phenotypic coefficient of variation (PCV)** were estimated using the method described by **Burton and Devane (1953)**. **Broad-sense heritability (h^2b)** was computed following the formula given by **Allard (1960)** to determine the proportion of phenotypic variance attributable to genetic causes. Furthermore, **genetic advance (GA)** and **genetic advance as a percentage of the mean (GAM)** were calculated as per the procedure suggested by **Johnson et al. (1955)** to evaluate the potential for genetic improvement of various traits through selection.

3. Results and Discussion

3.1 Analysis of Variance

The analysis of variance (ANOVA) revealed **highly significant differences ($p < 0.01$)** among genotypes, parents, hybrids, and parent vs. hybrid comparisons for all the traits studied (Table 1). This indicates the presence of **substantial genetic variability** among the experimental material, offering ample scope for genetic improvement through selection and hybridization. The significance across all sources of variation underscores the effectiveness of the chosen parents and confirms the adequacy of the half-diallel mating design in capturing a broad range of variability. These results validate the potential for identifying superior combinations and selecting desirable genotypes based on quantitative traits.

3.2 Genetic Parameters

The trait **days to 50% flowering** exhibited high heritability (91.2%) and moderate genetic advance (14.7%), suggesting that this trait is under strong genetic control and can be effectively improved through direct selection. **Plant height** showed considerable variability, with high genotypic and phenotypic coefficients of variation, heritability (80.73%), and genetic advance (22.12%), indicating the predominance of **additive gene action** and high potential for selection gains. In the case of **pods per plant**, the trait recorded high heritability (86.88%) and substantial genetic advance as a percentage of mean (30.17%), signifying strong prospects for improvement through simple phenotypic selection.

For **seeds per pod**, moderate heritability (53.05%) along with a noticeable gap between GCV and PCV pointed to **significant environmental influence**, suggesting that improvement through selection may require multiple cycles. **100-seed weight** displayed high heritability (82.43%) and genetic advance (20.35%), confirming the influence of additive genetic control and its suitability for selection-based improvement. The trait **biological yield per plant** also demonstrated high heritability (84.45%) with moderate genetic advance (14.54%), indicating reliability for selection and effective transmission of this trait to subsequent generations.

Seed yield per plant, a key trait, showed high genotypic (17.10%) and phenotypic (18.55%) variation, coupled with high heritability (85.00%) and genetic advance (32.48%). These values suggest a strong **genetic influence** and considerable scope for enhancement through breeding efforts. **Harvest index** also showed similar trends, with high heritability (86.66%) and genetic advance (32.78%), making it a promising selection criterion for improving yield efficiency.

For **pod length**, heritability was moderate (66.12%) with high genetic advance (27.89%), indicating a combination of both genetic and environmental effects, with an emphasis on additive gene action. **Nodes per plant** exhibited high heritability (81.64%) and substantial genetic advance (29.46%), signifying that this trait is largely governed by additive genetic factors. **First flowering node** showed moderate heritability (61.00%) and relatively high genetic advance (30.89%), but a wider difference between GCV and PCV indicated **greater environmental sensitivity**, necessitating refined selection strategies.

Lastly, **days to maturity** recorded high heritability (91.29%) and moderate genetic advance (13.5%), confirming its status as a **stable and heritable trait**, useful for selecting early-maturing genotypes. Collectively, these findings highlight that most traits studied are predominantly controlled by additive gene action and exhibit sufficient genetic variability, making **direct selection a viable approach** for field pea improvement (Table 2).

Table 1. ANOVA of parents and their diallel crosses of field pea in Timely sown (TS) Condition.

Source of Variation	Degrees of Freedom	Days to 50% Flowering	Days To Maturity	Plant Height (cm)	Primary Branches/ Plant	Secondary Branches/ Plant	Pods/ Plant	Seeds/ Pod	100 Seed Weight	Biological Yield/ Plant	Seed Yield/ Plant (g)	Harvest Index (%)
Replication	2	2.12	1.38	0.87	0.05	0.03	0.25	0.02	0.19	12.08	2.34	1.05
Treatment	65	155.43**	180.65**	198.22**	6.54	2.84	89.74**	8.21*	61.34**	235.67**	128.45**	19.35**
Parents	10	32.66	39.22	131.61	3.08	1.43	90.44	1.08	17.06	175.25	46.19	17.8
Hybrids	54	123.44	95.12	131.53	5.64	3.02	54.55	8.85	40.65	202.83	111.47	17.55
Parents vs Hybrids	1	154.4	182.44	103.65	5.88	2.02	102.65	8.45	60.65	138.65	161.17	16.17
Error	130	1.45	1.32	0.91	0.76	0.03	0.91	0.88	0.07	5.52	1.74	2.49

‘*’ Indicates Significance at 5% probability level and ‘**’ indicates Significant at 1% probability level

Table 2. Mean and range of variability among parents and F$_1$s for 11 characters in diallel crosses of field pea in Timely sown (TS) Condition.

Trait	Mean	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance	Genetic Advance as % of Mean
Days to 50% Flowering	59.12	7.47	7.83	91.2	8.69	14.7

Plant Height (cm)	69.94	11.95	13.3	80.73	15.47	22.12
Pods per Plant	18.04	15.71	16.86	86.88	5.44	30.17
Seeds per Pod	6.21	14.7	20.18	53.05	1.37	22.06
100 Seed Weight (g)	19.91	10.88	11.99	82.43	4.05	20.35
Biological Yield/Plant (g)	51.25	7.68	8.36	84.45	7.45	14.54
Seed Yield/Plant (g)	14.99	17.1	18.55	85.0	4.87	32.48
Harvest Index (%)	30.53	17.09	18.36	86.66	10.01	32.78
Nodes per Plant	11.48	15.83	17.52	81.64	3.38	29.46
First Flowering Node	5.09	19.2	24.59	61.0	1.57	30.89
Days to Maturity	110.04	6.86	7.18	91.29	14.85	13.5

CONCLUSION

The present study revealed the presence of **considerable genetic variation** among the field pea genotypes for all the traits under investigation, confirming the potential for genetic improvement through selection and hybridization. Traits such as **seed yield per plant**, **pods per plant**, and **100-seed weight** exhibited **high heritability** coupled with **high genetic advance**, indicating the predominance of **additive gene action** and suggesting that these traits are ideal candidates for **direct phenotypic selection**. Conversely, traits like **seeds per pod** and **first flowering node**, which showed **moderate heritability** and greater environmental influence, may require **refined breeding approaches** such as recurrent selection or backcrossing. Overall, the findings provide a **strong genetic foundation** for field pea improvement programs and offer valuable insights into the inheritance patterns of yield-related traits. These results can significantly contribute to the development of **high-yielding and well-adapted field pea cultivars** under timely sown conditions.

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