Morphological Characterization of Field Pea (*Pisum sativum* L) Genotypes for Yield and its Atributting Traits

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ABSTRACT

Forty-eight field pea genotypes were evaluated in the Kharif season (2021-2023) at Tirhut College of Agriculture, Dholi, Dr. RPCAU, Bihar. The objective of this experiment was to identify stable and high yielding field pea genotypesthrough their overall mean values. The study was conducted using randomized block design with three replications. Observations were taken for 14 quantitative characters that included 35 crosses obtained through line x tester mating design, their parents and one check. The general mean of almost all the characters studied has performed to be higher than the check (Rachana) except for number of secondary branches, days to maturity, pod length, number of seeds per pod, number of pods per plant and number of nodules per plant. Among the parents HUPT 1810, PANT P 462 and within the crosses IPFD 19-9 X IPF 18-7, RFPG 111 X IPF 18-7 and KPF 14-29 X IPF-18-7 showed better results for yield based on the mean performance, indicating that these genotypes can be used for breeding to produce superior genotypes in the region.

Introduction

Pea (*Pisum sativum* L.), that is among the pulses, is a leguminous plant with in Papilionoiaceae subfamily and a member of the dicotyledons class. Its chromosome numberis 2n=14. It is extensively cultivated in cooler climates and is native to South Western Asia. The two types of peas *i.e.,* Field pea and garden pea are traditionally grown all over the world. They can also be referred as dry pea and table pea respectively.

In India, field pea contributes significantly about 3% of the over-all area used for pulses and approximately 5% of the entire amount generated. As per the statistical data it is grown in 0.98 million hectares with 0.89 million tonnes annual production and 912.0 kg per ha productivity in 2021–22 (www.indiaagristat.com). Field pea has a productivity of 866/kg hectare. Madhya Pradesh, Jharkhand, Assam, Maharashtra, and Bihar are indeed the principal field pea producing states.

Low productivity caused by the lack of varieties appropriate for year-round cultivation that are location-specific is one of the main obstacles to pea production. Hence, evaluation of the pea germplasm is urgently required to identify high-yielding geno-

types that may be used in their current form for commercial production or that can be included in future breeding initiatives to increase yield (Galal *et al.,* 2019). With these factors in consideration, the current study was undertaken to evaluate the mean performance of 48 field pea genotypes through yield and its attributing traits.

Materials and Methods

The current study was conducted at Tirhut College of Agriculture, Dholi, Dr. RPCAU, Bihar. The experiment was performed during the *rabi* of 2021–2022 to generate crosses and 2022–2023 to evaluate the parents and crosses. Dholi is 55 meters above MSL and is geographically located at 25.9 ^{0}N latitude and 85.9 ^{o}E longitude.

Seven lines namely, VL 42, RFPG 111, TRCP 8, HUPT 1810, KPF 14-29, DDR-23, IPFD 19-9 and five testers namely, IPF-18-7, PANT P 436, PANT P 462, APARNA and HFP 1545 were chosen due to their phenotypic variability. Thirty-five crosses and their twelve progenitors, including the popular check variety RACHANA, were utilized as the experimental materials.

The observations were recorded for fourteen characters *i.e.,* Days to 50% flowering, Number of primary branches, Number of secondary branches, Plant height, Number of pods per plant, Number of seeds per plant, Days to maturity, Pod length, 100 seed weight, Grain yield per plant, Harvest index, Number of nodules per plant, Nodules fresh weight and Nodules dry weight.

Results and Discussion

The mean performance of parents, hybrids and check recorded on 14 characters is presented in Table 1. The key findings from the experiment are outlined below, along with the conclusions obtained.

Days to 50% flowering

The general mean of the genotypes studied for the following trait is 66.83. Among the lines, the highest mean value is recorded for KFP 14-29 (73.33) and lowest for TRCP8 (65.33). Similarly, among the testers, the highest mean value is recorded for APARNA (67.33) and lowest for PANT P 436 (61.67).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses IPFD 19-9 X PANT P 462 (71.00) and HUPT 1810 X APARNA (63.00) respectively. The mean value for the check (RACHANA) is 65.00.

Number of primary branches

The general mean of the genotypes studied for the following trait is 7.24. Among the lines, the lowest mean value is recorded for KFP 14-29 (6.33) and highest for TRCP8 (8.33). Similarly, among the testers, the highest mean value is recorded for APARNA (7.33).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses HUPT 1810 X PANT P 462 (9.33) and RFPG 111 X APARNA (5.33) respectively. The mean value for the check (RACHANA) is 6.67.

Number of secondary branches

The general mean of the genotypes studied for the following trait is 14.94. Among the lines, the highest mean value is recorded for DDR 23 and IPFD 19-9 (16.00) and lowest for VL 42 (9.33). Similarly, among the testers, the highest mean value is recorded for IPF 18-7 (17.67) and lowest for APARNA (14.67).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses HUPT 1810 X PANT P 436 (20.33) and TRCP 8 X PANT P 436 (8.33) respectively. The mean value for the check (RACHANA) is 19.67.

Plant height

The general mean of the genotypes studied for the following trait is 90.63. Among the lines, the highest mean value is recorded for RFPG 111 (162.33) and lowest for DDR 23 (54.00). Similarly, among the testers, the highest mean value is recorded for IPF 18-7 (141.33) and lowest for APARNA (53.66).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses VL 42 X PANT P 436 (150.66) and HUPT 1810 X APARNA (49.66) respectively. The mean value for the check (RACHANA) is 50.33.

Days to maturity

The general mean of the genotypes studied for the following trait is 118.15. Among the lines, the highest mean value is recorded for HUPT 1810 (124.67) and lowest for KFP 14-29 (118.67). Similarly, among

Table 1a. Mean performance of 48 pea genotypes

S. No	Genotypes	Days to 50% flowering	Number of primary branches	Number of secondary branches	Plant height	Days to maturity	Pod length	Number of seeds per pod	Number of pods per plant
	LINES								
1	VL 42	71.67	7.66	9.33	140.33	121.00	5.20	4.33	21.33
2	RFPG111	69.00	7.33	8.66	162.33	123.00	5.50	5.33	32.33
3	TRCP8	65.33	8.33	10.66	130.33	121.67	5.37	5.67	40.67
4	HUPT 1810	70.67	7.33	15.00	138.33	124.67	6.17	3.33	47.67
5	KFP 14-29	73.33	6.33	15.33	56.67	124.00	7.80	6.67	19.33
6	DDR-23	69.00	7.00	16.00	54.00	118.67	6.37	5.33	27.67
7	IPFD 19-9	70.00	7.66	16.00	55.33	122.00	8.90	4.67	17.67
	Mean	69.85	7.38	13.00	105.33	122.14	6.47	5.05	29.52
	TESTERS								
8	IPF-18-7	63.33	6.67	17.67	141.33	123.67	4.93	3.67	26.00
9	PANT P 436	61.67	6.67	16.00	128.33	120.33	5.20	5.67	15.67
10	PANT P 462	65.33	6.67	17.33	64.00	117.33	6.53	4.33	23.33
11	APARNA	67.33	7.33	14.67	53.66	115.67	6.77	4.67	15.00
12	HFP 1545	67.00	6.67	16.33	55.66	117.00	7.37	6.67	20.33
	Mean	64.93	6.80	16.40	88.60	118.80	6.16	5.00	20.07
	CROSSES								
13	VL42 X IPF 18-7	64.33	7.67	17.00	113.33	114.33	4.97	6.33	27.33
14	VL 42 X PANT P 436	65.33	6.33	14.00	150.66	116.33	6.60	5.33	21.67
15	VL 42 X PANT P 462	69.00	6.33	17.67	74.66	111.33	6.90	4.33	27.00
16	VL 42 X APARNA	70.33	7.67	11.00	78.66	121.67	6.97	5.00	20.67
17	VL 42 X HFP 1545	67.33	8.33	14.00	93.66	121.33	6.33	5.33	22.67
18	RFPG 111 X IPF 18-7	64.67	7.33	12.00	149.00	117.67	5.73	4.67	33.00
19	RFPG 111X PANT P 436	69.33	6.33	10.33	135.33	111.33	6.53	5.67	28.00
20	RFPG 111 X PANT P 462	69.33	7.33	16.67	74.00	118.33	7.10	3.67	32.67
21	RFPG 111 X APARNA	69.33	5.33	14.00	62.33	116.67	7.27	5.67	26.33
22	RFPG 111 X HFP 1545	70.00	7.33	14.67	113.33	112.67	6.83	6.67	25.33
23	IPFD 19-9 X IPF 18-7	66.67	7.33	19.67	126.66	123.67	5.40	5.67	41.67
24	IPFD 19-9 X PANT P 436	64.67	6.33	17.33	120.66	119.67	5.33	6.67	33.67
25	IPFD 19-9 X PANT P 462	71.00	7.67	17.33	69.66	118.67	6.57	5.67	31.00
26	IPFD 19-9 X APARNA	63.33	7.33	18.33	84.66	114.00	6.93	5.33	27.33
27	IPFD 19-9 X HFP 1545	65.00	6.33	18.00	80.66	110.00	6.33	3.67	32.33
28	KPF 14-29 X IPF-18-7	66.00	5.67	11.67	139.33	112.33	6.13	3.33	43.00
29	KPF 14-29 X PANT P 436	65.00	6.33	14.00	134.33	120.33	5.60	4.67	31.33
30	KPF 14 -29 X PANT P 462	65.67	7.67	14.67	75.33	122.67	6.63	5.00	41.67
31	KPF 14-29 X APARNA	64.67	7.00	15.33	106.00	115.67	5.93	3.67	31.33
32	KPF 14-29 X HFP 1545	63.33	7.33	11.00	68.66	121.67	6.30	4.00	31.33
33	TRCP X IPF 18-7	63.67	6.67	9.33	108.33	113.00	6.73	6.33	24.00
34	TRCP 8 X PANT P 436	65.33	8.67	8.33	74.66	118.33	6.13	3.67	18.00
35	TRCP 8 X PANT P 462	66.67	7.67	11.33	56.66	117.67	5.87	4.00	26.00
36	TRCP 8 X APARNA	66.67	6.67	13.33	58.00	114.00	7.30	4.67	19.33
37	TRCP8 X HFP 1545	70.33	8.33	9.00	54.33	120.67	7.17	4.67	21.33
38	HUPT 1810 X IPF 18-7	69.33	7.67	16.33	111.33	123.00	7.37	5.67	30.33
39	HUPT 1810 X PANT P 436	65.67	8.33	20.33	90.33	113.00	5.60	3.67	26.33
40	HUPT 1810 X PANT P 462	65.33	9.33	17.33	55.00	116.67	6.33	5.67	32.67
41	HUPT 1810X APARNA	63.00	7.00	18.67	49.66	122.33	6.03	3.67	25.00
42	HUPT 1810 X HFP 1545	66.67	8.00	14.67	53.66	117.33	7.20	5.67	30.33
43	DDR 23 X IPF 18-7	69.67	7.33	19.33	106.00	113.67	6.93	5.33	21.33
44	DDR 23 X PANT P 436	68.33	7.67	15.67	81.66	114.67	5.17	5.00	19.67
45	DDR 23 X PANT P 462	64.67	8.33	15.67	62.00	122.33	7.10	3.67	25.33
46	DDR 23 X APARNA	65.00	6.00	17.00	56.33	117.00	7.53	4.33	19.00
47	DDR 23 X HFP 1545	64.67	8.33	19.67	51.00	118.67	8.83	4.00	21.67
48	RACHANA (CHECK)	65.00	6.67	19.67	50.33	119.67	7.47	6.67	16.67
	Overall Mean	**66.83**	**7.24**	**14.94**	**90.63**	**118.15**	**6.48**	**4.94**	**26.94**
	C.D 0.05	**1.72**	**1.07**	**1.83**	**7.95**	**5.69**	**0.77**	**1.03**	**2.31**

Table 1b. Mean performance of 48 pea genotypes

S. No.	Genotypes	100 seed weight	Grain yield per plant	Harvest index	Number of nodules per plant	Nodules fresh weight	Nodules dry weight
	LINES						
1	VL 42	15.33	15.41	20.79	22.43	1.97	0.65
2	RFPG111	11.87	16.70	31.34	19.90	1.30	0.44
3	TRCP8	21.55	22.05	29.69	17.50	1.98	0.64
4	HUPT 1810	14.75	24.79	33.80	23.73	2.20	0.62
5	KFP 14-29	11.94	14.19	33.17	20.67	1.30	0.37
6	DDR-23	12.99	17.90	32.51	23.43	2.11	0.49
7	IPFD 19-9	13.56	14.89	33.88	19.47	0.36	0.44
	Mean	14.57	17.99	30.74	21.02	1.60	0.52
	TESTERS						
8	IPF-18-7	14.77	15.54	24.81	21.87	0.76	0.24
9	PANT P 436	14.97	11.74	17.90	18.20	1.66	0.56
10	PANT P 462	16.34	16.51	22.75	21.77	1.15	0.33
11	APARNA	18.29	12.13	24.23	18.61	1.29	0.59
12	HFP 1545	12.92	15.35	31.19	18.77	1.26	0.26
	Mean	15.46	14.26	24.17	19.84	1.22	0.39
	CROSSES						
13	VL42 X IPF 18-7	10.99	17.61	32.08	21.73	2.12	0.51
14	VL 42 X PANT P 436	13.49	15.64	25.11	18.60	1.47	0.32
15	VL 42 X PANT P 462	15.28	18.27	40.37	21.41	1.70	0.34
16	VL 42 X APARNA	14.65	15.48	30.51	18.53	0.37	0.27
17	VL 42 X HFP 1545	12.78	15.93	37.71	19.53	2.03	0.60
18	RFPG 111 X IPF 18-7	13.52	22.46	28.54	18.63	2.51	0.92
19	RFPG 111X PANT P 436	12.92	17.50	28.05	18.60	1.35	0.53
20	RFPG 111 X PANT P 462	17.95	19.81	24.96	19.30	1.03	0.36
21	RFPG 111 X APARNA	12.15	17.16	33.70	17.57	0.72	0.18
22	RFPG 111 X HFP 1545	11.15	16.41	37.18	19.13	0.73	0.38
23	IPFD 19-9 X IPF 18-7	10.55	22.51	41.80	17.53	2.84	0.91
24	IPFD 19-9 X PANT P 436	10.07	20.29	33.55	18.50	1.74	0.81
25	IPFD 19-9 X PANT P 462	11.57	17.50	45.27	18.30	1.04	0.58
26	IPFD 19-9 X APARNA	13.78	18.87	26.38	17.13	1.77	0.45
27	IPFD 19-9 X HFP 1545	18.98	21.21	34.08	17.53	1.23	0.68
28	KPF 14-29 X IPF-18-7	16.37	21.56	41.27	20.60	2.76	0.36
29	KPF 14-29 X PANT P 436	14.57	20.28	29.62	18.90	1.12	0.82
30	KPF 14 -29 X PANT P 462	9.90	21.12	27.89	18.60	1.66	0.46
31	KPF 14-29 X APARNA	18.80	18.82	30.99	18.13	0.86	0.53
32	KPF 14-29 X HFP 1545	14.99	17.73	33.52	17.57	2.95	0.36
33	TRCP X IPF 18-7	11.89	16.73	27.21	16.67	2.84	0.35
34	TRCP 8 X PANT P 436	20.79	14.72	35.42	15.93	1.90	0.35
35	TRCP 8 X PANT P 462	16.94	17.54	50.24	17.90	1.27	0.45
36	TRCP 8 X APARNA	13.10	13.13	35.35	16.43	1.55	0.17
37	TRCP8 X HFP 1545	14.94	16.92	18.73	17.27	1.56	0.92
38	HUPT 1810 X IPF 18-7	10.87	17.82	27.99	21.60	1.53	0.35
39	HUPT 1810 X PANT P 436	15.69	16.58	18.70	19.77	1.31	0.58
40	HUPT 1810 X PANT P 462	11.72	17.34	23.51	21.77	2.56	0.56
41	HUPT 1810X APARNA	15.41	16.60	20.34	18.87	2.17	0.43
42	HUPT 1810 X HFP 1545	10.85	16.72	24.66	19.83	1.87	0.24
43	DDR 23 X IPF 18-7	19.65	20.76	26.12	22.87	1.40	0.79
44	DDR 23 X PANT P 436	14.95	14.96	23.86	22.30	2.17	0.30
45	DDR 23 X PANT P 462	16.12	16.79	24.37	20.67	1.85	0.54
46	DDR 23 X APARNA	14.68	15.92	24.79	20.37	1.11	0.41
47	DDR 23 X HFP 1545	14.48	14.57	29.81	21.50	1.25	0.51
48	RACHANA (CHECK)	13.98	14.50	22.85	23.80	0.90	0.47
	Overall Mean	**14.37**	**17.39**	**29.85**	**19.58**	**1.60**	**0.49**
	C.D 0.05	**1.63**	**1.99**	**4.18**	**1.80**	**0.21**	**0.06**

S204

Eco. Env. & Cons. 29 (November Suppl. Issue) : 2023

the testers, the highest mean value is recorded for IPF 18-7 (123.67) and lowest for APARNA (115.67).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses IPFD 19-9 X IPF 18-7 (123.67) and IPFD 19-9 X HFP 1545 (110.00) respectively. The mean value for the check (RACHANA) is 119.67.

Pod length

The general mean of the genotypes studied for the following trait is 6.48. Among the lines, the highest mean value is recorded for IPFD 19-9 (8.90) and lowest for VL 42 (5.20). Similarly, among the testers, the highest mean value is recorded for HFP 1545 (7.37) and lowest for IPF 18-7 (4.93).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses DDR 23 X HFP 1545 (8.83) and VL 42 X IPF 18-7 (4.97) respectively. The mean value for the check (RACHANA) is 7.47.

Number of seeds per pod

The general mean of the genotypes studied for the following trait is 4.94. Among the lines, the highest mean value is recorded for KFP 14-29 (6.67) and lowest for HUPT 1810 (3.33). Similarly, among the testers, the highest mean value is recorded for HFP 1545 (6.67) and lowest for IPF 18-7 (3.67).

Of the thirty-five crosses studied, the highest mean value is obtained for the crosses RFPG 111 X HFP 1545 and IPFD 19-9 X PANT P 436 (6.67) and the lowest value for KPF 14-29 X IPF 18-7 (3.33). The mean value for the check (RACHANA) is 6.67.

Number of pods per plant

The general mean of the genotypes studied for the following trait is 26.94. Among the lines, the highest mean value is recorded for HUPT 1810 (47.67) and lowest for IPFD 19-9 (17.67). Similarly, among the testers, the highest mean value is recorded for IPF 18-7 (26.00) and lowest for APARNA (15.00).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses KPF 14-29 X IPF 18-7 (43.00) and TRCP 8 X PANT P 436 (18.00) respectively. The mean value for the check (RACHANA) is 16.67.

100 Seed weight

The general mean of the genotypes studied for the following trait is 14.37. Among the lines, the highest mean value is recorded for TRCP 8 (21.55) and low-

est for RFPG 111 (11.87). Similarly, among the testers, the highest mean value is recorded for APARNA (18.29) and lowest for IFP 1545 (12.92).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses TRCP 8 X PANT P 436 (20.79) and KPF 14-29 X PANT P 436 (9.90) respectively. The mean value for the check (RACHANA) is 13.98.

100 Grain yield per plant

The general mean of the genotypes studied for the following trait is 17.39. Among the lines, the highest mean value is recorded for HUPT 1810 (24.79) and lowest for KFP 14-29 (14.19). Similarly, among the testers, the highest mean value is recorded for PANT P 462 (16.51) and lowest for PANT P 436 (11.74).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses IPFD 19-9 X IPF 18-7 (22.51) and TRCP 8 X APARNA (13.13) respectively. The mean value for the check (RACHANA) is 14.50.

Harvest index

The general mean of the genotypes studied for the following trait is 29.85. Among the lines, the highest mean value is recorded for IPFD 19-9 (33.88) and lowest for VL 42 (20.79). Similarly, among the testers, the highest mean value is recorded for HFP 1545 (31.19) and lowest for PANT P 436 (17.90).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses TRCP 8 X PANT P 462 (50.24) and HUPT 1810 X PANT P 436 (18.70) respectively. The mean value for the check (RACHANA) is 22.85.

Number of nodules per plant

The general mean of the genotypes studied for the following trait is 19.58. Among the lines, the highest mean value is recorded for HUPT 1810 (23.73) and lowest for TRCP 8 (17.50). Similarly, among the testers, the highest mean value is recorded for IPF 18-7 (21.87) and lowest for PANT P 436 (18.20).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses DDR 23 X IPF 18-7 (22.87) and TRCP 8 X PANT P 436 (15.93) respectively. The mean value for the check (RACHANA) is 23.80.

Nodules fresh weight

The general mean of the genotypes studied for the

following trait is 1.60. Among the lines, the highest mean value is recorded for HUPT 1810 (2.20) and lowest for IFPD 19-9 (0.36). Similarly, among the testers, the highest mean value is recorded for PANT P 436 (1.66) and lowest for IPF 18-7 (0.76).

Of the thirty-five crosses studied, the highest and lowest mean values are obtained for the crosses KPF 14-29 X HFP 1545 (2.95) and VL 42 X APARNA (0.37) respectively. The mean value for the check (RACHANA) is 0.90.

Nodules dry weight

The general mean of the genotypes studied for the following trait is 0.49. Among the lines, the highest mean value is recorded for VL 42 (0.65) and lowest for KPF 14 -29 (0.37). Similarly, among the testers, the highest mean value is recorded for APARNA (0.59) and lowest for IPF 18-7 (0.24).

Of the thirty-five crosses studied, the highest mean value is obtained for the crosses RFPG 111 X IPF 18-7 and TRCP 8 X HFP 1545 (0.92) and the lowest value is TRCP 8 X APARNA (0.17). The mean value for the check (RACHANA) is 0.47.

Based on the mean performance of genotypes, within the lines HUPT 1810 had performed best for the quantitative traits like Grain yield per plant, number of pods per plant, pod length, number of nodules per plant and nodules fresh weight. Whereas among the testers APARNA had performed better for traits like plant height, days to maturity, 100 seed weight, number of pods per plant and nodules dry weight. Similar results were found by Ceyhan *et al*. (2008), Parihar *et al*. (2014), Jaiswal *et al*. (2015) and Pratap *et al*. (2021).

The crosses HUPT 1810 X PANT P42 for characters like number of pods per plant and number of secondary branches, TRCP 8 X PANT P 436 for 100 seed weight and harvest index, RFPG 111 X HFP 1545 for number of seeds per pod, KPF 14-29 X IPF 18-7 for number of pods per plant had shown highest mean performances thus considered to perform better. For the main trait *i.e.,* Grain yield per plant the parents HUPT 1810, PANT P 462 and within the crosses IPFD 19-9 X IPF 18-7, RFPG 111 X IPF 18-7 and KPF 14-29 X IPF-18-7 showed better results. The results are in akin with the findings of Yadav *et al*. (2010), Punia *et al*. (2011), Kosev (2015), Kumar *et al*. (2017), Ali *et al*. (2021) and Tasnim *et al*. (2022).

Conclusion

The highest mean performance was observed in the parents TRCP 8, IPFD 19-9, APARNA, IPF 18-7 and HUPT 1810 for the almost all the characters over the check RACHANA included in the study. Hence, these genotypes can be selected as promising parents to develop high yielding progeny for yield improvement in field pea.The cross combinations IPFD 19-9 X PANT P 462, IPFD 19-9 X IPF 18-7, TRCP 8 X PANT P 436, DDR 23 X HFP 1545 and RFPG 111 X IPF 18-7 showed highest mean for yield and its attributing traits. These cross combinations with better performance for yield and its attributing traits can be used in further breeding programmes to release commercial hybrids.

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