



RESEARCH ARTICLE

Enhancing yield potential in vegetable pea through multi-flowering trait: Genetic variability and principal component analysis

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Abstract

Vegetable pea (*Pisum sativum* L. var. *hortense*) is a nutritionally and economically important legume, yet productivity gains have remained limited despite expanded cultivation. This study evaluated 50 pea genotypes along with multiflowered genotypes for yield potential relative to commercially grown single- and double-podded varieties. Significant genetic variability was observed for key agro-morphological and yield-related traits, with yield per plant ranging from 78.0 g (single-podded VRPSel-17) to 176.0 g (multi-podded VRPM-901-5). Traits including days to 50% flowering, total flowers per plant, branches per plant, pods per plant, plant height, and yield per plant exhibited high phenotypic and genotypic coefficients of variation, heritability, and genetic advance, indicating strong genetic control and substantial potential for improvement through selection. Notably, pods per plant, total flowers per plant, and branches per plant showed strong positive correlations with yield, highlighting their utility as reliable selection indices. Principal component analysis revealed that the first three components accounted for 61.54% of total variation, with PC1 associated with total flowers, pods per plant, and ten pod weight; PC2 with yield per plant, seeds per pod, and pod length; and PC3 with pod width and days to picking. Collectively, yield- and pod-associated traits constituted the primary contributors to genetic divergence, enabling the effective discrimination and selection of superior genotypes. The present findings identify critical target traits and superior multi-flowering genotypes VRPM-901-5, BSW-136, BSW-2, VRP-343, and VRPE-52 for use in breeding programs aimed at enhancing pea productivity.

Keywords: Pea, multi-flowering, genetic variability, heritability, yield/plant, and selection indices

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Introduction

Vegetable pea (*Pisum sativum* L. var. *hortense*) is an important crop of the Leguminosae family, having diploid chromosome number of $2n = 2x = 24$. It is widely cultivated across temperate and subtropical regions for both its fresh green pods and dry seeds. Historically, pea holds a pivotal place in the history of genetics, being the model crop used by Gregor Mendel in his foundational experiments on inheritance (Mendel, 1865). Beyond its genetic importance, pea continues to offer multifaceted value-nutritional, agronomic, and economic. The crop is utilized in various forms, including fresh, frozen, and canned products, making it highly versatile in culinary use (Nasir et al., 2024). Due to its adaptability, high protein content, and economic relevance, pea cultivation is widespread globally, particularly in Europe, North America, Asia, and Australia (Millar et al., 2019). Recent studies have also emphasized its role in managing lifestyle diseases such as diabetes, cardiovascular disorders, certain cancers, and degenerative conditions and make it crop of international importance with high export potential (Kumari & Deka, 2021; Sharma et al., 2023). India ranks as the

second-largest producer of green peas globally, after China. In 2022-23, green peas were grown on 0.59 million hectares, producing 6.5 million tonnes with a record productivity of 11.0 tonnes per hectare (Agriculture Statistics at a Glance, 2022). Since 1990-91, pea production in India has grown nearly 7.6-fold (from 0.85 to 6.50 million tonnes), whereas productivity has increased about 2.3 times, from 4.8 to 11.0 MT/ha (Agricultural Statistics at a Glance, 1991-2023). Despite the remarkable expansion in area and production, the pace of productivity growth has remained relatively modest. As India's predominantly vegetarian population increasingly relies on plant-based protein sources like peas, the crop plays a crucial role in ensuring national food and nutritional security. Therefore, focused efforts are needed to develop high-yielding varieties with novel agronomic traits to overcome the current yield plateau and meet future demands.

Flowers have significant agricultural and economic impact, as much of the human and livestock food is the product of flowers (Stewart *et al.*, 2016). With very limited variation in the flower number/node, most of pea genotypes generally have single or double flower/node, and multi-flowers (MF *i.e.* bearing more than two flowers or pod on a single peduncle) is rarest trait reported in *Pisum* (Devi *et al.*, 2018a; Mishra *et al.*, 2020). Several economically important legumes typically bear only 1-2 FPP, as seen in pea (*L*; 1-2) and chickpea (*Cicer arietinum*; 1-2), and lentils (*Lens culinaris* Medik., 2-3). Breeders and researchers consistently value this trait for its agricultural and evolutionary significance, recognizing its variability among cultivars and environmental conditions (Mishra *et al.*, 2021; Hole and Hardwick, 1976). The ICAR-Indian Institute of Vegetable Research (ICAR-IIVR), Varanasi, has taken a leading role in developing distinct multi-flowering (MF) pea genotypes since 2015-16 onward. Notable examples include 'VRPM-905-1' (INGR19077), which produces 3 to 5 pods per peduncle, and 'VRP-500' (INGR15009), which typically bears 3 pods per peduncle, both have been officially registered with the National Bureau of Plant Genetic Resources (NBPGR), New Delhi. Among these, 'VRPM-901-5' has shown exceptional yield potential, reaching up to 227 quintals per hectare (Devi *et al.*, 2021). These findings suggest that the MF trait holds significant promise for boosting pod and seed yields in peas and potentially other legume crops.

The present study aimed to evaluate the yield performance of selected multi-flowering genotypes developed from a stable population of multi-flowered recombinant inbred lines (RILs). These genotypes were compared with commercially cultivated single- and double-podded varieties to assess their productivity and suitability for pea improvement programs. Furthermore, genetic variability, correlation analysis, and principal component analysis (PCA) were conducted to identify the most responsive traits contributing to overall variation.

Materials and Methods

Experimental site and material

The present study was conducted during the *Rabi* season of 2024-25 at the Experimental Farm of ICAR-Indian Institute of Vegetable Research (IIVR), Varanasi (25°18'21" N, 82°52'37" E; 83 m AMSL). The experiment was laid out in a randomized block design (RBD) with three replications. A total of 50 genotypes-including single-, double-, and multi-podded types-were evaluated for yield performance.

Data observation and statistical analysis

The data was recorded on 12 agronomical traits. The traits recorded included DTF (days to 50% flowering), DTP (days to picking), TFP (total flowers per plant), BPP (branches per plant), PPP (pods per plant), PL (pod length, cm), PW (pod width, cm), PH (plant height, cm), SPP (seeds per pod), TPW (ten pod weight, g), YPP (pod yield per plant, g), and SP (shelling percentage). The heritability (h^2) was categorized as low when it ranges from 0 to 40%, moderate when it lies between 40 to 60%, and high when it is above 60%. Similarly, genetic advance (GA) as percentage of mean is classified as low when it is 0 to 10%, moderate from 10 to 20%, and high when it exceeds 20%. All the statistical analysis were done with R SOFTWARE.

Results and Discussion

The analysis of variance (ANOVA) was performed to assess the significance of genotypic differences among the 50 pea genotypes for various horticultural traits. The results revealed highly significant differences ($p < 0.01$) among genotypes for all the traits studied, including days to 50% flowering, days to picking, pod length, pod width, seeds per pod, total flower production, pods per plant, branches per plant, yield per plant, and shelling percentage. Similar observations were reported by Devi *et al.* (2023), who also found wide genetic variation in pea germplasm for flowering, pod, and yield-related traits.

Mean performance of genotypes

The evaluation of 50 pea genotypes revealed significant variability across phenological, morphological, and yield-related traits, indicating strong scope for genetic improvement. Earliness and maturity traits showed wide variation. Days to 50% flowering ranged from 32.3 to 69.0 days in double-podded genotypes, with early lines such as Kashi Udai, Kashi Nandini, and VRPE-30 suitable for early harvesting. Multi-podded genotypes flowered relatively later (45.0–68.0 days), while the single-podded VRPSel-17 (52.0 days) showed intermediate behaviour. Days to picking ranged from 70.0 to 96.3 days (mean 84.0 days). Double-podded types exhibited wider adaptability, whereas multi-podded genotypes matured later (mean 91.4 days) due to prolonged pod filling. This variability supports breeding for diverse maturity groups (Table 1).

Table 1: Mean comparison of single, double and multi-podded genotypes of peas for various horticultural traits

S. No.	Genotypes	Pod bearing	DTF	DTP	BPP	PH	TFP	PPP	PL	PW	TPW	SPP	YPP	SP
1.	AP3	Double podded	37.67	77.7	2.28	66.83	19.43	14.67	8.86	1.36	73.40	8.40	96.76	48.2
2.	Arka Kartik	Double podded	51.33	90.0	3.22	85.22	20.93	14.70	7.59	1.06	68.43	6.47	96.61	46.6
3.	Arkel	Double podded	38.00	77.7	1.78	71.50	15.53	11.67	9.27	1.04	71.13	6.60	73.12	44.9
4.	BHU-15	Multi-podded	68.00	96.0	1.83	79.23	40.00	18.23	8.11	1.15	56.03	7.47	85.71	46.2
5.	BSW-2	Multi-podded	45.00	91.7	2.60	113.20	54.40	32.53	7.10	1.33	52.33	5.47	133.33	43.8
6.	BSW-72	Multi-podded	54.00	90.0	2.67	100.13	30.33	18.87	6.60	1.23	51.83	6.27	114.70	49.7
7.	BSW-74	Multi-podded	54.00	88.9	2.03	121.17	33.50	22.97	6.63	1.17	47.13	6.70	124.43	46.6
8.	BSW-136	Multi-podded	50.00	82.6	3.10	54.97	43.97	29.90	7.27	1.30	53.60	6.43	145.67	48.3
9.	EC865920 (2)	Multi-podded	65.00	88.7	2.44	73.28	26.77	16.97	7.71	1.21	60.97	7.30	88.99	42.3
10.	EC865921 (3)	Multi-podded	65.67	95.7	2.22	79.51	28.60	12.40	7.70	1.21	54.13	6.67	61.73	44.0
11.	EC865925 (7)	Multi-podded	62.00	96.0	2.56	77.50	55.67	23.80	7.90	1.16	57.13	7.27	106.37	47.8
12.	EC865944 (26)	Multi-podded	64.00	93.0	1.28	80.39	37.97	20.47	7.30	1.15	59.83	7.00	97.47	46.5
13.	EC866018 100	Multi-podded	63.00	93.0	1.39	79.76	37.53	21.47	7.77	1.18	65.13	7.00	106.77	41.4
14.	Kashi Ageti	Double podded	38.67	75.0	2.22	70.56	14.93	11.93	8.76	1.32	86.23	8.07	89.89	48.9
15.	Kashi Dhanvi	Double podded	39.33	71.0	1.56	54.50	17.87	12.33	8.64	1.29	76.27	8.20	98.00	50.6
16.	Kashi Mukti	Double podded	38.00	76.7	1.78	53.72	14.80	11.60	9.27	1.42	73.10	7.33	72.35	48.3
17.	Kashi Nandini	Double podded	33.33	72.7	1.39	50.78	15.43	9.80	8.52	1.25	74.17	6.40	70.44	47.4
18.	Kashi Purvi	Double podded	36.33	71.3	1.28	63.11	14.73	11.47	8.85	1.23	76.80	8.20	73.27	49.5
19.	Kashi Samridhi	Double podded	69.00	96.3	2.56	64.28	26.20	22.00	7.24	1.33	65.40	6.93	117.47	45.5
20.	Kashi Shakti	Double podded	54.00	89.0	1.94	73.28	25.93	16.13	9.27	1.28	72.80	7.53	100.58	46.0
21.	Kashi Tripti	Double podded	53.33	85.0	1.83	93.39	24.87	20.07	9.92	1.76	75.10	7.07	132.05	50.2
22.	Kashi Udai	Double podded	33.00	70.0	1.28	38.39	14.33	8.47	8.16	1.30	75.53	7.33	63.25	48.4
23.	PC-531	Double podded	50.00	88.7	1.78	63.78	25.00	18.33	10.18	1.16	72.00	8.53	103.61	51.0
24.	PMRNIL-1	Double podded	59.33	94.7	1.28	52.90	24.87	16.77	8.83	1.33	72.77	7.93	101.63	48.4
25.	PMRNIL-2	Double podded	59.00	94.0	2.21	59.75	29.17	18.43	8.00	1.71	85.40	7.83	127.90	47.9
26.	PMRNIL-3	Double podded	66.00	93.7	1.63	69.17	20.00	17.07	7.59	1.77	68.80	7.33	89.07	48.9
27.	PMRNIL-4	Double podded	58.00	95.3	1.50	64.44	29.33	17.00	7.56	1.81	69.70	7.87	83.57	48.2
28.	PMRNIL-5	Double podded	58.33	94.3	1.93	64.14	18.73	16.43	8.14	1.77	72.27	7.83	91.83	47.2
29.	VL Matar-13	Double podded	52.00	82.0	2.00	64.44	29.33	17.47	9.62	1.33	78.37	8.73	118.74	46.0
30.	VRP-343	Double podded	55.00	88.3	2.55	67.28	27.20	20.73	8.45	1.38	83.73	7.53	147.19	48.2
31.	VRP-386	Double podded	60.00	87.2	2.44	94.89	49.53	17.67	7.06	1.01	79.60	8.33	126.37	46.0
32.	VRP-500	Multi-podded	56.00	85.3	1.95	67.95	28.60	14.40	7.64	1.30	64.10	8.13	89.62	47.0
33.	VRP-918	Double podded	39.33	75.0	1.33	65.39	20.93	16.67	8.44	1.03	61.47	7.27	96.19	48.6
34.	VRPE-17	Double podded	45.00	82.0	2.11	52.06	23.00	18.67	8.30	1.26	65.27	6.60	110.06	44.5
35.	VRPE-19	Double podded	36.33	75.3	1.67	55.44	15.87	10.93	7.42	1.23	82.97	7.33	83.30	47.4
36.	VRPE-30	Double podded	34.00	75.0	1.50	45.72	15.20	12.80	8.28	1.30	72.70	7.67	88.87	47.3
37.	VRPE-49	Double podded	35.00	78.3	1.83	50.67	15.60	12.93	8.64	1.32	78.13	8.00	97.27	44.7
38.	VRPE-52	Double podded	38.67	76.0	1.67	59.45	21.80	19.33	8.48	1.33	88.40	7.67	133.67	48.7
39.	VRPE-60	Double podded	43.33	82.3	1.89	79.22	26.40	20.20	8.48	1.23	64.90	7.27	106.57	45.7
40.	VRPE-64	Double podded	32.33	76.7	1.83	59.11	19.40	13.93	8.25	1.18	65.80	7.67	88.51	47.3
41.	VRPE-66	Double podded	42.33	73.7	2.84	62.28	20.67	14.93	10.00	1.08	73.70	9.00	91.97	50.6
42.	VRPE-115	Double podded	34.00	75.3	2.00	59.22	26.27	21.00	8.79	1.12	72.77	8.73	124.26	52.6
43.	VRPE-916	Double podded	41.00	79.0	1.44	65.06	17.60	12.60	8.48	1.10	71.63	7.53	84.92	44.9
44.	VRPE-953	Double podded	40.33	79.3	2.28	61.28	20.40	19.13	8.49	1.21	82.80	7.80	115.70	49.9

Cont...

45.	VRPE-955	Double podded	42.00	76.3	2.22	69.17	28.73	13.00	8.86	1.29	77.60	8.37	91.64	47.9
46.	VRPE-964	Double podded	46.33	82.7	2.17	68.56	25.90	18.93	8.54	1.32	74.53	7.47	126.98	40.8
47.	VRPM-107	Double podded	53.00	83.0	2.50	77.50	22.93	14.10	10.65	1.35	84.37	9.73	115.16	51.0
48.	VRPM-501	Multi-podded	61.00	89.7	2.61	64.67	34.70	17.87	8.64	1.48	75.60	7.27	118.63	47.8
49.	VRPM-901-5	Multi-podded	55.00	86.3	3.07	55.33	62.80	37.47	7.90	1.27	55.17	6.80	176.00	47.8
50.	VRPSel-17	Single podded	52.00	82.3	2.80	103.27	34.13	21.83	6.80	1.17	49.00	6.53	78.00	47.6
CV (%)			4.87	3.8	14.11	8.95	14.90	5.90	4.45	6.24	5.66	5.33	12.87	6.2
Mean			49.15	85.19	2.05	69.34	26.96	17.46	8.30	1.34	69.80	7.50	103.12	47.88
CD 5%			3.87	4.18	0.46	10.05	6.50	3.71	0.59	1.16	6.39	0.64	21.50	4.90

Plant architecture traits also varied considerably. Multi-podded genotypes showed higher vegetative vigor, with greater plant height and branching (e.g., BSW-74, BSW-136), supporting enhanced assimilate production. Double-podded types displayed wider variation in plant height (38.39–94.89 cm) and moderate branching, with promising entries like Arka Kartik and VRPE-66. The single-podded VRPSel-17 exhibited tall stature and good branching, indicating that podding habit does not restrict vegetative growth. Reproductive traits such as total flower production (TFP) and pods per plant (PPP) showed marked differences. TFP ranged from 14.33 to 62.80 (mean 26.96), with multi-podded genotypes outperforming others (mean 38.69), as seen in VRPM-901-5. PPP ranged from 8.47 to 37.47 (mean 17.46), with multi-podded genotypes again dominating due to higher pod-bearing nodes. However, efficient flower-to-pod conversion in some double- and single-podded lines highlights their breeding value. Pod traits reflected contrasting yield strategies. Pod length ranged from 6.60 to 10.65 cm, with double-podded genotypes producing longer pods (e.g., VRPM-107, PC-531), desirable for market preference. Pod width ranged from 1.01 to 1.81 cm, with double-podded types showing superiority in seed packing.

In contrast, multi-podded genotypes had relatively smaller pods but compensated through higher pod numbers. Seed traits further demonstrated variability. Seeds per pod ranged from 5.47 to 9.73, with double-podded genotypes such as Kashi Ageti and Kashi Dhanvi performing consistently well. Ten-pod weight ranges from 47.13 to 88.40 g (mean 69.80 g), indicating good selection potential. Multi-podded genotypes, though slightly lower in seeds per pod, offset this through higher pod numbers. Yield per plant averaged 103.12 g, with multi-podded genotypes recording the highest yields, particularly VRPM-901-5 (176.00 g). Double-podded genotypes showed moderate to high yields, while the single-podded type remained below average. Shelling percentage exceeded 50% in several genotypes, indicating efficient seed recovery. Overall, multi-podded genotypes excelled in yield, whereas double-podded types were superior in pod size and seed traits, offering complementary potential for breeding improved cultivars.

Phenotypic and genotypic coefficients of variation (PCV and GCV)

Based on the classification proposed by Sivasubramanian and Madhavamenon (1973), traits exhibiting high genotypic

Table 2: Assessment of genetic variability, heritability, and potential genetic gain for yield traits in 50 vegetable pea genotypes

<i>Trait</i>	<i>GCV (%)</i>	<i>PCV (%)</i>	<i>Heritability</i>	<i>Genetic advance</i>
Days to 50% flowering (DTF)	22.13	22.66	95.3	44.52
Days to picking (DTP)	3.40	4.54	56.1	5.24
Total flower produced (TFP)	40.66	43.30	88.1	78.64
Branches per plant (BPP)	23.95	27.79	74.3	42.53
Pods per plant (PPP)	30.61	33.31	84.4	57.95
Pod length (PL)	10.54	11.44	84.8	20.01
Pod width (PW)	5.30	53.66	0.98	1.08
Plant height (PH)	23.36	25.02	87.1	44.93
Seeds per pod (SPP)	10.17	11.48	78.4	18.56
Ten pod weight (TPW)	14.47	15.54	86.7	27.76
Yield per plant (YPP)	21.30	24.89	73.2	37.55
Shelling percentage (SP)	18.45	19.52	89.51	17.23

GCV: Genotypic Coefficient of Variation (%) and **PCV:** Phenotypic Coefficient of Variation (%).

(GCV) and phenotypic coefficients of variation (PCV) (>20%) included days to 50% flowering, total flowers produced, branches per plant, pods per plant, plant height, and yield per plant. These traits showed a high degree of genetic variability, suggesting greater potential for improvement through selection. Traits such as pod length, seeds per pod, and ten pod weight displayed moderate GCV and PCV values (10–20%), indicating moderate variability, which also offers scope for genetic enhancement, though to a lesser extent compared to high variability traits (Table 2).

Heritability and genetic advance

Most traits in the present study exhibited high heritability (>60%), indicating a strong genetic influence on trait expression. Traits such as days to 50% flowering (95.3%), total flowers produced (88.1%), branches per plant (74.3%), pods per plant (84.4%), pod length (84.8%), plant height (87.1%), seeds per pod (78.4%), ten pod weight (86.7%), and yield per plant (73.2%) all fell under the high heritability group. Among these, most also showed high genetic advance (>20%), highlighting the predominance of additive gene action and suggesting that these traits can be effectively

improved through selection. Traits like days to picking, with moderate heritability (56.1%) and low genetic advance (5.24%), suggest a greater environmental influence and limited selection gain. Similarly, pod width showed very low heritability (0.98%) and low genetic advance (1.08%), implying that this trait is largely governed by environmental factors and may not respond well to selection. Similar findings were reported by Aziz *et al.* (2021), who observed high heritability coupled with substantial genetic gain for traits such as seeds per pod, branches per plant, and pod yield, suggesting the predominance of additive gene effects and highlighting their suitability for improvement through selection.

Correlation of traits

The traits pod per plant, total flowers per plant, and branches per plant showed significant and strong positive correlations with yield per plant, making them reliable selection indices for yield improvement (Table 3). Notably, total flowers per plant showed a highly significant positive correlation with branches per plant, pods per plant, and plant height at both genotypic and phenotypic levels. This indicates that plants

Table 3: Inter-trait relationship analysis based on genotypic (g) and phenotypic (p) correlations

Trait		DTP	TFP	BPP	PPP	PL	PW	PH	SPP	TPW	YPP	SP
DTF	G	0.379 **	0.559 **	0.285 *	0.414 **	-0.350 *	0.093 ^{NS}	0.416 **	-0.160 ^{NS}	-0.382 **	0.244 ^{NS}	-0.002 ^{NS}
	P	0.261 **	0.508 **	0.242 **	0.354 **	-0.321 **	-0.013 ^{NS}	0.378 **	-0.152 ^{NS}	-0.350 **	0.187 *	-0.007 ^{NS}
TFP	G		1.000 **	0.522 **	0.859 **	-0.443 **	-1.049 **	0.464 **	-0.328 *	-0.575 **	0.624 **	0.027 ^{NS}
	P		1.000 **	0.405 **	0.753 **	-0.398 **	-0.084 ^{NS}	0.406 **	-0.285 **	-0.484 **	0.509 **	0.025 ^{NS}
BPP	G			1.000 **	0.543 **	-0.212 ^{NS}	-1.130 **	0.362 **	-0.178 ^{NS}	-0.284 *	0.535 **	-0.043 ^{NS}
	P			1.000 **	0.450 **	-0.157 ^{NS}	-0.139 ^{NS}	0.291 **	-0.138 ^{NS}	-0.198 *	0.423 **	-0.033 ^{NS}
PPP	G				1.000 **	-0.382 **	-0.936 **	0.393 **	-0.403 **	-0.545 **	0.794 **	0.096 ^{NS}
	P				1.000 **	-0.317 **	-0.015 ^{NS}	0.332 **	-0.357 **	-0.463 **	0.790 **	0.078 ^{NS}
PL	G					1.000 **	0.359 *	-0.403 **	0.677 **	0.619 **	-0.080 ^{NS}	-0.135 ^{NS}
	P					1.000 **	0.034 ^{NS}	-0.354 **	0.556 **	0.523 **	-0.051 ^{NS}	-0.118 ^{NS}
PW	G						1.000 **	-0.867 **	0.530 **	0.730 **	-0.767 **	-0.363 **
	P						1.000 **	-0.008 ^{NS}	-0.029 ^{NS}	0.101 ^{NS}	0.034 ^{NS}	-0.067 ^{NS}
PH	G							1.000 **	-0.369 **	-0.529 **	0.206 ^{NS}	0.440 **
	P							1.000 **	-0.312 **	-0.465 **	0.143 ^{NS}	0.369 **
SPP	G								1.000 **	0.668 **	-0.051 ^{NS}	0.000 ^{NS}
	P								1.000 **	0.562 **	-0.068 ^{NS}	-0.023 ^{NS}
TPW	G									1.000 **	-0.035 ^{NS}	-0.229 ^{NS}
	P									1.000 **	0.013 ^{NS}	-0.201 *
YPP	G										1.000 **	-0.035 ^{NS}
	P										1.000 **	0.056 ^{NS}
DTP	G											0.023 ^{NS}
	P											0.043 ^{NS}

*: Significant at $p \leq 0.05$; **: Significant at $p \leq 0.01$; P: phenotypic correlation; G: genotypic correlation; DTF: days to 50% flowering; DTP: days to picking; TFP: total flower per plant; BPP: branches per plant; PPP: Pods per plant; PL: pod length (cm); PW: pod width (cm), PH: plant height (cm); Seeds per pod (SPP); TPW: Ten pod weight (g); YPP: pod yield per plant (g), and SP: shelling percentage.

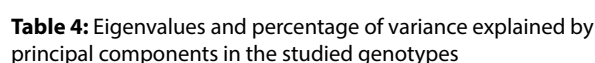


Table 5: Percentage contribution of different traits to principal components (PC1-PC12) in the studied genotypes

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
DTF	8.26	0.26	13.69	2.82	11.86	31.04	2.71	0.64	0.10	27.47	0.74	0.41
TFP	17.01	4.12	0.01	0.53	0.35	6.44	4.06	0.21	0.20	34.27	31.57	1.25
BPP	8.07	10.12	0.07	0.29	7.10	4.56	50.08	1.75	15.66	0.75	1.49	0.06
PPP	16.95	7.83	0.03	0.17	6.11	0.68	4.50	2.96	0.03	1.82	4.04	54.88
PL	9.85	13.25	0.01	4.21	0.44	0.47	0.93	64.46	0.17	1.80	4.17	0.24
PW	0.64	1.52	23.93	3.40	53.88	3.58	10.72	0.07	1.97	0.01	0.23	0.05
PH	9.98	3.05	4.27	13.83	0.40	3.77	18.92	0.74	37.86	3.47	3.34	0.38
SPP	8.20	15.02	0.35	11.30	1.73	16.15	0.23	4.78	8.60	13.46	19.18	1.00
TPW	12.74	10.55	2.79	1.87	0.32	1.30	0.03	20.25	20.50	0.62	19.37	9.65
YPP	7.28	25.86	1.92	2.50	3.59	9.36	3.54	0.98	5.30	1.43	7.43	30.82
DTP	0.12	5.07	40.10	6.43	13.17	16.56	1.12	2.40	0.07	12.69	1.03	1.25
SP	0.91	3.36	12.83	52.65	1.04	6.10	3.17	0.77	9.55	2.20	7.41	0.02

Where DTF: days to 50% flowering; DTP: days to picking; TFP: total flower per plant; BPP: branches per plant; PPP: Pods per plant; PL: pod length (cm); PW: pod width (cm), PH: plant height (cm); Seeds per pod (SPP); TPW: Ten pod weight (g); YPP: pod yield per plant (g), and SP: shelling percentage.

and plant height contributed more toward the lower-right quadrant, grouping genotypes such as BHU-02, BHU-26, and VRP-Sel-17. Outlier genotypes like VRPM-901-5 and BSW-74 indicated unique trait combinations. Collectively, the analysis highlights that yield- and pod-related traits were the key drivers of genetic divergence among the studied genotypes.

Conclusion

This study evaluated multi-flowering genotypes against single- and double-podded varieties, revealing significant genetic variability in agro-morphological and yield traits. Yield per plant ranged from 78.0 to 175.7 g. Traits including days to 50% flowering, total flowers, branches, pods per plant, plant height, and yield exhibited high PCV, GCV, heritability, and genetic advance, indicating strong genetic control. Pods per plant, total flowers, and branches showed strong positive correlations with yield, making them key selection indices. PCA highlighted yield- and pod-related traits as major contributors to divergence. These findings identify critical target traits and superior multi-flowering genotypes VRPM-901-5, BSW-136, BSW-2, VRP-343, and VRPE-52 for use in breeding programs aimed at enhancing pea productivity.

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सारांश

सब्जी मटर एक पोषण एवं आर्थिक दृष्टि से महत्वपूर्ण दलहनी फसल है, किंतु इसके खेती क्षेत्र में विस्तार होने के बावजूद उत्पादकता में अपेक्षित वृद्धि नहीं हो सकी है। इस अध्ययन में 50 मटर जीनोटाइपों तथा बहु-पुष्पी जीनोटाइपों का मूल्यांकन उनकी उपज क्षमता की तुलना व्यावसायिक रूप से उगाई जाने वाली एकल-फली एवं द्वि-फली किस्मों से किया गया। प्रति पौधा उपज 78.0 ग्राम (एकल-फली प्ररूप वीआरपीसेल-17) से लेकर 176.0 ग्राम (बहु-पुष्पी प्ररूप वीआरपीएम-901-5) तक दर्ज की गई। %50 पुष्पन तक के दिन, प्रति पौधा कुल पुष्पों की संख्या, प्रति पौधा शाखाओं की संख्या, प्रति पौधा फलियों की संख्या, पौधे की ऊँचाई तथा प्रति पौधा उपज जैसे लक्षणों में उच्च फीनोटाइपिक एवं जीनोटाइपिक परिवर्तन गुणांक, उच्च आनुवंशिकता तथा उच्च आनुवंशिक प्रगति प्राप्त हुई, जो इन लक्षणों पर मजबूत आनुवंशिक नियंत्रण तथा चयन द्वारा सुधार की पर्याप्त संभावना को दर्शाती है। विशेष रूप से, प्रति पौधा फलियों की संख्या, प्रति पौधा कुल पुष्पों की संख्या तथा प्रति पौधा शाखाओं की संख्या का प्रति पौधा उपज के साथ सशक्त धनात्मक सहसंबंध पाया गया, जिससे ये लक्षण चयन के विश्वसनीय सूचक सिद्ध हुए। प्रधान अवयव विश्लेषण (प्रिंसिपल कंपोनेंट एनालिसिस) से ज्ञात हुआ कि प्रथम तीन प्रधान अवयवों ने कुल आनुवंशिक परिवर्तनशीलता का %61.54 भाग स्पष्ट किया। प्रथम प्रधान अवयव (प्रथम प्रिंसिपल कंपोनेंट) का संबंध प्रति पौधा कुल पुष्पों की संख्या, प्रति पौधा फलियों की संख्या तथा दस फलियों के भार से था। द्वितीय प्रधान अवयव (द्वितीय प्रिंसिपल कंपोनेंट) का संबंध प्रति पौधा उपज, प्रति फली बीजों की संख्या तथा फली की लंबाई से था, जबकि तृतीय प्रधान अवयव (तृतीय प्रिंसिपल कंपोनेंट) का संबंध फली की चौड़ाई तथा तुड़ाई तक लगने वाले दिनों से था। समग्र रूप से, उपज एवं फलियों से संबंधित लक्षण आनुवंशिक विविधता के प्रमुख योगदानकर्ता सिद्ध हुए, जिन्होंने श्रेष्ठ जीनोटाइपों की प्रभावी पहचान एवं चयन को संभव बनाया। वर्तमान अध्ययन के निष्कर्ष मटर की उत्पादकता बढ़ाने हेतु प्रजनन कार्यक्रमों के लिए महत्वपूर्ण लक्ष्य लक्षणों की पहचान करते हैं तथा श्रेष्ठ बहु-पुष्पी जीनोटाइप—VRPM-901-5, BSW-136, BSW-2, VRP-343 एवं VRPE52—को भावी संकरण एवं सुधार कार्यक्रमों में उपयोग के लिए उपयुक्त अभिभावक सामग्री के रूप में सुझाते हैं।