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RESEARCH ARTICLE



Genetic variability, character association and multivariate analysis in garden pea (*Pisum sativum* L.) for quality and biochemical traits

Anchal Thakur¹, Yashpal Singh Bisht^{1*}, Shalini Singh² and Poonam Devi¹

Abstract

Seventeen garden pea genotypes were examined to check the magnitude of genetic variability, character association, principal component analysis and diversity. From the analysis, variation among the genotypes for all the characters was found to be highly significant. The estimates of PCV were found to be greater than the GCV for all the characters, demonstrating that the effect of environment is also a factor in the apparent variation in addition to genotypes. The highest GCV as well as PCV values have been observed in the case of total phenols followed by green pod yield/plant, total sugars, number of first fruiting nodes and shelling percentage. All the characters showed a high magnitude of heritability. Further, substantial heritability coupled with a high genetic advance in percent of mean was observed for total phenols, i.e., 94.90 and 80.57%, respectively. Based on genotypic and phenotypic correlation and path coefficient, number of pods/plants, shelling percentage, number of first fruiting node and 100-green seed weight are the most promising selection indices for yield improvement. The six PCs accounted for 96.42% (54.60, 21.92, 6.97, 6.00, 3.73 and 3.20) of the variation. PC-I was a combination of days to first flowering, days to 50% flowering, plant height, number of nodes per plant, number of first fruiting nodes, days to first picking, number of pods per plant, pod width, 100 gm seed weight and TSS. Therefore, for the successful breeding program to improve the yield of garden pea germplasm, these characteristics must be used in a direct selection of genotypes. **Keywords:** Correlation, Genetic advance, Path coefficient analysis, Pea, Variability.

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Introduction

Pea (*Pisum sativum* L.) 2n = 2x = 14 belongs to the Leguminosae family (Fabaceae) and is one of India's most important annual herbaceous legume crops due to its use as a fresh vegetable, canned, processed or dehydrated and dry seeds are consumed as the pulse. Peas are cultivated herbs with a branched tap root system and their seeds are nonendospermous with thick cotyledons. It is grown as mainly in the plains of North India as a winter vegetable and as a summer vegetable in the hills. Although the precise origin and progenitor of peas are unclear, the Mediterranean area of Southern Europe and Western Asia is considered as the centre of origin of peas (Matlob and Adaiy, 2002). Based on the genetic diversity, Vavilov identified the Near East, the Mediterranean, Abyssinia, and Central Asia as the likely centers of origin.

Due to its importance as an important vegetable crop for hilly regions, the unavailability of high-yielding variety, sufficient genetic variation and proper evaluation widen the gap between expected and actual production. For this reason, it is crucial to have enough genetic variety, which is also a necessary requirement for crop improvement programs in order to produce progenies with high yields (Tiwari and Lavanya, 2012). To find the source of a trait's

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genes among the germplasm that is accessible, genetic variability evaluation is required (Chakraborty and Haque, 2000). The more the heritable variance, the greater the potential for character modification by selection mechanisms (Sharma and Bora, 2013). The components of variability, like the phenotypic and genotypic coefficient of variation, heritability, and genetic advance, are important tools for judging heterogeneity in the population, which makes evaluation and selection for improvement easier. Also, heritable traits will be helpful for breeders because selection for traits with high heritability will be effective and will bring about improvement through selection. Correlation studies allow us to investigate the magnitude and direction of one character's association with another. Correlation analysis does not provide a cause-and-effect link; instead, it shows the pattern of association of component qualities with yield and the overall influence of a given trait on yield. However, correlation does not reveal the causeand-effect relationship in distinct characteristics, so the path coefficient approach is used to divide the effects into direct and indirect categories independently. By using path coefficient analysis, genotypic correlation may be divided into the direct and indirect effects of various characteristics on yield (Mahbub et al., 2015). The present experiment was, therefore, conducted to know the extent of variability, the nature and the magnitude of association among different traits with an overall goal of identifying the variety/line that is most suitable for growth.

Materials and Methods

The experimental material constituted of 17 pea genotypes namely Him Palam Meethi Phalli-1, Him Palam Meethi Phalli-2, Him Palam Matar-1, VL Sabji Matar-13, VL Sabji Matar-14, VL Sabji Matar-15, Pusa Pragati, Palam Triloki, PB-89, Arkel, Lincoln, AP-3, KSP-110, Nirali, Vasundra, Him Palam Matar-2 and Azad Pea-1 along with standard checks during Rabi, 2022-23 at the Experimental Research Farm Kakhali, Eternal University, Baru Sahib, Sirmaur, Himachal Pradesh. Three replications with a Randomised Block Design (RBD) were used to set up the experiment. In a well-prepared open field, each genotype was cultivated with a spacing of $30 \times$ 10 cm. To grow a healthy crop, all suggested horticultural practices and plant protection measures were followed. Five plants were chosen at random from each genotype in each replication to record the parameters viz. days to first flowering, days to 50% flowering, plant height, number of nodes per plant, number of first fruiting node, length of first fruiting node, internodal length, days to first picking, number of pods per plant, pod length, pod width, fresh weight of individual pod, number of seeds per pod, 100 seeds weight, shelling percentage, green pod yield per plant, moisture content, total soluble solids, total sugars and total phenols.

The ANOVA for all the characters was calculated as suggested by Panse and Sukhatme (1967). The method outlined by Burton and de Vane (1953) was used to compute the phenotypic and genotypic coefficient of variation. Heritability in the wide sense (h²) was calculated using Falconer's (1981) formula. Robinson et al. (1949) provided the method used to quantify genetic advance (GA). In addition, the genetic progress expressed as a percentage of the mean was calculated using the Johnson et al. (1955) approach. The phenotypic and genotypic Mahalanobis correlation coefficients were found by statistical analysis of the mean values (Al-Jibouri et al., 1958). In accordance with Dewey and Lu (1957), the correlation coefficients have been divided into measures of direct and indirect effects using route coefficient analysis.

Results and Discussion

Each of the nineteen variables in the garden pea genotypes showed a significant variance according to the ANOVA (Table 1), suggesting that there is variability among the genotypes, which is a fundamental need to bring about genetic advancement in a crop. The results are in harmony with the findings of Bahadur and Devi (2021); Singh et al. (2019); Barcchiya et al. (2018); Pandey et al. (2017) and Kumar et al. (2015). The data obtained from the mean performance study (Table 1) revealed highly significant differences, showing the existence of adequate variability for all the traits among the genotypes evaluated. The results revealed that the genotype VL Sabji Matar-15 was earliest for first flowering (49.00) and 50% flowering (49.67), whereas genotype Azad Pea-1 was late (95.00 & 104.00 respectively). With respect to plant height, PB-89 was recorded to be the shortest (74.80 cm) and Arkel was found to be the tallest (104.80 cm). The genotype Azad Pea-1 had a maximum number of nodes/plant (21.87), whereas the minimum number of nodes/plant was reported in genotype Pusa Pragati (13.00). Similarly, a minimum number of first fruiting nodes was observed in genotype VL Sabji Matar-13 (7.60) and a maximum in genotype Azad Pea-1 (14.13). The genotype Him Palam Matar-1 had a minimum internodal length (5.43 cm), whereas it was maximum in genotype Arkel (7.37 cm). Similarly, the genotype KSP-110 took a minimum of days to first pick (127.00), whereas the maximum days were taken by genotypes Him Palam Meethi Phalli-2 and Him Palam Matar-1 (152.33). The highest and the lowest number of pods/plants were produced by the genotypes VL Sabji Matar-15 (26.47) and Palam Triloki (9.07), respectively. The genotype VL Sabji Matar-13 was recorded with a maximum pod length (10.08 cm), whereas a minimum value was observed with genotype Azad Pea-1 (6.13 cm). Similarly, maximum pod width was observed with genotype Him Palam Meethi Phalli-1 (1.53 cm) while Nirali showed minimum pod width (1.14 cm). The maximum fresh weight of individual pod was found in genotype Him Palam Meethi

Table 1: Analysis of variance and component of genetic variation in pea

Characters	Range		11000	CCV(0)		h2/h)	CAM
Characters	Min.	Мах	wean	GCV (%)	PCV (%)	TF(D)	GAINI
Days to first flowering	49.00	95.00	65.84	19.68	20.03	96.50	39.83
Days to 50% flowering	49.67	104.00	74.33	19.83	20.20	96.40	40.10
Plant height (cm)	74.80	104.80	88.91	8.42	11.14	57.20	13.12
Number of node/plant	13.00	21.87	17.96	10.03	14.45	48.10	14.33
Number of first fruiting node	7.60	14.13	10.35	20.58	22.80	81.50	38.26
Internodal length (cm)	5.43	7.37	6.24	6.50	10.10	41.40	8.62
Days to first picking	127.0	152.33	136.88	5.23	6.47	65.40	8.71
Number of pod/plant	9.07	26.47	18.15	25.61	34.49	55.10	39.16
Pod length (cm)	6.13	10.08	8.77	10.17	13.16	59.80	16.20
Pod width (cm)	1.14	1.53	1.25	7.40	9.20	64.60	12.25
Fresh weight of individual pod (g)	3.86	8.52	6.54	15.51	18.46	70.60	26.86
Number of seeds/pod	5.10	8.00	6.50	9.16	17.27	28.10	10.01
100-seeds weight (g)	36.30	63.27	46.21	13.39	15.67	73.10	23.58
Shelling percentage (%)	33.43	73.77	46.73	20.19	20.81	94.10	40.34
Green pod yield/plant (g)	50.73	145.93	85.37	27.47	34.54	63.20	44.99
Moisture content (%)	70.88	84.20	78.07	3.60	4.93	53.40	5.42
Total soluble sugar (°brix)	14.07	16.53	15.46	3.73	5.78	41.80	4.97
Total sugar (%)	3.47	7.97	5.94	26.24	26.89	95.20	52.74
Total phenol (%)	0.17	0.78	0.52	40.14	41.20	94.90	80.57

Phalli-1 (8.52 g) and the minimum was recorded in check Azad Pea-1 (3.86 g). The highest number of seeds/pod was found in Him Palam Matar-1 (8.00), while Arkel had the least number of seeds/pod (5.10). Only one genotype Him Palam Meethi Phalli-1 (63.27 g) was found significant for higher 100 green seed weight and lower was reported in VL Sabji Matar-14 (36.30 g). The highest shelling (%) was recorded in Pusa Pragati (73.77%), whereas the lowest was found in Vasundhra (33.43%). In addition, the maximum green pod yield/plant was reported in genotype Pusa Pragati (145.93g), whereas the minimum was observed in genotype Palam Triloki (50.73 g). Moisture content was found to be maximum in Azad Pea-3 (84.20) and minimum in Him Palam Meethi Phalli-2 (70.88). The highest total soluble solids were found in check Him Palam Matar-2 (16.53 °B), whereas the lowest TSS was found in Azad Pea-1 (14.07 °B). The highest sugar content was found in check Him Palam Matar-2 (7.97) whereas VL Sabji Matar-13 (3.47) was found to be the lowest in sugar content. With respect to phenol content, the highest phenolic content was observed in Arkel (0.78), whereas the lowest was found in Him Palam Matar-1 (0.17).

It was found that for every character, the estimates of the phenotypic coefficient of variation (PCV) were greater than

the estimates of the genotypic coefficient of variation (GCV), suggesting that in addition to genes, the environment also plays a role in apparent variation. The highest phenotypic and genotypic coefficients of variation were found for total phenols (41.20 & 40.14 respectively). A similar result was also reported by Lal et al. (2018); Gudadinni et al. (2017); Kumar et al. (2015). Moderate PCV along with GCV was recorded for days to first flowering, days to 50% flowering, and a number of nodes per plant. The phenotypic and genotypic coefficients of variations were lower for plant height. Low GCV and PCV for these traits indicated that the genotypes taken for the present study were similar for these traits.

In the present study, heritability ranged from 28.10 (number of seeds/pod) to 96.50% (days to first flowering). High heritability estimates (> 60%) were observed for days to first flowering, days to 50% flowering, total sugars, total phenols, shelling percentage, number of first fruiting nodes, 100-green seed weight, fresh weight of individual pod, days to first picking, pod width and green pod yield/plant. Heritability was moderate for pod length, plant height, number of pods/plant and moisture content, whereas the number of nodes/plant, total soluble solids and number of seeds/pod exhibited low heritability estimates. Similar

			sof Ph		du	Nffn	=	Dfp	ddN	Ы	Pd	Мр	Nsp	100sw	Sp	Мс	Tss	Ts	Τp
	0	0.98** 1.0	00																
D50f	P	.98** 1.(00																
	ט	0.09	J. 1. (00															
Рh	Р	0.07 0.0).1 70	00															
	ט	0.71** 0.6	58** 0.6	59** 1	00.														
Nnp	P).48** 0.4	19** 0. <u>5</u>	59** 1	00.														
	ט).67** 0.4	53** 0.2	25 0	.70**	1.00													
Nffn	P).57** 0.5	55** 0.5	30* 0	.55**	1.00													
	י ט	0.79** -0.	·'0 **08'	43** -(0.32*	-0.48**	1.00												
=	ح	0.51** -0.	.52** 0.1	16 L	0.19	-0.34*	1.00												
	ט).58** 0.6	20** 0.4	48** 0	.64**	0.92**	-0.59**	1.00											
Dfp	P).49** 0.5	51** 0.5	31* 0	1.46**	0.66**	-0.35**	1.00											
	ט	0.2	27* 0.5	51** 0	.51**	0.16	-0.13	0.29*	1.00										
Npp	P).26 0.1	17 0.5	35* 0	.18	0.16	-0.05	0.08	1.00										
	ט	0.73** -0.	.72** -0.)- **69	0.95**	-0.75**	0.29*	-0.58**	-0.03	1.00									
Ы	- 4	0.55** -0.	.56** -0.	23 -(0.39**	-0.56**	0.18	-0.36	-0.08	1.00									
	ט).06 0.1	17 0.0	J5 -(0.06	0.13	-0.12	0.32*	-0.40**	-0.30*	1.00								
Pd	P	0.0	12 0.1	10	0.02	0.11	0.11	0.15	-0.10	-0.11	1.00								
	ט	0.36** -0	.27 -0.	.74** -(0.74**	-0.30*	0.03	-0.23	-0.63**	0.31*	0.73**	1.00							
Мp	- 4	0.29* -0.	.23 -0.	36"* -(0.42**	-0.21	-0.08	-0.17	-0.44**	0.42**	0.58**	1.00							
	ט	0.26 -0.	.24 -0.	49** -(0.03	0.31*	-0.57**	0.40**	-0.32*	0.35**	-0.13	0.43**	1.00						
Nsp	ح	0.13 -0.	.12 -0.	25 -(0.17	0.12	-0.25	0.12	-0.05	0.13	0.04	0.31*	1.00						
	5	0.159** 0.1	51** -0.	0 60.	.15	0.32*	-0.25	0.24	0.05	-0.50**	0.74**	0.37**	-0.33*	1.00					
100sw	P	0.52** 0.5	52** -0.	01 0	111	0.24	-0.14	0.26	-0.05	-0.24	0.57**	0.38*	-0.23	1.00					
	ט	0.39** -0.	42** -0.	11	0.49**	-0.13	0.10	-0.20	0.08	0.30*	-0.04	0.09	0.15	-0.44**	1.00				
Sp	ط	·0.37** -0.	40** -0.	04 -(J.28 *	-0.07	0.06	-0.14	0.04	0.23	-0.03	0.08	0.05	-0.31*	1.00				
	ט	0.49** -0.	.55** 0.(۲ - ۱	0.19	-0.55**	0.55**	-0.90**	-0.18	0.04	-0.43**	-0.24	-0.79**	-0.38**	0.26	1.00			
Мс	۔ م	0.20 -0.	.26 0.1	16	0.15	-0.14	0.10	-0.27	0.51**	0.11	0.04	0.03	-0.11	-0.02	0.38**	1.00			
	5	0.14 0.2	24 -0.	.27* 0	1.16	-0.03	-0.20	0.14	-0.13	0.02	0.34*	0.27	0.57**	0.10	-0.61**	-0.58**	1.00		
Tss	ط	0.35° -0.	.41** -0.	01 -(0.15	-0.40**	0.44**	-0.52**	-0.15	0.04	-0.15	-0.08	-0.04	-0.30*	0.19	60.0	1.00		
	ق	·0.16 -0.	.12 0.1	16 0	107	0.00	0.12	-0.14	-0.26	-0.26	0.32*	0.22	0.08	0.04	-0.05	-0.01	0.67**	1.00	
Ts	Р	0.	12 0.0	34 0	.02	-0.01	-0.12	0.11	-0.07	0.06	0.11	0.17	0.11	0.21	-0.31*	-0.03	-0.37**	1.00	
	ق	0.23 -0.	.25 -0.	- 44**	0.66**	-0.48**	0.52**	-0.64**	-0.22	0.22	-0.10	0.21	-0.28*	0.12	-0.19	0.36**	0.30*	0.12	1.00
d	ط	0.15 -0.	.11 0.	12 0	0.06	0.01	0.07	-0.07	-0.16	-0.17	0.27*	0.19	0.06	0.07	-0.04	0.35**	-0.03	0.40**	1.00
	י ט	0.23 -0.	.31* 0.(1 80	0.40**	-0.31*	0.29*	-0.42**	0.44**	0.16	-0.09	-0.04	-0.30*	-0.10	0.45**	0.22	-0.29	0.40	0.14
Gpyp	٩	0.06 -0.	r.0 0.	47** 0	.33*	-0.03	0.15	-0.06	0.43**	0.07	0.13	-0.10	-0.13	-0.09	0.37**	0.38**	0.10	-0.17	0.09
** Note: DF DFP- Days t	F- Days t o first pi	to first flowerir cking, NPP- Nu	ום, D50F- Da umber of poc	lys to 50% f ds per plant	lowering, F t, PL- Pod Ie	יH- Plant He פחמלה (cm),	eight (cm), N PD- Pod wic	NP- Number Ith (cm), WP-	of nodes p Fresh weig	er plant, NFI iht of individ	^c N- Number lual pod (g),	of first fruiti NSP- Numbe	ng node, LFF er of seeds p	⁻ N- Length o er pod, 100S	f first fruitiní ∛W- 100-gre€	g node (cm), en seed weig	lL- Internod ht (g), SP- Sł	al Length (nelling per	(cm), centage
(%),MC- Ma	isture cc	intent (%), TSS	- Total solub	do colide (°h	viv) TC. To	10 24 COLO 1-1	LITTE OF VI	100								•	5	5	•

Table 3:	Estima	ites of dire	ect and in	direct effec	ct of geno	typic and p	henotypic	correlation	n coefficier	nts betwee	en differe	nt traits ir	n garden p	ea					
Traits		DFFF	D50F	Ηd	NNP	NFFN	Π	DFP	NPP	PL	PD	WP	NSP	100SW	SP	MC	TSS	TS	TP
DFFF	ט	0.22	0.21	0.02	0.15	0.14	-0.17	0.13	0.09	-0.16	0.01	-0.08	-0.06	0.13	-0.08	-0.11	0.03	-0.03	-0.05
	٩	-0.13	-0.13	-0.01	-0.06	-0.07	0.07	-0.06	-0.03	0.07	-0.01	0.04	0.02	-0.07	0.05	0.05	-0.01	0.02	0.03
D50F	ט	-0.43	-0.44	-0.03	-0.29	-0.27	0.35	-0.26	-0.12	0.32	-0.07	0.12	0.10	-0.27	0.18	0.24	-0.10	0.05	0.11
	٩	-0.26	-0.26	-0.02	-0.13	-0.15	0.14	-0.13	-0.04	0.15	-0.03	0.06	0.03	-0.14	0.11	0.11	-0.03	0.03	0.06
Hd	ט	0.14	0.09	1.47	1.02	0.37	0.64	0.70	0.75	-1.02	0.08	-1.09	-0.72	-0.14	-0.17	0.11	-0.40	0.24	-0.64
	٩	0.003	0.003	0.05	0.03	0.01	0.01	0.01	0.02	-0.01	0.01	-0.02	-0.01	0.00	-0.002	-0.001	0.002	0.01	-0.02
NNP	ט	1.21	1.15	1.18	1.70	1.19	-0.55	1.09	0.87	-1.61	-0.10	-1.26	-0.05	0.25	-0.83	-0.32	0.28	0.12	-1.11
	٩	-0.01	-0.01	-0.01	-0.02	-0.01	0.004	-0.01	-0.004	0.01	0.000	0.01	0.004	-0.002	0.01	0.003	0.000	-0.001	0.01
NFFN	ט	2.61	2.46	0.98	2.75	3.92	-1.90	3.62	0.62	-2.96	0.50	-1.19	1.23	1.27	-0.50	-2.16	-0.13	0.02	-1.88
	٩	0.09	0.09	0.05	0.09	0.16	-0.05	0.10	0.03	-0.09	0.02	-0.03	0.02	0.04	-0.01	-0.06	-0.001	0.001	-0.07
Ч	ט	-1.07	-1.07	0.59	-0.44	-0.65	1.35	-0.80	-0.17	0.40	-0.17	0.04	-0.77	-0.33	0.13	0.74	-0.27	0.16	0.70
	٩	0.08	0.09	-0.03	0.03	0.06	-0.17	0.06	0.01	-0.03	-0.02	0.01	0.04	0.02	-0.01	-0.07	0.02	-0.01	-0.06
DFP	ט	-0.45	-0.47	-0.37	-0.50	-0.72	0.46	-0.78	-0.23	0.45	-0.25	0.18	-0.32	-0.19	0.15	0.70	-0.11	0.11	0.50
	٩	0.02	0.02	0.01	0.02	0.03	-0.02	0.04	0.004	-0.02	0.01	-0.01	0.01	0.01	-0.01	-0.02	0.01	-0.003	-0.02
NPP	U	0.47	0.32	0.59	09.0	0.18	-0.15	0.34	1.17	-0.03	-0.46	-0.73	-0.37	0.05	0.09	-0.21	-0.15	-0.30	-0.26
	٩	0.19	0.12	0.24	0.13	0.11	-0.04	0.06	0.70	-0.05	-0.07	-0.31	-0.04	-0.04	0.03	-0.11	-0.05	-0.11	-0.13
PL	ט	0.72	0.71	0.69	0.94	0.75	-0.29	0.58	0.03	-0.99	0.29	-0.31	-0.35	0.49	-0.30	-0.04	-0.02	0.26	-0.22
	٩	-0.06	-0.06	-0.03	-0.04	-0.06	0.02	-0.04	-0.01	0.11	-0.01	0.05	0.02	-0.03	0.03	0.01	0.01	-0.02	0.02
PD	U	0.13	0.40	0.12	-0.14	0:30	-0.29	0.76	-0.93	-0.70	2.35	1.71	-0.30	1.75	-0.11	-1.02	0.80	0.76	-0.23
	٩	-0.01	-0.03	-0.03	0.01	-0.03	-0.03	-0.08	0.03	0.03	-0.25	-0.14	-0.01	-0.14	0.01	0.04	-0.03	-0.07	0.03
WP	ט	0.05	0.03	0.10	0.10	0.04	00.0	0.03	0.08	-0.04	-0.09	-0.13	-0.06	-0.05	-0.01	0.03	-0.03	-0.03	-0.03
	٩	-0.02	-0.01	-0.02	-0.02	-0.01	-0.004	-0.01	-0.02	0.02	0.03	0.05	0.02	0.02	0.004	-0.004	0.01	0.01	0.01
NSP	U	-0.27	-0.25	-0.51	-0.03	0.33	-0.59	0.42	-0.33	0.37	-0.13	0.45	1.04	-0.35	0.15	-0.82	0.59	0.09	-0.29
	۵.	0.02	0.02	0.03	0.02	-0.02	0.03	-0.02	0.01	-0.02	-0.01	-0.04	-0.13	0.03	-0.01	0.01	-0.01	-0.01	0.02
100SW	U	0.87	0.90	-0.14	0.22	0.48	-0.36	0.35	0.07	-0.74	1.09	0.55	-0.49	1.48	-0.65	-0.57	0.15	0.06	0.18
	٩	0.13	0.13	-0.002	0.03	0.06	-0.03	0.06	-0.01	-0.06	0.14	0.10	-0.06	0.24	-0.08	-0.07	0.05	0.02	0.03
SP	U	-0.98	-1.06	-0.29	-1.23	-0.32	0.24	-0.50	0.20	0.77	-0.11	0.23	0.37	-1.12	2.52	0.65	-1.54	-0.14	-0.48
	٩	-0.09	-0.10	-0.01	-0.07	-0.02	0.01	-0.03	0.01	0.06	-0.01	0.02	0.01	-0.08	0.24	0.05	-0.08	-0.01	-0.04
MC	ט	-0.04	-0.04	0.01	-0.01	-0.04	0.04	-0.07	-0.01	0.00	-0.03	-0.02	-0.06	-0.03	0.02	0.08	-0.04	0.00	0.03
	٩	-0.01	-0.02	0.00	-0.01	-0.02	0.02	-0.02	-0.01	0.002	-0.01	-0.003	-0.002	-0.01	0.01	0.04	-0.01	-0.001	0.01
TSS	U	0.19	0.31	-0.36	0.21	-0.04	-0.26	0.18	-0.17	0.02	0.45	0.35	0.75	0.13	-0.80	-0.76	1.31	0.87	0.39
	٩	-0.01	-0.02	-0.01	-0.003	0.001	0.02	-0.02	0.01	-0.01	-0.01	-0.02	-0.01	-0.03	0.04	0.05	-0.13	-0.05	-0.03
TS	U	0.43	0.33	-0.46	-0.20	-0.01	-0.33	0.38	0.71	0.73	-0.89	-0.61	-0.23	-0.12	0.15	0.03	-1.85	-2.77	-0.33
	٩	-0.07	-0.05	0.06	0.03	0.003	0.03	-0.03	-0.07	-0.08	0.12	0.09	0.03	0.03	-0.02	-0.02	0.18	0.45	0.05
Ъ	ט	-0.49	-0.52	-0.92	-1.39	-1.01	1.10	-1.36	-0.47	0.46	-0.21	0.44	-0.59	0.25	-0.40	0.77	0.62	0.25	2.11
	۵.	-0.03	-0.03	-0.04	-0.05	-0.05	0.04	-0.06	-0.02	0.02	-0.01	0.02	-0.02	0.01	-0.02	0.04	0.03	0.01	0.12
GРҮР	U	-0.23	-0.31	0.08	-0.40	-0.31	0.29	-0.42	0.44	0.16	-0.09	-0.04	-0.30	-0.10	0.45	0.22	-0.29	0.40	0.14
	٩	-0.20	-0.26	0.16	-0.15	-0.14	0.10	-0.27	0.51	0.11	0.04	0.03	-0.12	-0.02	0.39	0.10	-0.03	0.35	0.11
Partial	ט	-0.05	0.14	0.12	-0.68	-1.19	0.39	0.33	0.51	-0.16	-0.20	0.01	-0.31	-0.15	1.13	0.02	-0.38	-1.12	0.29
ž	٩	0.03	0.07	0.01	0.003	-0.02	-0.02	-0.01	0.36	0.01	-0.01	0.002	0.02	-0.01	0.01	0.004	0.004	0.16	0.01
**Note: DF DFP- Days ((%).MC- Mc	F-Days to first p visture c	to first flow icking, NPP. ontent (%),	/ering, D50F - Number of TSS- Total so	- Days to 50% ⁶ pods per plá Juble solids	% flowering, ant, PL- Pod (°brix). TS- Tc	PH- Plant Hei length (cm), F otal sugars (%	ght (cm), NN PD- Pod widtl), TP- Total pl	P- Number of (cm), WP- Fi nenols (%), G	[:] nodes per p esh weight o PYP- Green p	olant, NFFN- of individual ood vield per	Number of pod (g), NS plant (g)	first fruiting P- Number	J node, LFFN of seeds pe	- Length of i pod, 100SV	īrst fruiting r /- 100-green	node (cm), seed weig	lL- Internc ht (g), SP-	dal Length Shelling pe	(cm), rcentage
							· · · · · · · · · · · · · · · · · · ·				() · · · · · · ·								

Table 4: Principal component analysis (PCA) of 17 pea genotypes based on different traits

Parameter	PC1	PC2	PC3	PC4	PC5	PC6
Eigen values	1.76	0.70	0.22	0.19	0.11	0.10
% of variance	54.60	21.92	6.97	6.00	3.73	3.20
Cumulative %	54.60	76.53	83.50	89.51	93.24	96.45
Characters	Eigen vector					
Days to first flowering	0.34	0.04	0.13	0.03	0.25	0.20
Days to 50% flowering	0.34	0.08	0.12	-0.01	0.22	0.18
Plant height (cm)	0.14	-0.33	0.11	-0.13	-0.32	-0.13
Number of node/plant	0.31	-0.18	0.08	0.00	-0.24	0.02
Number of first fruiting node	0.33	0.00	-0.11	0.05	-0.24	-0.17
Internodal length (cm)	-0.23	-0.15	0.26	-0.10	-0.20	-0.27
Days to first picking	0.33	0.03	-0.22	0.01	-0.11	-0.14
Number of pods/plant	0.10	-0.30	-0.02	0.08	0.16	0.39
Pod length (cm)	-0.28	0.04	-0.24	0.09	0.09	0.16
Pod width (cm)	0.05	0.16	-0.06	-0.55	0.06	-0.22
Fresh weight of individual pod (g)	-0.15	0.32	-0.20	-0.35	0.13	-0.11
Number of seeds/pod	0.00	0.20	-0.47	0.16	-0.23	0.03
100-green seed weight (g)	0.16	0.19	0.20	-0.36	0.33	-0.02
Shelling percentage	-0.15	-0.19	-0.35	-0.01	0.21	-0.14
Green pod yield/plant (g)	-0.15	-0.21	-0.19	-0.19	0.12	0.34
Moisture content (%)	-0.21	-0.19	0.29	0.07	0.02	-0.22
Total soluble solids (°B)	0.04	0.26	0.02	-0.12	-0.40	0.42
Total sugars (%)	-0.04	0.06	0.06	-0.34	-0.45	0.22
Total phenols (%)	-0.19	0.19	0.40	0.05	0.04	0.10

findings were reported by Bahadur and Devi (2021); Gudadinni et al. (2017), Devi et al. (2018), Singh et al. (2019) and Devi et al. (2018).

The highest value of genetic advance was shown by green pod yield/plant, while pod width exhibited the lowest value. The high expected genetic advance expressed as a percentage of the mean (>30%) was observed for total phenols followed by total sugars, green pod yield/plant, shelling percentage, days to 50% flowering, days to first flowering, number of pods/plant and number of the first fruiting node. Genetic advance expressed as a percentage of mean was found to moderate for total soluble solids, moisture content, internodal length and days to first picking. High heritability and GCV, along with high genetic advance as a percentage of the mean, were found for the green pod yield/plant (g) and number of first fruiting nodes. These characteristics could be further enhanced through individual plant selection.

Character correlations were made at both genotypic and phenotypic levels, illustrated in Table 2. Character expression appears to be greatly influenced by genetic variation, as indicated by the GCV, which was often greater than the corresponding PCV. The correlation studies revealed that green pod yield/plant showed significant and positive correlation with number of pods/plant and shelling percentage at genotypic as well as phenotypic levels whereas, internodal length, only at a genotypic level and plant height and number of nodes/plant at phenotypic level only. These characters may be considered as selection criteria for higher yield since these were mutually and directly associated with green pod yield/plant. The number of first fruiting nodes showed a significant and positive correlation with days to first flowering, days to 50% flowering, and number of nodes/plant at both the levels and with plant height at the phenotypic level only. Days to first picking also showed a significant and positive correlation with days to first flowering, days to 50% flowering, plant height, number of nodes/plant and number of first fruiting nodes at both levels. The number of pods/plants showed a significant and positive correlation with plant height at both the levels and days to first flowering, days to 50% flowering, number of nodes/plant, and days to first picking at the genotypic level



Figure 1: Biplot of pea based on first two components

only. The number of seeds/pods showed a significant and positive correlation with the fresh weight of individual pods at both the levels and number of first fruiting nodes, days to first picking and pod length at the genotypic level only. 100seed weight showed a significant and positive correlation with days to first flowering, days to 50% flowering, pod width and fresh weight of individual pods at both levels. The results were in close harmony with the findings of Meena et al. (2017); Katoch et al. (2016); Tofiq et al. (2015); and Kumar et al. (2015). Therefore, understanding the relationships between features and their intercorrelations may be regarded as the most precise indices for effective pea improvement.

Path coefficient analysis was used to further investigate the genotypic and phenotypic correlations since correlation coefficients are a measure of an easy relationship between variables. Green pod yield/plant served as the dependent variable and all other characteristics served as independent variables in the genotypic and phenotypic path coefficient analyses (Table 3). In this investigation, path coefficient analysis indicated that green pod yield/plant revealed a very high direct positive effect on a number of first fruiting nodes followed by shelling percentage, 100-green seed weight and number of pods/plant, both at genotypic and phenotypic levels. These traits were also correlated positively with green pod yield/plant. In order to improve the green pod yield in garden peas, direct selection for these traits will be successful. The results may be used to develop an appropriate selection criterion for a garden pea breeding program for genetic improvement to develop genotypes with high yields. Similar results were also reported by Bahadur and Devi (2021), Singh et al. (2019); Lal et al. (2018).

Based on the analysis, the first six principal components (PCs) accounted for 96.42% of the total variability of 17 peas germplasm. The proportion of variance for the first six components was 54.60, 21.92, 6.97, 6.00, 3.73 and 3.20, respectively. Only the first component having an eigenvalue greater than 1 had great variation. The eigenvalue was less than 1 for the rest of the components and counted less towards total variability. PC-I showed positive association towards days to first flowering, days to 50% flowering, plant height, number of nodes per plant, number of first fruiting nodes, days to first picking, number of pods per plant,

pod width, 100 gm seed weight and TSS. Whereas, PC-II positively associated with days to first flowering, days to 50% flowering, number of node/plant, days to first picking, pod length, pod width, fresh weight of individual pod, number of seeds/pod, 100-seed weight and TSS. Similar findings were reported by Hanci and Cebeci (2018). For the first two principal components, the explained variation among all the pea genotypes was graphically represented in a scattered plot (Figure 1). The study highlights the eigenvector's significant connection between factors with similar signs and their combined impact on improving the qualities under consideration. Analyzing the first and second dimensions shows that almost all attributes show discrimination and add a substantial amount to the total variability. A notable number of features stand out because of their exceptionally high factor loadings, including days to first flowering, days to 50% flowering from the first quadrant, pod weight, pod length from the second guadrant, moisture content, internodal length from the third guadrant, plant height, and number of nodes/plant from the fourth quadrant. This emphasizes that a significant amount of the differences observed in peas can be attributed to these particular characteristics. Selection efforts should thus be directed particularly at these emphasized qualities in order to enhance peas genetically (Yadav et al., 2024).

Conclusion

All of the features under research showed considerable differences from one another, indicating great diversity among the genotypes of garden peas in the current analysis. The most significant yield-contributing factors were found to be green pod yield per plant, number of pods per plant, number of first fruiting nodes, and shelling percentage. These factors should be included in the selection criteria for future garden pea breeding programs. These findings were based on the values of GCV and PCV, heritability, genetic advance as a percentage of mean, character association, and path analysis. Of these, the number of pods/plant and the shelling% were positively and substantially connected with the green pod yield/plant. It also showed a direct influence on the number of the first fruiting node, followed by the shelling percentage, the 100-green seed weight, and

the number of pods/plants. 96.42% of the variance was explained by the first six principal components (PCs).

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सारांश

षोध के तहत सभी विषेशताओं में एक-दूसरे से काफी अंतर दिखाई दिया, जो वर्तमान विष्लेशण में मटर के जीनोटाइप के बीच महान विविधता का संकेत देता है। सबसे महत्वपूर्ण उपज-योगदान कारक प्रति पौधा हरी फली की उपज, प्रति पौधा फली की संख्या, पहले फलने वाले नोड की संख्या और छिलका प्रतिषत पाया गया। इन कारकों को भविश्य के मटर प्रजनन कार्यक्रमों के लिए चयन मानदंडों में षामिल किया जाना चाहिए। ये निश्कर्श जीसीवी और पीसीवी के मूल्यों, आनुवंषिकता, माध्य के प्रतिषत के रूप में आनुवंषिक उन्नति, चरिल संघ और पथ विष्लेशण पर आधारित थे। इनमें से, प्रति फलियों पौधों की संख्या और छिलकाः सकारात्मक रूप से और पर्याप्त रूप से प्रति पौधा हरी फली की उपज से जुड़े हुए थे। इसने पहले फलने वाले नोड की संख्या, उसके बाद छिलके के प्रतिषत, 100-हरे बीज के वजन और प्रति पौधा फली की संख्या पर भी सीधा प्रभाव दिखाया। 96.42: विचरण को पहले 6 प्रमुख घटकों (पीसी) द्वारा समझाया गया था।