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# Genetic Variability Parameters for Quantitative Traits in Farmers' Pea (*Pisum sativum* var. *arvense* L.) Varieties

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ABSTRACT: The experiment was conducted to assess the genetic variability parameters for eleven quantitative traits in 22 farmers' Pea varieties during *rabi* 2019-2020 in randomized block design (RBD) with 3 replications. The ANOVA for all the characters showed 1% level of significance. On an average phenotypic and genotypic coefficient of variation were high for plant height, number of pods per plant, number of effective nodes, number of seeds per plant, harvest index, 100-seed weight and yield per plant. This indicated the presence of sufficient variability among the characters. High heritability coupled with high genetic advance as percent of mean, was observed in characters *viz.*, yield/plant, 100-seed weight, number of pods/plant, harvest index, plant height, number of effective nodes, number of seeds/pod and width of pods, which indicated the preponderance of additive gene action. The yield per plant had significant and positive direct association with days to maturity, width of pods and harvest index. Therefore, emphasis should be made on these traits in selection program to evolve high yielding genotypes in farmers' varieties of pea.

Keywords: Correlation, Farmers' varieties, Field-pea (*Pisum sativum* var. *arvense* L.), Genetic variability, Pathcoefficient analysis.

### INTRODUCTION

Field-pea (*Pisum sativum* var. *arvense* L.) with a chromosome number of 2n=2x=14; is a self-pollinated, *rabi* crop that belongs to the family *Fabaceae* (*Leguminaceae*) and sub-family *Papilionaceae*. In 2019, production of pea in India, went up to 8.1 LT and a productivity to 13,378 Kg/ha (FAO Stat., 2019). Uttar Pradesh is one of the leading states in the production of Pea, which comprises 46.37% of the total production of pea in India, followed by Madhya Pradesh and Bihar (Annual Report, 2017-18). But still, the major share of import belongs to pea (39%). In the year 2019-20, 1.5 LMT of pea was imported with a minimum import price of Rs. 200/kg.

The population data of India suggested that there would be 1613.30 million individuals by 2030 (Jadhav *et al.*, 2018). This indicates that in coming decades, India will be the most populous country in the world. Unfortunately, the growth in production and productivity of pulses has lagged behind the population growth rate. Moreover, the elite genitors used to compose new populations for selection are closely related, contributing to the yield plateau. To overcome this limit, it is necessary to broaden the genetic basis of the cultivars using diverse germplasm such as wild relatives or traditional varieties.

The latter being more practical because they are more easily crossed with elite germplasm to accelerate the recovery of modern plant types in the breeding lines. Also, the evaluation of the genetic variability of accessions of landraces can provide the basic information necessary to help gene-banks multiply and properly conserve these genetic resources (Brondani et al., 2006). This genetic variability is very important for the sustainability of small farmers, as despite the low vield capacity, these varieties present high yield stability. The genetic heterogeneity of farmers' varieties contributes to production system resilience in response to biotic and abiotic stresses lowering the risk of overall crop failure (Ceccarelli, 2012). Farmers' varieties sometimes outperform formal sector improved varieties, especially when deployed in difficult environments and in systems where farmers cannot afford inputs that are recommended to boost the performance of formal sector improved materials (Burdon and Jeirsoz, 1990). However, traditional knowledge and variability are being lost at an alarming rate. Very few information is available on the landraces of Pea. Therefore, the information about genetic variability parameters for quantitative traits will helps us to exploit the farmers' varieties for the development of a superior variety.

#### MATERIALS AND METHODS

The experimental materials for the present study consists of twenty-two farmers' varieties of pea,

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collected from different villages of Uttar Pradesh and were obtained from Directorate of Research, Sam Higginbottom University of Agriculture, Technology and Sciences (SHUATS), Prayagraj. They were grown under Randomized Block Design (RBD) with three replications during *Rabi* 2019-2020. The experimental field was divided into 3 blocks of equal size and 5 lines containing single genotype. Eleven quantitative traits were recorded during the study on five randomly selected plants in each entry of each replication for all the characters except days to flowering, days to maturity which were recorded on plot basis. Further, the data were subjected to following statistical analysis.

- 1. Analysis of Variance (Fisher, 1918)
- 2. Variability parameters (Burton, 1952);
- 3. Heritability (Burton and Devane, 1953);

4. Genetic advance (Lush, 1940 and Johnson et al., 1955).

5. Correlation coefficient Analysis (Al-Jibouri et al., 1958).

6. Path coefficient Analysis (Dewey and Lu, 1959) In the present study, GCV and PCV was classified according to Sivasubrahmanian and Menon (1973) classification, wherein if coefficient of variation is less than 10%, it is considered low, if it is between 10 and 20%, it is moderate and at more than 20% it is high.

The study of heritability and GAM was done accordance to the Johnson *et al.*, (1955) classification; as low if (<30%), medium for (30-60%) and high for (>60%).

## **RESULTS AND DISCUSSION**

**Genetic variability.** The Analysis of Variance revealed that the mean sum of squares due to genotypes showed high significant differences at 1% level of significance (as manifested in Table 1). Hence, there is an ample of scope for the selection of promising lines from the present gene pool for yield and its components in farmers' varieties of field pea.

			Mean Sum of Squares	
Sr. No.	Parameters	Replications	Treatments	Error
		( <b>df=2</b> )	( <b>df</b> = 21)	(df=42)
1.	Days to 50% flowering	4.11	129.19**	2.03
2.	Days to maturity	0.42	31.33**	3.41
3.	Plant height	8.36	8485.00**	4.76
4.	Number of pods per plant	0.79	65.07**	0.61
5.	Length of pods	0.18	1.87**	0.36
6.	Width of pods	0.01	0.07**	0.007
7.	Number of effective nodes	0.57	18.11**	1.04
8.	Number of seeds per pod	0.03	2.98**	0.12
9.	Harvest index	0.55	321.31**	1.16
10.	100 - seed weight	0.08	70.45**	0.15
11.	Yield per plant	0.006	48.78**	0.08

 Table 1: Analysis of Variance for eleven quantitative parameters in farmers' Pea varieties.

\*\* Significant at 1% level \* Significant at 5% level

The mean value for yield per plant ranged from 1.53 (PMRA- 502) to 17.42 g (PMKK-232) with grand mean value of 5.17 g. On the basis of *per se* performance genotypes PMKK-232 (17.42 g) followed by PKKK-227 (13.86 g), PSAK-307 (11.16 g), PRAV-230 (7.73 g) and PLCM-225 (5.89 g) were the best performers, as depicted in Table 2.

From Table 3, it was manifested that although PCV values were higher than GCV for all the traits under study indicating the influence of environment on studied characters, but their difference is reasonably small, suggesting that these characters are highly controlled by genetic factor than the environmental cause. Singh et al. (2019) reported the similar results in pea. On an average PCV and GCV were high for plant height, number of pods per plant, number of effective nodes, number of seeds per plant, harvest index, 100seed weight and yield per plant. While moderate values of PCV and GCV were found in pod length and pod width. High to moderate values of GCV and PCV suggest that there was sufficient variability present among the characters, which offer the scope of genetic improvement in farmers' varieties of pea through effective selection. The result further revealed that the selection in pea could be made on the basis of phenotypic performance, offering scope for crop improvement. Also, it may be feasible to determine the amount of heritable variation and the relative degree to which a character is transmitted from parent to offspring, by estimate of heritability. The results are in conformity with the findings of Meena *et al.* (2017); Kumar *et al.* (2019); Singh *et al.*, (2019); Yimam *et al.* (2021).

Heritability and Genetic advance as percent of mean (GAM). The estimates of heritability were high for most of the characters, ranged from 73.20 % for days to maturity to 99.83 % for plant height, as manifested in Table 3. Moderate heritability was shown by length of pods (58.04%) (Meena *et al.*, 2017), indicating considerable potential for the development of high yielding varieties through desirable selection in succeeding generations. Since, the estimates of broad sense heritability include both additive and non-additive gene effects. Therefore, a character exhibiting high heritability may not necessarily give high genetic advance.

Sr. No.	Farmers' varieties	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Length of pods (cm)	Width of pods (cm)	Number of effective nodes	Number of seeds per pod	Harvest index (%)	100 - seed weight (g)	Yield per plant (g)
1.	PLCM-225	86	117.33	248.1	9.67	6.03	1.35	7.37	4.1	29.45	14.2	5.89
2.	PSAB-309	79.67	120.33	248.27	15.5	6.17	1.11	10.53	5.07	23.14	16.19	3.53
3.	PRRA-370	73.33	120.67	107.07	7.27	6.06	0.9	5.2	5.3	19.32	12.49	2.21
4.	PRRA-370 A	75	120.67	161.24	6.67	5.07	0.96	4.73	4.13	13.4	11.63	1.85
5.	PBCM-250	80	119.33	257.73	9.1	4.87	1.05	6.9	3.43	16.49	12.69	2.2
6.	PSLM-226	79.67	119.33	119.5	8.23	4.9	0.96	7.67	3.6	35.1	19.18	3.85
7.	FSAB-428	79.33	120.33	270.53	5.27	5.77	1.29	3.9	4.07	27.52	21.99	5.41
8.	FAIV 425	86.33	121.33	189.03	13.77	5.2	0.98	8.13	5.17	29.93	13.17	3.83
9.	PARB-223	78.67	118	175.87	11.87	4.73	0.92	10.1	6.3	35.71	23.18	3.86
10.	PATK-278	73	118	150.37	25.69	5.9	1	13.93	3.93	15.69	12.7	2.49
11.	PARA-308 (2)	69.33	118.33	215.27	15.93	5.23	0.96	7.7	5.87	38.74	12.46	3.08
12.	PRBJ-229	80.33	120	104.13	12.75	5.17	0.94	7.4	3.8	28.57	8.12	3.61
13.	PKKKK-228	77	120.33	163.27	15.47	5.07	0.71	11.37	4.87	53.79	10.59	3.38
14.	PRAV-230	79.33	120.33	206.17	16.3	5.83	1.1	8.67	4.2	35.64	12.17	7.73
15.	PAKA-230	72	119.33	160.4	13.4	5.5	0.85	11.5	5.53	49.33	7.76	4.33
16.	PSAK-307	81	122.67	200.07	14.27	5.53	1.09	9.2	4.43	29.17	9.77	11.16
17.	PSRA-358	67.33	120	252.8	9.4	5.2	0.96	7.2	4.6	25.14	10.24	5.42
18.	PKKK-227	80.33	130.33	126.27	8.1	3.13	1.07	7.97	2.83	41.53	5.13	13.86
19.	PMKK-232	81	129.33	113.87	6.13	3.17	0.99	6.4	2.63	41.23	5.52	17.42
20.	PARB-223 A (3)	70.33	119.67	220.47	14.43	5.13	0.9	8.7	6.07	33.08	12.29	3.55
21.	PARA-501	80.67	122.33	169.07	13.2	5.1	0.89	12.06	5.57	37.3	10.37	3.54
22.	PMRA-502	97.67	123.33	129.8	8.6	4.5	0.64	7.35	4.47	33.59	4.48	1.53
	Mean	78.51	120.97	181.33	11.88	5.15	0.98	8.36	4.53	31.49	12.11	5.17
	Range Lowest	67.33	117.33	104.13	5.27	3.13	0.64	3.9	2.63	13.4	4.48	1.53
	Range Highest	97.67	130.33	270.53	25.69	6.17	1.35	13.93	6.3	53.79	23.18	17.42
	C.V.	1.81	1.53	1.2	6.59	11.71	8.77	12.21	7.51	3.43	3.22	5.56
	S.E.	0.82	1.06	1.26	0.45	0.35	0.05	0.59	0.19	0.62	0.22	0.16
	C.D. 5%	2.35	3.04	3.59	1.28	0.99	0.14	1.68	0.56	1.78	0.64	0.47

Table 2: Mean performance of genotypes for eleven quantitative characters in farmers' pea varieties.

Table 3: Genetic variability parameters of eleven quantitative characters of twenty-two farmers' Pea

varieties.

Sr. No.	Parameters	Phenotypic variance	Genotypic variance	GCV (%)	PCV (%)	ECV (%)	Heritability (%)	Genetic Advance (%)	Genetic advance as percent of mean (%)
1.	Days to 50% Flowering	44.42	42.39	8.29	8.49	1.81	95.4	13.10	16.69
2.	Days to maturity	12.72	9.31	2.52	2.95	1.53	73.2	5.38	4.45
3.	Plant height	2831.51	2826.75	29.32	29.34	1.2	99.8	109.43	60.35
4.	Number of pods per plant	22.09	21.49	39.07	39.62	6.59	97.2	9.41	79.36
5.	Length of pods	0.87	0.5	13.77	18.07	11.71	58.0	1.11	21.61
6.	Width of pods	0.03	0.02	15.14	17.49	8.77	74.9	0.27	26.98
7.	Number of effective nodes	6.73	5.69	28.52	31.02	12.21	84.5	4.52	54.01
8.	Number of seeds per pod	1.07	0.95	21.51	22.78	7.51	89.1	1.90	41.83
9.	Harvest index	107.88	106.72	32.8	32.98	3.43	98.9	21.16	67.20
10.	100 -seed weight	23.58	23.43	39.98	40.11	3.22	99.4	9.94	82.09
11.	Yield per plant	16.31	16.23	77.93	78.13	5.56	99.5	8.28	160.14

High heritability coupled with GAM was recorded for yield per plant, 100-seed weight, number of pods per plant, harvest index, plant height, number of effective nodes, number of seeds per pod and width of pods (Georgieva *et al.*, 2016; Singh *et al.*, 2019; Luthra *et al.*, 2020). Therefore, the traits are under the control of additive gene action. Hence desirable improvement in seed yield of pea can easily be achieved on implementation of effective selection scheme for above mentioned traits.

High heritability with moderate GAM was obtained for days to 50% flowering, therefore there is a predominance of additive and non-additive gene active in the expression of this traits on the performance of farmers' variety in the given environmental condition. This trait can be improved in FVs of Pea by mass selection and other breeding methods based on progeny testing. Similar results were reported by Saxesena *et al.* (2014).

High heritability with low GAM was recorded for days to maturity (Lal *et al.*, 2011; Yimam *et al.*, 2020). Thus, it is controlled by non-additive gene action and so selection of this trait may not be rewarding. This character can be improved by inter-mating superior genotypes of segregating population with FVs (Lal *et al.*, 2011).

**Correlation coefficient analysis.** As per Table 4(a), it was observed that yield per plant had highly significant and positive association at phenotypic level with days to maturity  $(0.70^{**})$  and harvest index  $(0.34^{**})$ , at 1 % level of significance and width of pods  $(0.29^{*})$  at 5% level of significance. Whereas, the character days to 50% flowering showed positive and non-significant association with yield per plant at the  $r_p = 0.09$ . On

contrary, yield per plant had negative significant association with number of seeds per plant ( $-0.52^{**}$ ), length of pods ( $-0.50^{**}$ ) and 100-seed weight ( $-0.35^{**}$ ), while negative and non- significant association with number of pods per plant (-0.23), plant height (-0.15), and effective nodes (-0.11).

As per Table 4(b), it was observed that grain yield per plant had significant and positive correlation at genotypic level with days to maturity (0.81\*\*), width of

pods  $(0.35^{**})$  and harvest index  $(0.35^{**})$ . Negative and significant correlation with yield per plant were shown by length of pods  $(-0.65^{**})$ , number of seeds per pods  $(-0.55^{**})$  and 100-seed weight  $(-0.35^{**})$ . Days to 50% flowering (0.09) is positively associated with this character, but non-significantly, while number of pods per plant (-0.24), plant height (-0.15) and number of effective nodes (-0.13) showed negative association non-significantly.

Table 4(a): Phenotypic correlation	coefficients among yie	eld and yield	components in f	farmers'	Pea varieties.
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	DF 50	DM	PH	PP	LP	WP	EN	SP	HI	100SW	YP
DF 50	1										
DM	0.28 *	1									
PH	-0.17	-0.38**	1								
PP	-0.25 *	-0.36**	0.06	1							
LP	-0.15	-0.65 **	0.37**	0.32**	1						
WP	-0.02	-0.09	0.49**	-0.10	0.27 *	1					
EN	-0.11	-0.17	-0.07	0.76**	0.15	-0.21	1				
SP	-0.29 *	-0.47**	0.21	0.32**	0.35**	-0.29 **	0.31*	1			
HI	0.05	0.25 *	-0.23	0.03	-0.35**	-0.32 **	0.30*	0.15	1		
100SW	-0.15	-0.53**	0.43**	0.01	0.38**	0.37 **	-0.06	0.30*	-0.25 *	1	
YP	0.09	0.70**	-0.15	-0.23	-0.50**	0.29*	-0.11	-0.52**	0.34**	-0.35**	1

DF (Days to 50% flowering), DM (Days to maturity), PH (Plant height), PP (Number of pods per plant), LP (Length of pods), WP (Width of pods), EN (Effective nodes), SP (Number of seeds per pod), HI (Harvest index), 100SW (100-seed weight), YP (Yield per pod).

Table 4(b): Genotypic correlation coefficients among yield and yield components in Pea.

	DF 50	DM	PH	PP	LP	WP	EN	SP	HI	100SW	YP
DF 50	1										
DM	0.31*	1									
PH	-0.17	-0.45**	1								
PP	-0.25*	-0.40**	0.07	1							
LP	-0.26*	-0.89**	0.49**	0.47 **	1						
WP	-0.01	-0.08	0.58**	-0.12	0.29*	1					
EN	-0.12	-0.19	-0.08	0.85**	0.16	-0.33**	1				
SP	-0.30*	-0.56 **	0.22	0.34**	0.51**	-0.36**	0.34**	1			
HI	0.06	0.31*	-0.23	0.03	-0.43**	-0.36**	0.33**	0.15	1		
100SW	-0.15	-0.63**	0.43**	0.02	0.50**	0.43**	-0.07	0.32**	-0.25 *	1	
YP	0.09	0.81**	-0.15	-0.24	-0.65**	0.35**	-0.13	-0.55**	0.35**	-0.35**	1

DF (Days to 50% flowering), DM (Days to maturity), PH (Plant height), PP (Number of pods per plant), LP (Length of pods), WP (Width of pods), EN (Effective nodes), SP (Number of seeds per pod), HI (Harvest index), 100SW (100-seed weight), YP (Yield per pod)

The traits *viz.*, days to maturity, width of pods and harvest index were found to possess positive significant association with yield per plant at both genotypic and phenotypic level. The results revealed that selection of these traits will help in selecting the genotypes of pea with high grain yield per plant. The findings are in agreement with the findings of Lal *et al.* (2011); Ali *et al.* (2019); Bahadur and Devi (2021).

**Path coefficient analysis.** The path coefficient analysis at the phenotypic level based on the yield as dependent

variable showed that days to maturity (0.507), width of pods (0.46), harvest index (0.341) and number of pods per plant (0.070) had positive direct effect on yield per plant. While, plant height (-0.026), number of effective nodes (-0.037), 100 seed weight (-0.082), length of pods (-0.110), days to 50% flowering (-0.127) and number of seeds per pod (-0.179) had negative direct effect on yield per plant, as manifested in Table 5 (a).

Table 5(a). Direct (uiazonai) and municet eneet of uniterent trans on view ber blant at bitenotyble iev	Table	5(a): I	Direct (	(diagonal)	and indirect	effect of	different	traits on	vield	per i	plant at	phenoty	pic lev	el.
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	DF 50	DM	PH	PP	LP	WP	EN	SP	HI	100SW
DF 50	-0.127	-0.036	0.021	0.031	0.019	0.002	0.013	0.036	-0.007	0.019
DM	0.143	0.507	-0.192	-0.18	-0.327	-0.045	-0.086	-0.236	0.129	-0.27
PH	0.004	0.009	-0.026	-0.001	-0.009	-0.012	0.002	-0.005	0.006	-0.011
PP	-0.017	-0.025	0.004	0.070	0.022	-0.007	0.054	0.022	0.002	0.0001
LP	0.017	0.071	-0.040	-0.035	-0.110	-0.029	-0.016	-0.038	0.038	-0.042
WP	-0.009	-0.042	0.231	-0.047	0.124	0.46	-0.098	-0.135	-0.149	0.171
EN	0.004	0.006	0.002	-0.028	-0.005	0.007	-0.037	-0.011	-0.011	0.002
SP	0.052	0.084	-0.038	-0.057	-0.063	0.052	-0.055	-0.179	-0.027	-0.054
HI	0.019	0.087	-0.08	0.011	-0.119	-0.109	0.101	0.052	0.341	-0.084
100SW	0.012	0.043	-0.035	-0.0001	-0.031	-0.030	0.005	-0.024	0.020	-0.082
YP	0.09	0.70**	-0.15	-0.23	-0.50	0.29*	-0.11	-0.52	0.34**	-0.35
Partial R <sup>2</sup>	-0.012	0.357	0.003	-0.016	0.055	0.137	0.004	0.093	0.117	0.028

DF (Days to 50% flowering), DM (Days to maturity), PH (Plant height), PP (Number of pods per plant), LP (Length of pods), WP (Width of pods), EN (Effective nodes), SP (Number of seeds per pod), HI (Harvest index), 100SW (100-seed weight), YP (Yield per pod).

The path coefficient analysis at genotypic level revealed the characters viz, width of pods (1.274), number of seeds per pod (0.481), number of pods per plant (0.225), and harvest index (0.135) had positive direct effect on seed yield. While number of effective nodes (-0.025), day to 50% flowering (-0.062), days to maturity (-0.139), plant height (-0.336), 100-seed weight (-0.442) and length of pods (-1.067) had

negative direct effect for genotypic path, as manifested in Table 5 (b).

The trait width of pods, number of pods per plant and harvest index had positive direct effect on seed yield, indicating the effectiveness of direct selection of these traits for grain yield improvement in pea (Ofga and Petros, 2017; Mohanty *et al.*, 2020; Bahadur and Devi, 2021; Kalapchieva *et al.*, 2021).

Table 5(b): Direct (diagonal) and indirect effect of different traits on yield per plant at genotypic level.

	DF 50	DM	PH	PP	LP	WP	EN	SP	HI	100SW
DF 50	-0.062	-0.019	0.011	0.016	0.016	0.0004	0.008	0.019	-0.003	0.009
DM	-0.043	-0.139	0.062	0.056	0.125	0.011	0.027	0.078	-0.043	0.088
PH	0.057	0.15	-0.336	-0.023	-0.167	-0.194	0.028	-0.075	0.079	-0.144
PP	-0.058	-0.090	0.015	0.225	0.10	-0.028	0.190	0.076	0.007	0.0005
LP	0.278	0.959	-0.529	-0.503	-1.067	-0.311	-0.174	-0.543	0.454	-0.536
WP	-0.009	-0.099	0.736	-0.158	0.371	1.274	-0.421	-0.460	-0.46	0.55
EN	0.003	0.005	0.002	-0.021	-0.004	0.008	-0.025	-0.008	-0.008	0.002
SP	-0.146	-0.272	0.108	0.163	0.245	-0.174	0.165	0.481	0.075	0.153
HI	0.008	0.042	-0.032	0.004	-0.058	-0.049	0.044	0.021	0.135	-0.033
100SW	0.067	0.280	-0.190	-0.001	-0.222	-0.191	0.031	-0.141	0.109	-0.442
YP	0.09	0.81**	-0.15	-0.24	-0.65	0.35**	-0.13	-0.55	0.35**	-0.35
Partial R <sup>2</sup>	-0.006	-0.113	0.051	-0.054	0.697	0.441	0.003	-0.266	0.046	0.156

DF (Days to 50% flowering), DM (Days to maturity), PH (Plant height), PP (Number of pods per plant), LP (Length of pods), WP (Width of pods), EN (Effective nodes), SP (Number of seeds per pod), HI (Harvest index), 100SW (100-seed weight), YP (Yield per pod).

## CONCLUSION

It is concluded that the farmers' pea varieties showed significant genetic variability for all the traits studied. On the basis of mean performance for seed yield variety PMKK-232 was found best followed by PKKK-227. High heritability coupled with high GAM was recorded for yield per plant, followed by 100-seed weight and number of pods per plant, indicating that these traits were under the control of additive gene action. Thus, selection for these traits will be effective. Correlation and path coefficient analysis also revealed positive significant association and direct effect on above mentioned characters on seed yield.

### FUTURE SCOPE

Hence, the characters *viz.*, days to maturity, width of pods, number of pods per plant and harvest index could be used as selection indices for further improvement in farmers' Pea varieties.

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**Conflict of interest.** The authors declare no conflict of interest.

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