

Heritability and Genetic Advance Analysis for Yield and Its Attributes in Garden Pea (*Pisum sativum* L.) over Environments

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ABSTRACT

The vegetable pea (*Pisum sativum* (L.) var. *hortense*) belonging to the illustrious Leguminosae family, subfamily Papilionaceae, and the discernible class of dicotyledons, it exudes nutritional prowess. As a self-pollinating gem, it boasts a diploid chromosome count of $2n=2x=14$. Narrow-sense heritability is a fundamental concept in quantitative genetics that

helps us understand the proportion of the phenotypic variation within a population that can be attributed to genetic differences between individuals. In this concept the present investigation has been carried out at the Main Experiment Station (MES) nestled within the Department of Vegetable Science, Acharya Narendra Deva University of Agriculture and Technology, Ayodhya during the *Rabi* seasons of 2020-21 (Y_1) and 2021-22 (Y_2), to estimate the extent of narrow sense heritability and genetic advance in garden pea. The observations were recorded for eighteen metric traits. The analysis of variance revealed the mean squares due to genotypes were highly significant for all the eighteen traits. During both Y_1 , Y_2 and season over pooled, high estimates of narrow sense heritability along with high genetic advance were noted for days to 50 % flowering, days to first picking, plant height, node to first pod appearance, nodes per plant, pod length, pod girth, number of seeds per pod, number of pods per 100 g, 100 green seed weight, non-reducing sugar and total sugars, while moderate to low range of heritability was observed for number of pods per plant, protein content, total soluble solids, reducing sugars, shelling percentage and green pod yield per plant.

Keywords Garden pea, Genetic advance, Narrow sense heritability, *Pisum sativum*, Genetic variability.

INTRODUCTION

The vegetable pea (*Pisum sativum* (L.) var. *hortense*)

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is a prominent crop in the lush vegetation of the plant kingdom. It is a member of the recognizable class of dicotyledons, the renowned Leguminosae family, and the subfamily Papilionaceae. It is a self-pollinating crop with $2n=2x=14$ diploid chromosomes. Garden pea, table pea, and vegetable pea are some of its popular names; in common use, it is called “Matar.” While growth takes place in the pleasant climate of 13–18°C, germination flourishes in the temperatures around 22°C (Rowland *et al.* 1994).

The main states that grow peas are UP, MP, Bihar, Assam, and Orissa. At a compound annual growth rate (CAGR) of 10.1%, the pea processed ingredients market is expected to generate approximately US\$5.0 billion in revenue by 2026 (ICAR-IIPR, Kanpur). According to Market Research Future (2022), the pea industry was projected to be worth USD 3.1 billion in 2021. The market for dried peas is expected to grow at a compound annual growth rate (CAGR) of 8.9% from its 2023 valuation of US\$5.05 billion to over USD 7.74 billion by 2028 (Market data Forecast 2022).

Genetic variation is the driving force behind the diversity observed within populations of living organisms. Whether it is the color of a flower, the size of a fruit, or a human's height, these traits are influenced by genetic factors. Narrow-sense heritability is a fundamental concept in quantitative genetics that helps us understand the proportion of the phenotypic variation within a population that can be attributed to genetic differences between individuals (Falconer and Mackay 1996).

Moreover, heritability influences the response to selection; traits with higher heritability values respond more predictably to selective breeding (Visscher *et al.* 2008). Accurately estimating heritability (h^2) is essential for understanding the genetic basis of traits and for making informed breeding decisions. Genetic advance is a concept that connects narrow-sense heritability with the progress achieved through artificial selection. It represents the increase in the mean value of a trait in the population after one generation of selection. Genetic advance helps breeders estimate the potential gain in a trait by selecting the best-performing individuals as parents for the next generation.

It provides a valuable tool for optimizing breeding strategies to achieve desired trait improvements (Meyer 2007).

With the above facts in view, the current inquiry was done in pea genotypes and their hybrids. The purpose was to unravel the estimates of narrow sense heritability and genetic advance in garden pea.

MATERIALS AND METHODS

The experiment was conducted during the *Rabi* seasons of 2020–21 (Y_1) and 2021–22 (Y_2). The purpose of this experiment was to explore the nuances of percentage-wise genetic advancement and narrow sense heritability at the Main Experiment Station (MES), Department of Vegetable Science at Acharya Narendra Deva University of Agriculture and Technology Kumarganj, Ayodhya. The crosses were made following diallel mating design. Geographically, the experimental field is located in a humid, subtropical region. At an elevation of 98 meters above mean sea level, at elevation of 24.47° and 26.54° N latitude and 81.84° and 83.58° E longitude. The sandy loam soil in this region, which is located beneath the Gangetic Alluvial Plains of Eastern Uttar Pradesh, is moderately fertile and has a pH range that gracefully spans from 7.5 to 8.5.

Ten different and promising lines/varieties of the vegetable pea made up the experimental material for this study (see Table 1 for specifics). The selection criterion was based on genetic diversity, which produced a population with potential. Furthermore, during the *Rabi* season of 2019–20, the group produced 45 F_1 hybrids under the guise of a diallel mating design, excluding the reciprocals. In order to evaluate the performance of 45 F_1 hybrids and their ten parental lines of vegetable pea, the experiments were carried out in a Complete Randomized Block Design (CRBD) with three replications set up during the years 2020–21 (Y_1) and 2021–2022 (Y_2). The crop was sown in single rows (3m) spaced at 30 cm apart with a plant to plant spacing of 10 cm. Every recommended tenet of agronomic care was diligently observed. A symphony of practices and protective measures, meticulously curated, unfurled to nurture the blossoming potential of these green denizens.

Table 1. List of parental lines with their salient features and collection sites.

Sl. No.	Parental lines	Collection site	Salient features of parental lines
1	Azad Pea-1	C.S.A.U.A. & T., Kanpur, (UP.)	Medium tall variety, medium in maturity, light green branched foliage, long pod size, green pod, high yielder.
2	Azad Pea-2	C.S.A.U.A. & T., Kanpur, (UP.)	Tall variety, late in maturity, powdery mildew resistant, light green foliage, branched, medium pod size, light green pod, good yielder.
3	Azad Pea-3	C.S.A.U.A. & T., Kanpur, (UP.)	Dwarf variety, good yielder, bold and wrinkled seeded, early in maturity, escape the powdery mildew disease with wider adaptability, long pod size, good yielder.
4	Azad Pea-4	C.S.A.U.A. & T., Kanpur, (UP.)	Tall variety, late in maturity, powdery mildew resistant, light green foliage, branched, medium pod size, light green pod, good yielder
5	Kashi Samridhi	I.I.V.R., Varanasi, (UP.)	Semi determinate plants, late in maturity, straight and slightly curved green pods, resistant to powdery mildew, good yielder.
6	Kashi Nandini	I.I.V.R., Varanasi, (UP.)	Dwarf, erect plants, early in maturity, straight and slightly curved at tip dark green and long pods, sweet taste, high yielder.
7	Kashi Mukti	I.I.V.R., Varanasi, (UP.)	Dwarf, erect plants, early in maturity, straight light green and long pods, resistant to powdery mildew high yielder.
8	Kashi Udai	I.I.V.R., Varanasi, (UP.)	Dwarf, erect plants, early in maturity, curved dark green and long pods, resistant to powdery mildew, high yielder.
9	NDVP-2	A.N.D.U.A. & T., Ayodhya, (UP.)	Dwarf, erect plants, late in maturity, straight light green and medium sized pods, good yielder.
10	NDVP-4	A.N.D.U.A. & T., Ayodhya, (UP.)	Dwarf, erect plants, late in maturity, straight light green and medium sized pods, good yielder.

Five competitive plants were tagged using a random filter within the scope of each replication for both parental and F_1 entries. These selected plants were appropriately marked and chosen, and it was obvious that they would be utilized to record observations. This observational table included a total of eighteen economic characteristics, including biochemical characteristics, viz., days to 50% flowering, days to first picking, plant height (cm), node to first pod appearance, nodes per plant, pod length (cm), pod girth (cm), number of seeds per pod, number of pods per plant, shelling percentage (%), number of pods per 100g, 100 green seed weight (g), protein content (%), total soluble solids, reducing sugars (%), non-reducing sugar (%), total sugars (%) and green pod yield per plant (g). For each year, Y_1 and Y_2 , as well as for the pooled data, the arithmetic mean of these five selected plants was computed. The data for days to 50% flowering was noted on plot basis. The statistical analyses were done for randomized block design, outlined by Panse and Sukhatme, (1967), the narrow sense heritability followed by Mather and Jinks (1971) and expected genetic advance, both in absolute terms and as a percentage of the mean, were estimated by formula suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

The variance analysis was done for each of the eighteen distinct attributes that have been depicted in Table 2. The table revealed the mean squares due to genotypes were highly significant for all the eighteen traits under investigation viz. days to 50% flowering (Y_1 - 126.47, Y_2 - 134.89, Pooled- 129.62), days to first picking (Y_1 - 202.90, Y_2 - 211.11, Pooled-205.41), plant height (Y_1 - 1387.72, Y_2 -1471.46, Pooled-1422.38), node to first pod appearance (Y_1 - 9.07, Y_2 -9.89, Pooled-9.33), nodes per plant (Y_1 - 17.80, Y_2 -16.35, Pooled-16.89), pod length (Y_1 - 3.59, Y_2 -3.54, Pooled-3.55), pod girth (Y_1 - 0.334, Y_2 -0.308, Pooled-0.310), number of seeds per pod (Y_1 - 12.39, Y_2 -4.72, Pooled-4.69), number of pods per plant (Y_1 - 7.60, Y_2 -7.47, Pooled-7.46), shelling percentage (Y_1 -35.40, Y_2 -36.30, Pooled-35.30), number of pods per 100g (Y_1 - 17.81, Y_2 - 17.85, Pooled-17.69), 100 green seed weight (Y_1 - 52.90, Y_2 - 58.04, Pooled-54.27), protein content (Y_1 - 12.39, Y_2 - 12.10, Pooled-12.16), total soluble solids (Y_1 - 6.29, Y_2 -6.50, Pooled-6.33), reducing sugars (Y_1 - 0.005, Y_2 -0.005, Pooled-0.005), non-reducing sugar (Y_1 - 1.52, Y_2 -1.19, Pooled-1.47), total sugars (Y_1 - 6.29, Y_2 -6.50, Pooled-1.62) and green pod yield per plant (Y_1 -274.60, Y_2 -314.46, Pooled-290.47) respectively.

Table 2. Analysis of variance (ANOVA) for a set of 10 x 10 diallel crosses for different traits in vegetable pea during Y₁, Y₂ and Pooled.

Source of variation	Replications			Genotypes			Parents		
d. f.	2			54			9		
Year	Y ₁	Y ₂	Pooled	Y ₁	Y ₂	Pooled	Y ₁	Y ₂	Pooled
days to 50% flowering	0.67	0.31	0.26	126.47**	134.89**	129.62**	155.26**	163.44 **	158.10**
Days to first picking	1.46	30.49**	9.15*	202.90 **	211.11**	205.41**	181.36**	191.63**	184.88**
Plant height	80.14	99.73 *	34.39*	1387.72**	1471.46 **	1422.38**	1621.38**	1613.03 **	1611.93**
Node to first pod appearance	0.26	0.32	0.053	9.07**	9.89 **	9.33 **	8.48**	10.11 **	9.23 **
Nodes per plant	4.81*	6.46 **	5.59**	17.80**	16.35 **	16.89**	35.32**	31.49 **	33.02**
Pod length	0.27 *	0.34 **	0.31 **	3.59**	3.54 **	3.55 **	2.79**	2.29 **	2.53 **
Pod girth	0.006	0.011	0.003	0.334**	0.308 **	0.31 **	0.278**	0.219 **	0.24 **
Number of seeds per pod	0.14	0.26	0.25 *	12.39**	4.72 **	4.69 **	9.68**	4.36 **	4.33 **
Number pf pods per plant	1.24	1.51 *	1.31*	7.60**	7.47 **	7.46 **	3.62**	3.00 **	3.19 **
Shelling percentage	31.01**	12.84 **	3.62*	35.40**	36.30 **	35.30 **	9.43*	7.72 **	8.21 **
Number of pods per 100 g	0.33	0.74	0.46	17.81**	17.85 **	17.69**	19.21**	19.48 **	19.21**
100 green seed weight	5.66	20.31 **	11.48 *	52.90**	58.04 **	54.27 **	24.41**	24.90 **	23.54 **
Protein content	0.14	0.28	0.023	12.39**	12.10 **	12.16**	9.68**	7.85 **	8.71 **
Total soluble solids	0.29	0.04	0.141	6.29**	6.50 **	6.33**	3.37**	3.25 **	3.26 **
Reducing sugars	0.001	0.001	0.001 *	0.005**	0.005 **	0.005 **	0.002**	0.002 **	0.002 **
Non reducing sugar	0.03	0.04	0.021	1.52**	1.49 **	1.47 **	0.91**	0.84 **	0.85 **
Total sugars	0.29	0.04	0.03	6.29**	6.50 **	1.62 **	3.37**	3.25 **	0.92 **
Green pod yield per plant	0.18	28.62 *	8.22	274.60**	314.46 **	290.47 **	52.33**	59.93 **	53.74 **

Table 2. Continued.

Source of variation	Hybrids			Parents vs. Hybrids			Error		
d. f.	44			1			108		
Year	Y ₁	Y ₂	Pooled	Y ₁	Y ₂	Pooled	Y ₁	Y ₂	Pooled
days to 50% flowering	123.38**	132.11 **	126.17 **	3.43	0.24	1.37	1.91	2.67	1.64
Days to first picking	211.78**	219.85**	214.20**	5.95	1.89	3.64	3.75	5.3	2.85
Plant height	1301.46**	1404.84 **	1345.38**	3080.20**	3128.50**	3104.28**	29.5	21.17	7.58
Node to first pod appearance	9.38**	10.05 **	9.54 **	0.47	1.25	0.82 *	0.27	0.4	0.16
Nodes per plant	13.01**	12.10 **	12.41**	70.75**	66.86 **	68.79**	1.04	1	0.9
Pod length	3.82**	3.85 **	3.83 **	0.59**	0.85 **	0.72 **	0.05	0.051	0.03
Pod girth	0.346**	0.323 **	0.33 **	0.331**	0.426 **	0.37 **	0.017	0.01	0.012
Number of seeds per pod	12.97**	4.83 **	4.81 **	11.07**	2.81 **	2.85 **	0.2	0.11	0.07
Number pf pods per plant	7.77**	7.90 **	7.76 **	36.03**	29.08 **	32.75 **	0.5	0.46	0.39
Shelling percentage	39.88**	39.98 **	39.38 **	71.55**	131.71 **	99.31 **	4.31	2.66	0.97

Table 2. Continued.

Source of variation	Hybrids			Parents vs. Hybrids			Error		
	44			1			108		
	Y ₁	Y ₂	Pooled	Y ₁	Y ₂	Pooled	Y ₁	Y ₂	Pooled
Number of pods per 100 g	17.92**	17.89 **	17.76 **	0.65	1.25	0.92	0.59	0.62	0.44
100 green seed weight	59.27**	65.73 **	61.26 **	28.88*	17.79 *	23.02 **	2.775	3.01	2.43
Protein content	12.97**	12.92 **	12.86 **	11.07**	14.39 **	12.71 **	0.2	0.22	0.069
Total soluble solids	6.69**	6.92 **	6.74 **	14.87**	17.28 **	16.06 **	0.14	0.16	0.135
Reducing sugars	0.005**	0.005 **	0.005 **	0.042**	0.042 **	0.042 **	0.0001	0.0001	0.0001
Non reducing sugar	1.64**	1.61 **	1.60 **	1.62**	1.76 **	1.68 **	0.016	0.03	0.013
Total sugars	6.69**	6.92 **	1.76 **	14.87**	17.28 **	2.26 **	0.142	0.16	0.012
Green pod yield per plant	274.05**	327.83 **	296.32 **	2299.19**	2017.11 **	2163.72 **	9.28	9.21	7.27

*, ** Significant at 5% and 1% level of probability, respectively.

Significance variance for most of these traits were also recorded by earlier workers Jafri *et al.* (2022) for days to 50% flowering, plant height, days to first picking, number of seeds per pod, and Towfiq *et al.* (2020) for number of pods per plant, green seeds weight.

Simultaneously, the estimates of heritability in the narrow sense (h^2_{ns}) and genetic advance, as percentage of the mean, was calculated, tabled within Table 3. Each observation was thoroughly stratified using the method described by Crumpacker and Allard (1962) in order to extract the essence of heritability (h^2_{ns}) estimates. They were divided into three different classes by this stratification: (i) High (>30%), (ii) Moderate (above 10% to 30%), and (iii) Low (<10%). High (>30%) estimates of heritability (ns) was observed for days to 50 % flowering (Y₁ - 73.06 %, Y₂ - 57.49 %, Pooled- 67.38 %), days to first picking (Y₁ - 74.37%, Y₂ - 64.91% and Pooled- 74.50 %), plant height (Y₁ - 38.53 %, Y₂ - 40.89 % and Pooled- 40.55%), node to first pod appearance (Y₁ - 45.81 %, Y₂ - 55.28 % and Pooled-52.36 %), nodes per plant (Y₁ - 71.50 %, Y₂ - 73.45 % and Pooled-74.24 %), pod length (Y₁ - 32.01 %, Y₂ - 32.29 % and Pooled-33.03 %), pod girth (Y₁ - 44.47 %, Y₂ - 57.41 % and Pooled-58.32 %), number of seeds per pod (Y₁ - 48.57 %, Y₂ - 46.07 % and Pooled-48.60 %), number of pods per 100 g (Y₁ - 61.06 %, Y₂ - 60.25 % and Pooled-63.93%), 100 green seed weight (Y₁ - 41.90 %, Y₂ - 43.07% and Pooled-46.03 %), non-reducing

sugar (Y₁ - 47.11 %, Y₂ - 37.63 % and Pooled-44.64 %) and total sugars (Y₁ - 44.74 %, Y₂ - 36.79 % and Pooled-42.82 %) respectively. For easy explanation the estimates of genetic advance, it was classified in three categories viz., (i) High (> 20%) (ii) moderate (> 10% to 20%) and (iii) low (< 10%). The table revealed the high values of genetic advance in per cent of mean for days to 50 % flowering (27.59, 28.17 and 27.91%), days to first picking (21.94, 22.13 and 22.13 %), Plant height (47.52, 48.60 and 48.55 %), node to first pod appearance (29.19, 29.29 and 29.54 %), nodes per plant (21.76, 20.94 and 21.39 %), pod length (27.68, 27.40 and 27.64 %), total soluble solids (20.98, 21.44 and 21.16 %), reducing sugars (34.14, 32.74 and 34.20 %), non-reducing sugar (36.67, 36.02 and 36.17 %), total sugars (36.31, 35.64 and 35.84 %) and green pod yield per plant (31.23, 33.92 and 32.57 %) in Y₁, Y₂ and over season (pooled). Number of seeds per pod in Y₁ (19.54 %) exhibited moderate genetic advance while in Y₂ (32.45 %) and over season pooled (32.75 %) high estimates of genetic advance in percent of mean were observed. A parallel finding can be seen in the studies by Mishra *et al.* (2014), Meena *et al.* (2017), Amin (2020) and Jafri *et al.* (2022) for the most of these traits under investigation. The high narrow-sense heritability (h^2_{ns}) and high genetic advance (GA) suggests that a substantial portion of the phenotypic variation in the population is indeed due to genetic differences. This indicates that the traits of interest are strongly influenced by

additive genetic factors rather than environmental or non-additive genetic effects. Moreover, a high genetic advance implies that selecting individuals with superior trait values will likely result in significant improvements in the population's mean trait value over just one generation of selection. Thus, the high estimates of heritability coupled with high genetic advance were observed for days to 50 % flowering, days to first picking, plant height, node to first pod appearance, nodes per plant, pod length, non-reducing sugar and total sugars in Y_1 , Y_2 and over season (pooled) while, number of seeds per pod showed high heritability coupled with high genetic advance in Y_2 and over season pooled while in Y_1 , it exhibited high heritability coupled with moderate genetic advance. Similar results have also been reported by Sureja and Sharma (2000) and Tiwari and Lavanya (2012) for these characters. Further, Dhangra *et al.* (2023) also recorded high proportion of GCV along with high heritability (bs) and high genetic advance as percentage of mean for the traits like days to 50% flowering, plant height, harvesting span, dry matter

and pod yield.

Moderate range of heritability (above 10% to 30%) was observed for number of pods per plant (Y_1 - 19.78 %, Y_2 -21.50 % and Pooled-21.23 %), protein content (Y_1 - 29.88 %, Y_2 -23.74 % and Pooled-27.56 %) and total soluble solids (Y_1 - 29.95 %, Y_2 -13.50 % and Pooled-21.84 %) respectively, while reducing sugars (10.10 % and 10.97 %) showed moderate heritability in Y_2 and over season pooled respectively. Whereas, moderate estimates of genetic advance were observed for pod girth (16.40, 15.97 and 16.24 %), shelling percentage (13.41, 14.36 and 14.84 %), number of pods per 100 g (25.73, 25.58 and 25.80 %), 100 green seed weight (17.99, 18.99 and 18.44 %) and protein content (19.54, 19.20 and 19.54 %) in Y_1 , Y_2 and over season (pooled). Afreen *et al.* (2017) and Amin (2020) noted similar results for pod girth, shelling percentage, number of pods per 100g, 100 green seed weight. Conversely, when narrow-sense heritability is high but genetic advance is low, it suggests that while a significant portion of phenotypic

Table 3. Estimates of heritability in narrow sense and genetic advance in percent of mean in vegetable pea over Y_1 , Y_2 and pooled.

Sl. No.	Parameters Characters	Heritability (h^2_{ns} %)			Genetic advance in per cent of mean		
		Y_1	Y_2	Pooled	Y_1	Y_2	Pooled
1	Days to 50% flowering	73.06	57.49	67.38	27.59	28.17	27.91
2	Days to first picking	74.37	64.91	74.50	21.94	22.13	22.13
3	Plant height	38.53	40.89	40.55	47.52	48.60	48.55
4	Node to first pod appearance	45.81	55.28	52.36	29.19	29.29	29.54
5	Nodes per plant	71.50	73.45	74.24	21.76	20.94	21.39
6	Pod length	32.01	32.29	33.03	27.68	27.40	27.64
7	Pod girth	47.47	57.41	58.32	16.40	15.97	16.24
8	Number of seeds per pod	48.57	46.07	48.60	19.54	32.45	32.75
9	Number of pods per plant	19.78	21.50	21.23	28.75	28.86	28.98
10	Shelling percentage	4.18	4.70	6.89	13.41	14.36	14.84
11	Number of pods per 100 g	61.06	60.25	63.93	25.73	25.58	25.80
12	100 green seed weight	41.90	43.07	46.03	17.99	18.99	18.44
13	Protein content	29.88	23.74	27.56	19.54	19.20	19.54
14	Total soluble solids	29.95	13.50	21.84	20.98	21.44	21.16
15	Reducing sugars	8.24	10.10	10.97	34.14	32.74	34.20
16	Non reducing sugar	47.11	37.63	44.64	36.67	36.02	36.17
17	Total sugars	44.74	36.79	42.82	36.31	35.64	35.84
18	Green pod yield per plant	3.33	2.60	3.10	31.23	33.92	32.57

variation is due to genetic differences, the potential for rapid trait improvement through selection is limited. As a result, other strategies, such as incorporating multiple traits in the selection process or considering the broader genetic context, might be necessary to achieve meaningful advancements. In this regard the high heritability coupled with moderate genetic advance were observed for pod girth and 100 green seed weight. These findings are in accordance with the earlier reports of Kumari *et al.* (2008), Tiwari and Lavanya (2012). Vinayaka *et al.* (2022) also noted moderate GCV and PCV, high heritability with moderate genetic advance and high genetic advance in percent over mean for shelling percentage, Total soluble solids showed high heritability with moderate genetic advance in percent over mean.

However, shelling percentage (Y_1 - 4.18 %, Y_2 - 4.70 % and Pooled-6.89 %) and green pod yield per plant (Y_1 - 3.33 %, Y_2 - 2.60 % and Pooled-3.10 %) showed low (<10%) range of heritability in Y_1 , Y_2 and over season (pooled) respectively, while reducing sugars (8.24 %) in Y_1 also exhibited low estimates of narrow sense heritability as shown in Table 3. These results agree with the observations taken by Sharma and Sharma (2012), Abbas (2015), Askandar *et al.* (2018). Additionally, if both narrow-sense heritability (h^2_{ns}) and genetic advance (GA) are low, it suggests that the phenotypic variation in the population is primarily influenced by environmental factors or non-additive genetic effects. The limited heritability indicates that the genetic component contributing to the trait is relatively small, making it difficult to achieve substantial gains through selection. In such cases, alternative strategies might be considered. Such a situation was also recorded for some of the traits as shelling percentage. Towfiq *et al.* (2020) also agreed to these results in their study.

Moreover, when narrow-sense heritability (h^2_{ns}) is low while genetic advance (GA) is high, it indicates that while the proportion of phenotypic variation due to genetic differences is small, the potential for significant improvement through selection exists. This might seem counterintuitive, but it can happen if the trait in question has a low heritability due to factors like non-additive genetic effects or strong gene-environment interactions. In this case, despite the limited

genetic contribution to the trait's variation, selecting the best-performing individuals can still lead to substantial gains in subsequent generations. Relatively, the present study revealed low heritability coupled with high genetic advance for reducing sugars and green pod yield per plant. Similar findings have also been reported by Afreen *et al.* (2017), Amin (2020) and Jafri *et al.* (2022).

CONCLUSION

The study confirmed the existence of exploitable genetic variation by demonstrating significant genetic variability among genotypes for each of the 18 attributes. Simple phenotypic selection can effectively improve some traits because of the high narrow-sense heritability and high genetic advance, these are days to 50% flowering, days to first picking, plant height, node to first pod appearance, nodes per plant, pod length, non-reducing sugar, and total sugars (across years and pooled). Moderately strong selection may also be used to target the number of seeds per pod that exhibit high heritability and moderate to high genetic advancement. The presence of both additive and non-additive gene effects is suggested by traits like pod girth and 100 green seed weight, which show high heritability but moderate genetic advancement. These traits may also react better to recurrent selection or hybridization followed by selection. The shelling percentage, which exhibits low heritability and poor genetic advancement, can be increased by using heterosis breeding or altering agronomic procedures instead of direct selection.

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