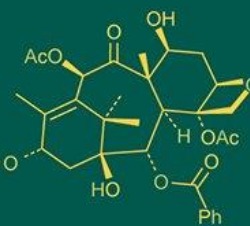
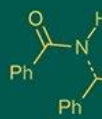


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Harnessing heritability and genetic advance for fruit yield and yield attributes from parents, F₁ hybrids and segregating generations in bottle gourd [*Lagenaria siceraria* (Mol) Standl]

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Abstract

The present investigation pertaining to study of narrow sense heritability and genetic advance for yield, yield attributes and quality traits in five genetically diverse parents were taken to produce F₁ hybrids and its subsequent segregating generations. The F₁ hybrids were developed at Centre for Vegetable Research, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during Kharif 2023 and subsequently F₁ hybrids along with their both the respective parents were sown in Summer 2024 to produce seed for F₂, BC₁ and BC₂ generations. All six populations were evaluated during Kharif 2024 at same location. Analysis of variance indicated that crosses showed highly significant differences for all characters which suggested the presence of sufficient variation of crosses for different traits thereby revealing existence of sufficient variation to analyze and interpret the results in terms of objectives under investigation. Low, medium and high estimates of narrow sense heritability and genetic advance were found in different plant characters under the study. Crosses ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25 of average fruit weight and some other crosses of yield attributes and quality characters also depicted high narrow sense heritability along with high genetic advance, so it indicated higher additive gene action and lower environmental factors in the expression of these traits with possibility of improvement through selection.

Keywords: Bottle gourd, F₁ hybrids, genetic advance, narrow heritability, segregating generations

Introduction

Bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] is one of the earliest domesticated vegetable crops belonging to the family Cucurbitaceae. It is a diploid species with a chromosome number of $2n = 2x = 22$ and is monoecious in nature. The crop exhibits a high degree of natural cross-pollination, ranging from 60 to 80 per cent, which contributes to extensive variability in morphological and yield related traits. Bottle gourd is cultivated primarily for its tender fruits, which are easily digestible and possess appreciable nutritional value, containing carbohydrates, minerals and vitamins. In certain tribal communities, dried bottle gourd fruits are traditionally used for making domestic utensils and musical instruments.

In India, vegetable cultivation forms an integral part of the horticultural sector and contributes substantially to agricultural growth and rural livelihoods. Recent estimates indicate that the horticultural area reached approximately 29.09 million hectares with a production of 367.70 million tonnes during 2024-25 (Anonymous, 2024) [3]. Despite this progress, average productivity in many regions remains below its attainable genetic potential. In Gujarat, bottle gourd cultivation is predominantly based on locally available landraces characterized by considerable genetic heterogeneity and lack of uniformity, resulting in inconsistent yield performance. Consequently, there exists a pressing need for systematic genetic improvement through scientifically designed breeding programmes.

Estimate of heritability serves as a useful guide to the plant breeder. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad-sense heritability) or additive (narrow-sense heritability) effects, which is the portion of genetic variation that is

fixable in pure lines. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to the relatively smaller contribution of the environment to the phenotype. Conversely, for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects.

Heritability in narrow sense (h_{ns}^2)

The narrow-sense heritability, which represents the portion of genetic variation fixable in pure lines, was estimated using the formula suggested by Warner (1952) [40].

The estimation was calculated as follows:

$$h_{ns}^2 (\%) = \frac{[2VF_2 - (VBC_1 + VBC_2)]}{VF_2} \times 100$$

Where,

h_{ns}^2 = Heritability in narrow sense

VF_2 = Variance of F_2 generation

VBC_1 = Variance of BC_1 generation

VBC_2 = Variance of BC_2 generation

Low, moderate and high heritability are not rigidly defined as they vary from character to character. In the present study, heritability percentages were categorized according to the criteria proposed by Robinson *et al.* (1949) [27]:

1. **Low heritability:** 0 - 30%
2. **Moderate heritability:** 30 - 60%
3. **High heritability:** > 60%

Genetic advance as per cent of mean

Genetic advance (GA) serves as a measure of the gain obtained from phenotypic selection for a particular character. High genetic advance coupled with high heritability estimates offers the most suitable condition for selection. The expected genetic advance at a 5 per cent level of selection intensity was estimated using the formula suggested by Johnson *et al.* (1955) [22]:

$$\text{Expected Genetic Advance} = K \cdot h_{(ns)}^2 \cdot \hat{\sigma}_p$$

Where,

$h_{(ns)}^2$ = Heritability in narrow sense

$\hat{\sigma}_p$ = Phenotypic standard deviation

K = Selection differential ($K = 2.06$ at 5% selection pressure)

Expected genetic advance as per cent of mean (expected genetic gain) was estimated using the following formula:

Expected Genetic Advance as % of mean =

$$\frac{\text{Genetic advance}}{\bar{X}} \times 100$$

Where, $\bar{X}$ = Mean of the character under experiment

The value of expected genetic advance for various characters was demarcated into three categories according to Johnson *et al.* (1955) [22]:

1. **Low genetic advance:** 0 - 10%
2. **Moderate genetic advance:** 10 - 20%

3. High genetic advance: > 20%

Narrow-sense heritability is more helpful in the selection of segregating populations, as it excludes non-fixable dominance and epistatic variances. For this reason, genetic advance was calculated on the basis of narrow-sense heritability to ascertain more reliable results regarding the improvement of fruit yield and its component traits in bottle gourd.

Methodology

The present investigation was conducted at the Centre for Vegetable Research, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat, during *Kharif* 2023, Summer 2024 and *Kharif* 2024. The experimental material comprised five parental lines, viz., GPBG 108, ABGS 11-24, ABGS 14-25, ABG 1 and NDBG 132, which were utilized to develop four crosses, namely GPBG 108 × ABGS 11-24, GPBG 108 × ABGS 14-25, ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25. Six basic generations, viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 , were developed following standard breeding procedures in bottle gourd. The F_1 hybrids were produced during *Kharif* 2023, F_2 generations were obtained by selfing the respective F_1 plants and backcross generations were developed during Summer 2024 by crossing F_1 plants with their respective parents. The list of pedigree and source of female and male parents used in crossing programme is given in Table 1.

Crossing programme

In bottle gourd, anthesis takes place during early morning hours. The female and male flower buds which were likely to open on the following day were selected and covered with butter paper bags during evening hours to avoid contamination by foreign pollen. On the day of anthesis, the bags were carefully removed in the morning hours. The pollen from freshly opened male flowers of the desired parent was collected and gently rubbed on the receptive stigma of the female flower. After pollination, the flowers were immediately covered again with butter paper bags and properly tagged indicating the name of the cross and date of pollination. For maintenance of parental lines and production of F_2 seeds, selfing was carried out by pollinating the female flower with pollen from the same plant and re-bagging the flower after pollination. The F_1 seeds of four crosses were produced. Then F_2 generation was developed by selfing F_1 plants, whereas backcross generations (BC_1 and BC_2) were developed by crossing F_1 with respective P_1 and P_2 parents. The seeds obtained from successful pollinations were extracted from fully mature fruits, dried properly and stored for further evaluation. List of crosses used for present experiment mentioned in Table 2.

Evaluation programme

All six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 of the four crosses were evaluated at the Centre for Vegetable Research, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar, Gujarat during *Kharif* 2024. The experimental material was evaluated in a Compact Family Block Design (CFBD) with three replications. Each replication was divided into four family blocks representing individual crosses and each family block consisted of six generations. Each block comprised eleven rows consisting

of one row each of P_1 , P_2 and F_1 , four rows of F_2 and two rows each of BC_1 and BC_2 generations. The crop was raised by following the recommended agronomic practices and

necessary plant protection measures to ensure successful crop growth and development.

Table 1: Bottle gourd parental lines and source of procurement

Sr. No.	Genotype	Source
1	GPBG 108	Main Vegetable Research Station, Anand
2	ABGS 11-24	Main Vegetable Research Station, Anand
3	ABGS 14-25	Main Vegetable Research Station, Anand
4	ABG 1	Main Vegetable Research Station, Anand
5	NDBG 132	Main Vegetable Research Station, Anand

Table 2: List of crosses used for generation mean analysis

Sr. No.	Cross designation	P_1	P_2	F_1	F_2	BC_1	BC_2
1	GPBG 108 × ABGS 11-24	GPBG 108	ABGS 11-24	$P_1 \times P_2$	F_1 selfed	$F_1 \times P_1$	$F_1 \times P_2$
2	GPBG 108 × ABGS 14-25	GPBG 108	ABGS 14-25	$P_1 \times P_2$	F_1 selfed	$F_1 \times P_1$	$F_1 \times P_2$
3	ABG 1 × ABGS 14-25	ABG 1	ABGS 14-25	$P_1 \times P_2$	F_1 selfed	$F_1 \times P_1$	$F_1 \times P_2$
4	NDBG 132 × ABGS 14-25	NDBG 132	ABGS 14-25	$P_1 \times P_2$	F_1 selfed	$F_1 \times P_1$	$F_1 \times P_2$

Results and Discussion

Analysis of variance for experimental design

Analysis of variance for generation means comprising six generations viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 was computed for twelve characters in four crosses of bottle gourd [*Lagenaria siceraria* (Mol.) Standl.] and the results are presented in Table 3. The analysis of variance between families (crosses) revealed that the mean squares due to crosses were highly significant for all the characters studied. Likewise, significant differences among generations were observed for all the characters in all the four crosses, indicating the existence of substantial variability among the

generations derived from the respective parental combinations.

The significant variation observed among generations suggested the presence of adequate genetic variability for fruit yield and its component traits, thereby providing sufficient scope for generation mean analysis and interpretation of gene effects. The existence of considerable variability among the generations may be attributed to the genetic divergence among the parental lines involved in the crosses. Such variability among the generations is essential for effective selection and genetic improvement of yield and its associated traits in bottle gourd.

Table 3: Analysis of variance between families and between progenies within family of six generations for different characters in bottle gourd

Sources	D.F.	Mean sum of squares					
		Days to first male flower appearance	Days to first female flower appearance	Node number at which first male flower appearance	Node number at which first female flower appearance	Number of branch per plant	Fruit length
Analysis of variance between families							
Replications	2	0.05	0.04	0.02	0.04	0.15	0.02
Crosses	3	9.12**	9.15**	10.68**	15.69**	0.81**	64.60**
Error	6	0.05	0.01	0.03	0.03	0.03	0.01
χ^2		NS	NS	S	S	NS	NS
Analysis of variance between progenies within family							
Cross-I (GPBG 108 × ABGS 11-24)							
Replications	2	0.02	0.07	0.37	0.25	0.33	0.11
Generations	5	19.50**	35.59**	18.64**	21.87**	98.35**	22.09**
Error	10	0.49	0.17	0.09	0.08	0.29	0.26
Cross-II (GPBG 108 × ABGS 14-25)							
Replications	2	0.50	0.01	0.28	0.50	0.23	0.06
Generations	5	8.92**	50.17**	7.17**	16.68**	105.53**	60.11**
Error	10	0.16	0.09	0.24	0.13	0.20	0.18
Cross-III (ABG 1 × ABGS 14-25)							
Replications	2	0.26	0.13	0.02	0.02	0.03	0.06
Generations	5	23.87**	88.28**	8.82**	21.75**	53.66**	10.60**
Error	10	0.19	0.04	0.04	0.03	0.13	0.58
Cross-IV (NDBG 132 × ABGS 14-25)							
Replications	2	0.39	0.21	0.04	0.04	0.94	0.10
Generations	5	67.10**	103.04**	14.16**	19.02**	117.69**	40.00**
Error	10	0.24	0.15	0.05	0.04	0.48	0.54

*, **, Significant at 5% and 1%, respectively;

Chi-square for Bartlett's test of homogeneity of error variances, S = Significant, HS = Highly significant and NS = non-significant

(Table 4.1 continued)

Sources	D.F.	Mean sum of squares					
		Fruit girth	Average fruit weight	Number of fruit per plant	Yield per plant	Moisture content	Total soluble solids
Analysis of variance between families							
Replications	2	0.003	0.001	0.02	0.002	0.01	0.001
Crosses	3	0.87**	0.134**	1.83**	0.30**	4.99**	0.13**
Error	6	0.01	0.001	0.02	0.001	0.07	0.002
χ^2		NS	HS	S	NS	NS	NS
Analysis of variance between progenies within family							
Cross-I (GPBG 108 × ABGS 11-24)							
Replications	2	0.04	0.002	0.04	0.011	0.60	0.003
Generations	5	13.86**	0.005**	11.08**	1.04**	34.36**	0.30**
Error	10	0.21	0.001	0.06	0.005	0.40	0.01
Cross-II (GPBG 108 × ABGS 14-25)							
Replications	2	0.02	0.004	0.04	0.001	0.26	0.01
Generations	5	10.94**	0.006**	5.11**	0.61**	4.58**	0.52**
Error	10	0.10	0.001	0.07	0.004	0.10	0.01
Cross-III (ABG 1 × ABGS 14-25)							
Replications	2	0.14	0.01	0.10	0.004	0.50	0.003
Generations	5	7.91**	0.12**	5.91**	0.54**	32.27**	0.60**
Error	10	0.09	0.01	0.16	0.01	0.42	0.003
Cross-IV (NDBG 132 × ABGS 14-25)							
Replications	2	0.01	0.001	0.31	0.01	0.01	0.02
Generations	5	5.90**	0.01**	2.18**	0.95**	21.66**	0.30**
Error	10	0.09	0.001	0.39	0.005	0.14	0.01

*, **, Significant at 5% and 1%, respectively;

Chi-square for Bartlett's test of homogeneity of error variances, S = Significant, HS = Highly significant and NS = non-significant

Days to first male flower appearance

Highest narrow-sense heritability was observed in ABG 1 × ABGS 14-25 with 76.25%, whereas the lowest heritability was observed in NDBG 132 × ABGS 14-25 with 6.02%. Highest genetic advance was observed in ABG 1 × ABGS 14-25 with 5.03% and lowest genetic advance was observed in NDBG 132 × ABGS 14-25 with 0.47%. High heritability coupled with low genetic advance was observed in ABG 1 × ABGS 14-25, which indicated non-additive gene action and selection may not be rewarding. Low heritability coupled with low genetic advance was observed in NDBG 132 × ABGS 14-25, which also indicated non-additive gene action and selection may not be rewarding. Similar observations were reported by Kandasamy *et al.* (2019) [23], Srirom and Yadav (2021) [34], Dubey *et al.* (2022) [13], Duhan *et al.* (2022) [14], Das *et al.* (2024) [9] and Suman *et al.* (2024) [35].

Days to first female flower appearance

Highest narrow-sense heritability was observed in GPBG 108 × ABGS 14-25 with 83.11%, whereas the lowest heritability was observed in ABG 1 × ABGS 14-25 with 40.11%. Highest genetic advance was observed in GPBG 108 × ABGS 14-25 with 5.65% and lowest genetic advance was observed in ABG 1 × ABGS 14-25 with 2.11%. High heritability coupled with low genetic advance was observed in GPBG 108 × ABGS 14-25, whereas moderate heritability coupled with low genetic advance was observed in ABG 1 × ABGS 14-25. These results indicated non-additive gene action and selection may not be rewarding. Similar findings were reported by Srirom *et al.* (2021) [34], Venkataraman *et al.* (2021), Dubey *et al.* (2022) [13], Duhan *et al.* (2022) [14], Harika *et al.* (2024) [18], Suman *et al.* (2024) [35], Das *et al.* (2024) and Kumar *et al.* (2025) [25].

node number at which first male flower appearance

Highest narrow-sense heritability was observed in GPBG 108 × ABGS 14-25 with 193.36%, whereas the lowest heritability was observed in ABG 1 × ABGS 14-25 with 3.84%. Highest genetic advance was observed in GPBG 108

× ABGS 14-25 with 209.67% and lowest genetic advance was observed in ABG 1 × ABGS 14-25 with 0.76%. High heritability coupled with high genetic advance was observed in GPBG 108 × ABGS 14-25, which indicated additive gene action and selection may be effective. Low heritability coupled with low genetic advance was observed in ABG 1 × ABGS 14-25, which indicated non-additive gene action and selection may not be rewarding. Similar findings were reported by Sharma and Sengupta (2013) [28], Deepthi *et al.* (2016) [11], Chikkeri *et al.* (2018) [6], Varalakshmi *et al.* (2018) [37], Kandasamy *et al.* (2021), Dubey *et al.* (2022) [13] and Harika *et al.* (2024). However, similar observations were also reported by Srirom *et al.* (2021) [34], Venkataraman *et al.* (2021), Bashir *et al.* (2024) [5] and Kumar *et al.* (2025) [25], who reported low or moderate heritability coupled with low or moderate genetic advance and suggested non-additive gene action and selection may not be rewarding.

Node number at which first female flower appearance

No estimable estimates of narrow-sense heritability and genetic advance were obtained for node number at which first female flower appearance in any of the four crosses. Therefore, meaningful interpretation regarding the nature of gene action and effectiveness of selection could not be made for this trait.

Number of branch per plant

For number of branch per plant, moderate narrow-sense heritability was observed in GPBG 108 × ABGS 14-25 with 58.51%, whereas no estimable heritability was observed in GPBG 108 × ABGS 11-24, ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25. Genetic advance was observed only in GPBG 108 × ABGS 14-25 with 9.17%. Moderate heritability coupled with low genetic advance was observed in GPBG 108 × ABGS 14-25, which indicated non-additive gene action and selection may not be rewarding. The results of the present investigations are in conformity with the findings of Dubey *et al.* (2022) [13], Duhan *et al.* (2022) [14],

Band *et al.* (2024) ^[4], Das *et al.* (2024) ^[9] and Harika *et al.* (2024) ^[18], who reported moderate or high heritability coupled with low genetic advance and suggested non-additive gene action and selection may not be rewarding.

Fruit length (cm)

No estimable estimates of narrow-sense heritability and genetic advance were obtained for fruit length in any of the four crosses. Therefore, meaningful interpretation regarding the nature of gene action and effectiveness of selection could not be made for this trait.

Fruit girth (cm)

In fruit girth, highest narrow-sense heritability was observed in GPBG 108 × ABGS 14-25 with 88.75%, whereas moderate heritability was observed in GPBG 108 × ABGS 11-24 with 57.98%. No estimable heritability was observed in ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25. Highest genetic advance was observed in GPBG 108 × ABGS 14-25 with 14.65% and lowest genetic advance was observed in GPBG 108 × ABGS 11-24 with 9.28%. High heritability coupled with moderate genetic advance was observed in GPBG 108 × ABGS 14-25, which indicated additive gene action and selection may be effective. Moderate heritability coupled with low genetic advance was observed in GPBG 108 × ABGS 11-24, which indicated both additive and non-additive gene action. Same results were reported by Sharma and Sengupta (2013) ^[28], Deepthi *et al.* (2016) ^[11], Chikkeri *et al.* (2018) ^[6], Varalakshmi *et al.* (2018) ^[37], Kandasamy *et al.* (2019) ^[13], Dubey *et al.* (2022) ^[13], Suman *et al.* (2024) ^[35] and Yogesh Kumar *et al.* (2025) ^[25], who reported high heritability coupled with high or moderate genetic advance and suggested additive gene action and effectiveness of selection.

Average fruit weight (g)

Highest narrow-sense heritability was observed in NDBG 132 × ABGS 14-25 with 93.64%, followed by ABG 1 × ABGS 14-25 with 92.23%, whereas the lowest heritability was observed in GPBG 108 × ABGS 11-24 with 22.22%. No estimable heritability was observed in GPBG 108 × ABGS 14-25. Highest genetic advance was observed in ABG 1 × ABGS 14-25 with 111.29%, followed by NDBG 132 × ABGS 14-25 with 74.31%, while the lowest genetic advance was observed in GPBG 108 × ABGS 11-24 with 18.34%. High heritability coupled with high genetic advance was observed in ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25, which indicated additive gene action and selection may be effective. Low heritability coupled with moderate genetic advance was observed in GPBG 108 × ABGS 11-24, which indicated non-additive gene action and selection may not be rewarding. Similar findings were reported by Sharma and Sengupta (2013) ^[28], Deepthi *et al.* (2016) ^[11], Varalakshmi *et al.* (2018) ^[37], Kandasamy *et al.* (2019) ^[23], Ahmad *et al.* (2022), Dubey *et al.* (2022) ^[13], Duhan *et al.* (2022) ^[14], Band *et al.* (2024) ^[4] and Das *et al.* (2024) ^[9]. However, similar observations were also reported by Srirom and Yadav (2021) ^[34], Venkataraman *et al.* (2021), Bashir *et al.* (2024) ^[5] and Suman *et al.* (2024) ^[35], who reported low or moderate heritability coupled with low or moderate genetic advance and suggested non-additive gene action and selection may not be rewarding.

Number of fruit per plant

Low narrow-sense heritability was observed in GPBG 108 × ABGS 11-24 with 11.51%, whereas no estimable heritability was observed in GPBG 108 × ABGS 14-25, ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25. Genetic advance was observed only in GPBG 108 × ABGS 11-24 with 2.32%. Low heritability coupled with low genetic advance was observed in GPBG 108 × ABGS 11-24, which indicated non-additive gene action and selection may not be rewarding. Similar observations were reported by Ahmad *et al.* (2022) ^[2], who reported low heritability coupled with low genetic advance and suggested non-additive gene action and selection may not be rewarding.

Yield per plant (kg)

Low narrow-sense heritability was observed in ABG 1 × ABGS 14-25 with 20.63%, whereas no estimable heritability was observed in GPBG 108 × ABGS 11-24, GPBG 108 × ABGS 14-25 and NDBG 132 × ABGS 14-25. Genetic advance was observed only in ABG 1 × ABGS 14-25 with 2.03%. Low heritability coupled with low genetic advance was observed in ABG 1 × ABGS 14-25, which indicated non-additive gene action and selection may not be rewarding. However, the findings are also supported by Varalakshmi *et al.* (2018) ^[37], Kumar *et al.* (2021) ^[24], Srirom and Yadav (2021) ^[34], Venkataraman *et al.* (2021) and Bashir *et al.* (2024) ^[5], who reported low heritability and suggested non-additive gene action and selection may not be rewarding.

Moisture content (%)

Highest narrow-sense heritability was observed in GPBG 108 × ABGS 11-24 with 78.58%, followed by NDBG 132 × ABGS 14-25 with 70.05%, whereas no estimable heritability was observed in GPBG 108 × ABGS 14-25 and ABG 1 × ABGS 14-25. Highest genetic advance was observed in GPBG 108 × ABGS 11-24 with 2.55% and lowest genetic advance was observed in NDBG 132 × ABGS 14-25 with 1.64%. High heritability coupled with low genetic advance was observed in GPBG 108 × ABGS 11-24 and NDBG 132 × ABGS 14-25, which indicated non-additive gene action and selection may not be rewarding. Similar findings were reported by Harika *et al.* (2024) ^[18] and Band *et al.* (2024), who reported high heritability for this trait.

Total soluble solids (Brix°)

Highest narrow-sense heritability was observed in GPBG 108 × ABGS 14-25 with 121.22%, followed by ABG 1 × ABGS 14-25 with 116.32% and NDBG 132 × ABGS 14-25 with 114.69%, whereas no estimable heritability was observed in GPBG 108 × ABGS 11-24. Highest genetic advance was observed in GPBG 108 × ABGS 14-25 with 17.97% and lowest genetic advance was observed in ABG 1 × ABGS 14-25 with 10.77%. High heritability coupled with moderate genetic advance was observed in GPBG 108 × ABGS 14-25, ABG 1 × ABGS 14-25 and NDBG 132 × ABGS 14-25, which indicated additive gene action and selection may be effective. Similar findings were reported by Suman *et al.* (2024), who reported high heritability coupled with high genetic advance and suggested additive gene action.

Table 4: Estimates of heritability and genetic advance for days to first male flower appearance, days to first female flower appearance, node number at which first male flower appearance, node number at which first female flower appearance, number of branch per plant and fruit length (cm) in four crosses of bottle gourd

Particulars	Estimates (%)					
	Days to first male flower appearance	Days to first female flower appearance	Node number at which first male flower appearance	Node number at which first female flower appearance	Number of branch per plant	Fruit length
Cross-I (GPBG 108 × ABGS 11-24)						
Heritability (ns) %	-	-	-	-	-	-
Genetic Advance %	-	-	-	-	-	-
Cross-II (GPBG 108 × ABGS 14-25)						
Heritability (ns) %	-	83.11	193.36	-	58.51	-
Genetic Advance %	-	5.65	209.67	-	9.17	-
Cross-III (ABG 1 × ABGS 14-25)						
Heritability (ns) %	76.25	40.11	3.84	-	-	-
Genetic Advance %	5.03	2.11	0.76	-	-	-
Cross-IV (NDBG 132 × ABGS 14-25)						
Heritability (ns) %	6.02	-	-	-	-	-
Genetic Advance %	0.47	-	-	-	-	-

" - " represent negative value

Table 5: Estimates of heritability and genetic advance for fruit girth (cm), average fruit weight (g), number of fruit per plant, yield per plant (kg), moisture content (%) and total soluble solid (°Brix) in four crosses of bottle gourd

Particulars	Estimates (%)					
	Fruit girth	Average fruit weight	Number of fruit per plant	Yield per plant	Moisture content	Total soluble solids
Cross-I (GPBG 108 × ABGS 11-24)						
Heritability (ns) %	57.98	22.22	11.51	-	78.58	-
Genetic Advance %	9.28	18.34	2.32	-	2.55	-
Cross-II (GPBG 108 × ABGS 14-25)						
Heritability (ns) %	88.75	-	-	-	-	121.22
Genetic Advance %	14.65	-	-	-	-	17.97
Cross-III (ABG 1 × ABGS 14-25)						
Heritability (ns) %	-	92.23	-	20.63	-	116.32
Genetic Advance %	-	111.29	-	2.03	-	10.77
Cross-IV (NDBG 132 × ABGS 14-25)						
Heritability (ns) %	-	93.64	-	-	70.05	114.69
Genetic Advance %	-	74.31	-	-	1.64	14.18

" - " represent negative value

Conclusion

The heritability estimates along with genetic advance is normally more helpful in predicting the gain under selection than heritability alone. High to moderate heritability coupled with moderate to high genetic advance was observed in node number at which first male flower appearance in cross (GPBG 108 × ABGS 14-25) and in average fruit weight in crosses (ABG 1 × ABGS 14-25) and (NDBG 132 × ABGS 14-25). It revealed that these crosses were controlled by additive genes and hence simple selections should lead to a fast genetic improvement of the genotypes used in the study. Some crosses showed high to medium narrow sense heritability coupled with low genetic advance, so bi-parental mating or few cycles of recurrent selection should be used for improvement in such characters. Crosses with low narrow sense heritability coupled with low genetic advance indicated presence of non-additive type of gene action and selection should not be rewarding for these characters.

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