ISSN 2515-8260 Volume 07, Issue 03, 2020

A STUDY ON BOTTLE GOURD HETEROSIS COMBINING CAPACITY AND GENE ACTION

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DOI:10.48047/ejmcm/v07/i03/621

Abstract

In the first experiment, 20 hybrids were produced using a line x tester mating pattern from a total of nine parents (five testers and four lines). In a randomized block design with three replicates, we analyzed the experimental materials for 16 characters. Variability was found between parents and hybrids for majority of the features analyzed, and analysis of variance confirmed substantial variations between genotypes for all traits. The highest mean fruit output per plant was found in the offspring of the ABG 1 and NDBG 132 (female) and DBG 5 and DBG 6 (male) hybrids. The most significant and desirable hybrids were NDBG 132 x DBG 5, Pusa Naveen x DBG 6, and ABG 1 x DBG 5 for fruit yield per plant, ascorbic acid, total sugar, fruit weight, and number of fruits per plant, and ABG 1 x DBG 5 for antioxidant activity.

Keywords: *Bottle, Gourd Heterosis, Combining Capacity, Gene Action.*

1. Introduction

The bottle gourd is a plant with a vinous, pubescent stem that is thick and five-angled. It's an annual plant with huge, round leaves made of oxalate and tendrils that may grow to be 15 metres in length and spread out horizontally or ascend vertically. The plant is monoecious, meaning that it produces distinct male and female flowers in the axils of its leaves. The pistillate blooms only have one pistil, and their ovary and peduncle are covered in hairs. Large, white, five-petaled corollas are carried on lengthy peduncles by the staminate blooms. Even though the flowers bloom at night, they could stay open until lunchtime the next day. across 60% and 80% of the pollen is transferred across different species.[1-2]

Both the length (10-90 cm) and the form (curved necked, cylindrical, long, flat-round, conical, pear-shaped, club-shaped, etc.) of a bottle gourd's fruit may vary widely. However, cylindrical, round-oval, and oblong forms predominate. In general, light green, green, or dark green in colour, with white pulp and big white soft seeds, are the most desirable hues for

commercially viable sensitive edible fruits. Although it looks like a berry, the ripe fruit has a rough skin.[3]

The bottle gourd is most often prepared as a vegetable. Additionally, it is used in the cooking of rayata, curries, juice, and pickle made from young fruits. The young leaves of the bottle gourd are a popular leafy vegetable in several parts of the world. Patients are encouraged to eat the fruits and vegetables in prepared forms because of their great digestibility. Bottle gourd dry shells have a long history of cultural significance as both a practical and decorative tool. Some musical instruments are crafted from dried bottle gourd fruits with thick, bitter skins.[4-5]

The minerals in bottle gourd are highly regarded. There are 96.1% water, 0.1% fat, 2.5% carbs, 0.2% protein, and 2.0% fibre in the edible part of fruit. The fruit provides a rich source of vitamins, which are essential for the human diet. Some people have found relief from constipation, coughing, and night blindness by eating the pulp of a bottle gourd, while others have used it as a poison antidote. When temperatures soar, you may relieve the pain in your feet and hands by rubbing the sliced surface of a tiny fruit.[6-7]

2. Literature review

Cavalli, L. L. (2020) Breeders rely heavily on heterosis breeding for crop development, since it has been universally recognised as a significant advancement in breeding methodology. The word "heterosis" is used to describe the occurrence of an increase or reduction in the mean value of an F1 population above its mid parental value as a result of a cross between two genetically different individuals. Relative heterosis (RH) or mid-parent heterosis is the most common name for this phenomenon. Since maize was the first crop to successfully commercialise heterosis, many other crops—including bajra, cotton, castor, sorghum, etc.—have followed suit, referring to the phenomenon as the stimulation of heterozygosis. Later on, a new word called "Heterobeltiosis" was proposed to characterise the rise or fall in the average value of F1 in comparison to its superior father.[8]

Dubois, M. & Smith, F. (2019) put out the idea of generic and specialised combination competence. They determined that a line's general combining ability (gca) was its typical performance in a set of hybrid crosses. The term "specific combining ability" (sca) is used to describe situations when certain cross combinations do much better or worse than would be predicted based on the average performance of the lines involved. The GCA is related to the

genes that have additive effects and can be fixed, whereas the SCA relies more on genes with dominance and epistasis and cannot. In order to create a successful breeding project, it is crucial to have a thorough understanding of the genetic diversity present in every crop you are working on.[9]

Dutta, O.P. (2018) Heritability is defined as the proportion of a trait's observed phenotypic variation that may be attributed to genetic factors. Therefore, heritability refers to the amount of phenotypic variation that may be attributed to genetics. This method of estimating heredity, called broad sense heritability, holds water when studying homozygous lines. Narrow sense heritability refers to the relative importance of the additive component of genetic variation relative to the total (phenotypic) variance in passing traits down through the generations. Heritability, therefore, is a measure of how much of a trait's variation may be attributed to genetics. The extent to which a given system can isolate genotypes in order to take advantage of genetic diversity is referred to as its heritability. Heritability estimations are helpful for plant breeders since they constitute the foundation for selecting for a desired phenotype.[10]

Fonesca, S., & Patterson, F. L. (2017) To learn about the specifics of the gene influences at play in character expression, generation mean analysis is an effective method. Generation mean analysis using first degree statistics is a typical method used to determine the nature of gene impact, and it is accurate and provides a detailed explanation of gene effects. Unlike generation mean analysis, which provides information on non-allelic gene actions operating in the inheritance of the traits, diallel analysis and lines x tester analysis in bottle gourd have generated information on the nature and relative magnitude of the genetic component of variation (additive and dominance).[11]

Ghevaria, P. K. & Dhameliya, H. R. (2016) Methods that offer information on mean effects of individual genes, interactions within gene of the same locus, and interactions among genes of various loci were necessary for assessing the degree of genetic influences on the expression of quantitative characteristics. It is preferable to effectively use the accessible genetic diversity in order to maximise the production potential. Further elucidation of the source and extent of genetic variation in a population may be gained by genetic study of quantitative features. In a crop development effort, the breeding strategy that is ultimately chosen depends crucially on the estimations of gene effects. In developing pure lines,

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additive gene effects are helpful, but in taking advantage of hybrid vigour, dominance and epistatic effects may be used.[12]

3. Methodology

3.1 Experimental material

In this study, we used a Line x Tester mating system, which resulted in 20 F1 offspring from four female "lines" and five male "testers" (Table 3.1). Main Vegetable Research Station, Anand Agricultural University, Anand, India, generated the seeds of 20 F1 hybrids and 9 parents by hand pollination and selfing, respectively, in the summer of 2019.

3.2 Crossing and selfing techniques

The 2019 harvest season was when the crossing and selfing efforts were made. The F1 seeds were from hand-pollinated hybridization. Bottle gourd anther dehiscence occurs between 11 a.m. and 2 p.m., while anthesis occurs between 5 p.m. and 8 p.m. for both staminate and pistillate flowers. For up to 30 hours after a flower opens, the stigma may still receive pollen. Only after 24 hours had passed after pollination was the fruit visible. Bandage cotton must be thoroughly wrapped around the male and female flower that is expected to blossom that evening before 10 a.m.

3.3 Experimental design

In Kharif of 2019, 20 F1 hybrids and 9 of their parents were tested using a randomized block design with three replicates. One 5-m-long row plot was used to show variation among genotypes. Row spacing was maintained at 2 m between rows and 1.5 m inside a row. To ensure a successful harvest, we used every strategy indicated.

Table: 3.1. Genotypes of the Proposed Study's Parents

Sr.no.	Parents	Origin/Source of seed
FEMALEPARENTS		
1.	ABG1	AAU,Anand(Gujarat)
2.	PusaNaveen	ICAR-IARI,(NewDelhi)
3.	NDBG517	NDUA&T,Faizabad(UttarPradesh)
4.	NDBG-132	NDUA&T,Faizabad(UttarPradesh)

MALEPARENTS		
1.	PunjabLong	PAU,Ludhiana(Punjab)
2.	Samrat	MPKV,Rahuri(Maharashtra)
3.	DBG5	RAU,Jaipur(Rajasthan)
4.	DBG6	RAU,Jaipur(Rajasthan)
5.	NDBG104	NDUA&T,Faizabad(UttarPradesh)

3.4 Cultural practices

Both the nursery and the field adhered to the prescribed packages of agronomic practices necessary to develop a healthy crop.

3.5 Statistical analysis

Statistics were performed using the character averages in the following sections:

- Variance analysis
- Heterosis estimation
- Analysis of combining skills

3.6 Generation mean analysis

3.6.1 Experimental Material

Four families, totaling six generations (P1, P2, F1, F2, B1, and B2), served as the experimental material. From these five parents, four distinct families were born: ABG 1, Pusa Naveen, NDBG-132, DBG 5, and DBG 6. From a total of nine lines utilized in a previous experiment, these five parental lines were chosen due to their geographical diversity and variety in fruit yield components and quality aspects including Total soluble sugar (%), Ascorbic acid (%), and Antioxidant activity (%).

Each family's F1 seeds came from an earlier experiment. These F1s and their parents were raised in a breeding programme that produced new F1s and back crossings (B1 and B2) in 2019–2020. Both the parents and the F1s were selfed in the same growing season to produce next-generation seeds.

3.6.2 Experimental design

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In the summer of 2020, researchers used a Compact Family Block Design with three replicates to analyse data from a set of experimental materials consisting of four families, each with six generations (P1, P2, F1, F2, B1, and B2). The families were organized into blocks defined by the four crosses, while the generations P1, P2, F1, F2, B1, and B2 within each family stood for independent experimental units. There were six family blocks, one each for the P1, P2, and F1 generations, two each for the B1 and B2 generations, and four for the F2 generation, to reflect the individual replication. The distance between rows was 2 metres, while the distance inside a row was 1.5 metres. Good crop production resulted from diligent adherence to all approved agronomic practices and plant protection measures.

3.6.3 Statistical methods

Statistical analysis was performed using the following topics on the character data received from the recorded observations:

- Variance analysis
- Genealogical impact prediction
- The effects of inbreeding depression, heritability (in the strict sense), and genetic progress may be estimated.

4. Results

The results of an analysis of variance conducted on all sixteen characteristics between parents and hybrids are shown in Table 4.1. Except for the amount of fruits per plant, the data showed that the mean squares owing to genotypes were statistically significant. For all variables except fruits per plant, this suggested that there was enough genetic variety in the materials. Further subdividing the mean squares attributable to genotypes yielded three groups: parents, hybrids, and parents vs hybrids. Except for days to first male flower, days to first female flower, first male flowering node, first female flowering node, days to first picking, fruit length, fruit girth, number of fruits per plant, and antioxidant activity, the analysis revealed significant differences between parents for all characters.

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Table 4.1: Comparison of parent and offspring means in an analysis of variance (mean squares) for a number of bottle gourd traits

Sourcesofvariation	df	DFMF	DFFF	FMFN	FFFN	DFP	LOP	FL	FG
Replications	2	3.89	5.03	1.52	0.10	7.79	8.19	2.19	6.08*
Genotypes (G)	28	12.90**	16.28*	3.87**	3.07**	18.79**	15.43**	58.33**	6.53**
Parents(P)	8	8.03	8.61	2.16	2.96	12.31	15.01**	1.92	0.53
Females(F)	3	3.44	5.97	0.20	1.64	0.97	5.02	2.11	0.17
Male (M)	4	13.20	11.98	4.07*	4.09*	18.24	24.68**	1.17	0.94
(Fvs M)	1	1.12	3.01	0.41	2.37	22.66	6.27	4.38	0.07
Hybrids(H)	19	11.05*	12.35	4.77**	3.17**	17.35	8.82*	84.10**	8.02**
ParentsvsHybrid	1	93.57**	152.62**	0.46	2.20	98.10**	144.37**	19.90**	28.81
Error	56	5.96	8.44	0.15	1.48	8.91	5.11	2.30	1.80

Sourcesofvariation	df	FW	NFPP	FY	TSS	TSG	AA	AAT	CC
Replications	2	0.01	0.87	0.69	0.05	0.02	0.19	0.0023	0.00
Genotypes (G)	28	0.04**	5.06	5.08**	0.62**	0.63**	9.19**	0.0110*	0.41**
Parents(P)	8	0.02**	0.77	0.90*	1.20**	0.92**	2.88**	0.0004	0.62**
Females(F)	3	0.01	0.45	1.90**	0.72**	1.38**	0.57*	0.0008	0.53**
Males (M)	4	0.03**	0.84	0.23	0.50**	0.54**	5.20**	0.0007	0.40**
(F Vs M)	1	0.01	1.44	0.58	5.41**	1.04**	0.25	0.0001	1.71**
Hybrids(H)	19	0.05**	5.04	3.44**	0.31**	0.48**	11.92**	0.0242*	0.33**
ParentsvsHybrid	1	0.01	3.96	66.34	1.68	1.18	7.44**	0.0012	0.05
Error	56	0.01	0.41	0.39	0.02	0.03	0.18	0.0058	0.01

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In Table 4.2, we see the amplitude of heterosis for 16 characters as expressed as a percent increase or reduction of F1 over better parent (heterobeltiosis) and over standard check, ABG 1 (standard heterosis). When estimating heterosis based on traits like days to first male flower, days to first female flower, first male flowering node, first female flowering node, and days to first picking, the parent with the lowest score was favoured. The following paragraphs provide a summary of the findings per character type..

Table 4.2: Days to first male blossom and days to first female bloom in heterobeltiosis (HB) and standard heterosis (SH).

Crosses	Daystofirstmaleflower		Daystofirstfemaleflower	
	BP(%)	SC (%)	BP(%)	SC(%)
ABG1×PunjabLong	-8.74*	-9.84*	-9.06	-11.00*
ABG 1×Samrat	-13.56**	-13.56**	-14.91**	-14.91**
ABG1×DBG5	7.07	1.29	1.89	-1.17
ABG1×DBG6	3.09	-3.02	4.27	-4.36
ABG1× NDBG104	-7.25	-9.90*	-9.01	-10.94*
PusaNaveen×PunjabLong	0.9	-4.31	-2.27	-6.75
PusaNaveen×Samrat	-2.31	-7.35	-3.02	-7.46
Pusa Naveen×DBG5	-3.39	-8.61*	-6.91	-11.17*
Pusa Naveen×DBG6	-2.99	-8.74*	-2.96	-10.99*
Pusa Naveen×NDBG 104	1.95	-3.31	0.62	-3.98
NDBG517× PunjabLong	-1.63	-3.84	-0.46	-5.98
NDBG517×Samrat	-3.81	-5.96	-0.68	-6.19
NDBG517× DBG5	-8.59	-13.52**	-9.03	-14.08**
NDBG517× DBG6	-1.52	-7.36	-2.84	-10.88*
NDBG517× NDBG104	-10.83	-13.31**	-9.01	-14.06**
NDBG132× PunjabLong	-7.16	-11.05*	-5.6	-10.83*
NDBG132×Samrat	-2.55	-6.63	-4.12	-9.44*
NDBG132× DBG5	2.58	-2.95	1.92	-3.73
NDBG132× DBG6	0.11	-5.82	0.31	-7.99
NDBG132×NDBG104	1.7	-2.56	-0.53	-6.05

S.E.±	**1.99**	**1.99**	**2.37**	**2.37**
Range	**-13.56to 7.07**	**-13.56to 1.29**	**-14.91to 4.27**	**-14.91to -1.17**
No. ofsignificantand+vecrosses	**-**	**-**	**-**	**-**
No. ofsignificantand-vecrosses	**2**	**8**	**1**	**10**

Heterobeltiosis varied from -13.56 (ABG 1 x Samrat) to 7.07% (ABG 1 x DBG 5), measured in days to first male bloom. Heterobeltiosis was only significantly negative in two hybrids, 13.56 (ABG 1 x Samrat) and 8.74 (ABG 1 x Punjab Long). Conversely, no hybrids showed any noticeable positive heterobeltiosis.

Generation mean analysis

Choosing parents for a crop improvement plan based only on their offspring's phenotypic performance may not always provide the best offspring. Segregating generations may produce inferior recombinants if phenotypically superior genotypes are used. Parentage decisions must, therefore, take genetic merit into account. To decode a complete genetic portrait of quantitative features, it is useful to examine the genetic components of variation.

Table 4.3 displays the results of an analysis of variance (ANOVA) performed on the means of the six generations (P1, P2, F1, F2, BC1, and BC2) that make up each cross.

Table 4.3: Comparative study of bottle gourd traits across four families and six generations

Source	df	Meansumofsquare							
		DFMF	**DFFF**	**FMFN**	**FFFN**	**DFP**	**LOP**	**FL**	**FG**
Betweenfamilycomparison									
Replication	2	0.66	0.55	0.00	0.00	0.45	0.61	1.10	0.04
Family	3	1.79	2.22	0.03	0.04	1.26	2.59	2.09	0.77**
Error	6	1.39	1.02	0.06	0.05	1.56	0.83	0.85	0.04
Betweenprogenieswithinfamilycomparison									
CrossI(ABG1xDBG5)									
Replication	2	0.05	0.16	0.68	0.53	0.28	1.54	20.82*	0.09
Generations	5	32.25*	14.24*	2.41**	2.55*	20.28*	23.45**	7.65	2.40*
Error	10	6.41	3.66	0.48	0.41	6.06	1.07	3.00	0.56
CrossII(PusaNaveenxDBG5)									
Replication	2	3.19	2.77	0.26	0.22	3.48	2.97	0.52	0.63
Generations	5	11.12*	7.93	0.33*	0.68*	9.22*	6.15**	5.98*	1.97*
Error	10	2.89	2.13	0.09	0.13	1.69	1.04	1.77	0.39
CrossIII(Pusa NaveenxDBG 6)									

Replication	2	18.04*	10.68	0.21	0.15	18.64	7.92	0.36	0.10
Generations	5	26.54**	19.37*	0.81*	1.05*	28.36*	18.72**	9.71*	2.55*
Error	10	4.17	5.79	0.16	0.30	6.09	2.69	2.22	0.75
CrossIV (NDBG132xDBG5)									
Replication	2	7.78	8.09	0.02	0.02	7.94	6.25	0.25	0.12
Generations	5	19.39**	16.65**	0.29*	0.21*	17.52*	15.25**	9.66*	2.70*
Error	10	2.54	2.03	0.08	0.06	3.79	1.69	1.92	0.80
Source	**df**	**Meansumofsquare**							
		FW	**NFPP**	**FY**	**TSS**	**TSG**	**AA**	**AAT**	**CC**
Betweenfamilycomparison									
Replication	2	0.00	0.00	0.03	0.01	0.00	0.00	0.002	0.00
Family	3	0.01	0.48**	0.59**	0.09**	0.01*	0.31**	0.015**	0.08**
Error	6	0.00	0.00	0.01	0.00	0.00	0.01	0.003	0.00
Betweenprogenieswithinfamilycomparison									
CrossI(ABG1xDBG5)									
Replication	2	0.00	0.01	0.02	0.00	0.00	0.10	0.001	0.00
Generations	5	0.01*	1.84**	2.52**	0.56**	0.59**	1.80**	0.022**	0.39**
Error	10	0.00	0.18	0.13	0.00	0.03	0.07	0.001	0.00
CrossII(PusaNaveenxDBG5)									
Replication	2	0.00	0.04	0.04	0.00	0.00	0.01	0.003	0.00
Generations	5	0.01*	2.16**	2.13**	1.25**	1.19**	2.25**	0.013**	0.44**
Error	10	0.00	0.25	0.36	0.00	0.03	0.05	0.001	0.00
CrossIII(Pusa NaveenxDBG 6)									
Replication	2	0.00	0.04	0.27	0.00	0.00	0.05	0.001	0.00
Generations	5	0.01*	3.67**	2.44**	1.47**	1.39**	2.89**	0.011**	0.56**
Error	10	0.00	0.29	0.21	0.00	0.01	0.06	0.003	0.00
CrossIV (NDBG132xDBG5)									
Replication	2	0.00	0.01	0.16	0.00	0.01	0.08	0.002	0.00
Generations	5	0.01*	0.72*	1.25*	0.16**	0.16**	1.25**	0.023**	0.12**
Error	10	0.00	0.19	0.26	0.01	0.01	0.02	0.002	0.00

Except for days to first male flower, days to first female flower, first male flowering node, first female flowering node, days to first picking, pedicel length, fruit length, and fruit weight, an analysis of variance showed significant differences across family comparisons for all parameters. Whereas, significant variations were seen between generations of all four crossings for all characteristics except fruit length in cross I and days to first female bloom in cross II, when compared using analysis of variance across generations within family comparisons. This meant that there was a wide enough range of materials to compare and contrast.

Table 4.4 displays the average generational performance of each family for a number of traits. P1 in family I had a mean value of 47.68, which was greater than P2's mean value of 45.66 by a little margin. F2 had a higher mean score (43.31 vs. 41.39), indicating no

inbreeding depression. The average of the first generation, or F1, or 41.39, was statistically equivalent to the average of the first two generations, or 47.58 and 45.66, respectively. Both B1 (45.29) and its recurrent parent P1 (47.68) had similar mean values. While the average of B2 was 38.60, the average of P2 was 45.66, suggesting the presence of epistasis gene activity.

Table 4.4: Statistics on bottle gourd mean values and standard deviations across six generations for several traits

Family	Generations						S.Em	C.D.(0.05)	C.V. (%)
	P_1	P_2	F_1	F_2	B_1	B_2			
Daystofirst maleflower									
I	47.68	45.66	41.39	43.31	45.29	38.60	1.46	4.61	5.80
II	45.94	44.16	40.47	44.22	42.46	44.73	0.98	3.10	4.90
III	46.04	42.85	38.38	44.57	44.00	39.65	1.18	3.12	4.80
IV	46.10	42.61	38.76	42.67	40.03	42.63	0.92	2.90	3.79
Daystofirst femaleflower									
I	52.05	50.46	46.06	48.18	50.03	47.60	1.11	3.48	3.90
II	50.50	48.83	45.99	49.03	47.33	49.59	0.80	2.66	3.01
III	50.76	47.76	43.40	49.46	49.05	47.52	1.39	4.38	5.02
IV	50.69	47.46	44.09	47.83	44.85	47.40	0.82	2.59	3.03
Firstmalefloweringnode									
I	8.14	8.35	6.32	8.07	9.04	7.87	0.40	1.27	8.77
II	8.43	8.25	7.48	8.26	7.93	8.02	0.18	0.57	6.90
III	7.40	8.77	7.65	8.35	7.75	8.31	0.23	0.74	5.05
IV	7.72	8.49	8.43	7.95	8.41	8.33	0.17	0.53	6.57
Firstfemalefloweringnode									
I	12.11	12.57	10.30	12.11	13.01	11.93	0.37	1.18	5.38
II	12.92	12.08	11.73	11.61	11.74	12.06	0.21	0.66	6.01
III	11.40	13.03	11.58	12.38	11.86	12.19	0.32	1.00	4.54
IV	11.96	12.53	12.45	11.95	12.51	12.23	0.14	0.45	6.77
Daystofirstpicking									
I	64.71	65.29	61.87	64.86	66.14	59.27	1.42	4.48	8.87
II	66.67	64.87	61.67	65.04	63.39	65.51	0.75	2.37	7.69
III	66.78	63.23	58.62	65.49	64.85	60.83	1.43	4.49	9.83
IV	66.79	63.42	60.01	63.73	60.78	63.47	1.12	3.54	6.30

Length ofpedicel									
I	17.51	14.85	12.75	13.20	14.02	8.99	0.60	1.89	7.63
II	15.27	13.55	11.25	13.78	12.48	14.47	0.59	1.86	7.50
III	14.24	11.58	8.80	14.18	14.16	9.47	0.95	2.99	13.50
IV	15.14	11.92	8.86	12.80	9.68	12.14	0.75	2.37	11.08
Fruitlength									
I	35.71	35.24	38.93	35.16	37.87	35.47	1.00	3.16	4.77
II	35.01	34.32	36.76	34.09	37.27	34.10	0.77	2.42	3.78
III	34.09	33.33	37.72	33.27	36.02	33.67	0.86	2.81	4.30
IV	33.98	33.20	37.60	33.09	35.89	34.66	0.80	2.52	4.01
Fruitgirth									
I	18.00	18.85	19.53	16.88	18.00	18.20	0.43	1.36	4.10
II	18.39	19.20	18.17	16.96	19.12	16.31	0.36	1.14	3.41
III	17.61	18.12	18.70	16.00	17.15	17.00	0.50	1.58	4.95
IV	17.47	18.02	18.61	15.82	17.02	17.31	0.52	1.64	5.18
Fruitweight									
I	0.69	0.76	0.88	0.83	0.81	0.80	0.04	0.11	7.88
II	0.70	0.76	0.81	0.72	0.85	0.73	0.03	0.09	6.37
III	0.70	0.64	0.82	0.70	0.71	0.71	0.03	0.10	7.43
IV	0.64	0.72	0.80	0.81	0.77	0.77	0.08	0.12	8.41
Numberoffruitsperplant									
I	5.02	5.26	7.15	6.01	5.36	6.14	0.25	0.77	7.30
II	4.90	5.69	7.43	8.48	5.91	6.38	0.29	0.93	8.30
III	4.73	3.91	5.67	6.80	5.87	6.59	0.31	0.98	9.62
IV	6.56	6.06	6.51	7.11	6.98	7.42	0.25	0.80	6.50
Fruit yieldperplant									
I	3.73	4.04	6.32	4.40	4.34	4.89	0.21	0.67	17.93
II	3.41	4.33	6.01	4.63	4.92	4.61	0.35	1.09	12.93
III	3.31	2.51	4.65	4.69	4.15	4.68	0.27	0.85	11.64
IV	4.20	4.35	5.22	5.65	5.38	5.66	0.30	0.94	10.22
Totalsolublesolids									
I	2.71	3.52	2.75	2.91	3.53	2.52	0.04	0.14	2.56

II	3.67	3.03	1.85	2.99	3.01	2.79	0.05	0.16	3.03
III	3.69	1.91	3.35	3.60	3.72	3.61	0.05	0.17	2.86
IV	3.17	3.66	3.39	3.08	3.03	3.16	0.07	0.23	3.87
Totalsolublesugar									
I	3.96	4.84	4.13	4.15	4.83	3.80	0.10	0.32	4.07
II	4.87	4.29	3.17	4.17	4.86	4.01	0.11	0.33	4.32
III	4.95	3.23	4.73	4.81	5.01	4.89	0.07	0.22	2.58
IV	4.37	4.92	4.71	4.43	4.36	4.38	0.07	0.23	2.74
Ascorbicacid									
I	5.50	7.30	6.64	5.54	6.59	5.47	0.16	0.49	4.38
II	6.28	6.02	4.78	5.68	7.29	5.30	0.13	0.42	3.19
III	6.85	4.87	7.59	6.38	7.37	7.01	0.15	0.46	3.83
IV	5.64	6.62	7.06	5.53	6.69	5.78	0.09	0.28	2.49
Antioxidantactivity									
I	0.06	0.08	0.08	0.06	0.07	0.06	0.00	0.00	3.85
II	0.05	0.07	0.06	0.08	0.06	0.04	0.00	0.00	3.01
III	0.08	0.06	0.08	0.07	0.08	0.08	0.00	0.01	4.46
IV	0.07	0.07	0.08	0.06	0.07	0.07	0.00	0.00	2.89
Chlorophyllcontent									
I	1.19	1.93	1.24	1.37	1.80	1.01	0.03	0.09	3.54
II	2.16	1.47	1.09	1.38	1.77	1.28	0.02	0.05	1.96
III	2.15	0.99	1.69	1.95	2.04	2.06	0.02	0.07	2.11
IV	1.62	1.88	1.91	1.42	1.46	1.59	0.04	0.13	4.33

P2 (with a mean value of 42.85) is substantially lower than P1 (with a mean value of 46.04) in family III. When compared to P1 (42.85 points) and P2 (46.04 points), the mean value of F1 (38.38) is much lower. B1's mean value (44.00) was comparable to that of P1, its recurrent parent, at 46.00. However, there was a large discrepancy between the means of B2 (39.65) and P2 (42.85), suggesting the presence of epistasis gene activity. The lack of inbreeding depression is shown by the much higher mean value of the F2 (44.57) generation compared to that of the F1 (38.38).

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In Family IV, there was a large disparity in parental income. Compared to the P1 (46.10) and P2 (42.61) generations, the F1 (38.76) generation had a much lower mean value. Both the F1 (38.76) and F2 (42.67) generations had considerably higher means, indicating no inbreeding depression had occurred. The B2 (42.63) generations were statistically equal to the mean value of F1 and their recurrent parent, indicating the existence of additivity of genes, whereas the B1 (40.03) generations were considerably lower with respective parents, revealing the potential of epistasis gene activity.

5. Conclusion

The hybrids NDBG 132 x DBG 5, Pusa Naveen x DBG 6, and ABG 1 x DBG 5, Pusa Naveen x DBG 5 demonstrated maximal standard heterosis and strong sca effects for fruit production per plant and its component qualities, making them attractive for commercial exploitation of heterosis. Multi-site research is needed before widespread production can begin. The kind of gene action involved in the manifestation of a trait determines the breeding system that may be used to increase that trait. It would be beneficial for the improvement of the characteristics under investigation if special care was taken with each individual cross throughout the segregating generations, since the kind and amount of gene effects varied for various characters within the same cross and for the same character across different crossings. In general, the pedigree selection approach may be used to enhance traits whose prevalence can be traced back to a fixable additive gene impact.

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