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Genetic studies in bitter gourd. (*Momordica charantia* L.)

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Abstract
The present investigation entitled "Genetic studies in Bitter gourd (*Momordica charantia* L.)" was undertaken during summer and *kharif* 2020-2021 by following generation mean analysis to obtain information on gene effects, heritability and genetic advance for various quantitative characters. Three possible crosses involving four parents (RHRBG-26, RHRBG-24, RHRBG-10 and RHRBG-29) with six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for each of these crosses were evaluated in randomized block design with two replications during summer 2021 at the All India Coordinated Research Project on Vegetable Crops, Department of Horticulture, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahmednagar (Maharashtra). All three types of gene actions *viz*., additive, dominance and epistasis (i, j and l) were present in most of the combinations for almost all characters under study and these characters can be improved by reciprocal recurrent selection. Duplicate type of epistasis were observed in all crosses for number of branches per vine, length of vine, days to first picking, days to last picking, length of fruit, weight of fruit, fruit fly and some crosses also showed duplicate type interaction in some remaining characters.
Complementary type epistasis was observed in the cross 2 (RHRBG-26 x RHRBG-10) days to appearance first male flower, node number at which first female flower appeared, days to 50% flowering, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield and downey mildew; cross 3 (RHRBG-26 x RHRBG-29) for days to appearance first male flower, days to 50% flowering, number of male flowers per vine, number of female flowers per vine, sex ratio and downey mildew in summer seasons and cross 1 (RHRBG-26 x RHRBG-26) for number of female flowers per vine, node number at which first male flower appeared, diameter of fruit, number of fruits per vine. The additive and additive x dominance effects were equally important in some combination for most of the characters. The heritability (broad sense) and genetic advance estimates were high for most of the characters.

Keywords: Genetic studies, gene action, heritability, genetic advance, bitter gourd

Introduction
Bitter gourd (*Momordica charantia* L.) is one of the most important vegetable grown throughout the tropical and subtropical regions of the world with native of Tropical Africa and Asia. The immature fruits are used afresh as well as in processed forms such as stuffed, pickled, sliced and dehydrated. The fruits are also called as bitter melon or balsam pear and harvested at developmental stages up to seed maturity. Fresh bitter gourd is an excellent source of vitamin-C (84mg/100g) which is one of the powerful natural antioxidant. As a rich source of antioxidants, flavonoids, and other polyphenol compounds, bitter gourd may help to reduce your risks for a number of health issues. It provides very low calories (17 cal per100g) (Chakrabarti, 2001) [2]. The fruits are bitter to taste due to the presence of substance called momordicine. Bitter gourd is also reported to use against diseases like paralysis, indigestion and vomiting pain and diabetes.
The estimates of gene effects and genetic variances will help in understanding the genetic potentiality of the population. The relative magnitude of the additive and dominance genetic variances will decide the breeding procedure to be followed for improving a given population. Our knowledge about the estimation of epistatic gene effects is rather limited and has usually been ignored by most of the workers dealing with quantitative characters. Understanding the nature of gene action could be helpful in predicting the effectiveness of selection in a population. A clear knowledge of the type of gene action, its magnitude and composition of genetic variance is of fundamental importance to a plant breeder. Yield is a complex character and is largely influenced by the genotype - environment interaction and understanding of the mode of inheritance of such complex quantitative character is essential for formulating effective selection procedures in order to improve the yield and its related characters. Bitter gourd shows a lot of variability in yield and yield contributing characters.

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For developing suitable cultivar the concrete breeding programme should be planned. For this purpose information regarding the nature of magnitude of genetic variation that exist in the breeding population is necessary. Although, bitter gourd is becoming a commercial crop but relatively less attention has been paid towards the improvement of existing germplasm available in different parts of the country.

Material and Methods
Parents and Hybrids
1. P_1 – RHRBG-26
2. P_2 – RHRBG-24
3. P_3 – Akole BG 4 – RHRBG-10
4. P_4 – Phule Green Gold – RHRBG-29

a. Experimental details
Design and Layout of experiment for Evaluation of six generation
1. No. of parents plants/replication: 10 vines/replication
2. No. of F_1 plant/replication: 10 vines/replication
3. No. of BC_1 and BC_2 plant/replication: 20 vines/replication of each BC_1 and BC_2
4. No. of F_2 plants/replication: 40 vines/replication
5. No. of replication: Two
6. Design: Randomized Block Design (RBD)
7. Genotypes: 18 (Six generations in each of three crosses)

Observations recorded
Number of branches per vine, length of vine, days to appearance first male flower, days to appearance first female flower, node number at which first male flower appeared, node number at which first female flower appeared, days to 50% flowering, number of male flowers per vine, number of female flowers per vine, sex ratio, days to first picking, days to last picking, length of fruit, diameter of fruit, weight of fruit, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield, downy mildew, powdery mildew and fruit fly.

Statistical analysis
The data will be analyzed by using the appropriate procedure to the Randomized Block design as described by Panse and Sukhatme (1995) [5].

Result and Discussion
1. Gene action
In the present study analysis of variance, scaling test and joint scaling test shows significant in all the crosses. Among the all the crosses cross 3 RHRBG-26 X RHRBG-29 shows highest length of vine, number of female flower per vine, length of fruit, diameter of fruit, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield was recorded. While days to appearance of first female flowers, node number at which first male and female flowers appeared shows minimum in six generation.

Six genetic parameters (m), (d), (h), (i), (j) and (l) were estimated by the generation means of parents, F_1, F_2 and back crosses (BC_1 and BC_2) of the F_2 to corresponding parents. Estimation of gene effects was worked out as per Hayman (1958). All the above estimates were calculated in all the three crosses for nineteen characters. All three types of gene actions *viz.*, additive, dominance and epistasis (i, j and l) were present in most of the combinations for almost all characters

under study and these characters can be improved by reciprocal recurrent selection.

All three types of gene actions *viz.*, additive, dominance and epistasis (i, j and l) were present in most of the combinations for almost all characters under study and these characters can be improved by reciprocal recurrent selection. Duplicate type of epistasis were observed in all crosses for number of branches per vine, length of vine, days to first picking, days to last picking, length of fruit, weight of fruit, fruit fly and some crosses also showed duplicate type interaction in some remaining characters.

Complementary type epistasis was observed in the cross 2 (RHRBG-26 x RHRBG-10) days to appearance first male flower, node number at which first female flower appeared, days to 50% flowering, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield and downey mildew; cross 3 (RHRBG-26 x RHRBG-29) for days to appearance first male flower, days to 50% flowering, number of male flowers per vine, number of female flowers per vine, sex ratio and downey mildew in summer seasons and cross 1 (RHRBG-26 x RHRBG-26) for number of female flowers per vine, node number at which first male flower appeared, diameter of fruit, number of fruits per vine. The additive and additive x dominance effects were equally important in some combination for most of the characters. Dominance x dominance gene effects were greater magnitude followed by additive x additive and additive x dominance for node at which first female flower appeared, days required for first harvest of fruit, fruit length, fruit weight, respectively in summer season. The selection for these characters should be postponed to later generation. The gene effects revealed that, there was predominance of dominance gene effects for most of the characters in most of the all combinations.

2. Heritability
In the present study, high estimates of broad sense heritability in all the three crosses *viz.* cross 1 (RHRBG-26 X RHRBG-24), cross 2 (RHRBG-26 X RHRBG-10), and cross 3 (RHRBG-26 X RHRBG-29) for all the characters in summer season. The characters *viz.*, number of branches per vine, length of vine, days to appearance first male flower, days to appearance first female flower, node number at which first male flower appeared, node number at which first female flower appeared, days to 50% flowering, number of male flowers per vine, number of female flowers per vine, sex ratio, days to first picking, days to last picking, length of fruit, diameter of fruit, weight of fruit, number of fruits per vine, fruit yield per vine, fruit yield per plot, fruit yield downey mildew and fruit fly showed high heritability. Similar results were reported by Choudhary *et al.* (1991) [3] in bitter gourd, Prasad *et al.* (2004) [6], Arvindkumar (2004) [1], Singh and Lal (2005),Tokardi *et al.* (2007) [8] in muskmelon, Kumar (2007) [4] in bottle gourd; Krishna Prasad and Singh (1992) [9] in cucumber.

High heritability (bs) with low genetic advance was recorded in all the three crosses *viz.* cross 1 (RHRBG-26 X RHRBG-24), cross 2 (RHRBG-26 X RHRBG-10), and cross 3 (RHRBG-26 X RHRBG-29) for number of branches per vine. Summing up it may be concluded that all the three crosses *viz.* cross 1 (RHRBG-26 X RHRBG-24), cross 2 (RHRBG-26 X RHRBG-10), and cross 3 (RHRBG-26 X RHRBG-29) were the best hybrid, which also exhibited considerable heterosis

for most of the economical yield contributing characters and these hybrids also showed better performance in F_2, BC_1, and BC_2 generation. Both additive and non additive gene effects were equally important in the inheritance of various economic characters in Bitter gourd. Therefore, in order to undertake crop improvement in this crop, heterosis breeding, progeny breeding recurrent and reciprocal recurrent selection would be effective.

Table 1: Estimates of gene effects for different characters in three crosses of bitter gourd during summer

Cross/ Characters	m	d	h	i	j	l	Type of Epistasis
No. of Branches / Vine							
Cross 1	12.42** (0.07)	0.24* (0.10)	-6.04** (0.39)	-7.51** (0.36)	0.74** (0.28)	11.11** (0.58)	D
Cross 2	13.33** (0.07)	0.71** (0.12)	-2.88* (0.44)	-5.47** (0.37)	2.75** (0.30)	7.71** (0.76)	D
Cross 3	12.11** (0.05)	1.31** (0.18)	-3.26** (0.46)	-4.68** (0.41)	2.08** (0.44)	4.94** (0.86)	D
Length of Vine (m)							
Cross 1	5.55** (0.08)	0.29* (0.14)	-0.006 (0.44)	-0.86* (0.42)	0.36 (0.33)	1.68* (0.70)	D
Cross 2	6.48** (0.08)	0.88** (0.12)	-2.47** (0.44)	-2.96** (0.41)	-1.07** (0.32)	4.72** (0.67)	D
Cross 3	4.97** (0.06)	1.91** (0.12)	4.67** (0.40)	3.14** (0.35)	3.38** (0.36)	-1.66* (0.67)	D
Days to Appearance First Male Flower							
Cross 1	53.42** (0.13)	-0.89** (0.35)	-8.42** (0.88)	-6.10** (0.86)	-1.03 (0.75)	10.35** (1.52)	D
Cross 2	52.84** (0.09)	-0.96** (0.15)	-3.67** (0.48)	-0.28 (0.45)	-2.31** (0.32)	-3.42** (1.11)	C
Cross 3	51.81** (0.07)	0.52** (0.15)	-1.57** (0.43)	1.12** (0.40)	-0.01 (0.33)	-1.98** (0.73)	C
Days to Appearance First Female Flower							
Cross 1	57.21** (0.13)	0.57** (0.20)	-4.07** (0.71)	-1.97** (0.65)	0.83 (0.49)	-0.72 (1.13)	C
Cross 2	55.24** (0.06)	-2.26** (0.21)	1.38** (0.52)	3.93** (0.49)	-4.63** (0.47)	-5.12** (0.95)	D
Cross 3	55.37** (0.07)	1.04** (0.21)	3.68** (0.55)	6.66** (0.51)	-3.46** (0.54)	-14.50** (1.00)	D
Fruit yield per vine (kg)							
Cross 1	2.10** (0.01)	0.05** (0.02)	-0.19** (0.07)	-0.66** (0.06)	-0.19** (0.05)	0.76** (0.10)	D
Cross 2	2.27** (0.01)	0.10** (0.01)	0.08 (0.04)	-0.64** (0.04)	-0.03 (0.04)	0.72** (0.07)	C
Cross 3	2.46** (0.01)	0.05** (0.02)	-1.08** (0.07)	-1.83** (0.07)	-0.26** (0.04)	3.16** (0.10)	D
Fruit yield per plot (kg)							
Cross 1	10.51** (0.07)	0.26** (0.08)	-1.01** (0.34)	-3.33** (0.32)	-0.98** (0.23)	3.85** (0.50)	D
Cross 2	11.34** (0.03)	0.48** (0.07)	0.38 (0.20)	-3.23** (0.18)	-0.16 (0.18)	3.63** (0.34)	C
Cross 3	12.28** (0.07)	0.25** (0.09)	-5.42** (0.34)	-9.15** (0.33)	1.29** (0.21)	15.78** (0.49)	D
Fruit yield (q/ha)							
Cross 1	140.07** (0.92)	3.43** (1.11)	-13.43** (4.59)	-44.40** (4.28)	-13.08** (3.02)	51.29** (6.64)	D
Cross 2	151.18** (0.41)	6.38** (0.91)	5.09 (2.70)	-42.97** (2.46)	-2.11 (2.45)	48.26** (4.59)	C
Cross 3	163.77** (0.93)	3.31** (1.22)	-72.26** (4.57)	-122.04** (4.43)	17.22** (2.83)	210.47** (6.51)	D
Downey Mildew (%)							
Cross 1	9.39** (0.21)	2.01** (0.28)	8.85** (1.08)	10.43** (1.02)	7.35** (0.62)	-22.32** (1.57)	D
Cross 2	11.35** (0.10)	1.87** (0.16)	-0.27 (0.58)	2.90** (0.50)	6.09** (0.44)	-9.37** (0.94)	C
Cross 3	11.13** (0.15)	0.96** (0.16)	-2.76** (0.79)	-1.19 (0.68)	2.83** (0.52)	-4.00** (1.18)	C
Fruit Fly (%)							
Cross 1	11.29** (0.13)	-1.03** (0.30)	5.63** (0.83)	7.57** (0.78)	-3.28** (0.68)	-17.42** (1.40)	D
Cross 2	10.21**	-0.35	0.66	2.60**	-1.23**	-3.01**	D

	(0.09)	(0.21)	(0.62)	(0.56)	(0.58)	(1.06)	
Cross 3	12.01** (0.50)	0.67** (0.18)	-6.16** (0.76)	-3.44** (0.70)	2.82** (0.49)	5.00** (1.12)	D

Table 2: Estimates of heritability (bs) and genetic advance in bitter gourd for different characters during summer

Cross/ Characters	Heritability (%)	Genetic advance	GA as % of mean
No. of Branches / Vine			
Cross 1	73.38	1.43	12.76
Cross 2	95.12	2.35	19.18
Cross 3	92.20	1.41	12.99
Length of Vine (m)			
Cross 1	96.99	0.92	17.07
Cross 2	87.69	0.86	14.26
Cross 3	97.88	1.83	32.11
Days to Appearance First Male Flower			
Cross 1	89.29	2.26	4.28
Cross 2	89.92	2.47	4.70
Cross 3	84.63	2.33	4.49
Days to Appearance First Female Flower			
Cross 1	72.31	1.48	2.61
Cross 2	97.41	2.92	5.22
Cross 3	95.19	2.88	5.14
Length of fruit			
Cross 1	84.41	1.36	6.66
Cross 2	85.91	2.40	11.44
Cross 3	**90.22**	**2.09**	**9.82**
Diameter of fruit			
Cross 1	95.25	0.71	20.01
Cross 2	67.07	0.35	9.67
Cross 3	92.12	0.81	21.18
Weight of fruit			
Cross 1	99.11	13.98	15.63
Cross 2	99.85	16.72	18.50
Cross 3	99.87	15.92	18.00
Number of fruits per vine			
Cross 1	93.96	2.58	12.04
Cross 2	95.98	3.10	13.63
Cross 3	95.71	3.90	16.04
Fruit yield per vine (kg)			
Cross 1	97.97	0.46	23.90
Cross 2	99.30	0.64	31.12
Cross 3	99.04	0.72	33.27
Fruit yield per Plot (kg)			
Cross 1	97.83	2.30	24.04
Cross 2	99.40	3.18	31.14
Cross 3	99.14	3.59	33.30
Fruit yield (q/ha)			
Cross 1	97.86	30.70	24.01
Cross 2	99.41	42.39	31.14
Cross 3	99.14	47.93	33.31
Downey Mildew (%)			
Cross 1	52.81	0.90	37.50
Cross 2	50.30	0.79	34.05
Cross 3	54.00	1.24	47.33
Fruit Fly (%)			
Cross 1	59.35	0.86	2.17
Cross 2	52.25	0.58	1.35
Cross 3	51.49	0.43	1.00

could be utilized in selection programme in the crosses 1(RHRBG-26 x RHRBG-24), 2 (RHRBG-26 x RHRBG-10) and 3(RHRBG-26 x RHRBG 29). The magnitude of dominance (h) gene effects were exhibited higher than additive (d) gene effects in all the three cross combinations for the nineteen characters.

All three types of gene actions *viz.*, additive, dominance and epistasis (i, j and l) were present in most of the combinations for almost all characters under study and these characters can be improved by reciprocal recurrent selection. Duplicate type of epistasis were observed in some crosses for Number of branches per vine, length of vine, days to first picking, days to last picking, length of fruit, weight of fruit, fruit fly and some crosses also showed duplicate type interaction in some remaining characters. Complementary type epistasis was observed in the some crosses.

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Conclusion
Analysis of genetic variance and gene effects reveled to know the nature and magnitude of gene effects for yield and its contributing characters. Contribution of additive gene effects was greater than dominance gene effects which is fixable and