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ESTIMATION OF GENE ACTION FOR YIELD AND ITS CONTRIBUTING TRAITS IN BITTER GOURD (*MOMORDICA CHARANTIA* L.)

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ABSTRACT

The present experiment was carried out to assess gene action in fifty-four genotypes comprising 15 parents and their fifty crosses through line × tester method. Analysis of variance exhibited significant differences among the genotypes for all the traits under studied. The data was collected for various morphological characters associated with yield and its contributing traits. In reference to estimates of additive variances (δ^2A) was lower than dominant variance (δ^2D) for different attributes all characters such as number of male flowers per plant, fruit weight, first fruit harvest, number of female flowers per plant, days to first fruit set, vine length, number of days to open first female flower, number of seeds per fruit, fruit length, number of days to open first male flower, number of fruits per plants, 100 seed weight, number of primary branches, fruit diameter, total soluble solids, sex ratio and fruit yield per plant . indication the presence of additive gene action.

Keywords : Gene action, Variance, Quantitative characters, Line × Tester analysis, Fruit yield and Bitter gourd (*momordica charantia* L.)

Introduction

Bitter gourd (*Momordica charantia* L.) $2n=2x=22$ is one of the important vegetable cum medicinal plant belongs to the family Cucurbitaceae, which is widely cultivated in Asia, Africa, the Caribbean, and South America (Grover and Yadav 2004). Bitter gourd contains about 25 calories, 1.2 g protein, 0.2 g fat, 5 g carbohydrate, 1.0 g fiber, 13 mg calcium, 32 mg phosphorus, 0.2 mg iron, 0.02 mg thiamine and 0.07 mg riboflavin per 100 grams of the bitter gourd fruit (Rose et al. 2014). Since, from last two decades' bitter gourd has occupied a special position among the vegetables because of its incomparable hypoglycemic action and nutraceutical values (Tan et al., 2016) and hence, bitter gourd is accepted as “Vegetable Insulin”.

Despite the presence of several valuable medicinal and nutritional attribute, the productivity of bitter gourd remains unsatisfactory to a large extent and are attributable to the limited research effort concentrated in this crop. Bitter gourd is predominantly cross-pollinated vegetable due to predominance of monoecious sex form and expresses very little inbreeding depression. Indian bitter gourd shows diverse morphological variation with respect to growth habit, maturity, fruit shape, size, colour, and surface texture and sex expression (Behera et al., 2006). Genetic improvement depends primarily on the effectiveness of selection among progenies that differ in genetic value. Therefore, from nutrient and health benefit considerations, it is desirable to improve the

crop in terms of yield and quality. Information on nature and magnitude of combining ability effects of parents and crosses may be of great value to the breeder in selecting the appropriate parents and crosses. In a hybridization programme, approach of selecting parents on the basis of per se performance does not necessarily lead to the best result (Labroo *et al.*, 2021). The studies on combining ability help to extract ideas about the nature and magnitude of gene action for particular traits which help in selecting diverse parents and hybrid combinations. In addition to this knowing the nature of gene action for different traits will be helpful to develop efficient crop improvement programme. General combining ability (gca) is due to additive and additive \times additive gene action and is fixable in nature while specific combining ability (sca) is due to non-additive gene action which may be due to dominance or epistasis or both and is non-fixable in nature. The presence of non-additive genetic variance is the primary justification for initiating the hybrid breeding programme (Pali and Mehta, 2014). In order to apply an optimum breeding strategy for targeted quantitative and quality traits, a genetic analysis of those traits needs to be performed. Line \times Tester design has been used extensively by several researchers to measure gene action for yield and yield components in bitter gourd.

The present investigation was, therefore, undertaken with a set of line \times tester crosses to elicit information about the nature and magnitude of gene action for yield and its components in bitter gourd so as to formulate suitable breeding strategy.

Materials and Methods

Crosses were developed through line \times tester mating design during summer season 2022-23 involving ten lines and five testers. During summer season 2023-24, all the 50 F₁s along with fifteen parents were sown which were then evaluated in randomized block design with three replications for yield and horticultural related traits at the Horticultural Research Centre, Department of Vegetable Science, College of Horticulture, Sardar Vallabhbhai Patel University of Agriculture & Technology, Modipuram, Meerut-250110 (U.P.), India. The following key traits were recorded for, Vine Length (m), Primary branches, First female flower initiation, First male flower initiation, Male flower per vine, Female flower per vine, Sex ratio, Fruit weight (Kg), Fruit length (cm) Fruit diameter (cm), Fruit flesh thickness (cm), First fruit set, Fruit per plant, No. of seeds per fruit, Hundred seed weight (g), Fruit yield per plant (kg), First fruit harvest and TSS (brix).

Genetic component and their magnitude

$$\text{Cov. Half sib (line)} = \frac{M_f - M_{fm}}{rm}$$

$$\text{Cov. Half sib (tester)} = \frac{M_m - M_{fm}}{rf}$$

Cov. Half sib (average) =

$$\frac{1}{r(2fm - f - m)} \left[\frac{(f-1)M_f + (m-1)M_m}{f+m-2} - M_{fm} \right]$$

$$(M_f - M_e) + (M_m - M_e) + (M_{fm} - M_e) + 6r \text{Cov. H.S. (average)} - r(f+m)$$

$$\text{Cov. F.S. (average)} = \frac{\text{Cov. H.S. (average)}}{3r}$$

Where,

M_f = Mean squares due to lines (females)

M_m = Mean squares due to testers (males)

M_{fm} = Mean squares due to line \times tester interactions

M_e = Mean squares due to error

r = Number of replications

f = Number of lines

m = Number of testers

$$\text{gca variance } (\sigma^2 \text{ gca}) = \text{COV. H.S. (average)} = \frac{1+F}{4} \sigma^2 A$$

Therefore,

Additive genetic variance ($\sigma^2 A$) = 2 Cov. H.S. (average), if $F = 1$ and ($\sigma^2 A$) = 4 Cov. H.S. (average), if $F = 0$

$$\text{sca variance } (\sigma^2 \text{sca}) = \frac{(M_{fm} - M_e)}{r}$$

$$\sigma^2 \text{sca} = \left[\frac{1+F}{2} \right]^2 \sigma^2 D$$

Therefore,

Dominance variance ($\sigma^2 D$) = $\sigma^2 \text{sca}$ with $F = 1$, and $\sigma^2 D = 4\sigma^2 \text{sca}$, if $F = 0$

Where,

F = Inbreeding coefficient

Results and Discussion

Genetic components and their magnitude. The estimates of GCA and SCA variance, predictability ratio, average degree of dominance, narrow heritability is given in Table-1.

The estimates of δ^2g due to males were found to be higher than δ^2g due to females for fruit length (0.93) and diameter (1.47) a comparison of relative magnitude of these expressed to focus that additive gene action. However, the δ^2g due to females showed higher than the δ^2g due to males for number of male flowers per plant (95.90), vine length (6.33), fruit weight (5.97), number of female flowers per plant (4.93), first fruit harvest (3.20), days to first fruit set (3.07), number of seeds per fruit (2.54), number of days to open first female flower (1.62), number of fruits per plant (1.39), number of days to open first male flower (0.99), 100 seed weight (0.65), number of primary branches (0.33), sex ratio (0.045), total soluble solids (0.041) and fruit yield per plant (0.02) which indicated that the predominance role of additive gene action. Singh (2012), Sit (2005), Sridhar (2015), Narender (2018), Verma (2014)

The estimates of δ^2s were found to be higher than the δ^2g (pooled) for all characters such as number of male flowers per plant (802), vine length (99.16), number of female flowers per plant (39.59), fruit weight (25.46), first fruit harvest (18.49), number of fruits per plant (14.15), days to first fruit set (8.47), number of days to open first male flower (7.09), number of days to open first female flower (6.86), number of seeds per fruit (3.63), fruit length (3.11), 100 seed weight (3.03), number of primary branches (2.51), fruit diameter (0.38), sex ratio (0.26) total soluble solids (2.63) and fruit yield per plant (0.07). In reference to estimates of additive variances (δ^2A) was lower than dominant variance (δ^2D) for different attributes all characters such as number of male flowers per plant (111.52), fruit weight (6.57), first fruit harvest (6.37), number of female flowers per plant (4.47), days to first fruit set (3.36), vine length (2.66), number of days to open first female flower (2.60), number of seeds per fruit (1.94), fruit length (1.845), number of days to open first male flower (1.55), number of fruits per plant (1.44), 100 seed weight (1.07), number of primary branches (0.29), fruit diameter (0.22), total soluble solids (0.07), sex ratio (0.05) and fruit yield per plant (0.01). indication the presence of additive gene action. The dominance variance (δ^2D) was higher than additive variance (δ^2A) for characters except characters viz., number of male flowers per plant (802), vine length (99.16), number of female flowers per plant (39.59), fruit weight (25.46), first fruit harvest (18.49), number of fruits per plant (14.15), days to first fruit set (8.47), number of days to open first male flower (7.09), number of days to open

first female flower (6.86), number of seeds per fruit (3.63), fruit length (3.11), 100 seed weight (3.03), number of primary branches (2.51), fruit diameter (0.38), sex ratio (0.26) and fruit yield per plant (0.07) which indicated as non-additive gene action. Average degree of dominance exhibited partial dominance for characters viz., number of primary branches (2.92), number of days to open first female flower (1.62), number of days to open first male flower (2.13), fruit weight (1.96), fruit length (1.20), fruit diameter (1.32), vine length (6.10), days to first fruit set (1.58), number of fruits per plant (3.12), number of seeds per fruit (1.36), fruit yield per plant (2.28), 100 seed weight (1.68), number of female flowers per plant (2.97), number of male flowers per plant (2.60), sex ratio (2.16), first fruit harvest (1.70) and total soluble solids (1.93). The mean degree of dominance was greater found unity for all traits under study. The predictability ratio was observed less than unity for all the characters. Alhariri (2020), Kumar (2015), Revati (2023), Laxuman (2012).

Narrow sense of heritability was observed for fruit length (35.35), fruit diameter (34.54), number of seeds per fruit (32.10), days to first fruit set (23.87), number of days to open first female flower (22.31), 100 seed weight (22.17), days to first fruit harvest (21.89), total soluble solids (19.44), fruit weight (16.97), sex ratio (16.64), fruit yield per plant (14.57), no of days to open first male flower (14.91), number of male flowers per plant (11.66), no of primary branches (9.96), number of female flowers per plant (9.61), no of fruits per plant (8.62) and vine length (1.76).

Conclusion

The study concluded that both additive and non-additive gene action are present for different trait in bitter gourd, and the knowledge of gene action is essential for formulating an efficient selection program. The results of the study can be used to develop a suitable breeding strategy for improving yield and its contributing traits in bitter gourd.

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Table 1: Estimate of genetic components and their magnitude for 17 quantitative characters in Bitter Gourd (*Momordica charantia* L.)

	NPB	NFFF	NFMF	FW(g)	FL(cm)	FD(cm)	VL(cm)	DFFS	NFPP
σ^2_g (female)	0.336	1.682	0.99	5.971	0.9	0.037	6.338	3.077	1.394
σ^2_g (Male)	0.053	1.109	0.67	1.949	0.933	0.147	-1.174	0.986	0.389
σ^2_g (pooled)	0.148	1.3	0.777	3.29	0.922	0.11	1.33	1.683	0.724
σ^2_s (sca)	2.515	6.868	7.097	25.464	3.113	0.385	99.166	8.47	14.15
σ^2_A	0.295	2.6	1.553	6.579	1.845	0.221	2.661	3.366	1.448
σ^2_D	2.515	6.868	7.097	25.464	3.113	0.385	99.166	8.47	14.15
Average Degree of Dominance	2.92	1.625	2.137	1.967	1.299	1.321	6.105	1.586	3.127
Heritability (Narrow Sense) %	9.962	22.319	14.917	16.978	35.351	34.544	1.762	23.878	8.629
Predictability Ratio	0.105	0.275	0.18	0.205	0.372	0.364	0.026	0.284	0.093

NPB= Number of Primary Branches, NFFF= Number of Days to Open First Female Flower, NFMF= Number of Days to Open First Female Male, FW= Fruit weight, FL= Fruit length, FD= Fruit Diameter, VL= Vine Length, DFFS= Days to First Fruit Set, NFPP= Number of Fruit Per Plant.

Countd.,

	NSPF	FYPP(kg)	100 SW	NFFPP	NMFPP	SR	FFH	TSS
σ^2_g (female)	2.542	0.022	0.659	4.93	95.903	0.045	3.205	0.041
σ^2_g (Male)	0.19	-0.001	0.476	0.892	35.69	0.02	3.191	0.032
σ^2_g (pooled)	0.974	0.007	0.537	2.238	55.761	0.028	3.196	0.035
σ^2_s (sca)	3.639	0.074	3.035	39.593	802.575	0.266	18.496	0.263
σ^2_A	1.948	0.014	1.074	4.477	111.522	0.057	6.392	0.07
σ^2_D	3.639	0.074	3.035	39.593	802.575	0.266	18.496	0.263
Average Degree of Dominance	1.367	2.285	1.681	2.974	2.683	2.162	1.701	1.933
Heritability (Narrow Sense) %	32.105	14.579	22.17	9.616	11.662	16.645	21.899	19.448
Predictability Ratio	0.349	0.161	0.261	0.102	0.122	0.176	0.257	0.211

NSPF= Number of Seed Per Fruit, FYPP= Fruit Yield Per Plant, 100SW= Seed Weight, NFFPL= Number of Female Flowers Per Plant, NMFPP= Number of Male Flowers Per Plant, SR= Sex Ratio, FFH= Frist Fruit Harvest, TSS= Total Soluble Solids.

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