



Plant Archives

Journal homepage: <http://www.plantarchives.org>

DOI Url : <https://doi.org/10.51470/PLANTARCHIVES.2024.v24.no.2.297>

ESTIMATION OF GENE ACTION FOR YIELD AND ITS CONTRIBUTING TRAITS THROUGH LINE \times TESTER ANALYSIS IN PUMPKIN (*CUCURBITA MOSCHATA*.)

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(Date of Receiving-27-06-2024; Date of Acceptance-07-09-2024)

ABSTRACT

The present experiment was carried out to assess gene action in fifty-four genotypes comprising fourteen parents and their forty crosses through line \times 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. Estimates of additive variance (δ^2A) were lower than dominant variance (δ^2D) for different attributes except *viz.*, days to first fruit set, days to first fruit harvest, fruit yield per plant, days to first male flower initiation, fruit diameter, vine length, number of female flowers per vine, TSS and fruit weight indicated as non-additive gene action.

Key words- Gene action, Variance, Quantitative characters, Line \times Tester analysis and Fruit yield, Pumpkin (*Cucurbita moschata* L.).

Introduction

Pumpkin (*Cucurbita moschata* L.) belongs to the family Cucurbitaceae and sub family Cucurbitoidae (Gbemenou *et al.*, 2022). It is highly cross-pollinated crop having chromosome number $2n=40$. The pollination may occur by majorly by bees. It is an annual vine crop having a climbing or trailing habit (Katyal and Chadha, 2000). It is widely cultivated in India, China, Malaysia, Taiwan and Bangladesh. It is distributed widely in Southeast Asia, tropical Africa, tropical South and Central America (Peru and Mexico), the Caribbean and most part of tropics. China and India lead the world production and other major producers are U.S., Egypt, Mexico, Ukraine, Cuba, Italy, Iran and Turkey (Ferriol and Pico, 2008). Pumpkin is made up primarily of pulp and seeds. Pumpkin pulp contains polysaccharides, amino acids, active proteins and

minerals. They provide an abundant supply of potassium, phosphate and magnesium, as well as lipids (Fernández-López *et al.*, 2020, Roongruangsri W. and Bronlund J. 2015). The pumpkin medicinal benefits include anti-carcinogenic (Zhang *et al.*, 2012), anti-diabetic (Chang *et al.*, 2014), anti-oxidant (Wu *et al.*, 2014) and hypolipidemic properties (Zhao *et al.*, 2014). The line \times tester analysis is one of the efficient techniques of evaluating large number of inbreeds as well as giving information on the relative importance of GCA effects of lines and testers and also SCA effects of pairs of parental genotypes for interpreting the genetic basis of significant plant traits (Mather and Jinks, 1982). Knowledge on the genetic system controlling the quantitative and quality traits is important for formulating an efficient selection program through the use of a

suitable mating design. The information about the relative contribution of components of variation viz., additive and non-additive, is essential for effective crop improvement program (Azhar and Ajmal, 1999). 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 × Tester design has been used extensively by several researchers to measure gene action for yield and yield components in pumpkin.

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

Materials and Methods

Crosses were developed through line x tester mating design during *rabi* season 2022-23 involving ten lines and four testers. During *rabi* season 2023-24, all the 40 F₁s along with fourteen 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 Vallabhbai Patel University of Agriculture & Technology, Modipuram, Meerut-250110 (U.P.), India. The following key traits were recorded for vine length (cm), number of primary branches, days to first female flower initiation, days to first male flower initiation, number of male flowers per vine, number of female flowers per vine, sex ratio, days to first fruit set, fruit weight (g), fruit length (cm), fruit diameter (cm), fruit flesh thickness (cm), number of fruits per plant, fruit yield per plant (kg), number of seeds per fruit, 100 seed weight (g) and TSS.

Genetic component and their magnitude

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

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

$$\text{Cov. Half sib (average)} = \frac{1}{r(2fm - f - m)} \left[\frac{(f - 1)Mf + (m - 1)Mm}{f + m - 2} - M_{fm} \right]$$

$$\text{Cov. F.S. (average)} = \frac{(Mf - Me) + (Mm - Me) + (M_{fm} - Me) + \frac{6r \text{ Cov. H.S. (average)} - r(f + m) \text{ Cov. H.S. (average)}}{3r}}$$

Where,

Mf= Mean squares due to lines (females)

Mm=Mean squares due to testers (males)

M_{fm}=Meansquares dueto line×tester interactions Me= Mean squares due to error

r=Numberofreplications f = Number of lines

m= Numberof 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 ($\sigma^2 D$)= σ^2_{sca} with F=1, and

$\sigma^2 D = 4\sigma^2_{\text{sca}}$, if F=0

Where,

F=Inbreeding coefficient

Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines (\%)} = \frac{S.S.(lines)}{S.S.(crosses)} \times 100$$

$$\text{Contribution of testers (\%)} = \frac{S.S.(testers)}{S.S.(crosses)} \times 100$$

$$\text{Contribution of line } \times \text{ testers} = \frac{S.S.(lines \times testers)}{S.S.(crosses)} \times 100$$

Results and Discussion

Genetic components and their magnitude. The estimates of GCA and SCA variance, predictability ratio, average degree of dominance, narrow heritability and proportional of lines, testers and lines x testers are given in Table 1 and Fig. 1a and 1b.

The estimates of $\delta^2 g$ due to males were found to be higher than $\delta^2 g$ due to females for number of seeds per fruit (6464.25), number of male flowers pe vine (586.88), days to first female flower initiation (14.9), Hundred seed weight (11.34), sex ratio (9.90), days to first fruit set (9.09), days to first male flower initiation (8.67), number of primary branches (2.23), fruit length (1.39), fruit diameter (0.99), number of fruits per plant (0.48), fruit weight (0.30), vine length (0.25), fruit flesh thickness (0.14) and TSS (0.11) a comparison of relative magnitude of these

Table 1: Estimate of genetic components and their magnitude for 18 quantitative characters in Pumpkin (*Cucurbita moschata* L.).

	VL	PB	FFFI	FMFI	MFPV	FFPV	SR	FW	FL
σ^2A	0.465	3.267	22.733	13.079	877.743	0.792	15.123	0.543	2.416
σ^2D	2.191	0.607	22.027	25.494	372.592	1.117	4.118	0.741	1.402
σ^2g (female)	0.182	0.143	2.533	1.208	68.857	0.426	1.724	0.191	0.747
σ^2g (male)	0.253	2.23	14.9	8.672	586.877	0.384	9.897	0.303	1.392
σ^2g (pooled)	0.232	1.634	11.367	6.539	438.871	0.396	7.562	0.271	1.208
σ^2s (sca)	2.191	0.607	22.027	25.494	372.592	1.117	4.118	0.741	1.402
Average Degree of Dominance	2.171	0.431	0.984	1.396	0.652	1.188	0.522	1.169	0.762
Predictability ratio	0.175	0.843	0.508	0.339	0.702	0.415	0.786	0.423	0.633
Contribution (line)	9.23	6.24	9.92	6.40	8.34	26.79	13.45	19.24	24.86
Contribution (tester)	10.29	73.97	35.50	24.23	58.02	19.83	61.77	24.69	33.74
Contribution (L x T)	80.48	19.79	54.58	69.37	33.65	53.38	24.78	56.07	41.40
Narrow sense heritability (%)	17.244	83.097	46.497	31.404	69.868	40.548	77.363	41.226	54.996
VL=Vine Length (m), PB=Primary branches, FFFI=First female flower initiation, FMFI=First male flower initiation, MFPV=Male flower per vine, FFPV=Female flower per vine, SR=Sex ratio, FW=Fruit weight (Kg), FL=Fruit length (cm)									

Contd...

	FD	FFT	FFS	FPP	NSPF	HSW	FYPP	FFH	TSS
σ^2A	1.684	0.27	17.765	0.954	9430.457	16.584	13.02	3.165	0.155
σ^2D	2.346	0.22	51.313	0.712	1739.459	1.894	32.919	34.8	0.842
σ^2g (female)	0.471	0.115	8.367	0.459	342.674	0.68	16.563	7.632	0.006
σ^2g (male)	0.99	0.143	9.088	0.484	6464.25	11.337	2.489	-0.838	0.106
σ^2g (pooled)	0.842	0.135	8.882	0.477	4715.229	8.292	6.51	1.582	0.077
σ^2s (sca)	2.346	0.22	51.313	0.712	1739.459	1.894	32.919	34.8	0.842
Average Degree of Dominance	1.18	0.902	1.7	0.864	0.429	0.338	1.59	3.316	2.331
Predictability ratio	0.418	0.552	0.257	0.573	0.844	0.898	0.283	0.083	0.155
Contribution % (line)	16.31	28.64	16.44	32.43	5.33	6.37	37.90	23.09	4.80
Contribution (tester)	24.75	28.94	13.05	28.01	74.84	79.73	4.85	1.34	11.38
Contribution (L x T)	58.93	42.42	70.51	39.57	19.83	13.90	57.25	75.56	83.82
Narrow sense heritability (%)	38.254	53.426	23.014	55.36	83.173	88.28	27.807	5.802	13.565
FD=Fruit diameter (cm), FFT=Fruit flesh thickness (cm), FFS=First fruit set, FPP=Fruit per plant, NSPF=No. of seeds per fruit, HSW=Hundred seed weight (g), FYPP=Fruit yield per plant (kg), FFH=First fruit harvest, TSS=TSS (brix).									

expressed to focus that additive gene action. However, the δ^2g due to females showed higher than the δ^2g due to males for fruit yield per plant (16.56), days to first fruit harvest (7.63) and number of female flowers per vine (0.43) which indicated that the predominance role of additive gene action.

The estimates of δ^2s were found to be higher than the δ^2g (pooled) for the characters such as days to first fruit set (51.31), days to first fruit harvest (34.8), fruit yield per plant (32.92), days to first male flower initiation (25.49), days to first female flower initiation (22.03), fruit diameter (2.35), vine length (2.19), fruit length (1.40), number of female flowers per vine (1.12), TSS (0.84), fruit weight (0.74), number of fruits per plant (0.71) and fruit flesh thickness (0.22). In reference to estimates of additive variances (δ^2A) was lower than dominant variance (δ^2D) for different attributes except characters such as days to first fruit set (51.31), days to first fruit

harvest (34.8), fruit yield per plant (32.92), days to first male flower initiation (25.49), fruit diameter (2.350), vine length (2.19), number of female flowers per vine (1.12), TSS (0.84) and fruit weight (0.74) 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 seeds per fruit (9430.46), number of male flowers per vine (877.740), days to first female flower initiation (22.73), hundred seed weight (16.58), sex ratio (15.12), number of primary branches (3.27), fruit length (2.42), number of fruits per plant (0.95) and fruit flesh thickness (0.27) which indicated as non-additive gene action. Same results were found by Yadav (2021), Singh (2019), Mohanty B.K. (2002) and Adarsh (2017).

Average degree of dominance exhibited partial dominance for characters *viz.*, days to first female flower initiation (0.98), fruit flesh thickness (0.90), number of

fruits per plant (0.86), fruit length (0.76), number of male flowers per vine (0.65), sex ratio (0.52), number of primary branches (0.43), number of seeds per fruit (0.43) and hundred seed weight (0.34). However, over dominance was observed for characters like days to first fruit harvest (3.32), TSS (2.33), vine length (2.17), days to first fruit set (1.7), fruit yield per plant (1.59), days to first male flower initiation (1.40), number of female flowers per vine (1.19), fruit diameter (1.18) and fruit weight (1.17). 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.

Narrow sense of heritability was observed for hundred seed weight (88.28%), number of seeds per fruit (83.17%), number of primary branches (83.09%), sex ratio (77.36%), number of male flowers per vine (69.87%), number of fruits per plant (55.36%), fruit length (55.00%), fruit flesh thickness (53.42%), days to first female flower initiation (46.50%), fruit weight (41.23%),

number of female flowers per vine (40.55%), fruit weight (38.25%), days to first male flower initiation (31.40%), fruit yield per plant (27.81%), days to first fruit set (23.01%), vine length (17.24%), TSS (13.57%) and days to first fruit harvest (5.80%).

Proportional contribution of lines, testers and line × tester for all the characters under study revealed that the proportional contribution of lines for all the characters ranged varied from 37.90% (fruit yield per plant) to 4.80% (TSS). The highest contribution of lines was recorded for fruit yield per plant (37.90%) followed by number of fruits per plant (32.43%), fruit flesh thickness (28.64%), number of female flowers per vine (26.79%), fruit length (24.86%), days to first fruit harvest (23.09%), fruit weight (19.24%), days to first fruit set (16.44%), fruit diameter (16.31%), sex ratio (13.45%), days to first female flower initiation (9.92%), vine length (9.23%), number of male flowers per vine (8.34%), days to first male flower initiation (6.40%), hundred seed weight (6.37%), number of primary branches (6.24%), number of seeds per fruit (5.33%) and TSS (4.80%).

The proportional contribution of testers for all the characters range varied from 79.73% (hundred seed weight) to 1.34% (days to first fruit harvest). The highest contribution of testers was observed for hundred seed weight (79.73%) followed by number of seeds per fruit (74.84%), number of primary branches (73.97%), sex ratio (61.77%), number of male flowers per vine (58.02%), days to first female flower initiation (35.50%), fruit length (33.74%), fruit flesh thickness (28.94%), number of fruits per plant (28.01%), fruit diameter (24.75%), fruit weight (24.69%), days to first male flower initiation (24.23%), number of female flowers per vine (19.83%), days to first fruit set (13.05%), TSS (11.38%), vine length (10.29%), fruit yield per plant (4.85%) and days to first fruit harvest (1.34%).

The proportional contribution of line × tester for all the characters range varied from 83.82% (TSS), 13.90% (hundred seed weight). The highest contribution of line × tester was observed for TSS (83.82%) followed by vine length (80.48%), days to first fruit harvest (75.56%), days to first fruit set (70.51%), days to first male flower initiation (69.37%), fruit diameter (58.93%), fruit yield per plant (57.25%), fruit weight (56.07%), days to first female flower initiation (54.58%), number of female flowers per vine (53.38%), fruit flesh

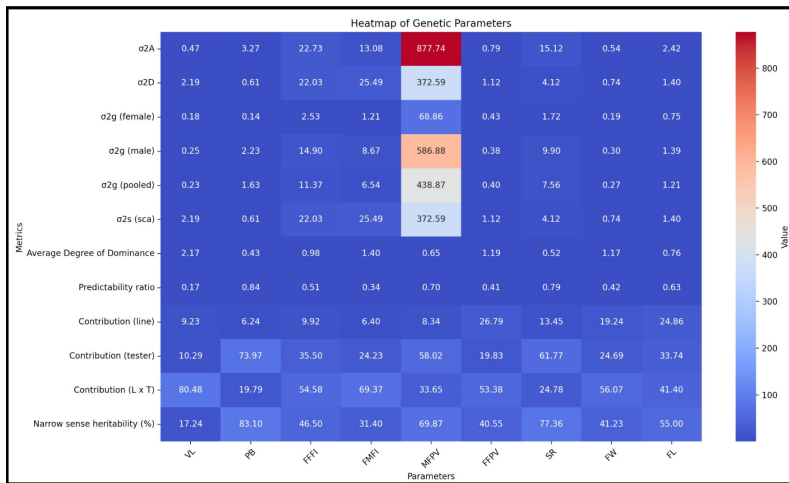


Fig. 1a: Heatmap of genetic components and their magnitude for 18 quantitative characters in Pumpkin (*Cucurbita moschata* L.).

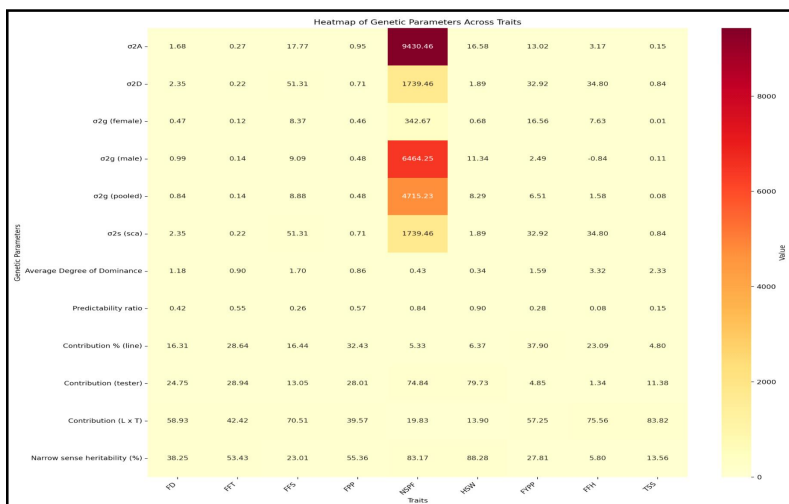


Fig. 1b: Heatmap of genetic components and their magnitude for 18 quantitative characters in Pumpkin (*Cucurbita moschata* L.).

thickness (42.42%), fruit length (41.40%), number of fruits per plant (39.57%), number of male flowers per vine (33.65%), sex ratio (24.78%), number of seeds per fruit (19.83%), number of primary branches (19.79%) and hundred seed weight (13.90%). Similar results were also reported earlier by Musnhi (2013), Mohanty (2001), Janakiram (1987) and Lawande (1991).

In Fig. 1a and 1b, the heat map employed color gradients to depict the magnitude of values, with darker colors often signifying greater values. This enables easy visual discovery of trends, such as which measures have the highest variations or contributions across distinct features. These findings give information on the genetic architecture of numerous qualities in the population. Traits such as NSPF and HSW exhibit substantial genetic diversity and heritability, making them suitable candidates for selection in breeding programs. The significant impact of the L × T (Line × Tester) interaction to the manifestation of numerous features indicates the necessity of specialized combining abilities.

Conclusion

The study concluded that both additive and non-additive gene action are present for different traits in pumpkin, 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 pumpkin.

Acknowledgement

The authors are indebted to the Department of Vegetable Science, College of Horticulture, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh (250110), for providing the necessary infrastructure to carry out the work.

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