

STUDIES ON HERITABILITY AND MULTIVARIATE ANALYSES IN BRINJAL (*SOLANUM MELONGENA* L.)

K. Chandra SHEKAR, P. ASHOK, K. SASIKALA
Department of Vegetable Science,
Horticultural College & Research Institute,
Venkataramannagudem near Tadepalligudem
W.G.Dt-534101 Andhra Pradesh, India

Received: January 26, 2012; Accepted: April 21, 2012

Summary

Thirty one accessions of brinjal were assessed for heritability and genetic divergence for fourteen characters. Highly significant differences were observed among the accessions. High phenotypic and genotypic coefficient of variation was observed for number of leaves per plant, leaf area index, number of fruits per plant, average fruit length, average fruit diameter, fruit yield per plant, fruit yield per plot, fruit yield per hectare. Almost all the characters exhibited high heritability except for plant height (51%) and moderate to low heritability was recorded for average fruit weight (24%). Highest genetic advance as percent of mean was observed for almost all the characters except for days to first flowering, days to first picking, plant height and average fruit weight recorded moderate to low genetic advance as per cent of mean. These thirty one accessions of brinjal were assessed for genetic diversity by adopting Mahalanobis (D^2) statistics considering fourteen characters were grouped into 6 clusters. Multivariate analyses revealed maximum divergence among the clusters signifying their role in exploitation of heterosis.

key words: Brinjal (*Solanum melongena* L.), heritability, genetic divergence

INTRODUCTION

Brinjal is one of the most important and popular vegetable crop grown throughout the year all over the India. Being primary centre of origin, India has accumulated a wide range of variability in this crop. In spite of large number of varieties available in India, only a few are promising. This fact draws the attention of plant breeder for its improvement. Assess-

ment of variability present in any crop species is essential pre requisite for formulating an effective breeding programme. The existing variability can be used to further enhance the yield level of the cultivars following the appropriate breeding strategies. Estimation of genetic variability does not give a clear indication of the possible improvement that can be achieved through selection and it should be used in conjunction with

heritability and genetic advance. Heritability is the measure of transmission of characters from generation to generation and estimates of heritability may be of some help to the breeder in selecting superior individuals and successfully utilizing them in breeding programme.

Hence an attempt has been made in the present investigation with the following objectives: to study variability and heritability for yield and yield components, and to estimate the genetic divergence in available germplasm.

MATERIALS AND METHODS

The experiment was conducted from July 2010 to February 2011 at the experimental farm of the Dept. of Vegetable Science, Horticultural College & Research Institute of Dr. Y.S.R. Horticultural University, Andhra Pradesh, India. Nursery beds were prepared with dimensions of 500×100×15 cm in length, width and height. Seed of 31 eggplant accessions were sown in rows spaced 12 cm apart. Fertilizers (N:P₂O₅:K₂O at 100:60:60 kg·ha⁻¹) were applied for the main field as per the recommendations of Chadha (2009). The recommended synthetic fertilizers were applied as Nitrogen (50 kg·ha⁻¹), Phosphorus (60 kg·ha⁻¹) and potash (60 kg·ha⁻¹), respectively, at main field preparation and a second application of 50 kg·ha⁻¹ of Nitrogen was applied at 40 days after transplanting. The experiment was arranged in a randomized complete block design with three replications in 3.0×2.4 m plots. Five-week-old seedlings of at least 15 cm with four leaves were transplanted manually at a spacing of

75×60 cm between and within rows. Plots were kept free from weeds by regular hand weeding. Five plants of each accession in each replication were randomly chosen and labeled for recording observations. Single plant observations were recorded on 14 quantitative characters (days to first flowering, days to first harvest, plant height, number of branches per plant, number of leaves per plant, leaf area index, number of marketable fruit per plant, average fruit length, average fruit diameter, average fruit weight, total number of harvests, fruit yield per plant, fruit yield per plot and fruit yield per hectare) and means of 10 plants were used for statistical analysis. Analysis of variance (ANOVA) was calculated according to Gomez and Gomez (1983). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953).

Phenotypic standard deviation

$$(\sigma_p) = \sqrt{\sigma_p^2} = \sqrt{\sigma_g^2 + \sigma_e^2}$$

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation } (\sigma_p)}{\text{General mean } (\bar{x})} \times 100$$

Genotypic standard deviation

$$(\sigma_g) = \sqrt{\sigma_g^2}$$

$$\text{GCV (\%)} = \frac{\text{Genotypic standard deviation } (\sigma_g)}{\text{General mean } (\bar{x})} \times 100$$

Heritability in broad sense was estimated as per Allard (1960).

$$h^2(b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

The range of heritability in broad sense [$h^2(b)$] classified as low (less than 30%), moderate (30-60%) and high (more than 60%) suggested by Johnson *et al.* (1955).

Genetic advance was estimated as per the formula proposed by Lush (1940) and Johnson *et al.* (1955).

Genetic advance

$$K \times \sigma_p \times h^2(b)$$

where,

K = Selection differential at 5 per cent selection intensity which accounts to a constant value 2.06

$h^2(b)$ = Heritability in broad sense

σ_p = Phenotypic standard deviation

Genetic advance as per cent of mean (GAM)

$$GAM = \frac{GA}{\text{Grand mean } (\bar{x})} \times 100$$

The range of genetic advance as per cent of mean was classified as low (less than 10%), moderate (10-20%) and High (more than 20%) suggested by Johnson *et al.* (1955).

The data collected on different characters were analyzed through Mahalanobis D^2 analysis to determine the genetic divergence among the accessions (Mahalanobis, 1928).

D^2 value between i^{th} and j^{th} accessions for 'P' characters was calculated as

$$D^2_{ij} = \sum_{t=1}^P (Y_i^t - Y_j^t)^2$$

where,

Y_i^t is uncorrelated mean value of i^{th} genotype for 't' characters

Y_j^t is uncorrelated mean value of j^{th} genotype for 't' characters

D^2_{ij} is D^2 between i^{th} and j^{th} accessions.

In all combinations each character was ranked based on their contribution towards divergence between two entries ($d_i = Y_i^t - Y_j^t$). Rank 1 is given to the highest mean difference and rank P to the lowest difference, where, P is the total number of characters. Percentage contribution towards genetic divergence was calculated using the following formula.

Percentage contribution of character

$$x = \frac{N \times 100}{M}$$

where,

N = Number of accessions combinations where the character was ranked first.

M = All possible combinations of number of accessions considered.

The grouping of accessions into different clusters was done by the method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster should, at least on an average, show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster. The accessions of the first cluster were then eliminated and the rest were treated in a similar way. This procedure was continued until all the accessions were included into one or other cluster.

For the measurement of intra-cluster distance, the formula used was $\Sigma D^2_i / n$ where, ΣD^2_i was the sum of distances between all possible combinations (n) of the populations included in a cluster. Average inter-cluster distance was measured by taking clus-

ters one by one and the distances from other clusters were calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the members of the other cluster divided by the product of number of accessions in both the clusters under consideration.

Average inter-cluster distance

$$\frac{D^2}{(n_1 \times n_2)}$$

where:

n_1 and n_2 are number of accessions of two clusters

D^2 = distance between two cluster.

RESULTS AND DISCUSSION

Highly significant differences were observed among the accessions for all the growth characters like number of leaves per plant, leaf area index, number of fruits per plant, average fruit length, average fruit diameter, fruit yield per plant. High GCV (genotypic coefficient of variation) and PCV (phenotypic coefficient of variation) values indicating large amount of variation and consequently more scope for their improvement through selection (Table 1).

Moderate PCV and low GCV values were recorded for the characters, plant height, number of branches per plant, average fruit weight and

total number of harvests which means that the extent of genetic variation observed was somewhat less for these characters among the accessions studied. There was much difference observed between GCV and PCV values in characters, suggesting the possible role of environment in influencing these traits. Kushwah and Bandhyopandhya (2005) and Sherly (2006) reported that difference between PCV and GCV was high for total number of branches for plant.

Low values of PCV and GCV were exhibited for the characters days to first flowering and days to first picking which means the extent of genetic variation observed was low for these characters among the accessions studied. Nearness between GCV and PCV values in almost all the growth characters indicating that these traits were less influenced by environment. Low values for PCV and GCV for days to first flowering was observed by Singh and Kumar (2005).

With the genotypic coefficient of variation alone, it is difficult to determine the relative amount of heritable and non-heritable components of variations present in the population. Estimates of heritability and genetic advance would supplement this parameter.

Table 1. Estimates of variability, heritability and genetic advance as per cent of mean for fourteen characters in 31 germplasm accessions of brinjal

Character	Mean $\pm$ S.E	Range		PCV (%)	GCV (%)	Heritability (%)	Genetic advance	Genetic advance as per cent of mean (%)
		min.	max.					
Days to 1 st flowering	49.78	39.73	56.93	9.43	9.30	97	9.41	18.90
Days to 1st picking	69.49	57.00	76.93	7.17	7.05	97	9.91	14.27
Plant height (cm)	98.96	80.44	118.15	10.63	7.61	51	11.10	11.21
Number of branches/plant	14.58	8.40	17.20	14.31	12.88	81	3.48	23.88
Number of leaves/plant	201.74	114.66	322.33	24.96	22.72	83	85.96	42.61
Leaf area index	5.02	3.14	7.39	28.85	28.49	98	2.91	57.95
Number of fruits/plant	17.76	11.00	30.33	28.47	26.93	89	9.32	52.48
Average fruit length (cm)	9.03	5.80	13.83	23.32	23.19	99	4.29	47.50
Average fruit diameter (cm)	3.80	2.13	6.61	25.27	24.92	97	1.92	50.62
Average fruit weight (g)	56.62	44.63	70.19	15.47	7.61	24	4.37	7.72
Total number of harvests	13.25	10.06	15.93	12.14	11.91	96	3.19	24.07
Fruit yield/plant (kg)	0.99	0.59	1.54	27.06	24.66	83	0.46	46.29
Fruit yield/plot (kg)	15.89	9.46	24.69	27.07	24.67	83	7.36	46.31
Fruit yield/ha (tones)	22.11	13.14	34.30	27.08	24.62	83	10.19	46.10

The heritability in broad sense ranged for the characters from 24 per cent for average fruit weight to 99 per cent for the average fruit length. In general the values of heritability in broad sense for most of the characters studied were high, indicating that the characters were least influenced by the environmental effects, but the selection for the improvement of such characters may not be useful, because broad sense heritability is based on genetic variance which includes both fixable (additive) and non fixable (dominance and epistatic) variances. While the plant height recorded moderate value of heritability (51%) and average fruit weight recorded low value of heritability (24%), indicating the role of non-additive gene action which includes dominance and epistasis.

Heritability estimates alone are not of any use in predicting the results about the selection unless it is accompanied by genetic advance (Johnson *et al.* 1955). The expected genetic advance (EGA) expressed as percentage of mean ranged from 7.72% (average fruit weight) to 57.95% (leaf area index).

In the present study high value of EGA was observed for the character leaf area index, followed by number of fruits per plant, average fruit diameter, average fruit length, fruit yield per plot, number of leaves per plant, total number of harvests, number of branches per plant, indicating the role of additive gene action and hence, selection is more effective. While moderate value of EGA was recorded for days to first flowering, days to first picking, plant height, indicating the role of non-additive gene action. The characters which were observed

high to moderate estimates of EGA are indicative of the fact that improvement could be quickly achieved in these characters through selection.

Low values of expected genetic advance were recorded for the character average fruit weight indicating the presence of both additive and non-additive gene action. Similar findings with high EGA were reported for the character by Mishra and Mishra (1990) and Lohakhare *et al.* (2008).

Generally high heritability accompanied with high genetic advance in a character suggests that the inheritance of such character is governed mainly by additive gene effects and therefore simple selection based on phenotypic performance of these traits may be effective. Characters like leaf area index, number of fruits per plant, average fruit diameter, average fruit length, fruit yield per plant, number of leaves per plant, total number of harvests and number of branches per plant were showing high heritability accompanied with high genetic advance. Thus, the expression of these traits is predominantly governed by additive gene effects and therefore selection based on phenotypic performance will be useful to improve these characters in future as suggested by Prasad *et al.* (2004).

Low heritability and low genetic advance were observed for the character average fruit weight. These results revealed the predominance of both additive and non-additive gene action in the above mentioned characters.

Genetic divergence (D^2 analysis)

The distributions of 31 accessions into 6 groups were presented in Table 2. Group IV and VI was the largest consisting of 7 accessions fol-

lowed by group II consisting of 6 accessions, Group I and III consisting of 4 accessions and group V consisting of 3 accessions. The accessions exhibited random pattern of distribution into various groups and the magnitude of D^2 values suggested that there was considerable amount of diversity in the accessions of brinjal under investigation indicating that forces such as genetic drift, natural

and artificial selection and exchange of genetic material might have played an important role in the diversity of accessions. According to Falconer (1981), larger the divergence between the accessions, higher will be the heterosis. Therefore, it would be desirable to attempt crosses between accessions belonging to distant clusters for getting highly heterotic crosses.

Table 2. Clustering of 31 brinjal accessions

Groups	No. of accessions	Accessions
I	4	IC090915, IC374912, IC127024, IC111404
II	6	IC298633, IC354612, IC090806, IC136245, IC13601, IC111074
III	4	IC427025, IC090942, DBT171, IC354564
IV	7	IC111443, IC345309, AR/04-477, IC136088, IC111444, IC90767, MR/04-02
V	3	IC111439, IC090093, IC111431
VI	7	IC089986, GULABI, IC285140, IC332508, IC427007, EC384565, IC111387

Selection should be based on characters contributing maximum D^2 values for further selection and choice of parents with in a group for hybridization. Highest contribution towards divergence (Table 3) in this regard was put forth by average fruit length (41.29%) followed by leaf area index (20.86%), days to first flowering (13.98%), average fruit diameter (12.04%), number of fruits per plant (0.43%), and number of leaves per plant (0.22%) respectively. Sherly and Shanthi (2007) conducted D^2 analyses and indicated that in order to select parents for hybridization, the material should be screened for average fruit diameter, number of fruits per plant and average fruit length.

Mean intra and inter cluster distances

The mean inter and intra cluster D^2 values were presented in the Table 4. The intra cluster D^2 values ranged from 195.830 to 333.276. The inter cluster D^2 values ranged from 342.626 to 1599.517. The maximum intra and inter cluster distance indicating the wider genetic diversity and also this might be due to limited gene exchange or selection practices among the accessions for diverse characters. Selection of parents from clusters I, III, IV and V for hybridization programme would help in achieving novel recombinants.

The intra cluster distance was minimum between cluster I and VI, cluster II and IV, cluster III and V and also the inter cluster distance was

minimum between cluster II, III and IV; indicating the close relationship and similarity for most of the characters of the accessions.

Table 3. Contribution of different characters towards genetic divergence in 31 accessions of brinjal

S. No.	Characters	Times ranked first	% contribution towards divergence
1	Days to 1st flowering	65	13.98
2	Days to 1st picking	0	0.00
3	Plant height (cm)	0	0.00
4	Number of branches/ plant	0	0.00
5	Number of leaves/ plant	1	0.22
6	Leaf area index	97	20.86
7	Number of fruits/ plant	2	0.43
8	Average fruit length (cm)	192	41.29
9	Average fruit diameter (cm)	56	12.04
10	Average fruit weight (g)	0	0.00
11	Total number of harvests	51	10.97
12	Fruit Yield/ plant (kg)	0	0.00
13	Fruit Yield/ plot (kg)	0	0.00
14	Fruit Yield/ ha (tones)	1	0.22

Table 4. Average intra and inter cluster D^2 values for fourteen characters in 31 germplasm accessions of brinjal

Groups	I	II	III	IV	V	VI
I	333.276	640.909	667.294	688.396	1599.517	1594.974
II		197.547	342.626	354.980	694.564	516.907
III			240.268	395.258	959.265	892.979
IV				195.830	542.589	821.676
V					279.969	558.127
VI						304.041

Bold and diagonal values indicate intra-cluster distances and remaining values indicate inter cluster distances

CONCLUSIONS

High estimates of PCV and GCV and high estimates of heritability coupled with high estimates of genetic advance for number of leaves per plant, number of branches per plant,

leaf area index, number of fruits per plant, average fruit length, average fruit diameter, fruit yield per plant, yield per plot and total number of harvests indicated that the variability available for these traits in the

germplasm was high and selection for these traits may be effective.

Selection and crossing of one or two accessions from the most divergent clusters I (IC090915, IC374912, IC127024, IC111404) and IV (IC111443, IC345309, AR/04-477, IC136088, IC111444, IC90767, MR/04-02) and clusters III (IC427025, IC090942, DBT171, IC354564) and V (IC111439, IC090093, IC111431) based on average fruit length and leaf area index may result in useful heterotic hybrids and desirable transgressive segregants.

REFERENCES

- Burton G.W., Devane E.H. 1953. Estimating the heritability in tall (*Festula arundinacea*) from replicated clonal material. *Agronomy Journal* 45: 478-481.
- Chadha K.L. 2009. Handbook of horticulture. Indian Council of Agricultural Research, Pusa, New Delhi.
- Falconer D.S. 1981. Introduction to quantitative Genetics Second Edition. Longman Group Ltd., Longman House, Burnt Mills, Harrow, Essex England.
- Gomez K.A., Gomez A.A. 1983. Statistical procedures for Agricultural Research. John Wiley & Sons, New York.
- Johnson H.W., Robinson H.F., Comstock R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy J.* 47: 314-318.
- Kushwah S., Bandhyopadhyaya B.B. 2005. Variability and correlation studies in brinjal. *Indian Journal of Horticulture* 62 (3): 210-212.
- Lohakare A.S., Dod V.N., Peshittiwari P.D. 2008. Genetic variability in green fruited brinjal. *The Asian Journal of Horticulture* 3(1): 114-116.
- Lush J.L. 1940. Intra-sire correlation on regression of off-spring on dams as a method of estimating heritability of characters. *Proceedings of American Society of Animal Production* 33: 292-301.
- Mahalanobis P.C. 1928. A statistical study at Chinese head measurement. *Journal of Asiatic Society of Bengal* 25: 301-307.
- Mishra S.N., Mishra R.S. 1990. Variability, heritability and genetic advance in the F₁ generation of a diallel cross in brinjal. *Indian Journal of Horticulture* 47: 93-96.
- Prasad M.N., Mehta S., Dikshit N., Nichal S.S. 2004. Genetic variability, genetic advance and heritability in brinjal (*Solanum melongena* L.). *Orissa Journal of Horticulture* 32(2): 26-29.
- Rao C.R. 1952. Advanced statistical methods in biometrical research. pp: 236-272. John Wiley and Sons Inc., New York.
- Sherly J. 2006. Evaluation of local types of brinjal (*Solanum melongena* L.). M.Sc., (Hort.) Thesis, Pandit Jawaharlal Nehru College of Agricultural and Research Institute, Karaikal, India.
- Sherly J., Shanthi A. 2007. Diversity studies in brinjal. *Haryana Journal of Horticultural Sciences* 36 (1/2): 162-163.
- Singh R.K., Chaudhary B.D. 1977. Biometrical methods in quantitative genetic analysis. Kalyani Publishers, New Delhi pp. 215-218.
- Singh O., Kumar J. 2005. Variability, heritability and genetic advance in brinjal (*Solanum melongena* L.). *Indian Journal of Horticulture* 62 (3): 265-267.

BADANIA DZIEDZICZNOŚCI I ANALIZY WIELOWYMIAROWE
U PSIANKI PODŁUŻNEJ (*SOLANUM MELONGENA* L.)

Streszczenie

Trzydzieści jeden nowych mieszańców psianki podłużnej oceniono pod względem stopnia dziedziczności i rozbieżności genetycznej dla czternastu cech. Zaobserwowano bardzo istotne różnice. Stwierdzono wysoki fenotypowy i genotypowy współczynnik zmienności dla liczby liści na jednej roślinie, wskaźnika powierzchni liści, liczby owoców na jednej roślinie, średniej długości owocu, średniej średnicy owocu, plonu owoców z jednej rośliny, plonu owoców z poletka, plonu owoców z hektara. Niemal wszystkie cechy wykazywały wysoki stopień dziedziczności z wyjątkiem wysokości rośliny (51%), a dla średniej masy owoców odnotowano umiarkowany/niski stopień dziedziczności (24%). Najwyższy postęp genetyczny wyrażony jako procent średniej stwierdzono prawie dla wszystkich cech z wyjątkiem liczby dni do pierwszego kwitnienia, liczby dni do pierwszego zbioru, wysokości roślin a dla średniej masy owoców odnotowano umiarkowany/niski postęp genetyczny. Te trzydzieści jeden nowych mieszańców psianki podłużnej oceniano pod kątem zróżnicowania genetycznego stosując statystykę Mahalanobisa (odległości D^2) biorąc pod uwagę czternaście cech podzielonych na 6 skupień. Analizy wielowymiarowe wykazały maksymalne rozbieżności pomiędzy skupieniami podkreślając ich ważną rolę w badaniach heterozji.