DOI : 10.58993/ijh/2025.82.1.5

Indian J. Hortic. 82(1), March 2025: 28-33

Genetic dissection of phenotypic variation in segregating populations of CGMS-based intraspecific hybrid of eggplant

Harnoor Kaur Dhillon, Madhu Sharma*, O.P. Meena, Karmvir Singh Garcha, Jiffinvir Singh Khosa, M.K. Sidhu and A.S. Dhatt

Department of Vegetable Science, Punjab Agricultural University, Ludhiana 141004, Punjab

ABSTRACT

Genetic diversity is pivotal for the success of crop improvement programs, particularly in mitigating the adverse impacts of existing abiotic and biotic stresses and climate change. Hitherto, in present study, an introgressed male sterile line D-PSB-A (*S/rfrf*) was crossed with restorer line R-2596 (*N/RfRf*) to develop six populations [P_1, P_2, F_1, F_2, BC_1 and BC_1] to establish selection criteria for recycling breeding, targeting the development of superior recombinants. All six populations were evaluated for yield attributing traits *viz.,* length, diameter and weight of fruit, fruit number/plant and seeds/fruit. High heritability beside high genetic advance was recorded for all traits except fruit length in BC_1 and fruit weight in BC_1 populations indicating prospects for improvement of these traits by simple selection. Based on overall performance BC_1 population was found to be superior for developing new strains of the restorer with the genetic constitution *S/RfRf*.

Key words: Brinjal, cytoplasmic male sterility, variability, heritability, fertility restorer.

INTRODUCTION

Eggplant or brinjal (*Solanum melongena* L.) is the fourth most important vegetable crop of the Solanaceous family after potato, tomato and chilli. It is a native of Indo-Burma region. Brinjal is pre-dominantly a warm weather crop with bushy growth habit and is chiefly cultivated in tropical and subtropical zones of the world. In India it is cultivated over an area of 0.74 million ha with a production of 12.78 million tonnes (FAOSTAT, 5). Brinjal has regional specificity for shape, size, colour, and texture of fruits. As a result, many varieties and hybrids are under cultivation in the country. Popularity of hybrid cultivars among growers could be due to large percentage of heterosis for yield (56.16%) and yield attributing traits (40.56-57.64%) (Sharma *et al.*, 13). Because of androgynous nature of the flower, hybridization in brinjal is mostly carried out through hand emasculation and pollination. This process is laborious, time consuming and requires skilled labour resulting in a higher seed cost. Sometimes purity of hybrid seed is also sacrificed in this process. However, exploiting male sterile lines can substantially reduce the expenses incurred on labour for flower emasculation and ensure genetic purity of the hybrid seed. Both genic (GMS) (Dhatt *et al.*, 4) and cytoplasmic genic male sterility (CGMS) systems (Kaur *et al.*, 8; Dhatt *et al.*, 4) prevail in brinjal and have been exploited for hybrid seed production. Both systems have their own advantages and disadvantages. GMS pollination control system is functionally stable over environmental factors. But male fertile plants need to be rouged out from hybrid seed production plots which limits use of GMS in hybrid seed production. Contrary to this CGMS system provides advantage of 100% male sterility (Kaur *et al.*, 8).

To initiate cytoplasmic male sterility-based hybridization programme, there is a pre-requisite of three lines, *viz.,* male sterile or A-line, maintainer or B-line and restorer or R-line. Cytoplasmic genic male sterility (CGMS) has been utilized progressively in hot pepper, a close relative of brinjal but its use in brinjal is restricted due to lack of good fertility restorer lines to act as pollen parents so that F_1 hybrids are fertile. Thus, there is great need to develop perfectly stable restorer lines with strong *Rf* allele (Nalla *et al.*, 12). Punjab Agricultural University, Ludhiana initiated CGMS-based hybrid breeding programme of brinjal in 2008 (Dhatt *et al.*, 4). Due to lack of sterility system in cultivated species *Solanum melongena*, it was introgressed from a wild species of brinjal, *viz.*, *S. aethiopicum* into elite breeding lines with diverse genetic backgrounds. Ten cytoplasmic male sterility (CMS) lines were developed by backcross breeding followed by selection (Garcha and Dhatt, 6). Concomitantly, work on restorer lines was also initiated. Genetic analysis of CMS/*Rf* systems revealed that fertility restoration is governed by a single dominant gene (Kaur *et al.*, 8). But a suspected penalty on fruit yield has been observed in some combinations (unpublished), which may be attributed

---

*Corresponding author: madhusharma@pau.edu to less compatibility of alien cytoplasm with the nuclear genes of *S. melongena*. However, the course of evolution this cytonuclear incompatibility can be overcome (Tuteja and Khadi, 18) through recycling breeding and/ or pure line selection wherein the frequency of favourable alleles could be enhanced in the population.

Effective selection can change the gene frequencies in the population and can help in development of genotypes with a good population mean and variation for the desired character. But the efficacy of selection is mostly determined by the degree of variability in the population and the heritability of the relevant attribute. Hence, assessment of existing variability for yield and yield attributing traits is of utmost importance to develop alloplasmic restorer lines with high yielding potential. In addition to variability, the extent of heritable variation present has a significant impact on genetic development. Heritability in plant breeding extends the predictive function by determining the probability of transmittance of a specific character from parent to its progeny. Genetic advance instead indicates the increase obtained by selection in a specific characteristic during a single breeding cycle under a certain selection pressure. Judgement solely based on heritability sightings is less reliable; nevertheless, assessment based on both heredity and genetic advancement is significant (Sharma and Swain, 14). As a result, understanding the level of genetic diversity, heritability, and genetic gain over selection is critical for determining the progress of a breeding effort. Therefore, this study was planned with the objective to estimate the differences in means, genotypic variances, heritability, and selection responses of an F_2 and first backcross generations of a cross between M-PSB-A and R-2596 of eggplant and to define criteria for selecting the best base population in a recycling breeding programme.

MATERIAL AND METHODS

The current study was carried out at Research Farm of Department of Vegetable Science, Punjab Agricultural University, Ludhiana, India. Seed parent D-PSB-A bearing the sterile cytoplasm was used to perform cross with pollen parent R-2596 harbouring fertility restorer gene(s) during 2020. Individual plants of F_1 were selfed and backcrossed in subsequent season of 2021 to produce F_2 and BC_1F_1 populations. Parents [D-PSB-A (P_1, A-line), D-PSB-B (maintainer, B-line) and R-2596 (P_2, R-line)], F_1, F_2, $BC_{1(F1XP2)}$ and $BC_{1(P1XF1)}$ populations were sown in July (2022) followed by transplanting in August. The crop was raised as per recommendations mentioned in package of practices (Anon., 1). Individual plants in segregating populations while fifteen random plants in parents (D-PSB-B and R-2596) and F_1 generation were evaluated for yield and yield attributing traits, *viz*., number of fruits/plant, fruit length (cm), fruit width (cm), fruit weight (g), and number of seeds/ fruit.

The phenotypic (PCV), genotypic (GCV) and environmental (ECV) coefficients of variation for all six traits were estimated using Burton and Devane's (2) formulas. PCV, GCV and ECV estimates were categorized according to Sivasubramanian and Menon (15). Broad sense heritability and genetic advance were computed in accordance with Lush (10) and Johnson *et al*. (7), respectively. Heritability and genetic advance as a per cent of mean estimates were categorized according to Johnson *et al*. (7). Number of superior plants per population were determined by the following formula (Nadarajan *et al*., 12):

Number of superior plants = [Mean + 2 $*$ (Standard deviation)]

RESULTS AND DISCUSSION

In the present study, the parental lines significantly differ with respect to fruit weight, number of fruits/plant and seed No./fruit (Table 1 and Fig. 1). The number of fruits/plant was found to be lowest in F_1 but thereafter showed comparative improvement in segregating generations with highest being recorded in first backcross with restorer parent R-2596 ($BC_{1(F1xP2)}$). Parental and segregating populations were at par in terms of days to flowering but varied significantly for days to fruiting. Fruiting was observed after 45 days of transplanting (DAT) in parental lines while segregating generations were late (70 DAT). Since the progenies are cross of an alloplasmic CMS line and a restorer line, placing nucleus of restorer into an alien cytoplasm might have showcased pleiotropic

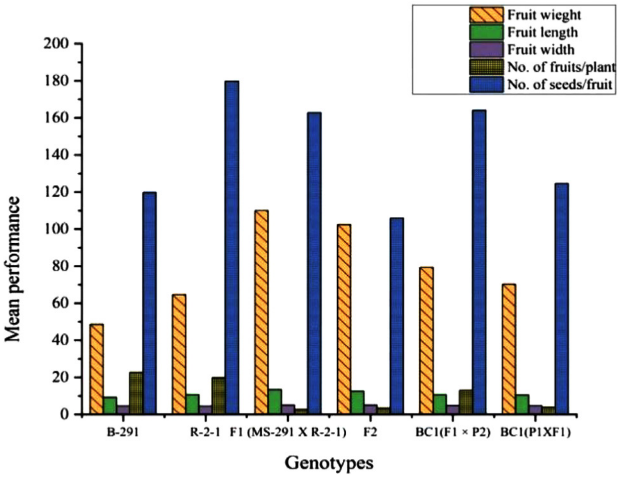

Fig. 1. Graphical representation of mean performance of six populations.

Table 1. Mean performance of genotypes for various quantitative traits.

Population	Fruit weight (g)	Fruit length (cm)	Fruit width (cm)	No. of fruits/plant	No. of seeds/fruit
D-PSB-B	48.60	9.14	4.50	22.60	119.69
R-2596	64.66	10.70	4.48	19.87	179.78
F_1	110.00	13.33	5.06	2.66	162.79
F_2	102.37	12.50	5.01	3.40	105.89
BC_1 (F_1 × P_2)	79.30	10.62	4.74	13.00	164.08
BC_1 (P_1XF_1)	70.23	10.47	4.65	3.90	124.58

*Since P_1 (D-PSB-A) is male sterile, therefore fruit characteristics of its maintainer line (D-PSB-B) are compared with other populations

effects. Variation in penetrance and expressivity was observed for anther dehiscence. Though no fixed pattern of inheritance was observed for anther dehiscence among segregating generations depicting non-mendelian nature of the trait. This could be due to maternal effects (Tiaz *et al.*, 17), unfavourable linkage or cytonuclear incompatibility. Mother's genes or of her environment (*e.g.* health) often tend to be greatest on juvenile traits and decline as the offspring gets older (Kearsey and Pooni, 9). Thus, delayed fruiting could be due to maternal effects. Floral abnormalities have been witnessed widely in alloplasmics of *Brassica napus* in form of petaloid anthers (*ogu* and *tour*), less or no nectaries (*tour*, *ogura*, *niger*, *lyr*), crooked style and low seed fertility (*tour*, *ogu* cytoplasm). These floral abnormalities make pollination difficult, resulting in inadequate realization of heterosis. However, such abnormalities can be rectified through backcross and pedigree breeding (Payal, 14).

Recombinant selection offers scope for improvement of alloplasmic lines. But fixing desirable recombinants from a segregating population needs to be based on scientific principles (Sravanthi *et al.*, 16) to attain realistic genetic gain. Effectiveness of selection relies on variation in a population and transmission percentage of character from parent to offspring. The developed base populations, *i.e.*, F_2, $BC_{1(F1XP2)}$ and $BC_{1(P1XF1)}$ exhibited significant variation for fruit weight, number of fruits/plant and number of seeds/ fruit indicating presence of variability. The F_2 population exhibited high PCV and GCV values (Table 2) for two (fruit weight and number of fruits/plant) out of five studied traits. Thus, scope for improvement of fruit length, fruit width and number of seeds/fruit through selection in F_2 population is limited. The heritability and genetic advance estimates were high for all the traits indicating role of additive gene action and thus these traits can be improved *via* selection in early generations. Similar results have been reported by Chouhan *et al*. (3). Number of fruits/plant and number of seeds/fruit give a direct idea of normal dehiscence and agronomic superiority of population. $BC_{1(F1XP2)}$ generation exhibited a rather higher variance than F_2 and $BC_{1(P1XF1)}$ populations for both the traits. Moderate influence of environment was observed in F_2 and $BC_{1(P1XF1)}$ population for number of fruits/ plant as compared to $BC_{1(F1XP2)}$. The reduction in magnitude of ECV with the recovery of genome of restorer parent; R-2596 indicated that backcrossing in this direction could be worthwhile as it enhanced the transmission percentage (99.20%) of restorer gene (Table 2). PCV and GCV values were high for fruit weight (Fig. 2) and number of fruits/plant (Fig. 3), while it was moderate for fruit length, width and number of seeds/fruit (Fig. 4.). ECV was low for all traits. Moderate PCV and GCV was observed in $BC_1(P_1 × F_1)$ for all traits except number of fruits/plant. Genetic gain was high for all the traits in all populations except fruit length and fruit weight in $BC_{1(F1XP2)}$ and $BC_{1(P1XF1)}$ populations.

Based on mean performance and variation, we also determined the superior plants in three populations that should be selected for further evaluation (Table 3). F_2 population had 10 superior

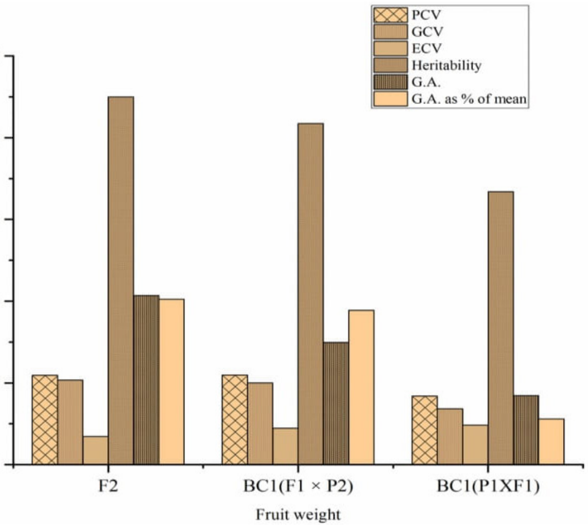

Fig. 2. Representation of components of variance, heritability and genetic advance for fruit weight.

Table 2. Generation variance and components for yield attributing traits of the cross D-PSB-A × R-2596 in eggplant.

Base population	Quantitative traits				
	Fruit weight (g)	Fruit length (cm)	Fruit width (cm)	No. of fruits/plant	No. of seeds/fruit
F_2					
PCV	21.85	14.25	15.46	86.65	13.39
GCV	20.73	13.43	14.32	84.65	13.32
ECV	6.91	4.77	5.83	18.54	1.27
Heritability (broad sense) (%)	89.99	88.80	85.75	85.44	99.11
Genetic advance (GA)	41.43	3.26	1.77	2.88	28.94
GA as per cent of mean (%)	40.47	26.07	27.31	84.75	27.33
$BC_1(F_1$ × $P_2)$					
PCV	21.95	11.81	16.12	54.55	14.62
GCV	20.06	10.34	14.89	54.33	14.59
ECV	8.92	5.70	6.16	4.84	0.81
Heritability (%)	83.49	76.71	85.35	99.20	99.68
Genetic advance (GA)	29.95	1.58	1.28	14.49	49.25
GA as per cent of mean (%)	37.77	15.09	27.11	108.94	30.01
$BC_1(P_1$ × $F_1)$					
PCV	16.77	12.99	14.29	86.91	12.19
GCV	13.70	11.67	12.84	85.40	12.14
ECV	9.66	5.70	6.29	16.17	1.27
Heritability	66.80	80.74	80.65	96.54	99.22
Genetic advance (GA)	16.90	2.26	1.10	3.92	31.03
GA as per cent of mean (%)	11.21	21.61	23.75	100.70	24.91

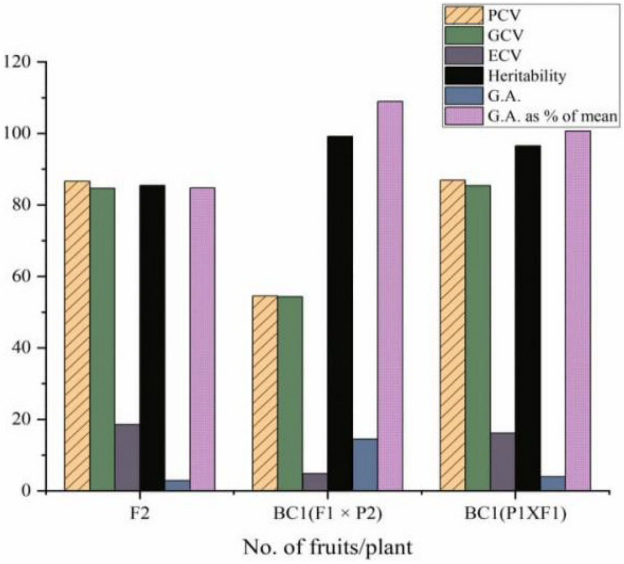

Fig. 3. Representation of components of variance, heritability and genetic advance for number of fruits/ plant.

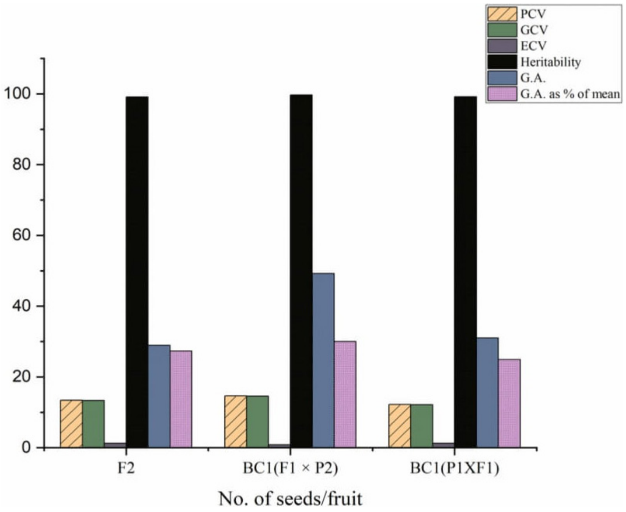

Fig. 4. Representation of components of variance, heritability and genetic advance for number of seeds/ fruit.

Table 3. Number of superior plants in evaluated segregating populations.

Trait	Population		
	F_2	BC_1 ($F_1 \times P_2$)	BC_1 ($P_1 \times F_1$)
Fruit weight	10.00	4.00	2.00
Fruit length	1.00	3.00	13.00
Fruit width	1.00	5.00	1.00
No. of fruits per plant	2.00	4.00	2.00
No. of seeds per fruit	3.00	15.00	9.00

plants for fruit weight while $BC_{1(F1XP2)}$ had 4 superior plants for number of fruits per plant. Based on overall evaluation it was concluded that selection and advancement of superior transgressive segregants from F_2 and $BC_{1(F1XP2)}$ would lead to development of heterotic homozygous recombinants with good pollen density, anther dehiscence and yield. Thus, both pure lines and near isogenic lines (NILs) can be developed from these populations. Among the three evaluated populations, $BC_{1(F1XP2)}$ showed better response to selection thus indicating that backcross breeding with stability analysis shall be adopted to overcome negative impacts of cytonuclear interactions and achieve new strains of restorer R-2596 with genetic constitution *S* (*RfRf*) rapidly and efficiently.

AUTHOR'S CONTRIBUTION

Conceptualization of research (MS, ASD, OPM); Designing of the experiments (MS, OPM); Contribution of experimental materials (ASD, MKS); Execution of field/lab experiments and data collection (HKD, OPM, JSK); Analysis of data and interpretation (HKD, JSK); Preparation of the manuscript (HKD, MS, MKS).

CONFLICT OF INTEREST

The authors declare that they have no conflict of interest in the publication.

ACKNOWLEDGEMENT

Financial support provided by Department of Science and Technology (DST), Government of India, New Delhi, India through Grant No. CRG/2021/008101 and lab facilities under PURSE/ FIST scheme, is gratefully acknowledged.

REFERENCES

1. Anonymous. 2022. *Package of Practices for Vegetable Crops*. Punjab Agricultural University, Ludhiana, 1-2 p.
2. Burton, G.W. and Devane E.H. 1953. Estimates of heritability in tall fescue. *Agron. J*. **45**: 478-81.
3. Chouhan, G., Kushwah, S., Singh, O. and Sharma, R. 2020. Genetic variability and correlation analysis for fruit yield and quality traits in bottle gourd. *Indian J. Hortic.* **77**: 287-92. https://doi.org/10.5958/0974-0112.2020.00039.0
4. Dhatt, A.S., Sidhu, M.K. and Garcha, K.S. 2023. Development of alloplasmic male sterile lines and their assessment for heterotic potential in eggplant (*Solanum melongena* L.). *J. Hortic. Sci. Biotechnol*. **99**: 95-105.
5. FAOSTAT. 2020. Food and Agriculture Organization. https://www.fao.org/fruits-vegetables-2020/resources/en/. Accessed 23 March 2020.
6. Garcha, K.S. and Dhatt, A.S. 2017. Evaluation of cytoplasmic male sterile (CMS) and maintainer lines for yield and horticultural traits in brinjal (*Solanum melongena* L.). *Veg. Sci*. **44**: 101-06.
7. Johnson, H.W., Robinson, H.F. and Comstock, R.E. 1955. Estimation of genetic and environmental variability in soybean. *Agron. J.* **47**: 314-18.
8. Kaur, K., Dhatt, A.S. and Sharma, M. 2021. Inheritance of alloplasmic fertility restoration in eggplant (*Solanum melongena* L.) *Genet. Resour. Crop. Evol*. **68**: 1949-60.
9. Kearsey, M.J. and Pooni, H.S. 1996. *The genetical analysis of quantitative traits*, Chapman and Hall. Springer, London, 286-83 p.
10. Lush, J.L. 1940. Intro-site correlation and regression of off spring corn as a method of estimating heritability of characters. *PNAS* **33**: 293-301.
11. Liu, C.Q., Li, G.Q., Yao, X.Q., Huang, L., Wu, X.Y. and Xie, Z.J. 2020. Characterization of *Ogura* CMS fertility-restored interspecific hybrids and backcross progenies from crosses between broccoli and rapeseed. *Euphytica* **216**: 194.
12. Nadarajan, N., Manivannan, N. and Gunasekaran, M. 2021. *Quantitative genetics and biometrical techniques in plant breeding*, Kalyani publishers, New Delhi, 79 p.
13. Sharma, T.K., Pant, S.C., Kumar, K., Kurrey, V.K., Pandey P.K. and Bairwa P.L. 2016. Studies

on heterosis in brinjal (*Solanum melongena* L.). IJBSM **7**: 964-69.

14. Sharma, A. and Swain, D. 2018. Estimation of genetic variability in advance breeding lines derived from inter-varietal crosses in chilli. *Indian J. Hortic.* **75**: 440–45.
15. Sivasubramanian, S. and Menon, P.M. 1973. Genotypic and phenotypic variability in rice. *Madras Agric J.* **60***:* 1093-96.
16. Sravanthi, R., Kumaresan, D., Saraswathi, R. and Sritharan, N. 2022. Genetic variability studies in early generation prebreeding restorer germplasm of the cross CBSN 25 × WRM 93-20. *Electron. J. Plant Breed.* **13**: 865-72. https://doi.org/10.37992/2022.1303.109.
17. Tiaz, L., Zeiger, E., Moller, I.M. and Murphy, A. 2015. Photosynthesis: The light reactions. **In**: *Plant Physiology and Development*. Sixth Edition. Sinauer Associates, Inc., Sunderland, Massachusetts, U.S.A, pp. 198-99.
18. Tuteja, O.P. and Khadi, B.M. 2008. Development and characterization of fertility restorers in cytoplasmic genetic male sterile lines of cotton (*Gossypium hirsutum* L.) derived from *Gossypium harknessii. Indian J. Genet*. **68**: 337-39.

(Received : July, 2024; Revised : March, 2025;
Accepted : March, 2025)