Genetic variability in CMS backcross generations and their maintainers in eggplant (*Solanum melongena* L.)

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Abstract: Twelve genotypes of eggplant in BC_3, BC_4 and BC_5 generations of CMS-lines derived from *Solanum aethiopicum* × *Solanum melongena* cross along with their maintainers were evaluated for eighteen quantitative characters at Punjab Agricultural University Ludhiana. Analysis of variance depicted significant variation (P ≤ 0.05) for all the characters in all generations. High PCV and GCV values were observed for fruit length, fruit girth, fruit weight, number of fruits plant^{-1} and yield plant^{-1} in all generations indicating high variability in the germplasm. High heritability coupled with high genetic advance was found for peduncle length, fruit length, fruit girth, fruit weight, number of fruits plant^{-1} and yield plant^{-1} in all generations indicating the predominance of additive gene action for these traits. Thus, selections can be made from present germplasm for the development of improved CMS inbred lines with varying fruit traits.

Keywords: CMS, Eggplant, GCV, Heritability, PCV, Percent GA

INTRODUCTION

Eggplant (*Solanum melongena* L.), popularly known as brinjal, aubergine or guinea squash is a diploid (2n=2x=24) and often cross-pollinated vegetable crop. It is an economically important horticultural crop especially in South - East Asia and, exploitation of genetic diversity is important for raising the yield levels. Selection of genotypes based on yield, as such is difficult as most of the yield related characters are inherited and being governed by the large number of cumulative, duplicate and dominant genes. Therefore, generation of variability, selection of superior genotypes from the variable genetic stock and development of superior genotypes remains a basic breeding strategy in crop improvement programmes (Appalaswamy and Reddy, 2004).

In eggplant, on the basis of fruit size even the varieties exhibit variability leading to classification of specie *melongena* into three botanical varieties *viz.*, *esculentum* (round or egg shaped fruits), *serpentinum* (long, slender fruits) and *depressum* (small fruits) (Choudhury,1976). Further, variability in colour like deep-purple, purple, light-purple, scarlet, green, white and striped is also present and, exploited as per consumers' preference. Accordingly, in heterosis breeding parents are also chosen based upon the size, shape, colour and clustering pattern of the fruits. There is a report of induced cytoplasmic male sterility (CMS) in eggplant through wide hybridization between *S. aethiopicum* and *S. melongena* (Khan and Issihiki, 2010). Male sterility is an established genetic tool that evaded

hand emasculation and pollination during hybrid seed production and, exploited world-wide in large number of field and vegetable crops (Fang *et al.,* 1997; Zhao and Gai, 2006; Chen *et al.,* 2008; Deol *et al.,* 2013; Shen Xian-hua *et al.,* 2013 and Islam *et al.,* 2015). Thus, we made an attempt to cross *S. aethiopicum* and *S. melongena* to induce non-pollen formation type of cytoplasmic male sterility. This was further transferred into diverse genetic backgrounds of different shapes, sizes, colours and clustering patterns to use in heterosis breeding programme. The genetic variability for agronomic and morphological traits have been reported by many workers in cultivated and wild relatives of eggplant (Prohens *et al.,* 2005; Rodríguez-Burruezo *et al.,* 2008; Muñoz-Falcón *et al.,* 2009; Prabhu *et al.,* 2009; Dhaka and Soni, 2012; Kumar *et al.,* 2013 and Singh *et al.,* 2014) but is not available among male-sterile lines of different genetic backgrounds. Therefore, in present study attempt was made to assess the information on magnitude of genetic variability in BC_3, BC_4 and BC_5 generations of CMS lines and their maintainers derived from interspecific cross of *S. aethiopicum* × *S. melongena*.

MATERIALS AND METHODS

Experimental site: The experiment was conducted at Vegetable Research Farm, Department of Vegetable Science, Punjab Agricultural University, Ludhiana which is 30˚ 54' N latitude and 75˚ 48' E longitude at a mean height of 247 meters above sea level. The mean maximum and minimum temperature show considera-

ble fluctuations during the summer, while minimum temperature falls below freezing point accompanied by frosty spells during winter. The average rainfall is about 500-700 mm, most of which is normally received from July-September.

Planting material and treatments: In this study BC_3, BC_4 and BC_5 progenies of twelve genotypes *viz.*, CB 99 - 231, SR 5, SR 93-213, SR 232, P 67, BL 12-4, BL 201, BL 214, BL 216, BL 219, BR 104 and MR 319 developed from cross of *S. aethiopicum* × *S. melongena* along with their respective maintainer recurrent parents were subjected to variability analysis. The maintainer genotypes and advanced backcross generations were evaluated for various morphological traits using phenotypic measures. Maintainers and sterile backcross generations were raised during 2015-16 at Vegetable Research Farm, Department of Vegetable Science, Punjab Agricultural University, Ludhiana. The experiment was laid in Randomized Complete Block Design with three replications for each generation. To ensure optimum fruit setting on cytoplasmic male-sterile lines, each flower was pollinated everyday with the pollen collected by the pollen collector. This process was continued for entire period of flowering (eight weeks). The data obtained from all the generations was assessed statistically for various yield and disease related traits *viz.,* plant height (cm), plant spread (cm), petiole length (cm), leaf length (cm), leaf width (cm), pedicel length (mm), calyx size (mm), petal length (mm), petal width (mm), stamen size (mm), pistil size (mm), days to 50% flowering, peduncle length (cm), fruit length (cm), fruit girth (cm), fruit weight (g), number of fruits plant[-1] and yield plant[-1] (kg).

Estimation of genetic parameters: Means of the data collected across seasons were subjected to analysis of variance using CPCS-1 (Cheema and Singh, 1990) and significant means were compared using least significant difference at P ≤ 0.05. Genetic parameters like genotypic variance (Vg) and phenotypic variance (Vp) were obtained according to Burton and Devance, (1953) as follows:

$$Vg = \frac{MSg - MSe}{r}$$

$$Vp = Vg + Ve$$

Where, MSg= mean square of genotypes, MSe= mean square of error, r = number of replications, and Ve = environmental variance

The mean values were used for genetic analyses to determine phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), according to Burton, (1952) as follows:

$$GCV(\%) = \frac{\sqrt{Vg}}{\bar{x}} \times 100,$$

$$PCV(\%) = \frac{\sqrt{Vp}}{\bar{x}} \times 100$$

Where, Vg= genotypic variance, Vp= phenotypic variance, and $\bar{x}$= genotypic mean

The broad sense heritability (H^2) and genetic advance (GA) was computed according to the procedure suggested by Johnson *et al.,* (1955) as follows:

$$H^2 = \frac{Vg}{Vp} \times 100,$$

$$GA = \sqrt{Vp} \times H^2 \times k$$

Where, k= differential selection constant (2.06) at 5% selection, Vp= phenotypic variance, Vg= genotypic variance, and H^2 = heritability in broad sense
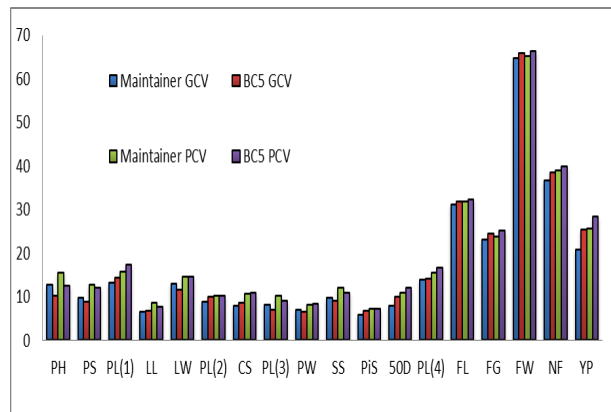

Fig. 1. *Phenotypic co-efficient of variation (PCV %) and Genotypic co-efficient of variation (GCV %) in maintainers and CMS BC$_5$ generation of eggplant genotypes.*
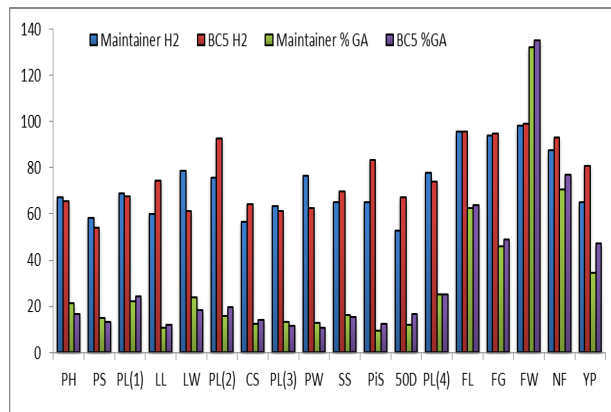
Fig. 2. *Heritability (H^2) and Genetic advance (%GA) in maintainers and CMS BC$_5$ generation of eggplant genotypes.*

Where, PH = plant height, PS = plant spread, PL(1) = petiole length, LL = leaf length, LW = leaf width, PL(2) = pedicel length, CS = calyx size, PL(3) = petal length, PW = petal width, SS = stamen size, Pis = pistil size, 50D = days to 50% flowering, PL(4) = peduncle length, FL = fruit length, FG = fruit girth, FW = fruit weight, NF = number of fruits plant[-1] and YP = yield plant[-1].

Table 1. Analysis of variance for various quantitative traits in three CMS backcross generations along with their maintainers in eggplant genotypes.

	df	PH	PS	PL(1)	LL	LW	PL(2)	CS	PL(3)	PW	SS	PiS	50D	PL(4)	FL	FG	FW	NF	YP
Maintainers																			
Replication	2	485.1	117.7	0.1	0.3	0.7	1.2	0.4	1.7	0.1	2.1	1.2	21.2	0.2	0.6	0.1	51.8	9.7	0.1
Genotypes	11	213.3*	170.4*	0.9*	3.1*	4.6*	8.5*	6.4*	6.6*	2.1*	4.3*	3.1*	52.7*	0.8*	21.6*	4.1*	6606.3*	504.5*	0.6*
Error	22	29.9	32.7	0.1	0.6	0.4	0.8	1.3	1.1	0.2	0.7	0.5	12.1	0.1	0.3	0.1	40.8	22.5	0.1
BC5																			
Replication	2	251.6	90.1	0.1	1.4	0.1	0.4	5.9	0.6	0.6	0.4	0.4	6.2	0.1	0.1	0.1	66.2	0.9	0.1
Genotype	11	162.4*	164.4*	1.1*	3.3*	4.2*	9.7*	6.9*	4.8*	1.9*	1.8*	3.6*	103.0*	1.0*	22.3*	3.9*	6455.2*	419.3*	0.6*
Error	22	24.3	36.3	0.1	0.3	0.7	0.3	1.1	0.8	0.3	0.2	0.2	14.3	0.1	0.3	0.1	21.9	9.9	0.1
BC4																			
Replication	2	66.0	31.1	0.1	0.2	0.5	0.3	4.5	0.7	0.3	0.1	1.2	6.3	0.1	0.2	0.1	60.6	4.9	0.1
Genotypes	11	228.8*	144.0*	0.9*	3.4*	4.2*	8.4*	7.3*	5.1*	1.5*	1.6*	3.8*	162.6*	1.1*	20.9*	4.2*	6272.5*	397.5*	0.5*
Error	22	36.7	32.4	0.1	0.6	0.3	0.4	1.0	1.1	0.4	0.3	0.6	11.3	0.1	0.5	0.1	18.8	7.6	0.0
BC3																			
Replication	2	250.4	133.4	0.1	0.1	1.5	0.8	1.8	0.1	0.4	0.5	0.1	17.5	0.4	0.1	0.1	56.7	0.4	0.1
Genotypes	11	284.1*	176.4*	0.8*	3.6*	4.7*	8.5*	7.1*	6.0*	2.3*	1.5*	4.0*	105.7*	1.0*	22.5*	3.5*	6082.4*	398.3*	0.6*
Error	22	35.5	21.0	0.2	0.8	0.6	1.5	0.8	0.9	0.3	0.2	0.8	17.6	0.1	0.3	0.1	33.2	8.1	0.0

*Significant at P≤0.05, Where, PH=plant height, PS=plant spread, PL(1)=petiole length, LL=leaf length, LW= leaf width, PL(2)=pedicel length, CS=calyx size, PL(3)=petal length, PW= petal width, SS=stamen size, PiS=pistil size, 50D=days to 50% flowering, PL(4)=peduncle length, FL=fruit length, FG=fruit girth, FW=fruit weight, NF=number of fruits plant^{-1} and YP=yield plant^{-1}

Table 2. Mean performance of the maintainers and CMS backcross generations of eggplant genotypes in field conditions.

	PH	PS	PL(1)	LL	LW	PL(2)	CS	PL(3)	PW	SS	PiS	50D	PL(4)	FL	FG	FW	NF	YP
Generation mean																		
Maintainer	61.7	70.0	3.9	14.0	9.1	18.1	16.2	16.5	11.2	11.3	16.0	46.2	3.7	8.6	5.0	72.3	34.7	2.0
BC5	66.8	73.5	3.8	14.7	9.3	18.0	16.1	16.2	11.0	8.1	15.8	54.6	3.8	8.5	4.6	70.2	30.3	1.7
BC4	68.9	74.4	3.8	14.8	9.4	18.1	16.0	16.0	10.9	8.1	15.6	56.1	3.9	8.5	4.6	69.4	29.6	1.7
BC3	71.4	75.7	3.8	14.9	9.5	18.0	16.0	15.9	10.7	8.1	15.5	57.9	3.9	8.5	4.5	67.7	28.6	1.6
Genotypic variance (%)																		
Maintainer	61.2	45.9	0.3	0.9	1.4	2.6	1.7	1.8	0.6	1.2	0.9	13.5	0.3	7.1	1.3	2188.5	160.7	0.2
BC5	46.0	42.7	0.3	1.0	1.2	3.1	1.9	1.3	0.5	0.5	1.1	29.6	0.3	7.3	1.3	2144.4	136.5	0.2
BC4	64.1	37.2	0.3	0.9	1.3	2.6	2.1	1.4	0.4	0.5	1.1	50.4	0.3	6.8	1.4	2084.5	130.0	0.2
BC3	82.9	51.8	0.2	1.0	1.4	2.4	2.1	1.7	0.7	0.4	1.1	29.4	0.3	7.4	1.1	2016.4	130.1	0.2
Phenotypic Variance (%)																		
Maintainer	91.0	78.6	0.4	1.4	1.8	3.4	3.0	2.9	0.8	1.9	1.3	25.6	0.3	7.4	1.4	2229.3	183.2	0.3
BC5	70.4	79.0	0.4	1.3	1.9	3.4	3.0	2.2	0.8	0.8	1.3	43.9	0.4	7.7	1.4	2166.3	146.3	0.2
BC4	100.7	69.6	0.4	1.5	1.6	3.1	3.1	2.4	0.7	0.7	1.6	61.7	0.4	7.3	1.5	2103.4	137.6	0.2
BC3	118.4	72.8	0.4	1.7	2.0	3.8	2.9	2.6	1.0	0.7	1.9	46.9	0.4	7.7	1.2	2049.6	138.1	0.2
Co-efficient of variation (%)																		
Maintainer	8.9	8.2	8.7	5.4	6.8	5.0	7.0	6.2	3.9	7.2	4.3	7.5	7.4	6.6	5.9	8.8	13.7	15.1
BC5	7.4	8.2	9.9	4.0	9.1	2.8	6.5	5.7	5.1	5.9	3.0	6.9	8.5	6.7	5.9	6.7	10.4	12.4
BC4	8.8	7.7	8.4	5.1	6.3	3.6	6.3	6.5	5.5	6.4	4.8	6.0	9.3	8.0	7.1	6.3	9.3	12.2
BC3	8.4	6.1	10.1	5.9	8.4	6.7	5.6	5.9	5.0	8.1	5.8	7.2	9.8	6.8	6.6	8.5	9.9	17.7

Where, PH=plant height, PS=plant spread, PL(1)=petiole length, LL=leaf length, LW= leaf width, PL(2)=pedicel length, CS=calyx size, PL(3)=petal length, PW= petal width, SS=stamen size, Pis=pistil size, 50D=days to 50% flowering, PL(4)=peduncle length, FL=fruit length, FG=fruit girth, FW=fruit weight, NF=number of fruits plant^{-1} and YP=yield plant^{-1}

Table 3. Variability parameters in different generations of eggplant genotypes for different quantitative traits.

	PH	PS	PL(1)	LL	LW	PL(2)	CS	PL(3)	PW	SS	PiS	50D	PL(4)	FL	FG	FW	NF	YP
Genotypic co-efficient of variability (%)																		
Maintainer	12.7	9.7	13.1	6.6	13.0	8.9	8.0	8.2	7.1	9.7	5.8	8.0	13.8	31.1	23.2	64.7	36.6	20.7
BC$_5$	10.2	8.9	14.3	6.8	11.5	9.9	8.7	7.1	6.6	9.0	6.7	10.0	14.2	31.8	24.4	65.9	38.6	25.5
BC$_4$	11.6	8.2	13.4	6.5	12.1	9.0	9.1	7.3	5.8	8.3	6.7	12.7	14.6	30.7	25.7	65.8	38.5	23.0
BC$_3$	12.8	9.5	12.1	6.5	12.3	8.6	9.1	8.2	7.6	8.1	6.6	9.4	14.0	31.9	23.7	66.4	39.9	25.3
Phenotypic co-efficient of variability (%)																		
Maintainer	15.5	12.7	15.7	8.5	14.7	10.2	10.6	10.3	8.1	12.1	7.2	11.0	15.6	31.8	23.9	65.3	39.0	25.6
BC$_5$	12.6	12.1	17.4	7.8	14.7	10.2	10.8	9.1	8.3	10.8	7.3	12.1	16.6	32.4	25.1	66.3	40.0	28.3
BC$_4$	14.6	11.2	15.8	8.3	13.6	9.7	11.0	9.7	7.9	10.5	8.2	14.0	17.3	31.7	26.6	66.1	39.7	26.0
BC$_3$	15.2	11.3	15.7	8.8	14.8	10.9	10.7	10.1	9.1	10.1	8.8	11.8	17.0	32.6	24.6	66.9	41.1	30.9
Heritability (%)																		
Maintainer	67.2	58.4	69.1	60.1	78.7	75.9	56.8	63.6	76.7	64.9	65.1	52.8	77.9	95.7	94.0	98.2	87.7	65.2
BC$_5$	65.4	54.1	67.8	74.4	61.4	92.7	64.2	61.3	62.5	69.8	83.5	67.4	73.8	95.8	94.6	99.0	93.2	80.8
BC$_4$	63.6	53.4	71.6	61.8	78.8	86.3	67.4	55.5	52.4	62.9	66.5	81.7	71.1	93.7	92.8	99.1	94.5	78.1
BC$_3$	70.0	71.2	59.0	55.5	68.2	61.8	72.0	65.7	70.0	64.4	56.1	62.6	67.2	95.6	92.8	98.4	94.2	67.3
Genetic advance																		
Maintainer	13.2	10.7	0.9	1.5	2.2	2.9	2.0	2.2	1.4	1.8	1.6	5.5	0.9	5.4	2.3	95.5	24.5	0.7
BC$_5$	11.3	9.9	0.9	1.8	1.7	3.5	2.3	1.9	1.2	1.3	2.0	9.2	1.0	5.5	2.3	94.9	23.2	0.8
BC$_4$	13.2	9.2	0.9	1.6	2.1	3.1	2.5	1.8	0.9	1.1	1.8	13.2	1.0	5.2	2.3	93.6	22.8	0.7
BC$_3$	15.7	12.5	0.7	1.5	2.0	2.5	2.5	2.2	1.4	1.1	1.6	8.8	0.9	5.5	2.1	91.8	22.8	0.7
Percent genetic advance over mean																		
Maintainer	21.4	15.2	22.3	10.6	23.8	15.9	12.5	13.5	12.8	16.2	9.7	11.9	25.1	62.7	46.2	132.1	70.6	34.4
BC$_5$	16.9	13.5	24.3	12.0	18.6	19.5	14.3	11.5	10.7	15.5	12.6	16.8	25.2	64.0	48.9	135.1	76.8	47.1
BC$_4$	19.1	12.3	23.3	10.6	22.1	17.2	15.3	11.1	8.6	13.6	11.3	23.6	25.3	61.1	50.9	135.0	77.2	41.9
BC$_3$	22.0	16.5	19.1	10.0	20.9	13.9	15.8	13.7	13.1	13.4	10.2	15.2	23.6	64.3	47.0	135.6	79.8	42.8

Where, PH=plant height, PS=plant spread, PL(1)=petiole length, LL=leaf length, LW= leaf width, PL(2)=pedicel length, PW= petal width, SS=stamen size, Pis=pistil size, 50D=days to 50% flowering, PL(4)=peduncle length, FL=fruit length, FG=fruit girth, FW=fruit weight, NF=number of fruits plant^{-1} and YP=yield plant^{-1}

Genetic advance percentage of mean (%GA) was calculated as follows:

$$GA(\%) = \frac{GA}{\mu} \times 100$$

Where, GA = genetic advance, and μ= grand mean

Categories of the coefficients of variation: Coefficients of variation were categorized according to Sivsubramanian and Menon, (1973) as: Low (0-10%), Medium (11-20%) and High (> 20%).Whereas, categories of heritability values were accordance to Robinson *et al.,* (1949) as Low (0-30%), Medium (31-60%) and High (> 60%). Further, the percent genetic advance (% GA) over mean was also classified as Low (<10%), Medium (10-20%), High (> 20%).

RESULTS AND DISCUSSION

Analysis of variance: The analysis of variance for eighteen quantitative traits of all the three backcross generations along with their maintainers in twelve genotypes is presented in Table 1. The results represented that mean sum of squares of the traits in three backcross generations of CMS-lines and their maintainers differed significantly (P≤0.05) demonstrating vast amount of variability for various growth and yield attributes. It depicts the transfer of cytoplasmic male-sterility into different backcross generations derived from diverse maintainers. This variability in different maintainers and CMS generations is very important in the development of diverse CMS lines (A-lines) for use in heterosis breeding of CGMS (cytoplasmic genetic male-sterility system) system. The selection could be made from these backcross populations for succeeding backcrosses with their respective recurrent parents for further improvement. The variability available for the eighteen traits under study in twelve genotypes was investigated using PCV, GCV, H^2 and genetic advance (Table 2, 3).

Estimation of variability parameters: Mean and variance values for all of the traits under study exhibited difference in alloplasmic male-sterile backcross generations of all the genotypes (BC$_3$, BC$_4$ and BC$_5$). The mean values of vegetative growth traits revealed that all male-sterile lines had more vegetative growth than their fertile counterparts (Table 2), which may be attributed to lesser fruit setting and yield plant^{-1} due to artificial pollination. But in BC$_5$, days to 50% flowering along with vegetative growth *viz.* mean plant height, plant spread, leaf length, leaf width were less compared to BC$_3$ and BC$_4$. Similarly, there was an increase in calyx size, petal length and width, pistil size, fruit weight, number of fruits plant^{-1} and yield plant^{-1} in BC$_5$ than BC$_3$ and BC$_4$ indicating desirable restoration of recurrent parental characters with advancement in backcross generations. Overall, the population mean of BC$_5$ was more near towards the recurrent parents mean compared to BC$_3$ and BC$_4$. Analysis

of genotypic and phenotypic variances resulted in differential genotypic contribution in hereditary character also imparting the importance of environmental variance in the phenotypic expression of the analysed traits. The highest proportion of genetic variance was presented in petiole length followed by peduncle length, fruit girth and yield plant^{-1} with least environmental influence in expression of these characters. Similar results of high genotypic variance ranging from 22.28 to 61296.0 and phenotypic variances ranging from 35.51 to 61319.20 for various traits have been observed in eggplant by Mili *et al.*, (2014).

Selection of desirable and appropriate parents is one of most important step in any successful breeding programme. Good cultivars are obtained only, if the parents used in the program were suitable. Therefore, emphasis was given to choose appropriate parents in order to obtain desirable genotypes. Use of agronomically superior, diverse and locally adapted genotypes in the breeding programme will ensure the recovery of high proportion of progenies with wide adaptation; thus the variability in parental genotypes for various morphological traits was studied.

The co-efficient of variations (GCV and PCV) for the various morphological traits reported in various generations are presented in Table 3. These co-efficient of variations were classified into low, moderate and high scale (Sivsubramanian and Menon, 1973). In all the generations; plant spread, leaf length, pedicel length, calyx size, petal length, petal width, stamen size and pistil size exhibited low GCV while high variability was exhibited by fruit length followed by fruit girth, mean fruit weight, number of fruits plant^{-1} and yield plant^{-1}. All other traits had shown an intermediate genotypic component of variation. The high GCV gives an indication of justifiable variability among the genotypes with respect to these characters and therefore gives scope for improvement through selection. In general, high PCV was there than the corresponding GCV for all traits under study (Figure 1). The variation between GCV and PCV depicts the predominant environmental role in expression of these characters. Selection for improvement of characters with high GCV will be rewarding in this situation. Similarly, high GCV and PCV for various traits in eggplant have been reported by many investigators *viz.,* Madhavi *et al.*, (2015) for number of fruits plant^{-1} (65.21, 65.62), fruit weight (59.32, 59.42), fruit yield plant^{-1} (55.36, 56.10) and fruit diameter (31.02, 31.43); Roychowdhury, (2011) for number of fruits plant^{-1} (41.76, 43.32) and fruit weight (36.10, 37.96); Lokesh *et al.,* (2013) for plant height (24.31, 24.75), plant spread (39.66, 39.68), fruit diameter (20.43, 20.68), fruit weight (31.92, 31.94) and fruit yield plant^{-1} (37.07, 37.26). Along with these, high variability coefficients in eggplant for number of fruits plant^{-1}, leaf width and fruit length were reported by Singh *et al.,* (2014) while

for fruit weight and number of fruits plant[-1] by Singh and Kumar (2005) and Mohanty (2002).

Estimation of heritability (H[2]) and genetic advance: The progress and success of any breeding program is dependent upon the degree and the nature of the variability present in in various traits *viz.*, genotypic and non-genotypic variation. Since most of the economic characters (e.g. fruit traits and yield) are governed by quantitative genes and have complex inheritance, various environmental conditions greatly influence them. The study of heritability and genetic advance is thus very important for estimating the scope of improvement with selection. Therefore, heritability (broad sense) was estimated and computed for different traits across three backcross generations of CMS lines along with their maintainers (Table 3). The heritability percentage was classified into low, medium and high according to Robinson *et al.,* (1949). The traits *viz.*, plant height, pedicel length, stamen size, peduncle length, fruit length, fruit girth, fruit weight, number of fruit plant[-1] and yield plant[-1] had high heritability (H[2]) values in all the generations (Table 3). In maintainer lines all characters exhibited high heritability (>60%) except plant spread (58.4) and calyx size (56.8), where moderate heritability was present. Similarly, in BC₅ generation only plant spread (54.1); in BC₄, plant spread (53.4) and petal length (55.5) and, in BC₃, petiole length (59.0), leaf length (55.5) and pistil size (56.1) exhibited moderated heritability, whereas high heritability was revealed by all other traits in all these backcross generations. No character in all the generations depicted low heritability.

The use of heritability estimates alone do not provide any indication of the genetic progress that would result from selection of best plants. However, along with phenotypic variance and selection intensity, these estimates can compute response to selection or genetic advance, which is more helpful in the selecting desirable and promising lines (Roham *et al.,* 2003).

The percent genetic advance over mean was also classified into three categories *viz.,* low, moderate and high. High %GA in all generations was found in case of days to 50% flowering, peduncle length and all yield related fruit traits *viz.* fruit length, girth, weight besides number of fruits and yield plant[-1] (Table 3). In maintainer lines highest genetic gain or % GA value was reported for fruit weight (132.1) followed by number of fruits plant[-1] (70.6), fruit length (62.7), fruit girth (46.2), yield plant[-1] (34.4), peduncle length (25.1) leaf width (23.8), petiole length (22.3) and plant height (21.4) while it was lowest for pistil size (9.7). Whereas, all other traits exhibited moderate percent genetic advance over mean. In all the CMS backcross generations also, highest %GA was found for fruit weight followed by number of fruits plant[-1], fruit-length, fruit-girth, yield plant[-1] and peduncle length. Along with these in BC₅ high percent genetic advance was also

found for petiole length, in BC₄ for days to 50% flowering, petiole length and leaf width while in BC₃ for plant height and leaf width. All other traits in all the backcross generations exhibited moderate percent genetic advance except petal width in BC₄. High heritability and high % GA was found for all the yield related traits in all the generations (Figure 2) which is an indication of prevalence of additive gene-action, where selection can be effective (Panse, 1957). In BC₅ generation plant spread, petiole length, peduncle length and all yield traits displayed high heritability along with high percent genetic advance demonstrating importance of selection for further improvement (Figure 2). While, all other traits displayed high heritability but low percent genetic advance indicating predominance of non-additive gene action, where hybridization for improvement could be followed and selection will not be effective. Similar results of high heritability and percent genetic advance in cultivated eggplant for number of fruits plant[-1] (92.9, 82.96), fruit weight (90.4, 71.33) and total yield (59.1, 23.82) were reported by Roychowdhary (2011). Senapati *et al*, (2009) for number of fruits plant[-1] (96.51, 73.26), fruit weight (96.01, 49.30) and fruit yield plant[-1] (92.76, 75.52); Vidhya and Kumar (2015) for fruit girth (96.34, 54.35), fruit weight (95.66, 48.96), fruit length (73.35, 37.48), no. of fruits plant[-1] (94.09, 40.52) and yield plant[-1] (87.43, 38.50). Apart from these studies, Singh and Kumar (2005) also reported high heritability and % GA for fruit weight, no. of fruits plant[-1] and yield plant[-1] while Golani *et al.* (2007) reported high heritability and % GA for fruit length, girth and weight.

Conclusion

Genetic variability was studied to find out the diversity among three generations of CMS lines along with their maintainers in twelve genotypes. There was significant difference among genotypes for all the traits studied in all the generations. Minute differences between PCV, GCV along with high estimates of heritability for most of the traits examined revealed the heritable nature of variability. Heritability and genetic advance as percent of mean was high for majority of yield contributing fruit traits in all the generations indicating predominance of additive gene action and selection will be effective for the improvement of these traits. Therefore, the CMS inbred lines that could be used as A-lines in CGMS hybrid development programme could be developed from the present germplasm.

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