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Variability in the Segregating Generation of Eggplant for Earliness and Yield

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Abstract: In the past, very little efforts have been taken for development of inbred lines of brinjal through the exploitation of genetic variability present in the exotic hybrids. F_2 generation obtained from the selfing of F_1 hybrid provides all possible variations. So, selection with particular objectives in F_2 generation is very much effective and selfing of those selected genotypes generation after generation helps to develop inbred lines (similar to the parental lines of the exotic hybrids). These inbreds with desired characters including high yield potential can be used as High Yielding Variety (HYV) as well as the parents for hybrid variety. To increase the genetic yield potential, the maximum utilization of the desirable characters for synthesizing of any ideal genotypes is essential. Variability in brinjal is expected to be immense as the fruits vary greatly in shape and size. The present investigation was undertaken at Department of Horticulture, Agricultural College and Research Institute, Madurai during 2011 to determine variability in segregants of eggplant (*Solanum melogena* L.). The crosses $L_5 \times T_4$ (Palamedu Local \times EP 65) and $L_4 \times T_1$ (Alagarkovil Local \times Annamalai) had the highest mean with high variability for individual fruit weight and fruit yield per plant. These crosses were best for using as a base population for further improvement in fruit yield and fruit weight as they had high heritability and genetic advance. Favorable low mean with high variability occurred for days to first flowering (earliness) in the crosses $L_5 \times T_2$ (Palamedu Local \times KKM 1) and $L_4 \times T_2$ (Alagarkovil Local \times KKM 1). Direct selection may be executed considering these genotypes for selection towards the development of early in flowering and high yielding brinjal variety.

Key words: *Solanum melogena*, brinjal, genetic advance, heritability, variability

INTRODUCTION

India is a major producer of brinjal in the world and is grown throughout the year. In achieving the nutritional security through vegetables, brinjal crop plays vital role. However, the present production and productivity of brinjal is not sufficient enough to meet the nutritional security of increasing population. There are regional preferences for fruit shape, size and color. Apart from this the external appearance of brinjal fruit has equal weightage as that of production. Considering this, efforts have been diverted equally on consumer preference in terms of fruit colour, appearance, shape and overall acceptability. It contains the alkaloid solanine in roots and leaves and there are medicinal uses for eggplant (Dhankhar and Singh, 1984). There is a need for increased production and productivity of eggplant. Exploitation of hybrid vigour or heterosis by intervarietal hybridization has been a very promising line of varietal improvement in many vegetables including tomato, chilli, sweet pepper

and brinjal. With ever-growing need to increase vegetable production in Asian countries and with increasing consumption of eggplant, vegetable breeders are showing greater interest in this vegetable. Unlike tomato and sweet pepper, brinjal has considerable regional preference for shape, size and colour of fruits. Therefore, brinjal breeders have to aim at evolving genotypes that are more preferred for each region and yet be efficient and show substantial increase over the existing types in respect to yield and other economic characters. This would mainly depend upon the nature, magnitude and inter-relationship of heritable variation. Variability is the most important characteristic feature of any population. Estimation of variability is an important prerequisite for realizing response to selection as the progress in the breeding depends upon its amount, nature and magnitude.

The genetic proportion of this variability measured in terms of Genotypic Coefficient of Variation (GCV) alone represents the heritable component of total variability.

Higher the GCV more will be chance for exploitation of that particular character in a selection programme. The genetic variability in terms of GCV alone is not sufficient for determination of amount of heritable variability. In addition, estimation of heritability and genetic advance as percent of mean is also needed to assess the extent of genetic gain expected from effective selection. As heritability in broad sense includes both additive and epistatic gene effects, it will be reliable only when it is accompanied with high genetic advance (Burton, 1952; Johnson *et al.*, 1955). This project was undertaken to examine the magnitude of variability, heritability, genetic advance and genetic advance as percent of mean for characters among the F_2 segregating generation.

MATERIALS AND METHODS

Experimental site: The study was carried out at the College Orchard, Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai, India, from May to October 2011.

Experimental materials: Seed from selfed F_1 hybrids were collected and utilized for the F_2 generation. Based on yield potential and other desirable traits, 10 F_2 s were selected out of 40 F_2 s for further evaluation.

Experimental design: The F_2 populations were arranged in a Randomized Complete Block Design with three replications.

Nursery and cultivation aspects: Seedlings were raised in raised nursery beds and precautionary measures were taken to avoid incidence of damping off by drenching 0.1% Carbendazim. Seedlings were sprayed with systemic insecticide to control sucking pests. The experimental plot for seedling transplantation was brought to fine tilth by ploughing and harrowing. Cow manure at the rate of 25 tonnes per ha was applied 20 days before transplanting. Thirty-five days old seedlings were transplanted with the recommended spacing of 60×60 cm to the main field during May 2011. Each cross consisted of 60 plants which were transplanted into a well drained loamy soil. Cultural operations were per the TNAU Crop Production Guide, 2005, under irrigation.

Data collected: Observations were recorded in all plants for plant height, days to first flowering, number of branches per plant, fruit length, fruit pedicel length, fruit

circumference, calyx length, number of fruit per plant, average fruit weight and fruit yield per plant in all the crosses viz., Alavayal Local×Annamalai ($L_1 \times T_1$); Alagarkovil Local×Annamalai ($L_4 \times T_1$); Alagarkovil Local x KKM 1 ($L_4 \times T_2$); Palamedu Local x KKM 1 ($L_5 \times T_2$); Palamedu Local x Punjab Sadabahar ($L_5 \times T_3$); Palamedu Local×EP 65 ($L_5 \times T_4$); Melur Local×KKM 1 ($L_6 \times T_2$); Keerikai Local×KKM 1 ($L_7 \times T_2$); Nilakottai Local×Annamalai ($L_8 \times T_1$) and Singampunari Local×Annamalai ($L_9 \times T_1$) for estimating variability parameters.

Data analysis: Data were subjected to Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV) calculated according to Burton (1952) and its scale by Sivasubramanian and Madhavamenon (1973). Broad sense heritability was estimated as per Lush (1940). Genetic advance was determined following Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Superior genotypes were identified in segregating generations for further study through selection. Selection in F_2 involves the principles choice of desirable crosses and selection of the best progenies within crosses. This strategy effectively capitalizes on transgressive variability available within a cross (Lerner, 1958).

Average and variability: The average response is the foremost consideration in selection (Kumar *et al.*, 1979). High or low average response can serve as a favorable index for selection. The genetic potential of a cross or family is measured not only by the average response and the extent of genetic variability (Allard, 1960). Eggplant possesses a wider range of variability and had a number of distinct local forms available all over the country. Average response and variability are not exclusive in deciding the selection of crosses or families within a cross but complement each other. Allard (1960) suggested that based on average response and variability the segregating population may be categorized as high average response and high variability, high average response and low variability, low average response and high variability and low average response and low variability. Selection in the high average response and high variability and less so in the high average response and low variability because they have potential to produce more transgressive segregants than other groups. Low average response and high variability are capable of producing more transgressive segregants which may be poor in performance. In certain characters

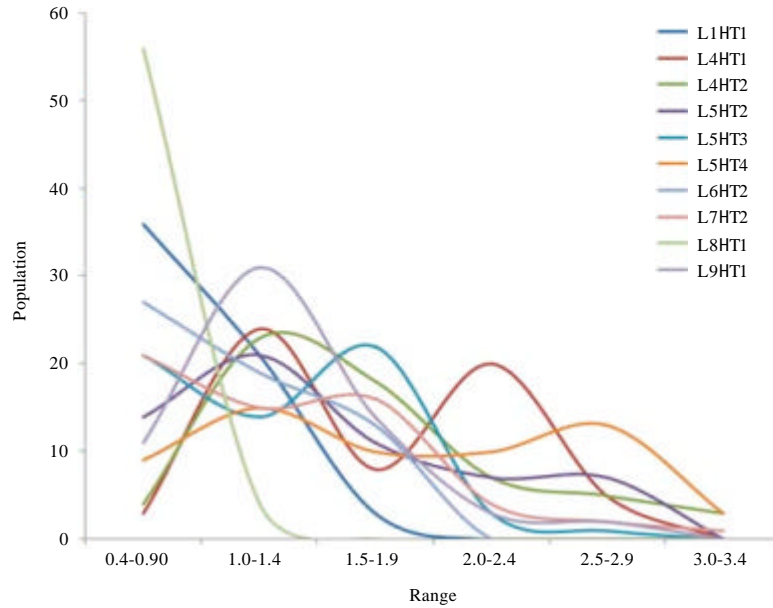


Fig. 1: Frequency distribution of segregating populations for fruit yield per plant

Table 1: Range, mean, variability, heritability, genetic advance and genetic advance as percent of average response for plant height (cm)

| Source | $L_1 \times T_1$ | $L_4 \times T_1$ | $L_4 \times T_2$ | $L_5 \times T_2$ | $L_5 \times T_3$ | $L_5 \times T_4$ | $L_6 \times T_2$ | $L_7 \times T_2$ | $L_8 \times T_1$ | $L_9 \times T_1$ |
|--|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|------------------|
| Range | 60.66-107.70 | 74.57-123.61 | 74.11-136.43 | 86.03-137.05 | 82.51-118.73 | 78.70-130.89 | 71.97-104.99 | 67.96-115.31 | 64.27-102.30 | 87.09-123.20 |
| Mean±SE | 85.52±2.08 | 102.29±2.02 | 97.97±2.26 | 110.66±1.98 | 98.53±2.25 | 99.11±1.95 | 90.43±1.93 | 92.97±2.00 | 81.19±5.03 | 100.03±4.98 |
| CV% | 13.33 | 14.01 | 14.39 | 12.23 | 10.79 | 12.28 | 9.26 | 13.12 | 12.15 | 8.20 |
| PV | 134.60 | 211.87 | 205.78 | 189.55 | 116.29 | 152.83 | 72.72 | 151.51 | 98.17 | 69.42 |
| GV | 128.09 | 205.75 | 198.08 | 183.61 | 108.70 | 147.11 | 67.13 | 145.49 | 60.15 | 32.17 |
| PCV | 13.56 | 14.23 | 14.64 | 12.44 | 10.94 | 12.47 | 9.42 | 13.23 | 12.20 | 8.32 |
| GCV | 13.23 | 14.02 | 14.36 | 12.24 | 10.58 | 12.23 | 9.05 | 12.97 | 9.55 | 5.67 |
| Heritability (%) | 95.00 | 97.11 | 96.00 | 96.87 | 93.47 | 96.26 | 92.30 | 96.03 | 61.27 | 46.34 |
| Genetic advance | 22.63 | 18.04 | 28.31 | 27.35 | 17.28 | 24.39 | 16.15 | 23.86 | 12.45 | 7.91 |
| Genetic advance as percent of average response | 26.59 | 28.46 | 29.03 | 24.82 | 21.07 | 24.73 | 17.93 | 26.18 | 15.40 | 7.95 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

where low average response is desirable the group will be more promising for selection of segregants. Range, mean, variability, heritability, genetic advance, genetic advance as percent of mean and frequency distribution were estimated out and the results are presented in the tables from Table 1-10 and Fig 1.

The crosses $L_5 \times T_2$ and $L_4 \times T_1$ had the highest average response with moderate variability for plant height. These two crosses also had a wide range for this trait. Genotypic and phenotypic co-efficients of variation were moderate. Their wide range of variation is suggest the scope for selecting superior and desired segregants for further improvement of plant height in brinjal. Similar findings

were reported by Naik (2007) and Ravishankar (2007). For days to first flowering, the crosses $L_5 \times T_2$ and $L_4 \times T_2$ had low average response and high variability. Low average response is beneficial for earliness. High variability and high average response for earliness was reported by Naik (2007). The crosses $L_5 \times T_3$ and $L_6 \times T_1$ had the highest average response with moderate variability for number of branches per plant. There is the ability to exploit variation for this character. For improvement of this trait specific crosses need to produce higher variability. Selection with considerable success may be crosses exhibiting high average response and moderate variability (Allard, 1960). Crosses $L_5 \times T_3$ and $L_4 \times T_1$ had the highest average

Table 2: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for days to first flowering

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 63.15-85.43 | 66.45-82.27 | 63.05-85.32 | 65.38-79.87 | 71.40-85.12 | 67.83-86.27 | 69.68-87.44 | 67.52-89.83 | 69.94-80.50 | 66.78-76.02 |
| Mean±SE | 73.76±1.34 | 75.18±1.62 | 72.98±1.66 | 71.88±1.48 | 79.11±1.53 | 79.90±1.42 | 76.50±1.51 | 75.63±1.77 | 76.66±1.82 | 74.53±3.88 |
| CV% | 7.07 | 6.08 | 7.11 | 4.94 | 3.34 | 5.91 | 5.69 | 6.16 | 10.18 | 7.19 |
| PV | 28.28 | 21.26 | 27.54 | 13.62 | 7.22 | 22.80 | 20.04 | 21.99 | 63.21 | 30.21 |
| GV | 25.56 | 17.32 | 23.37 | 10.33 | 3.69 | 19.77 | 16.58 | 17.28 | 58.23 | 7.53 |
| PCV | 7.20 | 6.13 | 7.19 | 5.13 | 3.39 | 5.97 | 5.85 | 6.20 | 10.37 | 7.37 |
| GCV | 6.85 | 5.53 | 6.62 | 4.47 | 2.42 | 5.56 | 5.32 | 5.49 | 9.95 | 3.68 |
| Heritability (%) | 90.38 | 81.47 | 84.87 | 75.87 | 51.13 | 86.73 | 82.76 | 78.57 | 92.12 | 24.94 |
| Genetic advance | 9.86 | 7.70 | 9.14 | 5.88 | 2.82 | 8.49 | 7.60 | 7.56 | 15.00 | 2.81 |
| Genetic advance as percent of average response | 13.42 | 10.29 | 12.57 | 8.02 | 3.57 | 10.67 | 9.97 | 10.03 | 19.68 | 3.78 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 3: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for number of branches per plant

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 11.72-19.79 | 12.70-23.03 | 20.69-25.47 | 22.48-27.50 | 19.06-22.67 | 17.63-27.98 | 16.41-27.36 | 20.27-24.90 | 18.94-24.88 | 18.87-27.32 |
| Mean±SE | 22.15±0.47 | 30.92±0.69 | 33.83±0.82 | 32.66±0.72 | 28.41±0.70 | 19.59±0.56 | 21.95±0.72 | 32.46±1.03 | 31.61±0.61 | 35.20±4.98 |
| CV% | 35.66 | 32.44 | 20.59 | 23.03 | 17.88 | 19.59 | 15.87 | 21.09 | 17.88 | 19.51 |
| PV | 64.46 | 104.52 | 49.76 | 59.39 | 27.39 | 27.77 | 13.41 | 48.46 | 33.04 | 69.42 |
| GV | 64.12 | 103.81 | 48.74 | 58.60 | 26.64 | 27.29 | 12.63 | 46.87 | 32.48 | 32.17 |
| PCV | 36.24 | 33.03 | 20.84 | 23.59 | 18.42 | 20.01 | 16.68 | 21.44 | 18.18 | 19.84 |
| GCV | 36.15 | 32.92 | 20.63 | 23.43 | 18.16 | 19.83 | 16.19 | 21.08 | 18.02 | 14.77 |
| Heritability (%) | 99.47 | 99.31 | 97.96 | 98.66 | 97.26 | 98.27 | 94.17 | 96.72 | 98.28 | 55.41 |
| Genetic advance | 16.38 | 20.82 | 14.17 | 15.60 | 10.44 | 10.63 | 7.07 | 13.80 | 11.60 | 7.91 |
| Genetic advance as percent of average response | 74.27 | 67.58 | 42.07 | 47.95 | 36.90 | 40.51 | 32.36 | 42.72 | 36.81 | 22.65 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 4: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for fruit pedicel length (cm)

| Crosses | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 2.48-5.63 | 3.08-5.68 | 2.69-5.14 | 2.71-5.24 | 3.00-5.72 | 2.41-4.98 | 3.08-5.32 | 2.53-4.45 | 2.83-5.09 | 2.81-4.71 |
| Mean±SE | 3.70±0.07 | 4.22±0.07 | 3.90±0.08 | 3.85±0.08 | 4.25±0.10 | 3.44±0.07 | 4.01±0.09 | 3.51±0.13 | 3.73±0.07 | 3.62±0.08 |
| CV% | 17.78 | 15.03 | 16.00 | 14.75 | 18.09 | 16.73 | 14.26 | 13.23 | 15.77 | 13.97 |
| PV | 0.45 | 0.42 | 0.40 | 0.33 | 0.60 | 0.34 | 0.33 | 0.22 | 0.35 | 0.27 |
| GV | 0.44 | 0.41 | 0.39 | 0.32 | 0.59 | 0.33 | 0.31 | 0.19 | 0.34 | 0.26 |
| PCV | 18.14 | 15.46 | 16.27 | 14.98 | 18.32 | 17.10 | 14.32 | 13.41 | 15.88 | 14.33 |
| GCV | 17.99 | 15.30 | 16.08 | 14.75 | 18.08 | 16.89 | 14.04 | 12.53 | 15.69 | 14.07 |
| Heritability (%) | 98.37 | 97.96 | 97.58 | 96.99 | 97.44 | 97.57 | 96.16 | 87.29 | 97.59 | 96.43 |
| Genetic advance | 1.34 | 1.32 | 1.26 | 1.15 | 1.57 | 1.16 | 1.11 | 0.84 | 1.18 | 1.04 |
| Genetic advance as percent of average response | 36.76 | 31.20 | 32.72 | 29.94 | 36.77 | 34.37 | 28.38 | 24.13 | 31.93 | 28.46 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 5: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for calyx length (cm)

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 2.54-4.72 | 3.15-5.56 | 2.79-4.61 | 2.92-4.28 | 2.46-5.76 | 1.76-4.20 | 1.76-3.64 | 1.56-5.09 | 1.68-4.16 | 1.82-4.18 |
| Mean±SE | 3.49±0.08 | 4.02±0.08 | 3.59±0.07 | 3.59±0.07 | 3.54±0.15 | 3.22±0.04 | 2.82±0.06 | 3.48±0.08 | 2.85±0.06 | 3.62±0.35 |
| CV% | 16.26 | 12.75 | 12.57 | 10.34 | 20.57 | 19.21 | 19.14 | 21.71 | 22.44 | 19.39 |
| PV | 0.33 | 0.27 | 0.20 | 0.14 | 0.54 | 0.39 | 0.30 | 0.58 | 0.42 | 0.36 |
| GV | 0.32 | 0.26 | 0.20 | 0.13 | 0.54 | 0.38 | 0.29 | 0.57 | 0.41 | 0.17 |
| PCV | 16.54 | 12.94 | 12.68 | 10.66 | 20.92 | 19.47 | 19.49 | 21.86 | 22.82 | 19.78 |
| GCV | 16.26 | 12.70 | 12.45 | 10.32 | 20.77 | 19.28 | 19.26 | 21.67 | 22.65 | 13.81 |
| Heritability (%) | 96.67 | 96.34 | 96.29 | 93.69 | 98.54 | 98.12 | 97.63 | 98.29 | 98.53 | 48.74 |
| Genetic advance | 1.15 | 1.04 | 0.93 | 0.72 | 1.51 | 1.25 | 1.10 | 1.53 | 1.31 | 0.58 |
| Genetic advance as percent of average response | 32.94 | 25.68 | 25.17 | 20.58 | 42.48 | 39.36 | 39.21 | 44.26 | 46.33 | 19.86 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 6: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for fruit length (cm)

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 4.18-7.22 | 4.55-8.67 | 4.84-7.31 | 5.01-7.65 | 4.28-9.31 | 5.28-11.32 | 5.44-11.76 | 5.73-11.89 | 5.54-9.32 | 3.92-8.94 |
| Mean±SE | 4.69±0.11 | 6.66±0.12 | 5.10±0.11 | 5.29±0.19 | 6.45±0.14 | 6.67±0.15 | 7.02±0.29 | 7.37±1.36 | 6.19±0.15 | 3.62±0.70 |
| CV% | 17.20 | 14.35 | 17.87 | 16.97 | 19.69 | 28.14 | 25.10 | 30.32 | 22.73 | 20.28 |
| PV | 0.67 | 0.95 | 0.87 | 0.82 | 1.68 | 3.64 | 3.22 | 5.10 | 2.06 | 1.40 |
| GV | 0.65 | 0.93 | 0.85 | 0.80 | 1.65 | 3.61 | 3.09 | 2.33 | 2.03 | 0.66 |
| PCV | 17.44 | 14.65 | 18.30 | 17.15 | 20.10 | 28.62 | 25.57 | 30.64 | 23.19 | 20.44 |
| GCV | 17.19 | 14.46 | 18.10 | 16.94 | 19.95 | 28.48 | 25.03 | 20.70 | 22.99 | 14.03 |
| Heritability (%) | 97.14 | 97.44 | 97.81 | 97.59 | 98.53 | 99.05 | 95.85 | 45.67 | 98.25 | 47.12 |
| Genetic advance | 1.64 | 1.96 | 1.87 | 1.86 | 2.62 | 3.89 | 3.53 | 2.12 | 2.91 | 1.14 |
| Genetic advance as percent of average response | 34.90 | 29.40 | 36.89 | 34.48 | 40.80 | 58.40 | 50.48 | 28.82 | 46.95 | 19.84 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 7: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for fruit circumference (cm)

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 8.13-16.89 | 11.65-21.72 | 11.65-18.84 | 12.07-20.47 | 9.08-14.43 | 11.58-25.28 | 8.97-22.61 | 9.68-17.68 | 6.85-11.13 | 6.99-14.52 |
| Mean±SE | 12.07±0.52 | 17.03±0.36 | 14.55±0.34 | 14.84±0.27 | 11.65±0.21 | 17.04±0.47 | 14.33±0.44 | 12.47±0.36 | 8.36±0.53 | 10.76±0.56 |
| CV% | 19.09 | 13.29 | 11.45 | 12.85 | 13.62 | 22.29 | 23.58 | 17.15 | 11.40 | 16.37 |
| PV | 5.50 | 5.31 | 2.83 | 3.77 | 2.60 | 14.87 | 11.56 | 4.88 | 0.94 | 3.18 |
| GV | 5.09 | 5.11 | 2.65 | 3.66 | 2.53 | 14.53 | 11.27 | 4.68 | 0.50 | 2.70 |
| PCV | 19.43 | 13.53 | 11.56 | 13.08 | 13.86 | 22.62 | 23.73 | 17.72 | 11.60 | 16.57 |
| GCV | 18.69 | 13.27 | 11.19 | 12.89 | 13.66 | 22.36 | 23.42 | 17.35 | 8.52 | 15.28 |
| Heritability (%) | 92.46 | 96.19 | 93.68 | 97.09 | 97.24 | 97.72 | 97.44 | 95.88 | 53.90 | 85.03 |
| Genetic advance | 4.45 | 4.55 | 3.23 | 3.86 | 3.22 | 7.73 | 6.70 | 4.36 | 1.06 | 3.10 |
| Genetic advance as percent of average response | 37.02 | 26.82 | 22.32 | 26.16 | 27.76 | 45.55 | 47.63 | 35.01 | 12.88 | 29.02 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 8: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for number of fruits per plant (cm)

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 18.69-41.00 | 17.00-40.68 | 18.28-39.78 | 18.54-36.70 | 17.82-40.30 | 14.84-42.32 | 16.52-41.86 | 18.39-52.94 | 20.00-44.44 | 19.79-54.43 |
| Mean±SE | 30.48±1.89 | 27.48±2.39 | 30.28±0.59 | 25.61±0.58 | 29.48±0.61 | 27.53±0.92 | 28.96±1.05 | 36.16±0.82 | 31.56±2.70 | 37.01±3.69 |
| CV% | 20.38 | 25.44 | 17.65 | 19.32 | 22.71 | 29.12 | 24.91 | 26.67 | 16.40 | 23.58 |
| PV | 39.75 | 50.42 | 29.77 | 25.82 | 46.35 | 65.58 | 52.60 | 95.82 | 27.84 | 78.68 |
| GV | 34.34 | 41.84 | 29.24 | 25.30 | 45.78 | 64.30 | 50.92 | 94.79 | 16.85 | 58.19 |
| PCV | 20.68 | 25.83 | 18.01 | 19.83 | 23.09 | 29.41 | 25.03 | 27.06 | 16.71 | 23.96 |
| GCV | 19.22 | 23.53 | 17.85 | 19.63 | 22.94 | 29.12 | 24.63 | 26.92 | 13.00 | 20.60 |
| Heritability (%) | 86.39 | 82.98 | 98.22 | 97.99 | 98.77 | 98.04 | 96.80 | 98.93 | 60.53 | 73.96 |
| Genetic advance | 11.17 | 12.08 | 10.99 | 10.20 | 13.80 | 16.29 | 14.39 | 19.86 | 6.55 | 13.44 |
| Genetic advance as percent of average response | 36.80 | 44.16 | 36.45 | 40.04 | 46.98 | 59.40 | 49.93 | 55.15 | 20.84 | 36.50 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 9: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for average fruit weight (g)

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 20.09-48.00 | 32.14-122.79 | 29.96-91.82 | 34.92-125.84 | 22.78-65.67 | 34.69-136.70 | 14.67-56.24 | 28.96-73.36 | 18.08-37.00 | 24.27-60.00 |
| Mean±SE | 32.73±4.22 | 65.30±1.35 | 55.95±1.29 | 60.16±0.94 | 43.50±0.98 | 73.21±1.28 | 37.33±4.02 | 39.46±2.93 | 24.23±3.40 | 35.81±5.62 |
| CV% | 22.48 | 32.41 | 28.01 | 38.12 | 25.02 | 40.69 | 26.87 | 40.73 | 20.14 | 19.63 |
| PV | 55.88 | 462.63 | 256.86 | 546.11 | 121.47 | 922.59 | 107.93 | 263.36 | 25.40 | 51.19 |
| GV | 29.13 | 459.85 | 254.34 | 544.76 | 120.00 | 920.12 | 83.64 | 250.41 | 8.01 | 3.67 |
| PCV | 22.83 | 32.93 | 28.64 | 38.84 | 25.33 | 41.48 | 27.82 | 41.11 | 20.79 | 19.97 |
| GCV | 16.49 | 32.83 | 28.50 | 38.79 | 25.18 | 41.42 | 24.49 | 40.09 | 11.68 | 5.35 |
| Heritability (%) | 52.14 | 99.40 | 99.02 | 99.75 | 98.79 | 99.73 | 77.50 | 95.08 | 31.56 | 7.70 |
| Genetic advance | 7.99 | 43.84 | 32.54 | 47.80 | 22.32 | 62.10 | 16.51 | 31.64 | 3.26 | 1.05 |
| Genetic advance as percent of average response | 24.52 | 67.44 | 58.42 | 79.81 | 51.56 | 85.23 | 44.42 | 80.53 | 13.52 | 2.95 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

Table 10: Range, mean, variability, heritability, genetic advance and genetic advance as percent of mean for fruit yield per plant (kg)

| Source | L ₁ ×T ₁ | L ₄ ×T ₁ | L ₄ ×T ₂ | L ₅ ×T ₂ | L ₅ ×T ₃ | L ₅ ×T ₄ | L ₆ ×T ₂ | L ₇ ×T ₂ | L ₈ ×T ₁ | L ₉ ×T ₁ |
|--|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|
| Range | 0.47-1.79 | 0.73-2.80 | 0.77-3.34 | 0.71-2.98 | 0.47-2.22 | 0.64-3.32 | 0.44-1.82 | 0.52-3.01 | 0.42-1.29 | 0.71-2.89 |
| Mean±SE | 0.99±13 | 1.75±0.15 | 1.71±0.05 | 1.54±0.04 | 1.30±0.03 | 1.92±0.10 | 1.07±0.10 | 1.36±0.06 | 0.76±0.12 | 1.32±0.23 |
| CV% | 28.61 | 32.67 | 37.16 | 40.60 | 37.01 | 37.66 | 38.72 | 42.81 | 24.58 | 32.60 |
| PV | 0.08 | 0.35 | 0.48 | 0.45 | 0.24 | 0.54 | 0.17 | 0.35 | 0.03 | 0.19 |
| GV | 0.05 | 0.32 | 0.41 | 0.40 | 0.23 | 0.52 | 0.16 | 0.34 | 0.01 | 0.11 |
| PCV | 29.17 | 33.86 | 37.77 | 41.28 | 37.67 | 38.28 | 39.14 | 43.55 | 24.95 | 33.13 |
| GCV | 24.25 | 32.18 | 37.60 | 41.12 | 37.48 | 37.69 | 37.36 | 43.19 | 14.89 | 25.43 |
| Heritability (%) | 6.91 | 90.33 | 99.10 | 99.20 | 99.03 | 96.92 | 91.13 | 98.36 | 35.64 | 58.91 |
| Genetic advance | 0.36 | 1.11 | 1.21 | 1.22 | 0.98 | 1.46 | 0.80 | 1.18 | 0.12 | 0.52 |
| Genetic advance as percent of average response | 41.54 | 63.01 | 77.11 | 84.36 | 76.85 | 76.44 | 73.48 | 88.25 | 18.32 | 40.21 |

SE: Standard error, CV: Coefficient of variation, PV: Phenotypic variance, GV: Genotypic variance, PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation

response for fruit pedicel length with moderate variability. High average response and moderate variability have the potential to produce more transgressive segregants that can attain homozygosity earlier than other groups (Premalakshmi, 2001). For calyx length low average response is desired. According to Prabhu (2005), short calyx length is associated with lesser incidence of fruit borer. Crosses L₆×T₂ and L₈×T₁ had the lowest average response for calyx length and moderate and high variability, respectively.

For fruit length the crosses L₇×T₂ and L₆×T₂ had the highest average response and high variability indicating greater genotypic and phenotypic variability among segregating generations and responsiveness of the attribute for further improvement through selection. High average response and high variability for fruit circumference occurred in the cross L₅×T₄; cross L₄×T₁ had high average response and moderate variability. The high average response and high variability indicated improved possibility for improvement through selection. Crosses L₉×T₁ and L₇×T₂ had the highest average response and variability for number of fruit per plant. These crosses can be a good source for selection of desirable recombinants for more fruit per plant. For individual fruit weight and fruit yield per plant crosses L₅×T₄ and L₄×T₁ had the highest average response with high variability with high genotypic and phenotypic co-efficient of variations. A greater possibility for selection is due to high average response, variability and wider range mean value.

Heritability and genetic advance: Heritability is a proportion of the genetic variance to total phenotypic variance and provides information whether a selection based on phenotype will be worthwhile. The genetic advance gives the extent of possible improvement in performance of populations at a selection intensity. For plant height all crosses had high heritability combined with high genetic advance as percent of average except

for crosses L₆×T₂, L₈×T₁ and L₉×T₁ which had low to moderate heritability and genetic advance. Days to first flowering had moderate to high heritability and low to moderate genetic gain indicating a high environmental influence on this character. Number of branches per plant and fruit pedicel length for crosses L₁×T₁ and L₄×T₁ were high for heritability coupled with high genetic advance as percent of mean. Expression of these characters may be attributed to additive gene effects which can be easily fixed in later generations. High heritability combined with high genetic advance as percent of mean for calyx length occurred in all crosses except L₉×T₁. The, crosses L₁×T₁, L₄×T₁, L₄×T₂, L₅×T₂, L₅×T₃, L₅×T₄, L₆×T₂, L₇×T₂ and L₈×T₁ offer excellent possibility for exercising simple selection for calyx length. Prabhu *et al.* (2009) reported that this trait was under control of non-additive gene action due to moderate heritability with low genetic gain. For fruit length, all crosses had high heritability and high genetic advance as percent of mean except for L₉×T₁ and L₇×T₂ where, as for fruit circumference, except L₈×T₁, all other crosses had high heritability and high genetic advance as percent of mean. Presence of a large number of additive factors and little non-additive genes for the above traits and therefore, these traits could be improved through simple selection. In the present study, numbers of fruit per plant in all crosses had high heritability and high genetic advance as percent of mean likely due to additive gene action and simple selection for this trait would be effective. For individual fruit weight and fruit yield per plant the crosses L₄×T₁, L₄×T₂, L₅×T₂, L₅×T₃, L₅×T₄, L₆×T₂ and L₇×T₂ had high heritability and high genetic advance as percent of mean (Table 9). These crosses may be utilized for improvement of these traits through simple selection programme.

Frequency of distribution: The frequency of distribution for plant height showed a polarization of population towards medium plant height. In most of the crosses, maximum distribution was in the class interval of 90.00 to

99.90 cm followed by 100.00-109.90 cm. In the following crosses viz., $L_1 \times T_1$, $L_7 \times T_2$ and $L_8 \times T_1$ 5, 2 and 11 out of 60 plants, respectively had a tendency towards the lower class interval of 60.00-99.9 cm indicating the lowest plant height. Three, seven and one plants in the crosses viz., $L_4 \times T_2$, $L_5 \times T_2$ and $L_5 \times T_4$, respectively were tall and fell in the frequency range of 130 to 140 cm among the population. The concentration on maximum frequencies for days to first flowering was observed near middle classes. The greater frequency in most of the crosses were in the class interval of 69.00 to 78.00 whereas the early in flowering was indicated by the class interval of 59.00-68.00. The late flowering was observed in the class interval of 79.00-88.00. In the crosses $L_7 \times T_2$ and $L_8 \times T_1$, only single plant showed a concentration towards the highest class interval of 89.00-98.00. Frequency distribution for number of branches per plant showed maximum concentration in the class interval of 13.00 to 17.00 followed by 18.00-22.00. All the crosses were noticed in the highest class interval of 23.00-27.00 except $L_1 \times T_1$, $L_5 \times T_2$, $L_5 \times T_3$ and $L_5 \times T_4$. The crosses viz., $L_1 \times T_1$, $L_4 \times T_1$, $L_5 \times T_3$, $L_5 \times T_4$, $L_6 \times T_2$, $L_7 \times T_2$, $L_8 \times T_1$ and $L_9 \times T_1$ were found in the lowest class interval of 8.00-12.00.

Frequency distribution for fruit pedicel length showed that the population towards middle class interval of 3.00 to 3.50 cm followed by $L_1 \times T_1$, $L_4 \times T_1$ and $L_5 \times T_3$ showed a polarization of population towards highest pedicel length while the population in all the crosses except $L_4 \times T_1$ and $L_9 \times T_2$ showed a lower class interval of 2.40 to 2.90. For calyx length the maximum number of plants was found in the class interval of 2.50-3.40 cm followed by the intervals of 3.50-4.40. The crosses $L_1 \times T_1$, $L_5 \times T_3$, $L_5 \times T_4$, $L_6 \times T_2$, $L_7 \times T_2$, $L_8 \times T_1$ and $L_9 \times T_1$ showed a polarization of population towards lower class interval while the crosses $L_4 \times T_1$ and $L_5 \times T_3$ showed that only single plant had a tendency towards the highest calyx length of 5.50-6.40. Frequency distribution for fruit length showed that the population towards the medium fruit length of 5.10-7.00 cm. The crosses $L_5 \times T_4$, $L_7 \times T_2$ and $L_6 \times T_2$ recorded that the population distributed in highest class interval of 11.10 to 12.00 cm while lowest fruit length was observed in the class intervals of 3.10-5.0 cm in all the crosses.

The frequency distribution for fruit circumference showed a polarization of population towards medium fruit size. In most of the crosses, the maximum distribution was in the class interval of 10.00 to 13.00 followed by 14.00-17.00 cm. In the following crosses $L_1 \times T_1$, $L_5 \times T_3$, $L_6 \times T_2$, $L_7 \times T_2$, $L_8 \times T_1$ and $L_9 \times T_1$ 15, 14, 3, 10, 53 and 25 plants out of 60 plants, respectively had a tendency towards the lower class intervals of 6.00-9.00. Eight and three plants in

the crosses $L_5 \times T_4$ and $L_6 \times T_2$ were highest and fell in the frequency range of 22.00 to 25.00 cm among the population. Frequency distribution for number of fruits per plant indicates nearly 50 per cent of population found in the middle classes (30.00-39.00) for the crosses viz., $L_5 \times T_3$, $L_8 \times T_1$, $L_9 \times T_1$, $L_1 \times T_1$, $L_4 \times T_2$ and $L_6 \times T_2$, respectively while the population of the crosses $L_4 \times T_1$, $L_5 \times T_2$ and $L_5 \times T_4$ (24, 29 and 22 plants) showed a tendency towards lower class intervals of 14.00 to 23.00. Less population of the crosses $L_7 \times T_2$ and $L_9 \times T_1$ were distributed in the class intervals of 50.00-59.00.

Frequency distribution for individual fruit weight showed a maximum concentration in the class intervals of 34.00 to 53.00 followed by 14.00 to 33.00. The population of the crosses viz., $L_4 \times T_1$ (1 plant), $L_5 \times T_2$ (3 plants), $L_5 \times T_3$ (1 plant) and $L_5 \times T_4$ (3 plants) showed a tendency towards highest fruit weight of 114.00-130.00 g. Except $L_1 \times T_1$ and $L_8 \times T_1$ all the other crosses were fell in the category of 54.00-73.00. Frequency distribution for fruit yield per plant showed that the concentration towards the class interval of 0.40 to 0.90 kg followed by the intervals of 1.00 to 1.40 kg. In three crosses $L_4 \times T_2$ (3 plants), $L_5 \times T_4$ (3 plants) and $L_7 \times T_2$ (1 plant) were produced the fruit yield exceeding 3.00 kg per plant. The fruit yield per plant was more than 2.00 kg were observed in all the crosses except $L_1 \times T_1$, $L_6 \times T_2$ and $L_8 \times T_1$.

CONCLUSION

At the outset comprehensive results obtained from the variability analysis in F_2 the crosses $L_5 \times T_4$ (Palamedu Local x EP 65) and $L_4 \times T_1$ (Alagarkovil Local x Annamalai) had the highest mean with high variability for individual fruit weight and fruit yield per plant. The above said crosses were found to be the best for using as a base population for further improvement in fruit yield and fruit weight as it has high heritability and genetic advance also. Favourable low mean with high variability was observed for days to first flowering in the crosses $L_5 \times T_2$ (Palamedu Local x KKM 1) and $L_4 \times T_2$ (Alagarkovil Local x KKM 1) which suggests that yield could be improved through selection for early flowering crosses.

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