# Evaluation of Genetic Variability and Frequency Distribution in the F₂ Segregating Population of Tomato Cross Anagha x IIHR 2896

**Bhaskar Reddy S.[1]\*, Beena Thomas[2], Anand S.[1], Ankitha M.O.[1] and Byrapuram Arani Jyothi[1,3]**
[1]*Research Scholar, Department of Plant Breeding and Genetics, College of Agriculture,*
*Vellayani, Kerala Agricultural University, Thrissur (Kerala), India.*
[2]*Assistant Professor, Department of Plant Breeding and Genetics, College of Agriculture,*
*Vellayani, Kerala Agricultural University, Thrissur (Kerala), India.*
[3]*Research Scholar, Department of Genetics and Plant Breeding, S.V. Agricultural College,*
*Tirupati, ANGRAU, Guntur (Andhra Pradesh), India.*

*(Corresponding author: Bhaskar Reddy S.\*)*
*(Received: 28 May 2023; Revised: 23 June 2023; Accepted: 17 July 2023; Published: 15 August 2023)*
*(Published by Research Trend)*

**ABSTRACT: Genetic variability and its hereditary components play a vital role in the selection of breeding material. A fundamental grasp of genetic diversity is essential for creating an superior variety. So, the F₂ population of the cross Anagha and IIHR 2896 was evaluated for frequency distribution and genetic parameters. The frequency distribution of the F₂ population showed positive skewness with platykurtic for all traits except number of days to first flowering and number of locules, which showed negative skewness and platykurtic distribution. Genetic variability results showed high GCV and PCV for traits like plant height, number of primary branches, plant spread, fruit weight, fruit volume, number of locules and fruit yield per plant. Higher heritability was recorded for all the traits whereas, high GAM was shown by all the traits except the number of days to first flowering and number days to first fruit harvest which showed low GAM. This indicates that the presence of high genetic variation, heritability and GAM for many characters will help in the improvement of those characters through direct and indirect selection.**

**Keywords:** GCV, PCV, GAM, Heritability, Skewness, Platykurtic distribution.

## INTRODUCTION

Tomato [(*Solanum lycopersicum* L.), (2n = 2n = 24)] is one of the most important self-pollinated and day-neutral vegetable crop grown widely throughout the world. It belongs to the Solanaceae family and is native to South America. It was first diversified in the Mexico-Peru-Equad or region and domesticated from its ancestor, *Solanum lycopersicum* var. *cerasiforme* (cherry tomato). Tomato is predominantly self-pollinated; but a certain percentage of cross-pollination may also occur. It grows as a series of branching stems. Most of the tomato plants have compound leaves. Both stem and leaves are covered with dense glandular hair. The flowers are borne in cymose inflorescence. Botanically, tomato fruit is known as berry. The fruit contains hollow spaces filled with seeds and moisture called locular cavities. Indeterminate types are tender perennials that die annually in temperate climatic conditions (they are originally native to tropical highlands); determinate varieties are annual in all climates.

To meet ever increasing demand for this vegetable, there is a need for the development of hybrids and varieties with improvement in yield, quality, and resistance to pests and diseases. Considering the potentiality of this crop, there is a scope for improvement and to development of varieties suited to specific agro-ecological conditions and for specific end use. Thorough knowledge regarding the amount of genetic variability existing for various characters is essential for initiating the crop improvement programme. With limited variability, much cannot be achieved and the breeder will have to enrich the germplasm or resort to creation of greater variability through hybridisation, mutation, and polyploidy breeding. Creation and utilization of variability using proper breeding procedures is a prerequisite for the genetic improvement of any crop. Generally, the amount of variability generated is higher in the early segregating generations than in the later generations. Assessment of genetic variation and degree of transmission of desirable characters are helpful in planning a sound breeding programme. In this regard, it is necessary to evaluate variability among the various plant characters in the partitioning of total variability into heritable and non-heritable components, which enables us to know whether the superiority of genetic advance is expected after selection (Robinson *et al.,* 1949).

The achievement of any crop improvement programme largely depends on the extent of genetic variability present in the base population. Naturally, in self-pollinated crops like tomato, the identification and

selection of superior segregants from the heterogeneous population in the early generation are essential. Based on the above facts, the present study was conducted to evaluate the genetic variability for yield and its attributing traits present in the $F_2$ population of cross Anagha × IIHR 2896.

## MATERIALS AND METHODS

The present study was conducted at the College of Agriculture, Vellayani, Thiruvananthapuram, Kerala during the month of January to April 2023. The experimental material consists of $F_2$ populations developed by involving the two parents *i.e.* Anagha, a bacterial wilt resistant variety released by KAU, Kerala and IIHR 2896 (resistant to ToLCV) line from IIHR, Bangalore. The $F_2$ population obtained by selfing $F_1$ along with $P_1$, $P_2$ and $F_1$ were planted in an unreplicated trial and assessed for yield and yield attributing traits. Each plant in the $F_2$ population was labelled and a total of 10 quantitative characters were recorded. The character studied were plant height (cm), number of primary branches, plant spread (cm), number of days to first flowering, number of days to first fruit harvest, number of fruits per plant, fruit weight, fruit volume, number of locules and fruit yield per plant.

**Statistical Analysis.** Statistical parameters such as mean, Vp, Vg, Ve and phenotypic and genotypic coefficients of variation (PCV and GCV) were computed based on the method suggested by Panse and Sukhatme (1961). Heritability in the broad sense was computed with the formula suggested by Lush (1940). The genetic advance as per cent of mean (GAM) was estimated by adopting the method suggested by Johnson *et al.* (1955). Skewness, the third-degree statistics and Kurtosis, the fourth-degree statistics were estimated as per Snedecor and Cochran (1974) to understand the nature of the distribution of 10 quantitative traits in the $F_2$ population of cross Anagha × IIHR 2896. All the above characters were calculated using Microsoft Excel.

## RESULT AND DISCUSSIONS

The study of frequency distribution such as coefficients of skewness (third-degree statistics) and Kurtosis (fourth-degree statistics) provides insight into the nature of gene action and the number of genes controlling the traits (Robson, 1956). The skewed distribution of a trait, in general, suggests that the trait is under the control of non-additive gene action, especially epistasis and influenced by environmental variables (Ponni *et al.,* 1977; Kimberg and Bingham 1998; Roy, 2000). The $F_2$ population exhibited a considerable amount of variability for all the characters. The mean performance, range, skewness and kurtosis of $F_2$ segregating generations of the cross Anagha × IIHR 2896 for yield and its attributing traits are presented in Table 1.

The frequency distribution of the $F_2$ population showed that characters such as plant height (0.198, 0.351), number of primary branches (0.396, 0.533), plant spread (0.478, -0.097), number of days to first fruit harvest (0.033, -0.966), number of fruits per plant

(0.339, 0.677), fruit weight (1.276, 1.519), fruit volume (1.093, 0.534) and fruit yield per plant (1.009, 0.071) showed positive skewness with platykurtic distribution. Traits observed with positive skewness indicate that more proportion of individuals are present at the low end of the distribution, but transgressive segregants are also obtained for positively skewed traits. Hence, the selection of single plants from transgressive segregants will improve positively skewed traits. The results indicate that the traits of the studies are governed by multiple genes with equal frequency with increasing or decreasing effects along with complementary epistasis on trait expression. The trait with positively skewed distribution requires an intense selection from the available variability to maximize the genetic gain. However, the number of days to first flowering (-0.019, -0.804) and the number of locules showed (-0.124, -0.732) negative skewness and platykurtic distribution. More genes are regulated in features of platykurtic distributions. Kurtosis is negative or near zero when there are no gene interactions and positive when they are present (Pooni *et al.,* 1977; Choo and Reinbergs 1982). The traits with negatively skewed distribution indicate the involvement of a large number of dominant genes with duplicate type of epistasis. This type of distribution will help to protect the individual plant from deleterious alleles arising from existing variability (Roy, 2000). The results are in agreement with the findings of Yogendra (2011); Rajeswari (2019); Sangamesh (2019) in tomato.

Genetic variability present in the population will help in the development of superior variety. Therefore, it is necessary to understand the amount of variability present. The results of mean, range, phenotypic variance, genotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability ($h^2$) and genetic advance as percent of mean (GA%) in the $F_2$ population of cross Anagha × IIHR 2896 are presented in Table 1. The results revealed that the genotypic variance is lower than that of phenotypic variance but the difference was very low. High PCV and GCV were shown by the traits like number of primary branches (32.29, 27.13), plant spread (30.50, 29.66), fruit weight (50.07, 49.80), fruit volume (48.08, 47.51), number of locules (27.26, 21.22) and fruit yield per plant (50.85, 50.10) indicating higher amount of variability for these traits. Plant height showed high PCV (20.78) and moderate GCV (19.33) and low PCV and GCV values were shown by number of days to first flowering (6.38, 4.96) and number of days to first fruit harvest (5.12, 4.09). The PCV is more than the GCV for all characters indicating the presence of environmental influence. However, it is low due to narrow difference between PCV and GCV. The character with high GCV can be used for the selection for further crop improvement. The level of PCV and GCV are depicted in Fig. 2. These findings were similar to Priyanka *et al.* (2017) for the characters like plant height, number of locules, fruit weight and fruit yield per plant. The results were inline with Mohanty (2003); Arvind *et al.* (2017); Verma *et al.* (2021); Nevani *et al.* (2022).

Heritability is a good index of the transmission of characters from parents to their off springs (Falconer, 1981). It helps in the selection of elite genotypes from diverse genetic populations. The results exhibited high heritability for all ten characters *i.e.,* plant height (86.57), number of primary branches (70.62), plant spread (94.57), number of days to first flowering (60.37), number of days to first fruit harvest (63.75), number of fruits per plant (87.98), fruit weight (98.94), fruit volume (97.62), number of locules (60.56) and fruit yield per plant (97.09). The level of heritability for all traits are depicted in Fig. 3. The results were in agreement with those of Meena *et al.* (2015); Ravindra *et al.* (2015); Sayeda *et al.* (2016); Bilal *et al.* (2017); Kumar and Yadav (2023).

Genetic advance as percent of mean was high for traits like plant height (37.06), number of primary branches (46.98), plant spread (59.42), number of fruits per plant (33.83), fruit weight (102.05), fruit volume (96.70), number of locules (34.01) and fruit yield per plant (101.70). However, traits such as number of days to first flowering (60.37) and number of days to first fruit harvest (63.75) showed low genetic advance as percent of mean. The level of genetic advance as percent of mean for all traits are depicted in Fig. 3. The traits like plant height (cm), number of primary branches, plant spread (cm), number of fruits per plant, fruit weight (g), fruit volume (ml), number of locules and fruit yield per plant (kg) showed high heritability with high genetic advance. This indicates the presence of additive gene effects and selection is effective for these traits. These findings are similar to the results of Shankar *et al.* (2013); Rai *et al.* (2016); Maurya *et al.* (2020); Akhter and Nanjine (2022).

**Table 1: Estimates of genetic parameters and frequency distribution for yield and its attributing traits in F2 segregating generations of the cross Anagha × IIHR 2896.**

| Sr. No. | Characters | Mean | Range | | Vp | Vg | PCV% | GCV% | h2 bs | h2 bs% | GA | GAM% | Skewness | Kurtosis | Kurtosis type |
| | | | Min | Max | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1. | Plant Height (cm) | 76.69 | 30 | 130 | 253.94 | 219.84 | 20.78 | 19.33 | 0.87 | 86.57 | 28.42 | 37.06 | 0.198 | 0.351 | P |
| 2. | Number of primary branches per plant | 3.63 | 1 | 8 | 1.37 | 0.97 | 32.29 | 27.13 | 0.71 | 70.62 | 1.71 | 46.98 | 0.396 | 0.533 | P |
| 3. | Plant spread | 44.36 | 10 | 90 | 183.05 | 173.12 | 30.50 | 29.66 | 0.95 | 94.57 | 26.36 | 59.42 | 0.478 | -0.097 | P |
| 4. | Number of days to 50% flowering | 35.06 | 31 | 40 | 5.01 | 3.02 | 6.38 | 4.96 | 0.60 | 60.37 | 2.78 | 7.94 | -0.019 | -0.804 | P |
| 5. | Number of days to first fruit harvest | 68.02 | 61 | 78 | 12.15 | 7.75 | 5.12 | 4.09 | 0.64 | 63.75 | 4.58 | 6.73 | 0.033 | -0.966 | P |
| 6. | Number of fruits per plant | 27.66 | 15 | 50 | 26.66 | 23.46 | 18.67 | 17.51 | 0.88 | 87.98 | 9.36 | 33.83 | 0.339 | 0.677 | P |
| 7. | Fruit weight | 45.78 | 16.17 | 133 | 525.46 | 519.88 | 50.07 | 49.80 | 0.99 | 98.94 | 46.72 | 102.05 | 1.276 | 1.519 | P |
| 8. | Fruit volume | 41.66 | 15 | 111 | 401.30 | 391.75 | 48.08 | 47.51 | 0.98 | 97.62 | 40.28 | 96.70 | 1.093 | 0.534 | P |
| 9. | Number of locules | 3.59 | 2 | 6 | 0.96 | 0.58 | 27.26 | 21.22 | 0.61 | 60.56 | 1.22 | 34.01 | -0.124 | -0.732 | P |
| 10. | Fruit yield per plant | 1.25 | 0.46 | 3.31 | 0.41 | 0.39 | 50.85 | 50.10 | 0.97 | 97.09 | 1.27 | 101.70 | 1.009 | 0.071 | P |
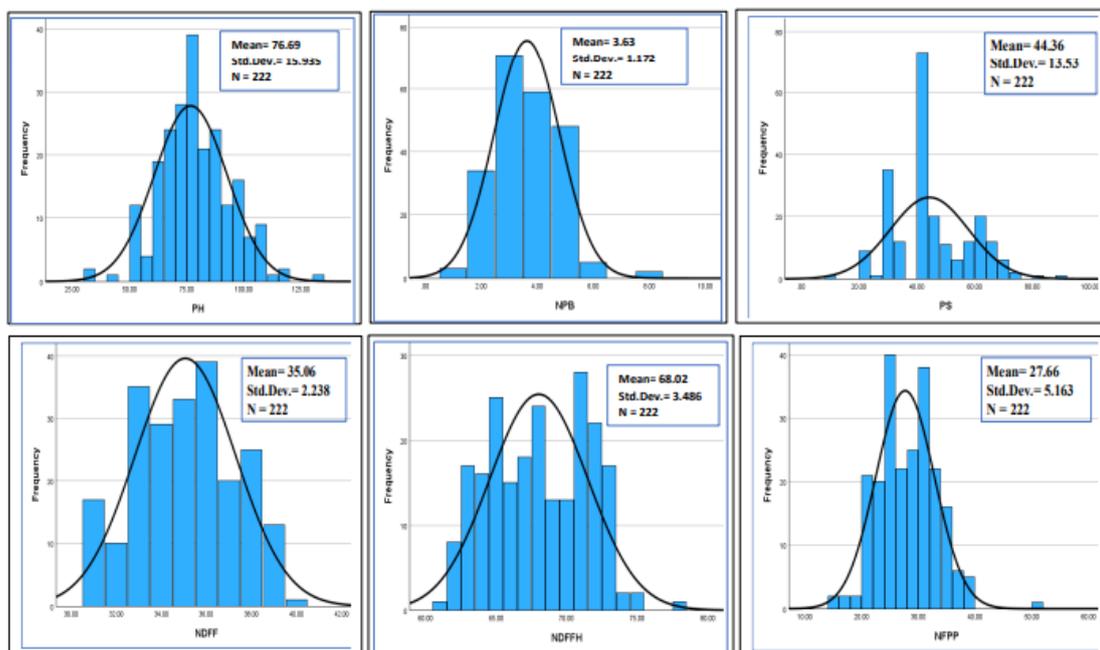


**Fig. 1.** Frequency distributions for Yield and its attributing traits in the F2 population of cross Anagha × IIHR 2896.
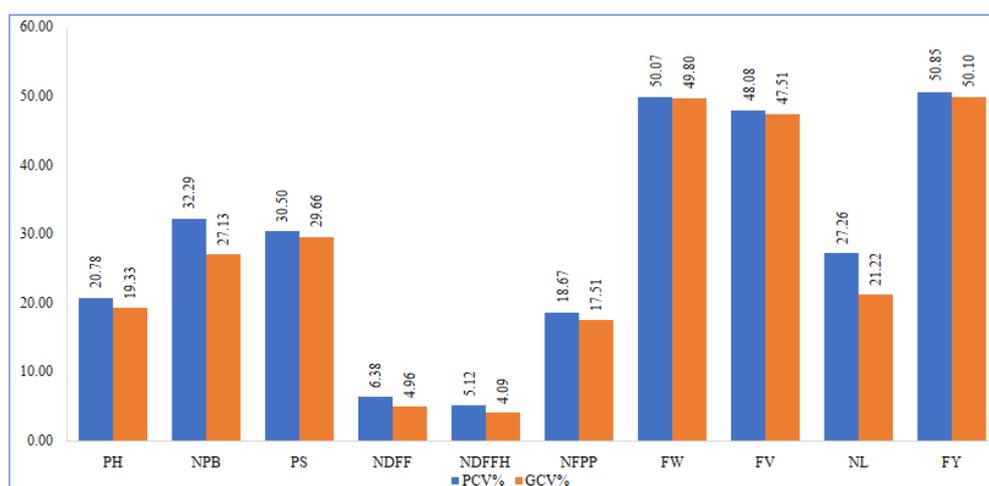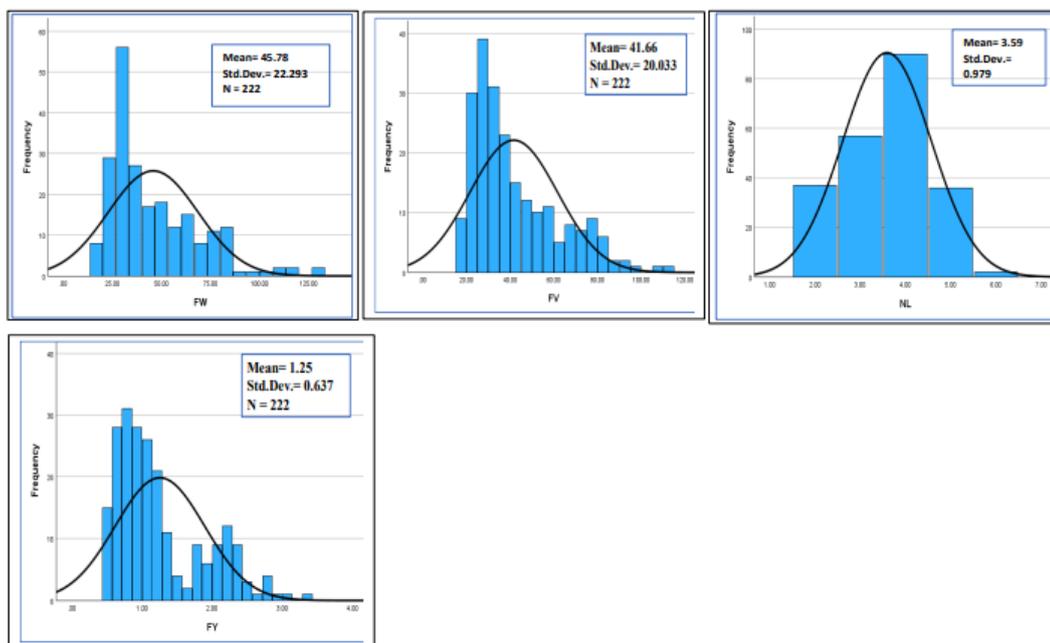
Fig. 2. PCV and GCV for yield and its attributing traits in segregating F2 population of cross Anagha × IIHR 2896.
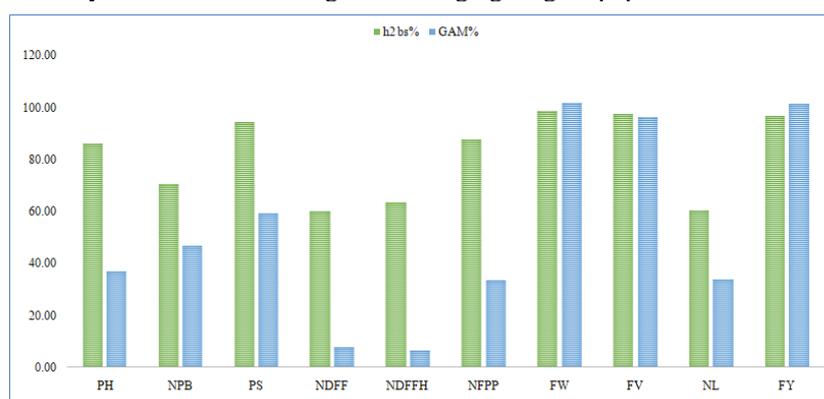


Fig. 3. Heritability and GAM for yield and its attributing traits in segregating F2 population of cross Anagha × IIHR 2896.

## CONCLUSIONS

Higher genetic variability is seen for plant height (cm), number of primary branches, plant spread (cm), number of fruits per plant, fruit weight (g), fruit volume (ml), number of locules and fruit yield per plant (kg).

However same characters showed a high amount of heritability coupled with genetic advance as percent of mean, which indicates that there is a greater scope for improvement in these characters through selection.

## FUTURE SCOPE

The study showed that there is an enormous amount of genetic variation in $F_2$ segregating population. Hence, through the application of specific breeding methods to harness the variation, it is possible to develop superior varieties of tomato with high yield and quality.

## REFERENCES

Akhter, S. and Najnine, F. (2022). Variability of Tomato (*Lycopersicon esculentum* L.) Genotypes for Higher Yield and Yield Contributing Traits. *North American Academic Research, 5*(2), 48-64.

Aravind, K. S., Ram, C. N., Yadav, G. C., Srivatsava, R. K., Chandra, D., Deepak, K. G., Pushpendra, K. and Prateek, K. (2017). Studies on genetic variability an genetic advance in tomato. *International journal of Pure and Applied Bioscience*, *5*(2), 908-912.

Bilal, A. K., Syeda, F. M., Mehboob, A., Mazhar, I., Ihsan, U., Maria. S., Adil. R. and Muhammad. S. (2017). Genetic analysis of F2population of tomato for studying quantitative traits in the cross between Coldera × KHT5. *International Journal of Plant Research, 7*(4), 90-93.

Choo, T. M., and Reinbergs, E. (1982). Analysis of skewness and kurtosis for detecting gene interaction in a double haploid population, *Crop Science, 22*, 231-235.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soybean. *Agronomy Journal, 47*, 477-483.

Kimberg, C. A. and Bingham, E. T. (1998). Population improvement in Lucerne (*Medicago sativa* L.): components of inbreeding depression are different in original and improved populations. *Australian Journal of Experimental Agriculture, 38*, 831-836.

Lav Kumar and G.C. Yadav. (2023). Estimations of Heritability in a Narrow Sense and Genetic Gain for Diverse Typescripts in Tomato (*Solanum lycopersicum* L.). *Biological Forum – An International Journal, 15*(2), 481-484.

Lush, J.L. (1940). Intra-sire correlation and regression of offspring on dams as a method of estimating heritability of characters. In: Proc. of "American Society of Animal Production". *33*, 293-301.

Maurya, S., Singh, A., Singh S. and Kumawat, O. M. (2020). Traits association analysis for yield and quality attributes of tomato (*Lycopersicon esculentum* L.). *Journal of Pharmacognosy and Phytochemistry, 9*, 1019–1023.

Meena, O. P., Bahadur, V., Shilendra, P. and Singth, D. (2015). Genetic association analysis for fruit yield and its contributing traits of indeterminate tomato (*Solanum lycopersicon* L.). germplasm in open field conditions. *The Journal of Agricultural Science, 7*(3), 148.

Mohanty, B. K. (2003) Genetic variability, correlation and path coefficient studies in tomato. *Indian Journal of Agricultural Research*, *37*(1), 68-71.

Panse, V. G. and Sukhatme, P. V. (1961). "Statistical Methods for Agricultural Workers," 2nd ed. Indian Council of Agricultural Research, New Delhi.

Pooni, H. S., Jinks, J. L. and Cornish, M. A. (1977). The causes and consequences of non-normality in pretending the properties of recombinant inbred lines. *Heredity, 38*, 329-338.

Priyanka, P. L., Vijay, B. and Puspha, G. (2017). Study on genetic variability, heritability, genetic advance in tomato (*Solanum lycopersicum* L.). *International Journal of Current Microbiology and Applied Science*, *6*(11), 1775-1783.

Rai, A.K., Vikram, A. and Pandav, A., (2016). Genetic variability studies in tomato (*Solanum lycopersicum* L.) for yield and quality traits. *International Journal of Agriculture, Environment and Biotechnology*, *9*(5), 739-744.

Rajeshwari Teli, A. (2019). Assessment of Genetic Variability in segregating population (F2) of cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*). M.Sc. thesis submitted to University of Agricultural and Horticultural Sciences, Shivamogga, 41pp.

Ravindra Kumar, S. K., Singh, K., Srivastava and Singh, R. K. (2015). Genetic variability and character association for yield and quality traits in tomato (*Lycopersicon esculentum* Mill). *Agriways*, *3*(1), 31-36.

Robinson, H. E. and Comstock, R. S. (1949). Biometrical studies of yield in segregating population of Korean lespedeza. *Agronomy Journal, 48*, 268-272.

Robson, D. S. (1956). The application of K4 statistics to genetic variance component analysis. *Biometrics, 12,* 433-444.

Roy, D. (2000). Plant breeding – The Analysis and exploitation of variability. PB: Narosa Publishing House. New Delhi. India. p.198.

Sangamesh Nevani, O. Sridevi, Lokesh Kumar Verma, Akshaya M., Shreyas A. and B.D. Biradar. (2022). Study of Genetic Variability, Correlation and Path coefficient Analysis in $F_2$ Segregating Population of Tomato (*Solanum lycopersicum* L.). *Biological Forum – An International Journal*, *14*(1), 1477-1482.

Sangamesh (2019). Assessment of genetic variability in $F_2$ tomato Population of cross, IIHR 2373 × Arka Alok (*Lycopersicon esculentum* L.). M.Sc. thesis submitted to University of Agricultural and Horticultural Sciences, Shivamogga, 51pp.

Sayeda, F. M., Bilal, A. K., Zaheer, U. K., Sajid, H. M., Ahmed, M. I., Maria, S. and Annum, S. (2016). Variability, Heritability and genetic advance in F2 population of cross between cultivated and wild tomato. *Food Science and Quality Management, 56*, 68-71.

Shankar, A., Reddy, R. V. S. K., Sujatha, M. and Pratap, M. (2013). Genetic variability studies in F1 generation of tomato (*Solanum lycopersicon* L.). *IOSR Journal of Agriculture and Veterinary Science*, *4*(5), 31-34.

Snedecor, G. W. and Cochran, W. G. (1974) Statistical Methods. 8th Edition, Iowa State University Press, Ames.

Verma, B., Kerketta, A., Sharma, D. and Bahadur, V. (2021). Studies on Genetic variability, Heritability, Genetic Advance and Trait Association in Tomato (*Solanum lycopersicum* L.). *Biological Forum – An International Journal, 13*(3), 101-104.

Yogendra, K. N. (2011). Development of tomato (*Solanum lycopersicum* L.) for extended shelf life through molecular marker approaches. *Ph.D. thesis* submitted to University of Agricultural Sciences, GKVK, Bengaluru, 137pp.

---