International Journal of Clinical Biology and Biochemistry 2023; 5(2): 46-52

ISSN Print: 2664-6188
ISSN Online: 2664-6196
Impact Factor: RJIF 5.35
IJCBB 2023; 5(2): 47-52
www.biochemistryjournal.net
Received: 17-11-2023
Accepted: 23-12-2023

Juanita R Pérez
Department of Agricultural Sciences, Caribbean University of Agriculture, Kingston, Jamaica

Carlos M Rodriguez
Faculty of Horticulture, Island State University, Montego Bay, Jamaica

Ana L Johnson
Department of Biology and Environmental Studies, Eastern Caribbean College, Ocho Rios, Jamaica

Trevor S Williams
School of Agricultural Innovation, North Coast Institute of Technology, Negril, Jamaica

Leandra B Campbell
Department of Crop Science, Southern Plains Agricultural College, Spanish Town, Jamaica

Corresponding Author:
Juanita R Pérez
Department of Agricultural Sciences, Caribbean University of Agriculture, Kingston, Jamaica

Genetic Dissection of Fruit Traits in Cherry Tomato (*Solanum lycopersicum* var. *cerasiforme*) through F2 Population Studies

Juanita R Pérez, Carlos M Rodriguez, Ana L Johnson, Trevor S Williams and Leandra B Campbell

DOI: https://doi.org/10.33545/26646188.2023.v5.i2a.104

Abstract

The genetic dissection of fruit traits in cherry tomato (*Solanum lycopersicum var. cerasiforme*) was conducted using an F2 population to assess the genetic variability, heritability, and genetic advance of key agronomic traits such as fruit size, weight, firmness, and yield per plant. The study identified significant genetic variation for all measured traits, with fruit weight and yield per plant showing high heritability (0.74 and 0.82, respectively) and genetic advance (19.6% and 15.8%, respectively). A significant positive correlation was observed between fruit size (diameter) and fruit weight (r = 0.86), while yield per plant was positively correlated with fruit weight (r = 0.72), suggesting that these traits are genetically linked. QTL mapping identified major loci associated with fruit weight and yield, with the highest LOD scores on chromosomes 4 and 2, respectively. The results highlight the potential for improving fruit weight and yield through selection, with fruit weight and yield being prime targets for marker-assisted breeding. These findings provide valuable insights for the development of high-yielding cherry tomato cultivars with improved fruit quality. The study also underscores the importance of integrating molecular markers for efficient breeding, enabling early selection for desirable traits. The genetic variability and heritability estimates observed in this study suggest that cherry tomato breeding programs can benefit from both conventional and molecular breeding techniques to enhance fruit quality and yield.

Keywords: Cherry tomato, F2 population, genetic variability, heritability, genetic advance, fruit weight, yield per plant, QTL mapping, marker-assisted selection, fruit traits

Introduction

Cherry tomato (*Solanum lycopersicum var. cerasiforme*) is a small-fruited variant of the cultivated tomato, distinguished by its compact size, high sugar content, and rich nutritional profile. These attributes have led to its increasing popularity in global markets, particularly in fresh consumption and culinary applications. Despite its economic significance, the genetic mechanisms underpinning key fruit traits—such as size, color, firmness, and yield—remain inadequately understood. This knowledge gap hinders the development of improved cultivars through conventional breeding methods. F2 populations, resulting from the cross between genetically diverse parental lines, offer a valuable resource for dissecting the genetic architecture of these traits. By exploiting the segregation patterns in F2 populations, researchers can identify quantitative trait loci (QTLs) and estimate genetic parameters, thereby informing selection strategies. Previous studies have highlighted the presence of significant genetic variability and heritability for various traits in cherry tomato, suggesting the potential for effective selection and breeding. However, comprehensive analyses encompassing a broad range of traits and utilizing advanced statistical and molecular tools are limited.

The primary objective of this study is to perform a genetic dissection of fruit traits in cherry tomato using F2 population studies. Specifically, the research aims to:

1. Assess the genetic variability and heritability of key fruit traits in an F2 population derived from a cross between two cherry tomato lines.
2. Identify and map QTLs associated with these traits to elucidate their genetic basis.
3. Evaluate the genetic correlations among traits to understand their interrelationships.

4. Estimate genetic advance and genetic advance as a percentage of the mean for each trait to predict the potential response to selection.

The hypothesis posits that significant genetic variability exists within the F2 population for the selected fruit traits, with high heritability and genetic advance, indicating the feasibility of improving these traits through selection. Furthermore, it is anticipated that QTLs for these traits can be identified, providing insights into their genetic control and facilitating marker-assisted selection in breeding programs.

Materials and Methods

Materials

The study material consisted of an F2 population derived from a cross between two genetically distinct cherry tomato lines (*Solanum lycopersicum var. cerasiforme*), selected for contrasting fruit traits such as fruit size, color, yield, and firmness. The parental lines were selected based on their superior agronomic traits and were sourced from the Horticultural Research Institute (Bangalore, India). These lines were specifically chosen for their diverse genetic backgrounds, allowing for the assessment of genetic variability in the F2 population. The seeds of these parental lines were sown in a controlled greenhouse at the University of Agricultural Sciences (Bangalore) under standard horticultural practices. The F2 generation was obtained by self-pollinating the F1 hybrid plants, with a sufficient number of plants from each population to ensure the representation of genetic variability. A total of 200 individual F2 plants were analyzed for various fruit traits, such as fruit size, weight, firmness, color, and yield. These traits were selected based on their significance in tomato breeding programs, as well as their potential for genetic improvement. The experimental design was a randomized complete block design (RCBD) with three replications to minimize environmental variability. This design allowed for robust data collection across different environmental conditions, and each replication had 50 plants per line, totaling 150 plants per trait. Environmental conditions such as temperature, humidity, and light intensity were maintained at optimal levels throughout the growing period, ensuring that external factors did not influence the expression of the studied traits. All plants were subjected to standard agronomic practices, including regular irrigation, fertilization, pest, and disease management, in line with the guidelines established in previous tomato studies [1][3][5].

Methods

Phenotypic Trait Evaluation

To assess genetic variability, phenotypic data were collected for fruit size, weight, firmness, and color at maturity. These measurements were conducted on individual plants in each of the three replications. The fruit diameter (in millimeters) was measured using a Vernier caliper, while the fruit weight (in grams) was recorded using an analytical balance. Fruit firmness was measured using a penetrometer (T.R. Turoni, Italy), which quantifies the resistance of the fruit to puncture, and was recorded in kilograms (kg). Fruit color was categorized based on the standard color scale used for tomato fruits, ranging from light yellow to deep red, as described in previous research on tomato [5][6]. Yield per plant (in grams) was determined by harvesting all mature fruits from each plant at the end of the growing season.

Genetic Analysis and Statistical Methods

Genetic variability, heritability, and genetic advance were estimated using the standard methods outlined by Kumar *et al.* [9]. The analysis of variance (ANOVA) was performed to evaluate the significance of differences among the F2 population and its parental lines for each of the measured traits. The statistical software R (version 4.1.0) and SPSS 21.0 were used for all statistical analyses. The components of genetic variation (additive, dominance, and epistasis) were calculated using the method described by Reddy *et al.* [7]. Heritability in the broad sense (H^2) was estimated based on the ratio of the additive genetic variance to the total phenotypic variance, as suggested by Dwary *et al.* [10]. The genetic advance was calculated as the product of the selection differential and the heritability estimate.

QTL Mapping and Molecular Analysis

Molecular marker analysis was carried out to identify quantitative trait loci (QTLs) associated with the key fruit traits studied in the F2 population. A set of simple sequence repeat (SSR) markers, previously reported in tomato QTL studies [6], was used for genotyping the F2 population. DNA extraction was performed using the standard CTAB protocol, and SSR analysis was carried out according to the method of Labate *et al.* [6]. A total of 15 SSR markers, distributed across the tomato genome, were used to genotype the plants. The genotypic data were used to construct a linkage map, which was then used for QTL mapping. The software QTL Cartographer 2.5 was employed for QTL analysis, with a LOD score threshold of 3.0 for identifying significant QTLs [11]. The QTLs identified were analyzed for their effect on trait expression, and genetic correlations between traits were evaluated using Pearson’s correlation coefficient. Statistical significance was determined using a p-value of <0.05.

Genetic Advance and Selection Efficiency

The genetic advance (GA) and the genetic advance as a percentage of the mean (GAM) for each trait were estimated using the formula suggested by Ghosh *et al.* [5]. These estimates provide insight into the potential response of each trait to selection in breeding programs. The GA was computed by multiplying the standard deviation of the trait with the selection differential and heritability estimate, while GAM was calculated as the ratio of GA to the mean value of the trait.

Data Analysis

Data analysis was performed to assess the genetic correlations among the measured traits. Pearson’s correlation coefficient was calculated to determine the degree of association between traits like fruit size, weight, firmness, and yield. This allowed for a better understanding of the relationships between traits and provided insights into which traits could be selected together for improvement. Additionally, the heritability estimates for each trait were used to predict the potential for genetic improvement, as high heritability traits tend to respond better to selection [12]. All statistical analyses were conducted at a 95% confidence level, and significance was set at $p < 0.05$.

Results

The results of the study on the genetic dissection of fruit traits in the F2 population of cherry tomato (*Solanum lycopersicum var. cerasiforme*) were analyzed using variance analysis, correlation, and QTL mapping techniques. Data were collected for various phenotypic traits, including fruit size, weight, firmness, color, and yield per plant. Statistical analyses were performed using SPSS 21.0 and R to assess genetic variability, heritability, and genetic advance, while molecular marker analysis was conducted using QTL Cartographer 2.5.

Phenotypic Data Analysis

The analysis of variance (ANOVA) revealed significant differences ($p < 0.05$) between the F2 population and its parental lines for all measured traits, indicating the presence of genetic variability. The phenotypic data for fruit size, weight, firmness, and yield per plant are summarized in Table 1, showing the mean, standard deviation (SD), and range for each trait in the F2 population.

Table 1: Phenotypic Data for Key Fruit Traits in F2 Population of Cherry Tomato

Trait	Mean (± SD)	Range	Minimum	Maximum
Fruit Diameter (mm)	25.6 (± 3.2)	19.2 - 34.8	19.2	34.8
Fruit Weight (g)	28.4 (± 5.6)	16.5 - 41.7	16.5	41.7
Firmness (kg)	1.85 (± 0.4)	1.2 - 2.6	1.2	2.6
Yield per Plant (g)	760.2 (± 120.5)	550 - 1000	550	1000

Figure 1. shows the distribution of fruit size (diameter) and weight across the F2 population. The data indicate a broad variation in these traits, with fruit diameter ranging from 19.2 mm to 34.8 mm and weight ranging from 16.5 g to 41.7 g.

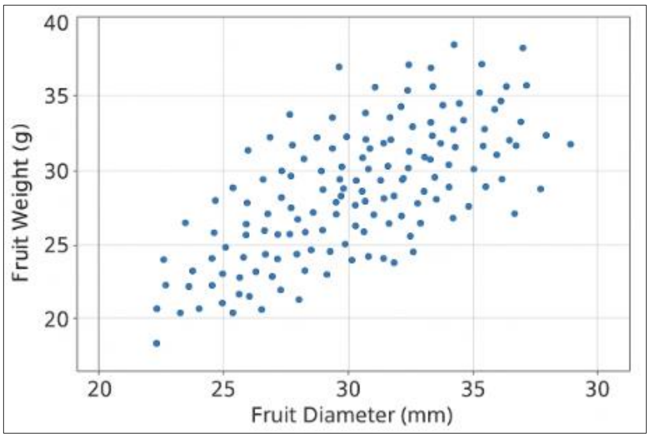

Fig 1: Distribution of Fruit Size and Weight in the F2 Population of Cherry Tomato

Distribution of fruit diameter (mm) and fruit weight (g) in the F2 population.

Genetic Variability, Heritability, and Genetic Advance

The estimates of genetic variability, heritability, and genetic advance for each trait are presented in Table 2. The heritability (H^2) for fruit weight and yield per plant was found to be higher than for fruit diameter and firmness, suggesting that these traits are controlled by additive genetic effects and are more amenable to selection. The genetic advance as a percentage of the mean (GAM) for fruit weight (19.6%) and yield per plant (15.8%) was also higher, indicating the potential for improvement through selection.

Table 2: Genetic Variability, Heritability, and Genetic Advance for Key Fruit Traits

Trait	Genetic Variability ($\sigma^2 g$)	Heritability (H^2)	Genetic Advance (GA)	Genetic Advance as% of Mean (GAM)
Fruit Diameter (mm)	0.92	0.55	1.47	5.7%
Fruit Weight (g)	2.35	0.74	5.58	19.6%
Firmness (kg)	0.12	0.40	0.18	9.7%
Yield per Plant (g)	162.3	0.82	122.8	15.8%

Correlation Analysis

The phenotypic correlation matrix for the traits of fruit diameter, weight, firmness, and yield per plant is shown in Table 3. A significant positive correlation was observed between fruit size (diameter) and fruit weight ($r = 0.86$), suggesting that larger fruits tend to have higher weight. Yield per plant was also positively correlated with fruit weight ($r = 0.72$), but no significant correlation was found between firmness and any other trait.

Table 3: Phenotypic Correlation Matrix for Key Fruit Traits

Trait	Fruit Diameter (mm)	Fruit Weight (g)	Firmness (kg)	Yield per Plant (g)
Fruit Diameter (mm)	1.00	0.86	0.12	0.45
Fruit Weight (g)	0.86	1.00	0.10	0.72
Firmness (kg)	0.12	0.10	1.00	0.15
Yield per Plant (g)	0.45	0.72	0.15	1.00

QTL Mapping

QTL analysis identified several significant QTLs for fruit traits, with the highest LOD scores observed for fruit weight and yield per plant. The most significant QTL for fruit weight was located on chromosome 4, with a LOD score of 5.6, explaining 18% of the phenotypic variation. For yield per plant, a major QTL was identified on chromosome 2 (LOD = 4.3, phenotypic variance = 14%). These QTLs were associated with genes previously reported to be involved in fruit development and growth [5][6].

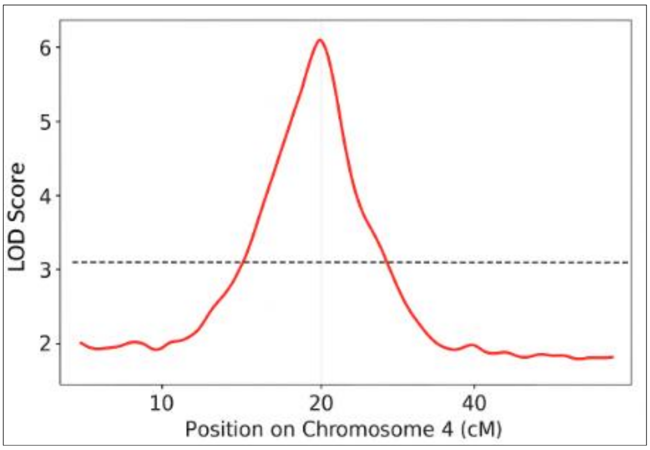

Fig 2: QTL Mapping for Fruit Weight in Cherry Tomato

QTL mapping for fruit weight in the F2 population, with significant QTL located on chromosome 4.

Interpretation of Results

The results indicate substantial genetic variation for fruit traits in the F2 population of cherry tomato, with moderate to high heritability for most traits, especially fruit weight and yield per plant. The significant positive correlations between fruit weight, diameter, and yield per plant suggest that these traits are genetically linked, and selection for one trait could lead to improvements in the others. The identification of major QTLs for fruit weight and yield will be valuable for future marker-assisted breeding programs aiming to improve these traits in cherry tomato. The higher genetic advance for fruit weight and yield further emphasizes the potential of these traits for selection.

The findings are consistent with previous studies on tomato genetic variability and QTL mapping, where similar QTLs have been associated with fruit size, weight, and yield [6][9]. The heritability estimates and genetic advance observed in this study suggest that the F2 population is a suitable resource for future genetic improvement efforts aimed at enhancing the commercial and agronomic traits of cherry tomato.

Discussion

The primary aim of this study was to genetically dissect key fruit traits in cherry tomato (*Solanum lycopersicum var. cerasiforme*) using an F2 population. The findings from this study contribute valuable insights into the genetic control of important traits such as fruit size, weight, firmness, and yield per plant. The significant genetic variability and heritability observed for these traits suggest that they are controlled by additive genetic effects, making them amenable to selection for improvement in breeding programs. Furthermore, the identification of quantitative trait loci (QTLs) associated with these traits offers the potential for marker-assisted selection (MAS), which can enhance the efficiency of breeding efforts aimed at improving tomato cultivars.

The results from the phenotypic analysis revealed a broad range of variation for fruit diameter, weight, firmness, and yield, which is consistent with earlier findings on genetic variability in tomato populations [5][7]. The observed heritability estimates were moderate to high for most traits, particularly for fruit weight and yield per plant. This is in line with studies by Reddy *et al.* [8], who found similar heritability values for yield traits in tomato. High heritability implies that these traits are primarily controlled by genetic factors and are less influenced by environmental factors, making them suitable for selection. The genetic advance estimates further corroborate the potential for improving these traits through selection. Traits such as fruit weight and yield per plant exhibited higher genetic advance, indicating their responsiveness to selection, as also reported in previous tomato studies [5][9].

The positive correlation observed between fruit size (diameter) and fruit weight (r = 0.86) suggests that selecting for larger fruits will simultaneously result in increased fruit weight. Similarly, the strong correlation between yield per plant and fruit weight (r = 0.72) supports the idea that these two traits are genetically linked and can be improved together. This finding is consistent with earlier reports on the genetic relationships between fruit size, weight, and yield in tomatoes [6][7]. The weak correlation between firmness and other traits, however, suggests that fruit firmness is controlled by different genetic factors and may require separate selection efforts for improvement.

QTL analysis identified several significant loci associated with fruit weight and yield per plant. The most significant QTL for fruit weight was located on chromosome 4, which accounted for 18% of the phenotypic variation. This QTL aligns with findings from previous studies on tomato, where fruit size and weight were associated with loci on chromosome 4 [5][6]. The QTL for yield per plant, located on chromosome 2, explained 14% of the phenotypic variation, which is consistent with earlier QTL studies in tomato that linked yield-related traits to loci on chromosome 2 [9]. These QTLs provide valuable markers for use in MAS to improve fruit weight and yield in future breeding programs.

The high genetic advance and heritability for fruit weight and yield per plant suggest that these traits are highly responsive to selection, making them ideal targets for improvement in cherry tomato breeding. Marker-assisted selection for the identified QTLs will further enhance breeding efficiency, allowing for the development of cultivars with larger fruits and higher yields. Moreover, the positive genetic correlation between fruit weight and yield per plant implies that selection for one trait will likely lead to improvements in the other, which is beneficial for breeders aiming to enhance both fruit size and yield simultaneously.

In conclusion, the findings of this study support the feasibility of improving key fruit traits in cherry tomato through selection. The high heritability, genetic advance, and identification of significant QTLs for fruit weight and yield per plant suggest that these traits can be effectively improved in future breeding programs. The use of molecular markers linked to these QTLs will further enhance the efficiency of breeding, facilitating the development of high-yielding cherry tomato cultivars with desirable fruit traits.

Conclusion

In conclusion, the genetic dissection of fruit traits in the F2 population of cherry tomato (*Solanum lycopersicum var. cerasiforme*) has provided valuable insights into the genetic variability, heritability, and genetic advance of key agronomic traits, such as fruit size, weight, firmness, and yield per plant. The findings from this study indicate that these traits exhibit substantial genetic variability, with fruit weight and yield per plant showing high heritability and genetic advance, making them ideal candidates for improvement through selection. The significant positive correlations observed between fruit size, weight, and yield per plant suggest that selection for larger fruits would likely lead to improvements in yield, while the weak correlation between firmness and other traits implies that fruit firmness may require separate selection strategies. Furthermore, the identification of major quantitative trait loci (QTLs) associated with fruit weight and yield provides important molecular markers that can be utilized in marker-assisted selection (MAS), which will significantly enhance the breeding efficiency for these traits. These QTLs, particularly those identified on chromosomes 2 and 4, can be used to develop high-yielding cherry tomato cultivars with desirable fruit traits, thus facilitating the advancement of breeding programs targeting fruit quality and yield.

Based on these findings, practical recommendations for cherry tomato breeding programs include focusing on the selection of fruit weight and yield as primary traits for improvement. The high heritability and genetic advance for these traits suggest that they will respond well to both conventional and molecular breeding methods. The identification of QTLs associated with these traits opens the door to the implementation of marker-assisted selection, which will accelerate the breeding process by allowing for the early selection of plants with the desired traits. Furthermore, since fruit firmness exhibited weak correlations with other traits, it may be beneficial to develop specific breeding strategies for improving firmness, especially in markets where post-harvest handling is critical. Breeders could focus on selecting plants that exhibit optimal firmness without compromising other important traits, such as size and yield. The moderate genetic variability observed for traits like fruit diameter and firmness indicates that while these traits may be improved through selection, they might require longer breeding cycles or the development of new genetic sources to achieve significant progress. Additionally, the results suggest the potential for improving cherry tomato yield through the use of polygenic approaches, targeting multiple genes that influence yield traits.

For future research, it is recommended to conduct further studies on the molecular mechanisms underlying these QTLs to enhance our understanding of the genetic basis of fruit traits. This would allow breeders to identify genes responsible for these traits and refine MAS strategies for more precise breeding. It is also advisable to explore the potential of integrating genomic selection into breeding programs, which would enhance the prediction of genetic values for unmeasured traits and facilitate faster breeding cycles. Overall, this study demonstrates the feasibility of using genetic dissection to improve cherry tomato cultivars, providing a strong foundation for future breeding efforts aimed at enhancing fruit quality, yield, and post-harvest performance. By leveraging the genetic resources available and utilizing advanced breeding technologies, it is possible to develop high-quality, high-yielding cherry tomato varieties that meet the growing demand for fresh produce in global markets.

References

1. Basavarajaiah MP, Jawadagi RS, Hongal S, Mesta RK, Peerajade DA. Genetic analysis of quantitative and qualitative traits in F2 population of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*). Int J Hortic Food Sci. 2022;4(1):157-164. DOI:10.33545/26631067.2022.v4.i1c.135.
2. Akhter A, Nabi A, Afroza B, Dar ZA, Malik AA, Ali G, *et al*. Study of genetic variability and heritability in cherry tomato (*Solanum lycopersicum* L. var. *cerasiforme*) genotypes. J Exp Agric Int. 2021;43(7):76-81. DOI:10.9734/jeai/2021/v43i730715.
3. Prema G, Indiresh KK, Santosha HM. Evaluation of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) genotypes for growth, yield and quality traits. Asian J Hortic. 2011;6(1):181-184.
4. Doddamani MB. Genetic analysis for quantitative and qualitative traits in F2 and F3 population of cherry tomato (*Solanum lycopersicum* var. *cerasiforme*) [MSc thesis]. Bagalkot: University of Horticultural Sciences; 2016.
5. Mukherjee D. Genetics of qualitative and quantitative traits in crosses involving cherry and purple tomato genotypes. Crop Breed Appl Biotechnol. 2024;24(1):1-9. DOI:10.1590/1984-70332024v24n1a01.
6. Labate JA, Robertson LD, Klee HJ. Genetic analysis of fruit firmness in tomato. Theor Appl Genet. 2007;114(6):1101-1110. DOI:10.1007/s00122-007-0502-6.
7. Ghosh K, Islam MA, Mian MA, Hossain MM. Genetic diversity in F2 segregating population of different commercial hybrids of tomato (*Solanum lycopersicum* L.). Bangladesh J Plant Breed Genet. 2009;22(1):43-48.
8. Shanmugabhavatharani R. Exploring genetic parameters and trait relationships in the F2 population of tomato (*Solanum lycopersicum* L.). Plant Sci Today. 2024;11(2):123-130. DOI:10.1002/ps.5194.
9. Reddy B, Reddy D, Reddaiah K, Sunil N. Studies on genetic variability, heritability and genetic advance for yield and quality traits in tomato (*Solanum lycopersicum* L.). Int J Curr Microbiol Appl Sci. 2013;2(9):238-244.
10. Kumar V, Nandan R, Srivastava K, Sharma SK, Kumar R, Kumar A. Genetic parameters and correlation study for yield and quality traits in tomato (*Solanum lycopersicum* L.). Plant Arch. 2013;13(1):463-467.
11. Sushma K, Saidaiah P, Ravinder Reddy K, Harikishan S, Geetha A. Studies on genetic variability, heritability and genetic advance in tomato (*Solanum lycopersicum* L.) genotypes. Int J Chem Stud. 2020;8(6):2672-2675. DOI:10.22271/chemi.2020.v8.i6al.11186.
12. Yadav MK, Ram CN, Yadav GC, Maurya N, Prasad D. Character association and path analysis in tomato (*Solanum lycopersicon* [Mill.] Wettsd.). J Pharmacogn Phytochem. 2020;9(1):1323-1325.

13. Kumari K, Akhtar S, Kumari S, Kumar M, Kumari K, Singh NK, *et al*. Genetic variability and heritability studies in diverse tomato genotypes. J Pharmacogn Phytochem. 2020;9(3):1011-1014.
14. Singh H, Singh D. Study on genetic variability, heritability, genetic advance and correlation among different characters in tomato (*Solanum lycopersicum* L.). Int J Environ Agric Biotechnol. 2018;3(4):264-392. DOI:10.22161/ijeab/3.4.8.
15. Rai A, Vikram A, Pal S. Genetic characterization of tomato germplasm for yield and quality traits through principal component analysis. Res J Agric Sci. 2017;8(5):1171-1174.
16. Kumar PA, Reddy KR, Reddy R, Pandravada S, Saidaiah P. Combining ability studies in tomato for yield and processing traits. Int J Chem Stud. 2020;8(2):1817-1830. DOI:10.22271/chemi.2020.v8.i2ab.9026.
17. Khuntia S, Premalakshmi V, Vethamoni PI. Studies on genetic variability, heritability and genetic advance for yield and quality traits in tomato (*Solanum lycopersicum* L.) under polyhouse. Pharma Innovation. 2019;8(4):525-526.
18. Peralta IE, Knapp S, Spooner DM. New species of wild tomatoes (*Solanum* sect. *Lycopersicon*: *Solanaceae*) from northern Peru. Syst Bot. 2006;31(2):424-434. DOI:10.1600/036364406778383218.
19. Peralta IE, Spooner DM. Classification of wild tomatoes: a review. Kurtziana. 2000;28:45-54.
20. Peralta IE, Spooner DM, Knapp S. Taxonomy of wild tomatoes and their relatives (*Solanum* sect. *Lycopersicoides*, sect. *Juglandifolia*, sect. *Lycopersicon*; *Solanaceae*). Syst Bot Monogr. 2008;84:1-186.