

## REVIEW

**Performance and Genetic Analysis of Cherry Tomato Genotypes in Zimbabwe****J. Dube and Maphosa, M**

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**Received** June 25, 2021; **Accepted** August 06, 2021; **Published** August 08, 2021**Copyright:** © 2021, J.Dube *et al.*,**\*Corresponding author:** Department of Crop and Soil Science, Lupane State University, Box 170, Lupane, Zimbabwe. Email: [thiousdube@gmail.com](mailto:thiousdube@gmail.com)**Abstract**

This study sought to explore avenues of strengthening tomato crop productivity through use of diverse germplasm sources through identification, characterisation and analysis of various traits that include: agronomic, morphological and fruit quality parameters. Furthermore, to estimate genetic advance for the purposes of an informed foundation for future crop improvement studies in tomato genotypes. Seven cherry tomato genotypes were grown alongside three popular commercial tomato varieties in Zimbabwe. The study established that most genotypes differed significantly ( $p \leq 0.05$ ) on their earliness to germination, branching ability, flower cluster development, earliness to maturity, vitamin C content, fruit acidity, fruit size, fruit weight and yield. Most cherry genotypes took less than 7 days to reach 50% emergence ahead of commercial genotypes. Higher branching ability scores ranging between 14 and 30 were recorded in cherry tomatoes. Cherry genotype 254 recorded higher Vitamin C levels of 35.2 mg/100g ahead of other cherry tomato genotypes yet line 126 was the most acidic recording 1.22% ahead of line 034 which recorded 1.03%. Line 063 recorded the highest fruit yield of 400 grams ahead of line 016 which recorded 386 grams. Observed higher phenotypic variances above genotypic variances across traits revealed the less impact of environment on trait heritability. Heritability estimates were higher for fruit clustering recording 97.8% ahead that for total harvested fruits per plant that recorded 95.3% implying the greater potential for crop improvements. Genotypic lines 063, 027, 016, 126, 254 and 034 can be recommended for possible use in cross breeding efforts for developing new improved tomato varieties because of their genetic potential for improved performances.

**Key words:** Genetic analysis, *Lycopersicon esculentum* var *cerasiforme*, tomato fruit**Introduction**

Tomato (*Solanum lycopersicum* L.) is an important warm season solanaceous crop grown world over for human consumption due to its high micro nutrient composition in a large variety of raw, cooked and processed food (FAO, 2015).

The Solanaceae family, which includes more than 3000 species with origins in both the Old eggplant coming from China and India, yet the new pepper/potato/tomato came from Central and South America (Bai and Lindhout, 2007). *Solanum lycopersicum* is the only domesticated species (Peralta *et al.*,

2006). Modern tomato varieties have suffered reduction in genetic variability mainly due to domestication bottlenecks known as domestication syndrome. The continuous selection of beneficiary alleles since tomato introduction has evolved a wide number of morphological and physiological traits in tomato resulting in compact growth habit, increased earliness, reduction and loss of seed dispersal plus limited fruit diversity (Paran and Van, 2007; Kulus, 2018). Genetic erosion resulting from restricted habitats, lack of information, hybrid sterility and pollen contamination are some of the key challenges related to domestication of modern tomato. During domestication, mutations associated with large fruit size were accumulated, fruit shape changes were manipulated from round shapes to tremendous shape variations (Bai and Lindhout, 2007). Seed is larger for domesticated genotypes than that of wild varieties.

Tomato breeding studies show a large variation between modern cultivated tomato and its semi-wild relatives that presents an exploitable opportunity for improving several traits. A lot of untapped diversity exist and can be best utilised for the betterment of human priorities (Bai *et al.*, 2007). More effort is needed to unravel the genetic potential of tomatoes and its wild relatives through breeding programmes. Cherry tomato (*Lycopersicon esculentum* var *cerasiforme*) is known to be of higher disease resistance, better sweetness, more succulent and higher carbohydrates resulting in more energy. Manganese, potassium, vitamin A, vitamin B-6, vitamin B-9, vitamin C, vitamin K, vitamin B-complex, calcium, copper, iron, magnesium, phosphorus and zinc are considered higher in cherry tomato making it of better nutritive value (Casals *et al.*, 2018). It also contains more carotenoids such as lycopene and phenolic compounds that are antioxidants (Zanfini *et al.*, 2017). High anti-oxidant content makes them better promising on the market because of their health benefits. The wide genetic diversity and variability in the genes of cherry tomato warrant their inclusion in breeding programmes for the cultivated tomato (Corado and Rao, 2017). Having stable genomes,

genetic variation within tomato species occurs both intraspecific, within cultivated tomato and interspecific between wild species (Kulus, 2018). The presence of many valuable genes from wild tomato has led to increased need to mine newer alleles from the interspecific gene pool and introgress them within the *Lycopersicum* plants (Branthome, 2010). Accordingly, the objective of this study was to characterize on agronomic, morphological, physiological and quality traits of selected cherry tomatoes of East African origin with a view to identify material for use locally as plant introductions and as sources of desirable genes for tomato improvement.

### Materials and methods

Seven cherry tomato accessions 016, 027, 032, 034, 063, 126 and 254 were grown alongside with three improved modern open pollinated varieties ‘Money Maker’, ‘Heinz’ and ‘Rodade’. The plants were characterized for germination duration, branch development, clustering ability, flowering ability and fruit development, earliness to maturity, pests and disease tolerance and yielding. Score shown on table 1 (qualitative traits of tomato genotypes on pests and disease) the symbol 0 stands for complete absence of pests and diseases yet symbol 10 represent severe pest or disease infestation.

### Genetic analysis of selected traits from the assemble germplasm

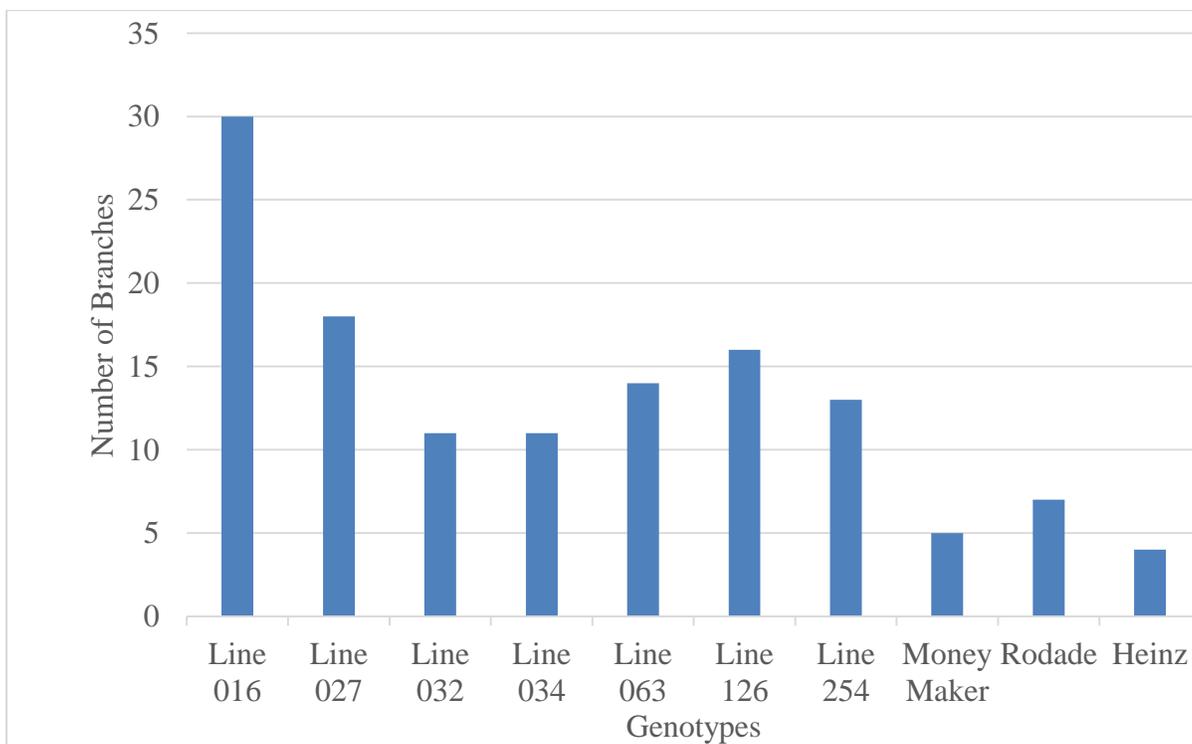
Performances for each individual genotype were monitored, observed and recorded for further analysis. Descriptive statistics generated from the ANOVA table through Genstat software were used in genetic analysis and estimate of genetic advance. Raw data from the ten randomly selected tomato plants from each genotypic line was subjected into GENSTAT (13th Edition) in order to carry out analysis of variances among traits. Coefficient of variation, Standard error of differences, Mean Square error, Standard error of means, Sum of squares,

Grand mean were determined for further use. Table 3, show results on variances obtained.

**Layout of the experiment**

Individual tomato genotypic plots each having fifteen plants were established. Each plot was replicated twice following a Randomised Complete Block Design. Tomato plants were grown to maturity with standard agronomic practices for observation.

**Results and Discussion**



**Figure 1 :** Branching habits across cherry tomato genotypes

Commercial varieties under study had fewer total branches numbering below 7 branches across genotypes. More branches per plant means more area for the production of leaves, whose quantity directly influence the efficiency of photosynthetic activity resulting in better growth and yields. These findings were in concurrence with findings by Kumar (2014) and Renuka *et al.*, (2014) who separately found out that cherry genotypic lines had branches ranging between 7.07 and 45.8.

**Germination duration**

Genotypes 063, 032, 126, 254 and Rodade were early to reach 50% germination since each took 7 days (most earliest) yet other lines, genotypes 027, Money Maker and Heinz were least, each taking 9 days. Earliness to germination is a good measure to show earliness to proper crop establishment which impact on plant development and yielding.

**Branching habit**

Higher branch numbers were recorded in genotypes 016 and 027 recording 30 and 18 branches respectively as shown in Figure 1.

**Flowering and clustering ability**

More flowers were recorded in line 027 (73 flowers). These results fits well with other research findings by Venkadeswaran *et al.*, (2018) and Mohamed *et al.*, (2012) who separately concluded that Cherry lines had a potential flower numbers ranging between 4.2 and 51.2. Both concluded that cherry tomato genotypes had fruit clusters averaging 17.07 in Pusa genotype against 13.8 in Pant genotype far ahead of most

commercial lines. Higher flower clustering ability shows the genetic potential which can be transferred to total number of developing and harvestable fruits per plant.

**Fruiting and yielding**

More visible fruits were recorded on cherry genotypes 027, 032, 126 and 063 ahead of commercial varieties. Fruit yield in cherry lines ranged between 179 g and 460 g/plant with line 063 recording the highest yields. The study results corroborated with findings by researchers Venkadeswaran *et al.*, (2018) and Tiwari and Upadhyay (2011) who established that some cherry tomato genotypes could yield between 326 g and 700 g/plant. The results were also in tandem with conclusions by Olaniyi *et*

*al.*, (2010) who found out that fruit yield per plant and total fruit yields per genotype varied significantly among different tomato genotypes.

**Maturity earliness**

Genotypes 016 and 063 each recorded 63 days to reach first full fruit maturity ahead of other genotypes. Findings were in tandem with previous research by Kumar (2018) and Jose *et al.*, (2018) who separately concluded similarly that Cherry tomato genotypes took between 56 and 76.69 days respectively to reach full maturity. Differences on qualitative traits shown on table 1.

Genotype	Days to 50% germination	Branches	Clusters	Flowers	Open flowers	Fruits	Disease incidence	Pest incidence	Pest type
016	8	30	40	32	6	107	2	0	Lm
027	9	18	43	73	34	83	0	2	Lm
032	8	11	20	44	22	69	1	2	Lm
034	8	11	20	33	12	19	2	1	Lm
063	7	14	33	60	19	54	0	3	Lm
126	7	16	30	36	10	57	2	5	Lm
254	7	13	20	32	11	29	3	2	Lm
Money Marker	8	5	4	20	2	1	1	3	Lm
Rodade	7	7	13	20	14	9	3	7	Lm, Bw
Heinz	9	4	11	9	8	10	2	8	Lm
<b>Mean</b>	7.8	13	23.4	35.9	13.8	43.8	1.6	3.3	
<b>Variance</b>	0.1	5.2	14.7	32.9	7.6	114.6	0.1	0.6	
Key: Lm- Leaf miner ( <i>Tuta absoluta</i> )      Bw - Boll worm ( <i>Heliothis</i> )      Lb-Leaf blight ( <i>Phytophthora infestas</i> )									

**Table 1:-** Qualitative Traits of 10 Selected Tomato Genotypes grown in Bubi District

Evaluation of ripe tomato fruits was on the basis of differences on external colour, differences on fruit diameters, length, weights (upon measuring) and chemical content where vitamin

C, fruit acidity and fruit pH levels were analysed in the laboratory through the titration process.

Genotype	Fruit colour	Fruit diameter (mm)	Fruit length (mm)	30 fruit weight (g)	Individual fruit weight (g)	Total harvested fruits	Average fruits per plant	Average yields (g/plant)
016	Red	20.1	65.7	140	4.6	167	84	386.4
027	Red	19.5	61.2	120	4.0	1041	95	380.0
032	Red	18.7	63.6	120	4.0	495	71	284.0
034	Red	22.1	73.9	210	7.0	536	49	343.0
063	Golden	19.9	60.4	220	7.3	752	63	460.0
126	Red	19.7	65.6	140	4.6	713	65	299.0
254	Golden	19.0	61.3	96	3.2	783	56	179.0
Money Marker	Red	35.7	112.0	250	25.0	76	9	225.0
Rodade	Red	55.2	118.4	840	84.0	58	7	588.0
Heinz	Red	58.6	179.2	850	85.0	34	4	340.0
Mean		28.8	86.13	298.6	23.0	465	50	348.0
SE±		6.9	7.7	36.0	4.4	3.5	3.4	36.3

SE-standard error

**Table 2.** Comparison of Tomato Fruit Parameters across Genotypes

**Fruit colour:** The most predominant fruit colour was red for five cherry genotypes yet only two cherry tomato lines (063 and 254) were golden as shown on figure 2.

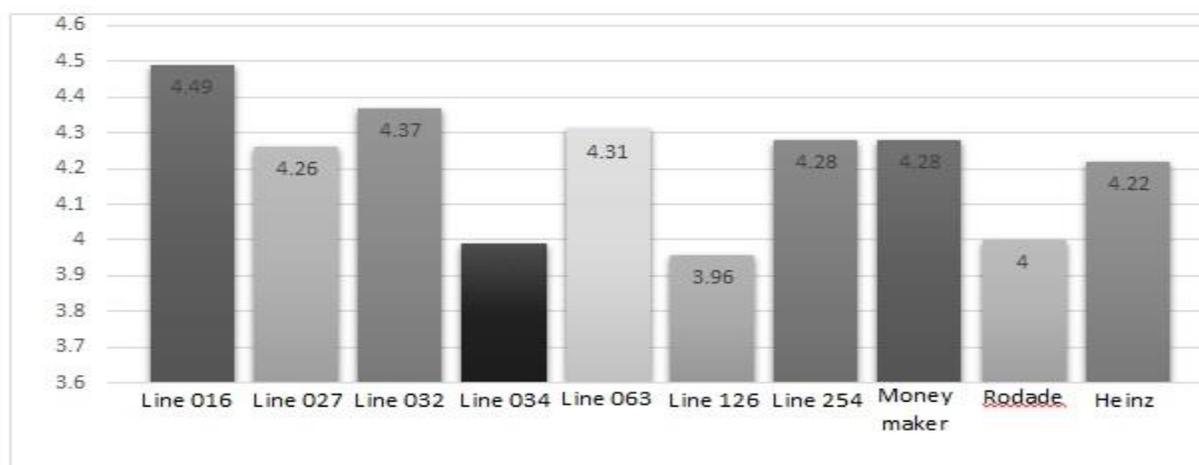


**Figure 2:** Diversity in fruit colour in cherry tomato germplasm evaluated in Zimbabwe

These results were in line with findings by Odour (2016) who studied 69 lines of Cherry tomato lines and established that 66 were red with only three being yellow.

**Fruit weight and size:** Cherry genotypes have relatively smaller weights per fruit with most lines weighing between 3.2 and 7.0 grams respectively, a direct product of fruit size (diameter and length). Line 034 recorded the highest fruit diameter of 22.1 mm against 18.7 mm for line 032 while fruit length ranged between 74 and 60.4 mm in cherry lines. Research results were agreeable to findings by Kumar (2018) who observed that there was wide variation in fruit diameter ranging between 16.3 and 41.7 mm yet fruit length ranged between 17.6 and 51.6 mm in Cherry tomato genotypes.

**Chemical composition:** Vitamin C content was greatest in genotypic line 254 with 35.2 mg whilst lines 016 and 063 recorded the lowest content each. These findings were in line with Salunkhe *et al.*, (1974) who concluded that some tomato genotypic lines contain an average of 35 mg/100 g of Vitamin C. Ascorbic acid (Vitamin C) is an important anti-oxidant which is protective to most diseases produced by reactive oxygen such as superoxide (Rawal *et al.*, 2016). Genotypes 126 and 034 recorded the highest acidity levels of 1.22% and 1.02% respectively. Low pH reduces the risk of pathogen growth in tomato thus delaying decay since micro-organisms that include *Bacillus coagulans* are completely growth inhibited at pH below 4.1 (Majid, 2007). Most cherry varieties had lower pH values (below 4.3) as shown on figure 3.



**Figure 3:** pH values for tomato genotypes evaluated in the characterization study

Results of lower pH values below 4.3 are most preferred because of their potential to reduce the risk of pathogenic growth of butyric, thermophilic and putrefactive anaerobic microorganisms were in line with conclusions by Salunkhe *et al.*, (1974).

#### **Genetic analysis of selected qualitative, quantitative traits and estimating genetic advance from the assemble germplasm**

Performances for each individual genotype were monitored, observed and recorded for further analysis. Descriptive

statistics generated from the ANOVA table through Genstat software were used in genetic analysis and estimate of genetic advance. Raw data from the ten randomly selected tomato plants from each genotypic line was subjected into GENSTAT (13th Edition) in order to carry out analysis of variances among traits. Coefficient of variation, Standard error of differences, Mean Square error, Standard error of means, Sum of squares, Grand mean were determined for further use. Table 3, show results on variances obtained.

Trait	Genetic Variance	GCV %	Phenotypic variance	PCV%	Environmental variance	ECV %	GCV/PCV Ratio	H <sup>2</sup>	GA	GA%
Branches	0.76	27.54	8.43	91.82	7.67	87.58	0.29	9.00	1.27	9.38
Yield g/plant	13.76	116.27	14.46	120.25	0.70	7.00	0.97	93.49	5.15	1.46
Clusters	24.89	157.76	25.44	159.50	0.88	29.66	0.99	97.84	6.98	29.83
50% Germination	0.09	9.50	0.18	13.50	0.09	9.49	0.70	49.53	0.42	5.41
Fruit Diameter	0.084	9.17	0.54	23.24	0.46	21.45	0.39	15.55	0.41	1.43
Fruit Length	2.91	53.98	6.49	80.57	3.58	59.83	0.67	44.89	2.39	3.00
Fruit weight	5.39	73.39	10.97	104.74	5.58	74.70	0.70	49.10	3.25	14.14
Fruits/plant	8.87	94.17	9.31	96.46	0.44	20.98	0.98	95.29	4.17	8.31
Open flowers	0.40	19.96	0.84	28.92	0.44	20.98	0.69	47.63	0.89	2.45
pH	10.16	100.8	20.32	203.2	10.16	100.00	0.50	50.00	4.46	1.00
Visible Fruits	0.43	20.81	1.78	42.22	1.35	13.50	0.49	24.28	0.92	2.07

**Table 3:-** Analysis of Variance for Quantitative Traits in Cherry Tomatoes

**Genotypic and phenotypic variance**

Genetic variance was found to be highly significant for most characters studied indicative of genetic differences. The number of plant branches scored 0.76, total clusters 24.89, fruit yield in grams per plant scored of 13.2, fruit weight 5.39, fruit pH 10.16 ahead of scores for open flowers and fruit diameter. These findings are in consonance with research results by Bhandari *et al.*, (2017) who concluded that fruit yield components had higher genetic variance. Heritability and higher genetic advance coupled with significantly positive correlation among the traits is considered key in selection when breeding (Ritongai *et al.*, 2018). Higher levels of genetic variance imply that there is high potential for crop improvement through breeding yet also the narrow difference obtained between genetic and phenotypic variance signify higher contribution of genetic components towards variability (Bhandari *et al.*, 2017). Higher GCV values were recorded for

such traits as the number of flower clusters per plant, yield in grams per plant, total harvested fruits per plant and fruit weight in the study. In this study, high PCV, GCV and genetic advance for yield per plant, number of fruits per plant were indicative of additive genetic effects and higher genetic variability in line with Savaranan *et al.*, (2019) and Kumar *et al.*, (2018).

**Heritability (H<sup>2</sup>) and Expected Genetic Advance (EGA):**

Clustering ability scored 97.84% ahead of total harvested fruits with 95.29% and fruit yield in grams per plant recording 93.49 % on broad sense heritability. Traits with higher heritability can be targeted for improvement through breeding techniques. The study find out that genotypic traits that included flower cluster numbers, fruit weight, number of branches per plant and total harvested fruits per plant were controlled by additive gene action since they recorded higher levels of both heritability and genetic advance as a per cent of mean (GAM). Traits for yield

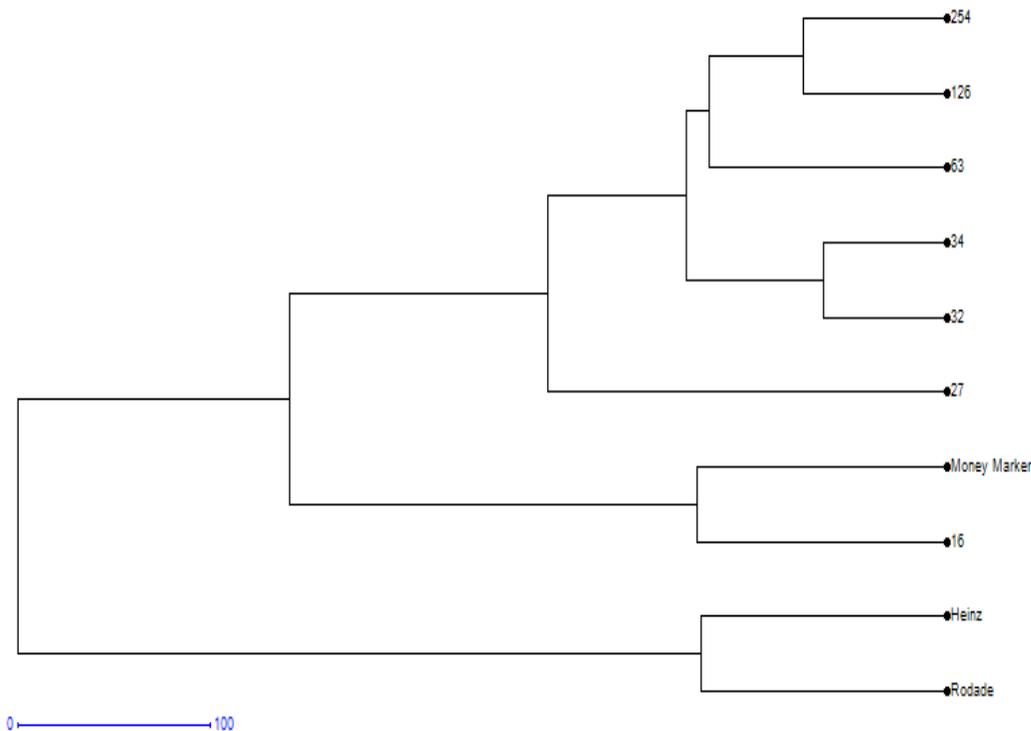
per plant, earliness to germination, fruit length and number of open flowers were controlled by non-additive gene action. Additivity effects meant that any additional gene enhances the expression of those specific traits and therefore selection is the most effective for additive variance. These results were in consonance with findings by Bhandari *et al.*, (2017); Saravanan *et al.*, (2019) and Tasisa *et al.*, (2018) who separately established that average fruit weight, number of branches, number of fruits per plant had both high heritability and high genetic advance.

**Environmental Coefficient of Variation:** Most of the yield traits had larger scores with yield per plant registering 116.12%, fruit length 53.98%, fruit weight 73.39%, total harvested fruits 94.17% and fruit clusters with above 100%.

The positive gap between genotypic and phenotypic coefficient of variation across traits in all genotypes explains the lesser influence of environment on the expression of individual traits findings also confirmed by Bhandari *et al.*, (2017).

**Cluster analysis for quantitative traits:**

The hierarchical cluster analysis performed to show the genetic relationship among the genotypes using a dendrogram constructed from genetic distance dissimilarity matrix (only bootstraps >50% (Figure 4). Of the ten tomato genotypes studied only two main heterotic groups were established. The first group had large fruits which included Heinz and Rodade while the second group with small fruits had eight genotypes being further subdivided into two distinct groups as shown on the dendrogram.



**Figure 4:** Dendrogram on Genetic diversity among ten tomato genotypes (7 cherry tomatoes and 3 commercial) based on UPGMA clustering of Euclidean similarity coefficient

## Conclusion

Therefore, the study shows that the intrinsic value in cherry tomato genotypes can be used as alternative in improving the genetic performance in commercial tomato breeding.

## References

1. Agarwal, S., and Rao, A. V. 2000. Tomato lycopene and its role in human health and chronic diseases, Canadian Medical Association Journal. 163(6), 23–26.
2. Anonymous. 2019. FAO Statistics, Food and Agriculture Organization of the United Nations, Rome, Italy.
3. Bai, Y. and Lindhout, P. 2007. Domestication and Breeding of Tomatoes: What have We Gained and What Can We Gain in the Future? Annals of Botany 100: 1085-1094.
4. Bhandari, H.R, Srivastava, K.S. and Reddy, G.E. 2017. Genetic Variability, Heritability and Genetic Advance for Yield Traits in Tomato (*Solanum lycopersicum* L.). International journal of Current Microbiology and Applied Sciences 6(7): 4131-4138. DOI: 10.20546/ijcmas.
5. Branthome, F. 2010. Trends in Tomato Products consumption compared to total Tomato consumption World Processing Tomato council (WPTC), Avignon, France.
6. Casals, J., Rivera, A., Sabat, J., Romero, R., and Sim, J. 2018. Cherry and Fresh Market Tomatoes: Differences in Chemical, Morphological, and Sensory Traits and Their Implications for Consumer Acceptance. Agronomy, volume 9 (1) 9.
7. Corrado, G. and Rao, R. 2017. Towards the genomic basis of local adaptation in Landraces. Diversity 9:1-12.
8. FAO, 2015. Running out of time, the Reduction of Women work burden in Agricultural production, Organization of United Nations (FAO) Rome.
9. FAO, 2019. Strategic analysis and intervention plan for fresh and industrial tomato in the Agro-Commodities Procurement Zone of the pilot Integrated Agro-Industrial Park in Central-Eastern Oromia, Ethiopia. ISBN 978-92-5-131710-5.
10. José, L. C., Vera-Guzman, A.M, Linares-Menéndez L.R., Carrillo-Rodríguez J. C., and Aquino-Bolaños, E.N. 2018. Agro-morphological Traits and Mineral Content in Tomato Accessions from El Salvador, Central America. Agronomy.
11. Kulus, D. 2018. Genetic resources and selected conservation methods of tomato. Journal of Applied Botany and Food Quality 91: 135-144.
12. Kumar, K., Sharma D., Singh, J., Sharma, T.K, Kurrey, V.K. and Minz R.R. 2018. Combining ability analysis for yield and quality traits in tomato (*Solanum lycopersicum* L.) Journal of Pharmacology and phytochemistry 7(6): 1002-1005

13. Kumar, R. Singh.,Srivastava, S.K. and Singh, R. K. 2015. Genetic variability and character association for yield and quality traits in tomato (*Lycopersicon esculentum*. Mill), Research and Education Developmet Society (REDS) 3 (1): 31-36.
14. Kumar, S., Chauhan MP, Tomar, A.and Kumar, R.K. 2018. Coeffiecient of variation (GCV and PCV), Heritability and genetic advance analysis for yield contributing characters in rice (*Oryza Sativa L.*) Journal of Pharmacognosy and Phytochemistry (7): 2161-216.
15. Majid, R. 2007. Genome Mapping and Molecular Breeding of Tomato. International Journal of Plant Genomics p.52
16. Mohamed, S.M, Ali, E.E., Mohamed, T.J. 2012. Study of heritability and genetic variability among different plant and fruit characters of tomato (*Solunum lycopersicum L.*) International Journal of Scientific and Technology 1(2): 55-58.
17. Odour, K.T. 2016. Agro-morphological and Nutritional characterisation of tomato landraces (*Lycopersicon species*) in Africa. Thesis.
18. Olaniyi, J. O., Akanbi, W.B., Adejumo, T.A. and Akande. O.G. 2010. Growth, Fruit yield and nutritional quality of tomato varieties. African Journal of Food Science 4(6), 398 – 402.
19. Peralta, I.E. and Spooner, D.M. 2006. Cherry improvement taxonomy: History, origin and early cultivation of Tomato. In Razdan, M and Matto, A. (Eds). Genetic Improvement of Solanaceous Crops Volume 2: Tomato, Science Publishers, Enfield, UK.
20. Rawal, R., Gautam, D.M., Gautam, I.M., Mishra, K., Hanson, A.A., Easdown, W., Huudges, J.A. and Keatinge, J.D.H. 2016. Fruit quality Characters of Tomato (*Solanum lycopersicum*) Genotypes, Differed by maturity stages. Conference Paper.
21. Renuka, D. M., Sadashiva, A. T., Kavita, B. T., Vijendrakumar, R. C., Hanumanthiah, M. R., Horticulture, C. and Karnataka, B. 2014. Evaluation of cherry tomato lines (*Solunum lycopersium var. cerasiforme*) for growth, yield and quality traits, Plant Archives.14 (1), 151–154.
22. Renuka, D. M., and Sadashiva, A. T. 2016. Heterosis for growth, yield and quality traits in Cherry Tomato (*Solunum lycopersicum var. cerasiforme*), Indian Institute of Horticultural Research (IIHR) 16(2), 654–658.
23. Ritongai, A.W., Chozin, M.A., Syukur, M. and Maharijaya A. 2018. Genetic variability, heritability, correlation, and path analysis in tomato (*Solanum lycopersicum*) under shading condition, Biological Journal of Biological Diversit. Volume 19 (4) : 1527-1531 DOI: 10.13057/biodiv/d190445.
24. Salunkhe, D.K., Jadhav, S.J. and Yu, M.H. 1974. Quality and Nutritional composition of Tomato fruit as

influenced by biochemical and Physiological changes.

Qualitus Plantarum. 24, 1/2: 85-113.

25. Saravanan, K.R, Vishnupriya, V., Prakash, M. and Anandan, R. 2019. Variability, Phytochemistry Heritability and Genetic Advance in tomato genotypes. Indian Journal Agriculture Research. 53(1) 2019: 92-95. DOI: 10.18805/IJARE.A-5030.
26. Tasisa, J., Mohammed, W., Hussien, S. and Kumar, V. 2018. Genetic Control of Inheritance of Fruit Quality Attributes in Tomato (*Solanum lycopersicum*) 7(2):120–128 Agriculture Research.
27. Tiwari, J. K. and Upadhyay, D. 2011. Correlation and path-coefficient studies in tomato
28. (*Lycopersicon esculentum Mill.*). Research Journal of Agriculture Science 2 (1): 63-68.
29. Venkadeswaran, E., Vethamoni, P.I., Arumugam, T., Manivannan, N. and Harish, S. 2018. Evaluation and selection of cherry tomato [*Solanum lycopersicum (L.) var. cerasiforme Mill.*] genotypes for growth and yield contributing characters. International Journal of Current Microbiology and Applied Sciences 7: 1155-1165.
30. Zanfini, A., Franchi, G. G., Massarelli, P., Corbini, G., and Dreassi, E. 2017. Phenolic compounds, carotenoids and antioxidant activity in five tomato (*Lycopersicon Esculentum mill*) cultivars. Ital Journal of Food Science 29, 90-4