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GENETIC VARIABILITY, CORRELATION AND PATH ANALYSIS IN TOMATO LEAF CURL VIRUS (ToLCV) RESISTANT ADVANCED BREEDING LINES OF TOMATO

Sampathkumar M.V.[1*], O. Sridevi[2], Sumangala Bhat[2] and P.V. Patil[3]
[1]Department of Genetics and Plant Breeding, University of Agricultural Sciences, Raichur – 584104, India
[2]Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad – 580005, India
[3]Department of Plant Pathology, University of Agricultural Sciences, Dharwad – 580005, India-
*Corresponding author E-mail: sampathkumar241999@gmail.com
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ABSTRACT

A field experiment was conducted during *Rabi* 2022 at the University of Agricultural Sciences, Dharwad, to assess genetic variability, trait associations and yield determinants in 47 advanced breeding lines resistant to Tomato Leaf Curl Virus (ToLCV), along with two commercial checks. The experiment was laid out in an alpha lattice design with three replications. High genotypic and phenotypic coefficients of variation were observed for number of fruits per plant (35.27% and 35.89%), number of clusters per plant (29.63% and 30.57%) and fruit yield per plant (24.04% and 25.47%), indicating substantial genetic variability. High heritability coupled with high genetic advance was recorded for number of fruits per plant (96.55% heritability and 71.40% GAM), clusters per plant (93.98% and 59.18%) and fruit yield (89.08% and 46.74%), suggesting predominance of additive gene action. Fruit yield showed significant positive correlations with number of fruits per plant (r = 0.743**), clusters per plant (r = 0.656**) and secondary branches (r = 0.287**). Path analysis revealed that number of fruits per plant exerted the highest direct effect (1.078) on yield, followed by average fruit weight (0.798). The results indicate that selection based on these traits would be effective for improving yield in ToLCV-resistant tomato breeding lines.

***Keywords* :** Advanced breeding lines, correlation, genetic variability, path analysis, ToLCV resistance, tomato.

Introduction

Tomato (*Solanum lycopersicum* L.), a member of the family Solanaceae (2n = 24), is one of the most economically important vegetable crops worldwide, valued for its nutritional quality, processing versatility and market demand (Rick, 1969). Despite continuous varietal development, tomato productivity is frequently constrained by biotic stresses, among which Tomato Leaf Curl Virus (ToLCV) is a major limiting factor in tropical and subtropical production systems. Breeding for ToLCV resistance using backcross breeding strategies enables the introgression of resistance genes into elite genetic backgrounds while retaining superior agronomic and yield attributes. However, yield in tomato is a complex quantitative trait governed by multiple interrelated component characters and strongly influenced by environmental factors (Kumar *et al.*, 2013; Ritonga *et al.*, 2018). Effective improvement of yield in ToLCV-resistant backgrounds requires a comprehensive understanding of genetic variability, heritability and interrelationships among yield and yield-related traits. Estimation of genetic parameters such as genotypic and phenotypic coefficients of variation, heritability and genetic advance provides insights into the nature and magnitude of inheritable variation and the potential response to selection (Burton and Devane, 1953; Johnson *et al.*, 1955). Correlation analysis elucidates the degree of association among traits (Al-Jibouri *et al.*, 1958), whereas path coefficient analysis partitions these relationships into direct and indirect effects, thereby identifying traits that exert the greatest influence on yield (Wright, 1921; Dewey and Lu, 1959). The present investigation was therefore undertaken to estimate genetic variability, character associations and path coefficients for yield and yield related traits in ToLCV-resistant advanced tomato breeding lines, with the objective of identifying effective selection criteria for yield improvement.

Materials and Methods

The experiment was conducted at the Botany Garden, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, during *Rabi* 2022. The experimental material comprised 49 genotypes, including 47 advanced breeding lines derived through backcross breeding for ToLCV resistance and two commercial checks (GPBT-8 and DMT-2 released from UAS, Dharwad). The trial was laid out in an alpha lattice design with three replications under open-field conditions. Each genotype was grown in a single row per replication, accommodating ten plants per row at a spacing of 60 cm × 60 cm. Observations were recorded on five randomly selected plants per genotype for the following traits: days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of clusters per plant, number of fruits per cluster, number of fruits per plant, average fruit weight (g), pericarp thickness (mm), total soluble solids (°Brix), number of locules per fruit, polar length of fruit (mm), equatorial length of fruit (mm), fruit shape index and fruit yield per plant (kg). Genotypic and phenotypic coefficients of variation were estimated following Burton and Devane (1953) and categorized as per Shivasubramanian and Menon (1973). Broad-sense heritability was calculated using the method of Weber and Moorthy (1952) and classified according to Robinson *et al.* (1949). Genetic advance and genetic advance as a percentage of mean were computed following Johnson *et al.* (1955). Phenotypic correlation coefficients were estimated following Al-Jibouri *et al.* (1958). Path coefficient analysis was performed by considering fruit yield per plant as the dependent variable, as proposed by Wright (1921) and Dewey and Lu (1959). Statistical analyses were performed using R software (version 4.3.1).

Results and Discussion

Genetic variability analysis for yield and yield attributing traits.

The success of crop improvement programme largely depends on the magnitude of genetic variability available in breeding populations. In the present study, substantial genetic variability was observed among the advanced breeding lines for most of the traits studied. High genotypic and phenotypic coefficients of variation were recorded for number of fruits per plant (GCV: 35.27%, PCV: 35.89%), number of clusters per plant (29.63%, 30.57%) and fruit yield per plant (24.04%, 25.47%), indicating the presence of considerable genetic variability. Similar findings have been reported in recent studies (Rasheed *et al.,* 2023; Singh *et al.,* 2025). For all traits, phenotypic coefficients of variation were marginally higher than corresponding genotypic coefficients, indicating limited environmental influence on trait expression, which is in agreement with earlier findings (Burton and Devane, 1953; Ritonga *et al.,* 2018). The narrow PCV-GCV gap for number of fruits per plant, number of clusters per plant, secondary branches per plant and fruit yield per plant suggests that these traits are predominantly governed by genetic factors and are amenable to effective phenotypic selection. High GCV and PCV values were recorded for number of fruits per plant, number of clusters per plant, plant height and fruit yield per plant, indicating the presence of substantial exploitable genetic variation in the backcross derived breeding lines. Moderate variability for primary branches per plant and average fruit weight suggests the availability of sufficient genetic diversity for selection, as also reported by Kumar *et al.* (2021) and Venkadeswaran *et al.* (2020) , whereas low variability for days to 50% flowering indicates limited scope for rapid improvement of earliness through simple selection. High heritability estimates were observed for number of fruits per plant (96.55%), clusters per plant (93.98%) and fruit yield per plant (89.08%). These traits also exhibited high genetic advance as percent of mean (71.40%, 59.18% and 46.74%, respectively), indicating predominance of additive gene action and effectiveness of direct selection (Johnson *et al.,* 1955; Robinson *et al.,* 1949). These findings are in agreement with earlier and recent reports (Saravanan *et al.,* 2019; Rasheed *et al.,* 2023). This combination strongly indicates the predominance of additive gene action and suggests that direct phenotypic selection in early generations would be effective for improving these traits in ToLCV-resistant backgrounds.

High heritability associated with low genetic advance, as observed for days to 50% flowering, implies a greater role of non-additive gene action and environmental influence. Improvement of such traits may therefore require heterosis breeding or selection in later generations. Plant height exhibited high heritability with moderate genetic advance, indicating the involvement of both additive and non-additive gene effects. Overall, the observed genetic variability confirms that the evaluated backcross derived advanced breeding lines constitute a valuable genetic resource for simultaneous improvement of yield and ToLCV resistance in tomato.

Association among yield and yield contributing traits

Fruit yield per plant exhibited strong positive and significant correlations with number of fruits per plant (r = 0.743**), number of clusters per plant (r = 0.656**) and number of secondary branches per plant (r = 0.287**). The strong association between fruit yield and number of fruits per plant indicates that fruit bearing capacity is a major determinant of yield performance in ToLCV-resistant tomato lines. Similar associations have been reported in recent studies (Kadyan *et al.,* 2023; Eppakayala *et al.,* 2025). Positive correlations between yield and number of clusters per plant and fruits per cluster further suggest that enhanced reproductive efficiency directly contributes to higher yield, which is consistent with findings of Maurya *et al.* (2020) and Rahimi *et al.* (2022). Conversely, a significant negative correlation was observed between number of fruits per plant and average fruit weight (r = -0.636**), indicating a trade-off between fruit number and fruit size, which is commonly observed in tomato (Kumar *et al.,* 2013). This indicates that balanced selection strategies are required to optimize both yield potential and market-preferred fruit size. Days to 50% flowering showed a significant negative correlation with number of fruits per cluster (r = -0.235**), suggesting that early flowering genotypes tend to produce more fruits per cluster which is advantageous for yield improvement and crop earliness. Plant height displayed mixed associations with yield-related traits, suggesting an indirect influence through plant architecture, as also reported by Sehgal and Kumar (2021). Collectively, the correlation analysis indicates that simultaneous selection for number of secondary branches per plant, number of clusters per plant, number of fruits per cluster, and number of fruits per plant would be effective for improving fruit yield in ToLCV-resistant tomato breeding lines.

Direct and indirect effects on fruit yield

Path coefficient analysis revealed that number of fruits per plant had the highest positive direct effect on yield (1.078), followed by average fruit weight (0.798), fruit shape index (0.725) and number of clusters per plant (0.190). These findings confirm this trait as the most critical selection criterion for yield improvement in the evaluated backcross derived lines. Similar results have been reported in recent studies (Suresh *et al.,* 2025; Ram Babu *et al.,* 2025). Although average fruit weight exhibited a strong positive direct effect, it showed a negative indirect effect *via* number of fruits per plant (-0.686), indicating a compensatory relationship between fruit size and number. Number of clusters per plant and number of fruits per cluster contributed both directly and indirectly to yield, primarily through their influence on number of fruits per plant, which is in line with earlier reports (Islam *et al.,* 2010; Sharma *et al.,* 2019). Days to 50% flowering and plant height exerted negative direct effects on yield, suggesting that delayed flowering and excessive vegetative growth may reduce yield, as also observed by Nevani and Sridevi (2021). The relatively low residual effect (0.28) indicates that the traits included in the path analysis explained a major proportion of the variability in fruit yield.

Conclusion

The present study demonstrated substantial genetic variability among ToLCV-resistant advanced tomato breeding lines derived through backcross breeding. High heritability coupled with high genetic advance for number of primary and secondary branches per plant, number of clusters per plant, number of fruits per plant, average fruit weight and fruit yield per plant indicates that these traits are predominantly governed by additive gene action and are amenable to effective phenotypic selection. Correlation and path coefficient analyses identified number of fruits per plant as the most influential trait affecting fruit yield, followed by average fruit weight and number of clusters per plant. Therefore, breeding strategies emphasizing these traits are expected to be most effective for improving yield in ToLCV-resistant tomato cultivars. The evaluated advanced breeding lines represent valuable genetic resources for the development of high-yielding, ToLCV-resistant tomato varieties, which is consistent with recent findings emphasizing the importance of such breeding materials.

Table 1: Mean, range and variability parameters for yield and yield attributing traits in advanced breeding lines of tomato.

Sl. No.	Character	Mean	Range		GCV	PCV	h^2 (%)	GA	GAM
			Min.	Max.					
1	Days to 50% flowering	48.22	44.00	56.00	5.01	5.59	80.48	4.47	9.27
2	Plant height(cm)	65.19	48.00	78.00	29.00	37.36	77.64	9.77	14.99
3	Number of primary branches	1.10	1.00	1.40	10.20	10.52	94.07	0.23	20.38

4	Number of secondary branches	5.53	3.60	8.00	12.76	13.60	88.01	1.36	24.66
5	Number of clusters per plant	16.24	7.80	32.00	29.63	30.57	93.98	9.60	59.18
6	Number of fruits per plant	41.99	20.20	94.00	35.27	35.89	96.55	29.98	71.40
7	Average fruit weight (g)	42.12	20.64	64.42	19.71	22.41	77.36	15.04	35.71
8	Fruit yield per plant (kg)	1.68	0.65	3.20	24.04	25.47	89.08	0.79	46.74

GCV: Genotypic coefficient of variation; PCV: Phenotypic coefficient of variation; GAM: Genetic advance as per cent of mean

Table 2: Phenotypic correlations among yield and yield attributing traits in advanced breeding lines of tomato

	DFF	PH	PB	SB	NC	NFC	NFP	AFW	FL	EL	FSI	LC	PT	TSS	YP
DFF	1	0.138	-0.134	0.069	0.054	-0.235**	-0.057	-0.04	0.105	-0.110	0.154	-0.232**	-0.262**	-0.090	-0.105
PH		1	-0.012	-0.040	0.042	-0.175*	0.054	0.099	0.146	-0.218**	0.280**	-0.256**	-0.152	0.003	0.130
PB			1	0.014	0.171*	-0.056	0.102	-0.135	0.055	-0.174*	0.172*	-0.182*	0.134	-0.107	0.018
SB				1	0.360**	0.306**	0.340**	-0.190*	-0.314**	-0.284**	-0.051	0.022	-0.055	0.080	0.287**
NC					1	0.236**	0.877**	-0.583**	0.042	-0.234**	0.185*	-0.309**	0.096	-0.048	0.656**
NFC						1	0.411**	-0.365**	-0.228**	-0.129	-0.091	-0.024	0.12	-0.11	0.250**
NFP							1	-0.636**	0.015	-0.185*	0.141	-0.264**	0.127	-0.083	0.743**
AFW								1	0.053	0.194*	-0.089	0.230**	-0.269**	0.285**	-0.006
FL									1	0.141	0.700**	-0.153	0.126	0.072	-0.010
EL										1	-0.601**	0.528**	0.059	0.060	-0.12
FSI											1	-0.486**	0.053	0.007	0.082
LC												1	0.015	0.208*	-0.167*
PT													1	0.250**	-0.071
TSS														1	0.088
YP															1

*, ** indicates significant at 5 per cent and 1 per cent level of probability, respectively.

DFF: Days to 50% flowering; PH: Plant height; PB: Primary branches; SB: Secondary branches; NC: Clusters per plant; NFC: Fruits per cluster; NFP: Fruits per plant; AFW: Average fruit weight; FL: Fruit length; EL: Equatorial length; FSI: Fruit shape index; LC: Locules per fruit; PT: Pericarp thickness; TSS: Total soluble solids; YP: Yield per plant

Table 3: Direct and indirect effects of different yield and yield attributing traits on yield in advanced breeding lines of tomato

	DFF	**PH**	**PB**	**SB**	**NC**	**NFC**	**NFP**	**AFW**	**FL**	**EL**	**FSI**	**LC**	**PT**	**TSS**	**YP**
DFF	**-0.052**	-0.002	0.002	-0.002	0.010	-0.006	-0.061	0.001	-0.068	-0.055	0.111	0.006	0.010	0.001	-0.105
PH	-0.007	**-0.018**	0.000	0.001	0.008	-0.005	0.059	0.079	-0.094	-0.108	0.202	0.007	0.005	0.000	0.130
PB	0.007	0.000	**-0.018**	0.000	0.033	-0.001	0.110	-0.108	-0.035	-0.086	0.116	0.005	-0.004	0.002	0.020
SB	-0.004	0.001	0.000	**-0.028**	0.068	0.008	0.367	-0.152	0.202	-0.140	-0.036	-0.001	0.002	-0.001	0.286**
NC	-0.003	-0.001	-0.003	-0.010	**0.190**	0.006	0.945	-0.466	-0.027	-0.115	0.134	0.008	-0.004	0.001	0.656**
NFC	0.012	0.003	0.001	-0.009	0.045	**0.026**	0.443	-0.292	0.148	-0.064	-0.062	0.001	-0.005	0.002	0.250**
NFP	0.003	-0.001	-0.002	-0.009	0.167	0.011	**1.078**	-0.508	-0.010	-0.091	0.102	0.007	-0.005	0.001	0.743**
AFW	0.000	-0.002	0.002	0.005	-0.111	-0.010	-0.686	**0.798**	-0.034	0.096	-0.065	-0.006	0.010	-0.004	-0.006
FL	-0.005	-0.003	-0.001	0.009	0.008	-0.006	0.016	0.043	**-0.643**	0.070	0.503	0.004	-0.005	-0.001	-0.011
EL	0.006	0.004	0.003	0.008	-0.044	-0.003	-0.199	0.155	-0.091	**0.493**	-0.434	-0.014	-0.002	-0.001	-0.121
FSI	-0.008	-0.005	-0.003	0.001	0.035	-0.002	0.152	-0.072	-0.450	-0.298	**0.725**	0.013	-0.003	0.000	0.087
LC	0.012	0.005	0.003	-0.001	-0.059	-0.001	-0.285	0.184	0.098	0.260	-0.351	**-0.027**	-0.001	-0.003	-0.166
PT	0.014	0.003	-0.002	0.001	0.019	0.003	0.137	-0.214	-0.084	0.027	0.053	-0.001	**-0.035**	-0.004	-0.083
TSS	0.005	0.000	0.002	-0.002	-0.009	-0.003	-0.089	0.228	-0.046	0.030	0.000	-0.006	-0.009	**-0.015**	0.086

Diagonal values indicate direct effects, off-diagonal value- indirect effect

Residual =0.28

DFF: Days to 50% flowering; PH: Plant height; PB: Primary branches; SB: Secondary branches; NC: Clusters per plant; NFC: Fruits per cluster; NFP: Fruits per plant; AFW: Average fruit weight; FL: Fruit length; EL: Equatorial length; FSI: Fruit shape index; LC: Locules per fruit; PT: Pericarp thickness; TSS: Total soluble solids; YP: Yield per plant

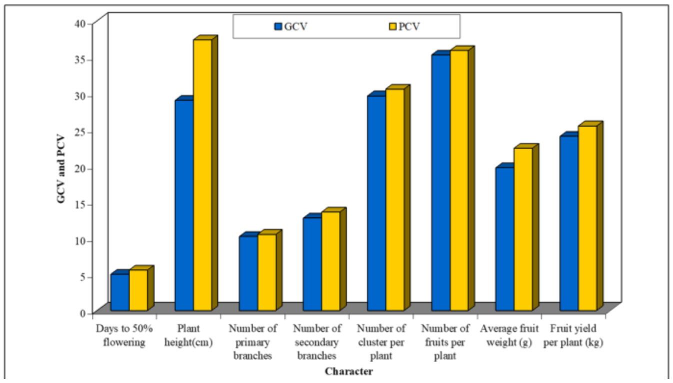

Fig. 1: GCV and PCV for yield and yield attributing traits in of advanced breeding lines of tomato

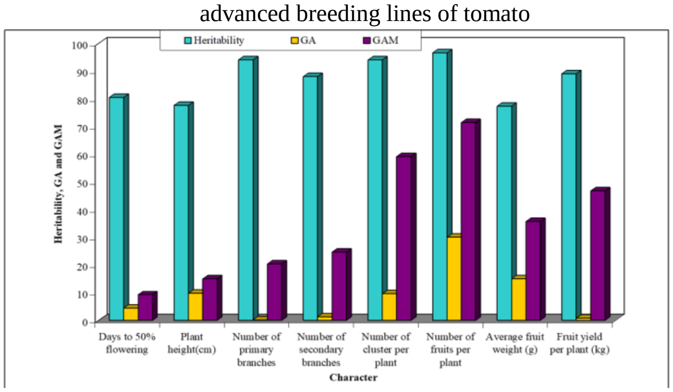

Fig. 2: Heritability, GA and GAM for yield and yield attributing traits in of advanced breeding lines of tomato

References

Al-Jibouri, H. A., Miller, P. A. and Robinson, H. V. (1958). Genotypic and environmental variances and covariances in upland cotton cross of interspecific origin. *Agronomy Journal*, **50**, 633–636.

Badge, S., Parate, S. R. and Ganvir, G. B. (2021). Correlation and path analysis studies for yield and quality traits in tomato (*Solanum lycopersicum* L.). *International Journal of Current Microbiology and Applied Sciences*, **10**(6), 144–151.

Burton, G. W. and Devane, E. M. (1953). Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*, **45**, 478–481.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal*, **51**(9), 515–518.

Eppakayala, K., Pidigam, S., Natarajan, S., Amarapalli, G. and Reddy, K. R. (2025). Correlation and path coefficient analysis studies in tomato germplasm (*Solanum lycopersicum* L.). *International Agronomy Journal*, **8**(12).

Heliyon. (2023). Exploring genotypic variability and interrelationships among growth, yield and quality traits in tomato genotypes. *Heliyon*, 18958.

Islam, B. M. R., Ivy, N. A., Rasul, M. G. and Zakaria, M. (2010). Character association and path analysis of exotic tomato (*Solanum lycopersicum* L.) genotypes. *Bangladesh Journal of Plant Breeding and Genetics*, **23**(1), 13–18.

Ismail, A. A., Khalifa, M. A. and Hamam, K. A. (2001). Genetic studies on some yield traits of durum wheat. *Asian Journal of Agricultural Science*, **32**, 103–120.

Johnson, H. W., Robinson, H. F. and Comstock, R. E. (1955). Estimates of genetic and environmental variability in soybean. *Agronomy Journal*, **47**(7), 314–318.

Kadyan, D., Srivastav, P., Kumar, J. and Singh, H. (2023). Genetic variability, correlation and path coefficient analysis in tomato (*Solanum lycopersicum* L.). *The Pharma Innovation Journal*, **12**(8), 2325–2329.

Kumar, D., Kashyap, A., Dogra, B. S., Sharma, D., Kumar, S., Shiwani, K., Chauhan, A. and Chandel, V. G. S. (2021). Diversity and association studies in various yield and quality traits in tomato (*Solanum lycopersicum* L.). *International Journal of Chemical Studies*, **9**(2), 873–879.

Kumar, D., Kumar, R., Kumar, S., Bhardwaj, M. L., Thakur, M. C., Thakur, K. S., Dogra, B. S., Vikram, A., Thakur, A. and Kumar, P. (2013). Genetic variability, correlation and path coefficient analysis in tomato. *International Journal of Vegetable Science*, **19**, 313–323.

Kumar, P. and Shukla, R. S. (2002). Genetic analysis for yield and its attributed traits in bread wheat under various situations. *JNKVV Research Journal*, **36**, 95–97.

Maurya, R. K., Singh, A. K. and Sai, A. (2020). Correlation and path analysis in tomato (*Solanum lycopersicum* L.) for yield and yield contributing traits. *Journal of Pharmacognosy and Phytochemistry*, **9**(3), 1684–1687.

Nevani, S. and Sridevi, O. (2021). Correlation and path coefficient analysis in tomato (*Solanum lycopersicum* L.). *Journal of Pharma Innovation*, **10**(7), 1522–1525.

Rahimi, S., Singh, B., Alam, K., Kumar, V. and Ahmad, M. (2022). Estimation of correlation and path coefficient studies in tomato (*Lycopersicon esculentum* Mill.). *Annals of Horticulture*, **15**(1), 102–107.

Ram Babu, D., Narigapalli, P., Hussain, Z., Singh, P. K., Lata, S. and Joshi, A. (2025). Dissecting genetic variability and trait interactions underlying yield improvement in tomato (*Solanum lycopersicum* L.). *International Agronomy Journal*, **8**(11).

Rasheed, A., Ilyas, M., Khan, T. N., Mahmood, A., Riaz, U., Chattha, M. B., Hassan, M. U., Wu, Z. and Qari, S. H. (2023). Study of genetic variability, heritability and genetic advance for yield-related traits in tomato (*Solanum lycopersicum* L.). *Frontiers in Genetics*, **13**, 1030309.

Rick, C. M. (1969). Origin of cultivated tomato: Current status of the problem. *Abstract XI*.

Ritonga, A. W., Chozin, M. A., Syukur, M., Maharijaya, A. and Sobir, S. (2018). Genetic variability, heritability, correlation, and path analysis in tomato (*Solanum lycopersicum*) under shading condition. *Biodiversitas Journal of Biological Diversity*, **19**(4), 1527–1531.

Robinson, H. F., Comstock, R. E. and Harvey, V. H. (1949). Estimates of heritability and degree of dominance in corn. *Agronomy Journal*, **41**, 353–359.

Saravanan, K. R., Vishnupriya, V., Prakash, M. and Anandan, R. (2019). Variability, heritability and genetic advance in tomato genotypes. *Indian Journal of Agricultural Research*, **53**(1), 92–95.

Sehgal, N. and Kumar, S. (2021). Variability and trait association analyses in bacterial wilt resistant genotypes of tomato (*Solanum lycopersicum* L.) under mid-hill conditions of Himachal Pradesh. *Indian Journal of Experimental Biology*, **59**(9), 617–625.

Sharma, P., Dhillon, N. S., Kumar, V. and Kumar, P. (2019). Correlation and path analysis for yield and its contributing traits in tomato (*Solanum lycopersicum* L.) under protected environment. *Journal of Pharmacognosy and Phytochemistry*, **8**(1), 447–450.

Shivasubramanian, S. and Menon, N. (1973). Heterosis and inbreeding depression in rice. *Madras Agricultural Journal*, **60**, 1139–1144.

Singh, A. P., Ram, C. N., Singh, A. K., Singh, N., Shukla, H. and Paswan, S. (2025). Genetic evaluation for variability, heritability and genetic advance in tomato (*Solanum lycopersicum* L.) genotypes. *International Journal of Agricultural Biochemistry*, **9**(7), 1–6.

Suresh, G. S. P., Evoor, S., Fakrudin, B., Jawadagi, R., Basavarajappa, M. P. and Vinaykumar, M. M. (2025). Correlation and path coefficient analysis in tomato genotypes for yield and quality traits. *Plant Cell Biotechnology and Molecular Biology*, **26**, 290–299.

Venkadeswaran, E., Vethamoni, P. I., Arumugam, T., Manivannan, N., Harish, S., Rani, E. A. and Sujatha, R. (2020). Genetic variability studies in cherry tomato [*Solanum lycopersicum* (L.) var. *cerasiforme* Mill.] for growth, yield and quality. *Electronic Journal of Plant Breeding*, **11**(4), 1222–1226.

Weber, C. R. and Moorthy, H. R. (1952). Heritable and non-heritable relationship and variability of oil content and agronomic characters in the F2 generation of soybean crosses. *Agronomy Journal*, **44**, 202–209.

Wright, S. (1921). Correlation and causation. *Journal of Agricultural Research*, **20**, 202–209.