



RESEARCH ARTICLE

Assessment of genetic variability and multivariate analysis for yield and quality improvement in an interspecific F_2 population of tomato (*Solanum lycopersicum* L.) under high-temperature stress

Agalya P¹, Vijai Selvaraj K S^{2*}, Beulah A³, Manikanda Boopathi N⁴, Bharathi A⁵ & Gurusamy K⁶

¹Department of Vegetable Science, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

²Department of Horticulture, Dr. M S Swaminathan Agricultural College and Research Institute Eachangottai, Thanjavur 614 902, Tamil Nadu, India

³Department of Post-harvest Technology, Horticultural College and Research Institute, Periyakulam 625 604, Tamil Nadu, India

⁴Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

⁵Department of Plant Breeding and Genetics Dr. M S Swaminathan Agricultural College and Research Institute Eachangottai, Thanjavur 614 902, Tamil Nadu, India

⁶Department of Food Process Engineering, Tamil Nadu Agricultural University, Coimbatore 641 003, Tamil Nadu, India

*Correspondence email - kshivajyselvaraj@tnau.ac.in

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Abstract

Heat stress is one of the major abiotic constraints limiting the productivity of tomato, especially at the reproductive stage. An interspecific F_2 population developed from the cross PKM 1 $\times$ *Solanum pimpinellifolium* L. was evaluated at the Vegetable Research Station, Palur, Tamil Nadu, India, to identify important traits associated with yield improvement under high temperature conditions. The population was evaluated for yield, physiological and quality traits through analyses of genetic variability, correlation, path coefficient and principal component analysis (PCA). Results indicated considerable genetic variability among the segregants; high heritability along with high genetic advance (GA) revealed the dominance of additive gene action, indicating the efficacy of direct phenotypic selection. The major determinants of fruit yield under heat stress were fruit weight (FW), fruit set percentage (FS), number of clusters per plant (NCP) and number of fruits per plant (NFP), as revealed by correlation and path coefficient analyses. Principal component analysis is an efficient method which revealed extensive genetic diversity and identified promising segregants with superior yield and heat tolerance. These results provide useful selection criteria and genetic resources for developing high-yielding, heat-tolerant tomato varieties adapted to future climate scenarios.

Keywords: correlation; fruit yield; genetic variability; heat stress; path coefficient analysis; principal component analysis; *Solanum pimpinellifolium*

Introduction

Tomato (*Solanum lycopersicum* L.) is one among the globally significant horticultural crops, which serves as a cornerstone of food security, nutrition and agricultural economies worldwide. Its cultivation spans diverse agro-climatic zones, underpinning both subsistence farming and large-scale commercial production. Global tomato production reached an impressive 186.1 million tonnes, harvested from approximately 4.97 million hectares (ha) of land, which translates to an average global productivity of 37.84 tonnes per ha(1).

This immense scale of production underscores its critical role in human diets, valued for its rich content of vitamins (notably vitamin C and provitamin A), minerals and potent antioxidants like lycopene, which are linked to numerous health benefits. However, global productivity is highly uneven, with significant regional disparities that highlight substantial yield gaps. For instance, India, the world's second-largest tomato producer, produced

20.425 million tonnes from 0.845 million ha during 2022–23, with an average productivity of 24.18 t ha⁻¹. This productivity remains well below the yield potential of > 60 t ha⁻¹ achievable under improved genetic, agronomic and environmental management practices (2).

This persistent yield gap is a major concern for agricultural scientists and policymakers, as it represents a significant loss in potential food and economic output. A primary driver of this yield gap, particularly in tropical and subtropical regions where much of the world's population resides, is the escalating threat of abiotic stresses, with heat stress emerging as a critical constraint intensified by anthropogenic climate change. Tomato is a thermosensitive crop, especially during its reproductive phase. Temperatures consistently exceeding 30 °C can severely disrupt key physiological processes, including pollen viability, stigma receptivity and ovule development, leading to poor pollination, flower and fruit abortion and ultimately, drastically reduced fruit setting and yield (3, 4). Projections from the Intergovernmental Panel on Climate Change (IPCC) and national agricultural research bodies, such as the Indian

Council of Agricultural Research (ICAR), indicate a continued rise in mean temperatures, with forecasts suggesting a 1.5–2.0 °C increase across major Indian tomato-growing regions by 2050. This trajectory poses an existential threat to stable tomato production, necessitating urgent and innovative breeding strategies to develop cultivars with enhanced resilience to high-temperature environments.

Conventional breeding has made significant strides, but the genetic base of modern cultivated tomatoes is relatively narrow due to historical domestication bottlenecks. To overcome this limitation and access a broader spectrum of adaptive traits, plant breeders have increasingly turned to wild relatives of *S. lycopersicum*. Among these, *Solanum pimpinellifolium* L., the putative progenitor of the cultivated tomato, is a particularly valuable genetic resource. Native to the arid coastal regions of Peru and Ecuador, *S. pimpinellifolium* has evolved under harsh environmental conditions and consequently possesses a remarkable array of beneficial traits, including exceptional tolerance to multiple abiotic stresses such as heat, drought and salinity as well as unique fruit quality attributes (5, 6).

The use of interspecific hybridisation between elite cultivated lines and *S. pimpinellifolium* offers a powerful avenue to introgress these critical adaptive genes into high-yielding backgrounds. Although *S. pimpinellifolium* is widely recognised as a valuable donor of heat tolerance in tomato breeding, most previous studies have focused mainly on germplasm screening, physiological characterisation, quantitative trait locus (QTL) mapping or development of advanced breeding populations. However, knowledge of the genetic architecture of yield, physiological and quality traits in segregating interspecific F_2 populations under natural high temperature stress in the field is still limited. The present study contributes to the existing knowledge by integrating genetic variability, heritability, correlation, path coefficient and principal component analyses (PCA) in a single interspecific F_2 population derived from PKM 1 $\times$ *S. pimpinellifolium*. This comprehensive strategy identifies key selection traits and superior segregants for simultaneous improvement of heat tolerance, yield and fruit quality, thus providing practical selection criteria for early-generation tomato breeding under high-temperature environments. This approach is designed to identify key selection indices and promising genotypes that combine high yield potential with the robust heat tolerance inherited from its wild ancestor, thereby contributing to the development of next-generation tomato varieties capable of sustaining productivity in a warming world.

Materials and methods

The reported work was undertaken at Vegetable Research Station, Palur, Cuddalore at 11°44'49" N latitude and 79°38'10" E longitude. The details of parent lines are mentioned in Table 1 and weather

parameters have been given in Supplementary Fig. 1.

Screening of tomato F_2 population for high temperature tolerance under field condition

An initial evaluation was conducted to screen the F_2 population of the cross PKM 1 $\times$ *S. pimpinellifolium* to identify the heat-tolerant F_2 population during the summer season of 2025 (February–May). The population was established at a spacing of 75 $\times$ 40 cm under field conditions and evaluated as an unreplicated early-generation breeding population, as each plant represented an individual segregant, making replicated evaluation impractical at this stage. To reduce environmental variance, all plants were cultivated under consistent agronomic conditions and exposed to the same natural high-temperature conditions ranging between 32–38 °C and observations were recorded on each individual F_2 plant. The primary objective of the evaluation was to identify superior segregants for advancement rather than to compare replicated genotypes. All 200 plants were considered as individual experimental units for trait evaluation and all suggested crop management measures were evenly applied throughout the cropping period. Twenty-two qualitative and quantitative traits encompassing vegetative growth, flowering behaviour, yield, quality and physiological attributes were evaluated, including plant height (PH), primary and secondary branches (SB), days to first flowering (DFF), days to 50 % flowering (DFPF), number of flowers per truss (NFT), number of fruits per cluster (NFC), number of clusters per plant (NCP), number of fruits per plant (NFP), average fruit weight (FW), fruit set percentage (FS), fruit yield per plant (FYP), total soluble solids (TSS), titratable acidity, total phenols, ascorbic acid, proline content, pollen viability, style protrusion, chlorophyll content, relative water content and electrolyte leakage. The parental lines PKM 1, *S. pimpinellifolium* and check variety Arka vikas together were also grown alongside the F_2 population under the same environmental conditions to facilitate comparison of trait expression and assessment of segregation patterns in the progeny population.

Statistical analysis

Statistical analyses were performed for twenty-two yield, quality and physiological characters to evaluate genetic variability characteristics, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance (GA) percent mean.

The estimates of GCV and CV were computed following the standard methodology (7).

$$GCV = \sqrt{\frac{\text{Genotypic variance}}{\text{Grand mean}}} \times 100$$

Table 1. Characteristic features of parental lines

Parents	Traits
PKM 1	PKM 1, a tomato variety with green shoulders created through induced mutagenesis from the indigenous cultivar Annanji, is developed and released by the Horticultural College and Research Institute, Periyakulam, Tamil Nadu Agricultural University. It is known for its high yield potential of 30–35 tonnes per hectare, as well as its adaptability to long-distance transportation and commercial marketing.
<i>Solanum pimpinellifolium</i>	<i>Solanum pimpinellifolium</i> regarded as the ancient wild relative of cultivated tomato, serves as a valuable genetic resource in tomato improvement programmes. Owing to its exceptional tolerance to abiotic stresses including heat, drought, salt and distinctive fruit quality attributes, particularly intense flavour. <i>Solanum pimpinellifolium</i> has been extensively utilised as a donor parent for the introgression of beneficial traits in modern tomato breeding strategies.

$$PCV = \sqrt{\frac{\text{Phenotypic variance}}{\text{Grand Mean}}} \times 100$$

Based on the classification, variability estimates were categorised as high when exceeding 20 %, moderate when ranging from 10–20 % and low when below 10 % (8).

Broad-sense heritability (h^2) was assessed by expressing genotypic variance as a fraction of total phenotypic variance according to the procedures and the estimates were expressed in percentage (9, 10).

$$\text{Heritability in broad sense } h^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

Heritability values are classified as high (> 60 %), moderate (30–60 %) or low (< 30 %) by which GA is computed (11).

Genetic advance (GA) was calculated by the following methodology (12).

$$GA = \frac{\sigma_g^2}{\sigma_p^2} \times k \times \sqrt{\sigma_p^2}$$

Where,

K = where the selection differential was considered as 2.06 at 5 % selection level

σ_g^2 = genetic variance

σ_p^2 = phenotypic variance

The GA expressed as percent of the population mean, was calculated (10).

$$GA \text{ as percent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

Genetic advance was classified according to the criteria proposed by early researchers (10).

Low	<10 %
Medium	10–20 %
High	>20 %

In addition, simple correlation coefficients among the studied traits were estimated by following the standard procedure (13). Pearson's correlation coefficients were tested for significance at the 5 % ($p < 0.05$) and 1 % ($p < 0.01$) probability levels. Significance levels are presented in the correlation matrix. Path analysis was carried out to partition the direct indirect component traits on yield and principal component was also analysed (14). The OPSTAT software and the R-based online package GRAPES were used to investigate correlation coefficients, path analysis and genetic variability.

Results and Discussion

Genetic variability studies

The assessment of genetic variability is fundamental for understanding the extent of variation present in a population and for predicting the effectiveness of selection in crop improvement programmes. In the present study, genetic variability parameters were estimated for twenty-two yield, physiological and quality traits to evaluate the scope for selection and genetic improvement. The calculated estimates of PCV, GCV, h^2 and genetic advance expressed

as a percent of the mean (GAM) are presented in Table 2 and their distribution is illustrated in Fig. 1. For all traits studied, PCV exceeded GCV, reflecting the contribution of environmental factors to the observed variability. Nevertheless, small differences between GCV and PCV for most traits indicate that environmental influence was relatively low and that genetic factors accounted for most of the variation. Comparable findings were reported in previous studies (15).

Elevated values of both PCV and GCV were recorded for SB (29.40 % and 22.49 % respectively), FW (28.05 % and 22.30 % respectively), NFP (24.47 % and 18.75 % respectively), FYP (21.81 % and 19.35 % respectively) and primary branches per plant (20.45 % and 8.36 % respectively). The high magnitude of variability observed for these traits indicates the existence of considerable genetic variation within the population and suggests significant scope for improvement through direct phenotypic selection. Similar results were previously recorded (16).

Moderate estimates of PCV and GCV were observed for NCP (15.58 % and 7.98 % respectively), electrolyte leakage (15.77 % and 8.79 % respectively), total phenols (14.02 % and 9.69 % respectively), style protrusion percentage (11.85 % and 9.04 % respectively), titratable acidity (11.66 % and 5.60 % respectively), pollen viability (11.51 % and 10.20 % respectively) and NFC (10.96 % and 10.25 % respectively). The moderate variability exhibited by these traits indicates the existence of exploitable genetic variation, although selection efficiency may be comparatively lower than that of highly variable traits (17).

Table 2. Genetic variability parameters for yield and related traits in the F_2 population of PKM 1 $\times$ *Solanum pimpinellifolium*

	PCV (%)	GCV (%)	Heritability	Genetic advance (%) (i = 5 %)
PH	9.73	7.01	52.00	10.42
DFF	7.44	4.49	36.40	5.59
PB	20.44	8.36	16.70	7.05
SB	29.40	22.49	58.50	35.43
DFFP	6.75	3.44	26.00	3.61
NFT	7.08	6.46	83.30	12.15
NFC	10.96	10.25	87.40	19.73
NCP	15.58	7.98	26.20	8.42
NFP	24.47	18.75	58.70	29.58
FW	28.05	22.30	63.20	36.51
FS	8.73	7.71	78.00	14.02
TSS	8.64	5.75	44.30	7.88
AA	10.86	6.61	37.10	8.29
TA	11.66	5.60	23.10	5.54
TP	14.02	9.69	47.70	13.79
PC	7.87	7.45	89.70	14.54
PV	11.51	10.20	78.50	18.61
SP	11.85	9.04	58.30	14.22
CC	7.60	6.96	83.90	13.12
RWC	6.78	3.74	30.50	4.25
EL	15.77	8.79	31.10	10.09
FYP	21.82	19.35	78.70	35.36

PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFFP: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids (°Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (μg/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

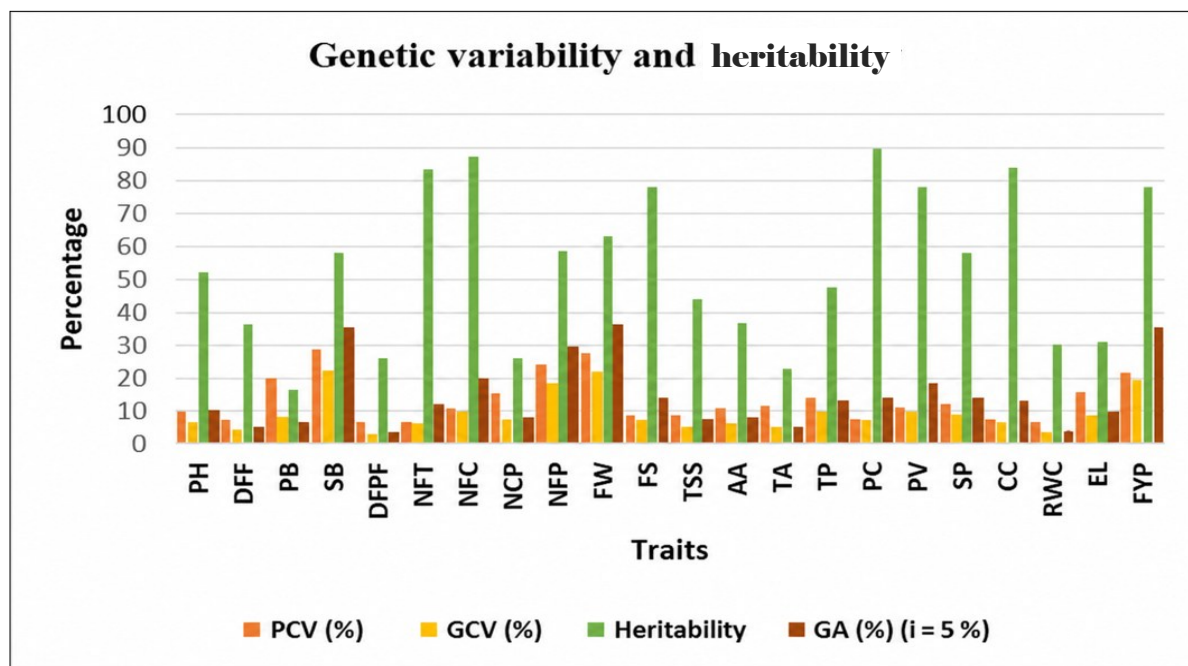


Fig. 1. Histogram of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad sense heritability (h^2) and genetic advance (GA) as per cent of mean. PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids ($^{\circ}$ Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (μ g/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

Low PCV and GCV values were recorded for PH (9.73 % and 7.01 % respectively), FS (8.73 % and 7.71 % respectively), TSS (8.64 % and 5.75 % respectively), proline content (7.87 % and 7.45 % respectively), chlorophyll content (7.60 % and 6.96 % respectively), DFF (7.44 % and 4.49 % respectively), NFT (7.11 % and 6.46 % respectively), relative water content (6.78 % and 3.74 % respectively) and DFPF (6.75 % and 3.44 % respectively). The low magnitude of variability for these traits indicates a relatively narrow genetic base and comparatively limited opportunity for improvement through selection. Similar observations were previously reported who also recorded low PCV and GCV for flowering in tomato and attributed them to restricted genetic variability, thereby limiting the effectiveness of phenotypic selection (18). Among the physiological traits, chlorophyll content and relative water content are important indicators of heat stress tolerance. Maintenance of higher chlorophyll under high temperature helps sustain photosynthetic efficiency and assimilate production, thereby supporting plant growth and fruit development. Likewise, higher relative water content reflects the ability of plants to maintain cellular hydration and turgor under heat stress, contributing to improved flowering, fruit set and yield. Although electrolyte leakage exhibited moderate variability, it is an important indicator of membrane stability under heat stress, where low electrolyte leakage reduces membrane damage and maintains cellular integrity. Therefore, these traits complement the yield-related traits and can serve as valuable selection criteria for identifying heat-tolerant tomato genotypes for breeding programmes.

Broad-sense heritability estimates varied considerably among the traits studied. High heritability was observed for proline content (89.7 %), NFC (87.4 %), chlorophyll content (83.9 %), NFT (83.3 %), FYP (78.7 %), pollen viability (78.5 %), FS (78.0 %) and FW (68.2 %). High heritability implies that most of the phenotypic variation arises from genetic rather than environmental effects. This agrees with previous studies (18–22). Heritability estimates derived

from a single-season, single-location F_2 population should be interpreted cautiously, as genotype $\times$ environment interactions could not be partitioned and may influence the magnitude of the estimates.

Genetic advance expressed as a percent of the mean (GAM) provides additional information regarding the nature of gene action governing trait inheritance. High GAM values were recorded for FW (36.50 %), SB per plant (35.43 %), FY per plant (35.35 %) and NFP (29.58 %). These traits have significant genetic variability and are likely to respond favourably to selection because of their high heritability and high GA. However, as h^2 includes additive, dominant and epistatic genetic effects, it cannot be utilised to conclusively determine the underlying gene action because the estimations were derived from an F_2 population. Therefore, regardless of the form of gene action, these qualities should be considered desirable targets for selection; however, assessment in advanced generations and in various contexts will be necessary to corroborate the genetic basis.

In general, the findings reveal considerable genetic variation for several economically important traits, particularly FYP, FW, NFP and branching characteristics. High estimates of heritability and significant GA observed for key yield-related traits indicate strong prospects for genetic improvement through selection in the studied population.

Correlation analysis

Correlation analysis is a useful statistical technique for assessing the magnitude and nature of associations among traits and for identifying the characters that contribute most effectively to yield improvement. The association among yield, physiological and quality traits was assessed through the correlation analysis. Fruit yield per plant was considered as the dependent variable and the results are summarised in Table 3 and correlogram displaying the correlation coefficients of yield, quality and physiological traits are depicted in Fig. 2.

Table 3. Correlation coefficients among growth, yield, quality and physiological parameters in the F₂ population of PKM 1 × *Solanum pimpinellifolium*

	PH	DFF	PB	SB	DFPF	NFT	NFC	NCP	NFP	FW	FS	TSS	AA	TA	TP	PC	PV	SP	CC	RWC	EL	FYP
PH	1	-0.684	0.668	0.536	-0.656	-0.096	0.7	0.626	0.649	0.633	0.807	0.534	0.456	0.556	0.497	0.485	0.431	-0.633	0.623	0.535	-0.455	0.873
DFF	-0.684	1	-0.607	-0.441	0.959	0.125	-0.508	-0.462	-0.499	-0.639	-0.614	-0.411	-0.386	-0.349	-0.387	-0.346	-0.358	0.548	-0.471	-0.444	0.27	-0.743
PB	0.668	-0.607	1	0.445	-0.569	-0.073	0.51	0.537	0.56	0.595	0.586	0.433	0.346	0.468	0.334	0.344	0.305	-0.489	0.5	0.478	-0.302	0.744
SB	0.536	-0.441	0.445	1	-0.459	-0.066	0.405	0.369	0.445	0.364	0.461	0.365	0.352	0.434	0.357	0.335	0.189	-0.537	0.307	0.362	-0.27	0.553
DFPF	-0.656	0.959	-0.569	-0.459	1	0.104	-0.489	-0.441	-0.483	-0.6	-0.58	-0.362	-0.364	-0.31	-0.373	-0.354	-0.344	0.527	-0.438	-0.435	0.279	-0.706
NFT	-0.096	0.125	-0.073	-0.066	0.104	1	0.388	-0.049	0.205	-0.321	-0.212	0.112	-0.028	0.073	0.034	-0.066	0.119	0.036	0.087	0.079	-0.074	-0.158
NFC	0.7	-0.508	0.51	0.405	-0.489	0.388	1	0.455	0.704	0.377	0.813	0.476	0.4	0.562	0.428	0.364	0.361	-0.508	0.548	0.506	-0.432	0.725
NCP	0.626	-0.462	0.537	0.369	-0.441	-0.049	0.455	1	0.762	0.183	0.524	0.363	0.393	0.527	0.44	0.323	0.426	-0.516	0.478	0.445	-0.387	0.627
NFP	0.649	-0.499	0.56	0.445	-0.483	0.205	0.704	0.762	1	0.116	0.62	0.452	0.391	0.52	0.427	0.345	0.442	-0.586	0.533	0.477	-0.458	0.623
FW	0.633	-0.639	0.595	0.364	-0.6	-0.321	0.377	0.183	0.116	1	0.604	0.341	0.323	0.301	0.298	0.379	0.196	-0.431	0.437	0.428	-0.198	0.776
FS	0.807	-0.614	0.586	0.461	-0.58	-0.212	0.813	0.524	0.62	0.604	1	0.445	0.447	0.55	0.438	0.431	0.322	-0.565	0.545	0.506	-0.421	0.871
TSS	0.534	-0.411	0.433	0.365	-0.362	0.112	0.476	0.363	0.452	0.341	0.445	1	0.401	0.399	0.297	0.435	0.264	-0.491	0.473	0.503	-0.334	0.513
AA	0.456	-0.386	0.346	0.352	-0.364	-0.028	0.4	0.393	0.391	0.323	0.447	0.401	1	0.398	0.364	0.41	0.284	-0.48	0.475	0.515	-0.462	0.464
TA	0.556	-0.349	0.468	0.434	-0.31	0.073	0.562	0.527	0.52	0.301	0.438	0.401	0.398	1	0.342	0.416	0.356	-0.495	0.426	0.484	-0.389	0.589
TP	0.497	-0.387	0.334	0.357	-0.373	0.034	0.428	0.44	0.427	0.298	0.438	0.297	0.364	1	0.364	0.407	0.407	-0.457	0.472	0.413	-0.43	0.455
PC	0.485	-0.346	0.344	0.335	-0.354	-0.066	0.364	0.323	0.345	0.379	0.431	0.435	0.41	0.416	0.364	1	0.3	-0.568	0.392	0.493	-0.478	0.491
PV	0.431	-0.358	0.305	0.189	-0.344	0.119	0.361	0.426	0.442	0.196	0.322	0.264	0.284	0.407	0.3	0.3	1	-0.311	0.378	0.333	-0.35	0.382
SP	-0.633	0.548	-0.489	-0.537	0.527	0.036	-0.508	-0.516	-0.586	-0.431	-0.565	-0.491	-0.48	-0.457	-0.568	-0.311	1	-0.612	-0.641	-0.641	0.514	-0.632
CC	0.623	-0.471	0.5	0.307	-0.438	0.087	0.548	0.478	0.533	0.437	0.545	0.473	0.475	0.426	0.472	0.392	0.378	-0.612	1	0.563	-0.452	0.598
RWC	0.535	-0.444	0.478	0.362	-0.435	0.079	0.506	0.445	0.477	0.428	0.506	0.503	0.515	0.484	0.413	0.493	0.333	-0.641	0.563	1	-0.538	0.59
EL	-0.455	0.27	-0.302	-0.27	0.279	-0.074	-0.432	-0.387	-0.458	-0.198	-0.421	-0.334	-0.462	-0.389	-0.43	-0.478	-0.35	0.514	-0.452	-0.538	1	-0.418
FYP	0.873	-0.743	0.744	0.553	-0.706	-0.158	0.725	0.627	0.623	0.776	0.871	0.513	0.464	0.589	0.455	0.491	0.382	-0.632	0.598	0.59	-0.418	1

PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids (°Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (µg/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

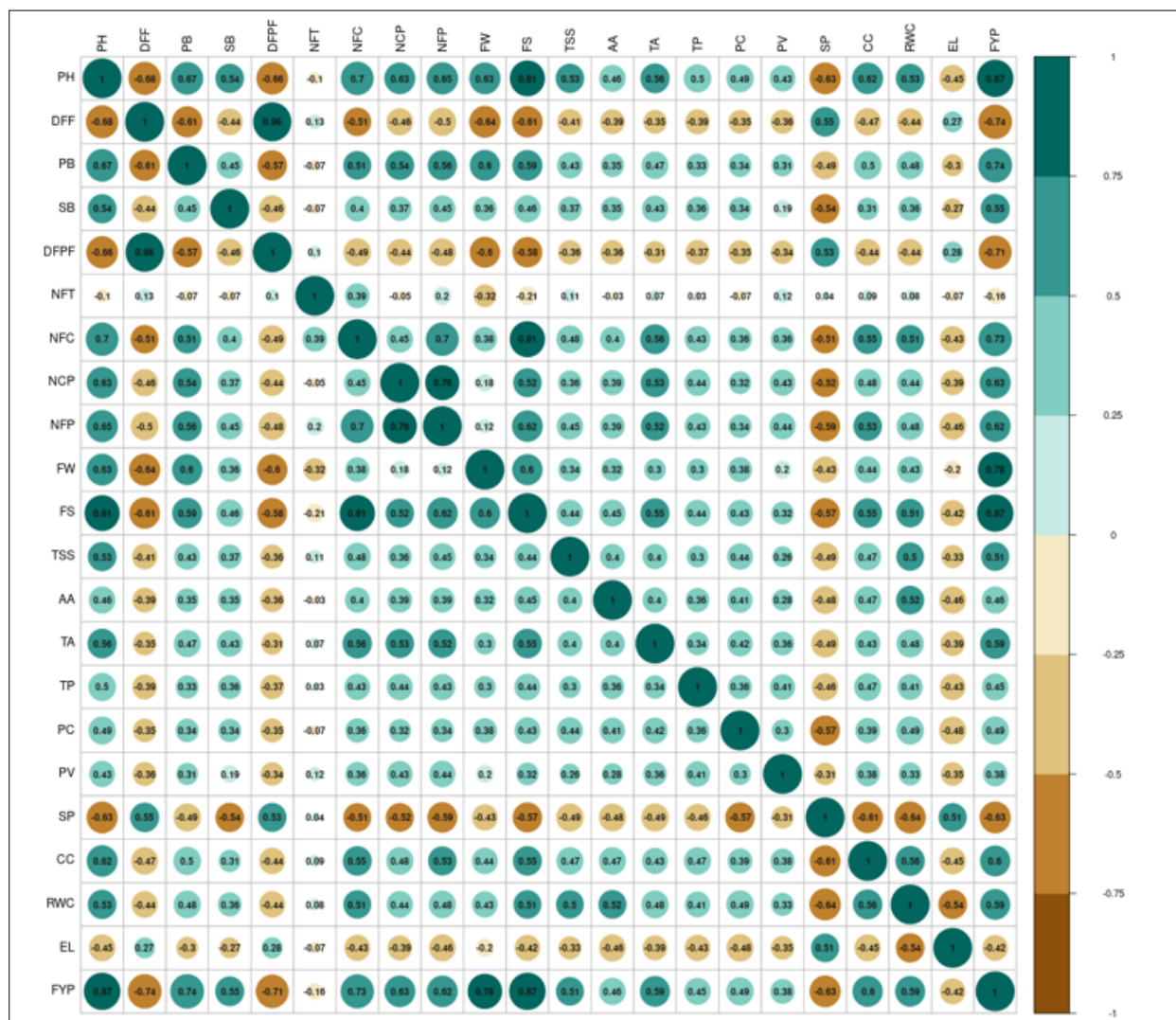


Fig. 2. Correlogram displaying the correlation coefficients of yield, quality and physiological traits. PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids ($^{\circ}$ Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (μ g/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

A pronounced and highly significant positive correlation was evident between FYP and several vegetative, physiological and quality traits. Among these, PH (0.873), primary branches per plant (0.744), chlorophyll content (0.598), relative water content (0.59), titratable acidity (0.589), SB (0.553), proline content (0.491) and total phenols (0.455) showed strong positive associations with FYP. These results suggest that vigorous vegetative growth, improved physiological status and enhanced reproductive fitness contribute substantially to yield improvement under heat stress conditions. The observed positive associations are consistent with those reported in earlier studies (23–25).

Among the yield component traits, FYP showed strong positive correlations with FS (0.871), FW (0.776), NFC (0.725), NCP (0.627) and NFP (0.623). These findings indicate that increased fruit setting, fruit size and fruit number are major contributors to higher yield. Similar trends were previously observed (26–29), who reported that fruit set and fruit-bearing traits are critical determinants of tomato productivity. Pollen viability (0.382) showed strong positive associations with FY per plant (30).

In contrast, DFF (-0.743) and DFPF (-0.706) indicated significant negative correlations with FYP. These results indicate that

early flowering genotypes tend to produce higher yields, particularly under heat stress conditions, where timely reproductive development is advantageous. The present outcome is consistent with earlier studies (31, 32). Number of flowers per truss (-0.158) showed negative association with yield (33). No. of flowers per truss exhibited weak and mostly non-significant correlations with most of the traits studied, suggesting a comparatively smaller contribution to yield variation.

Likewise, style protrusion percentage (-0.632) and electrolyte leakage (-0.418) were negatively associated with FYP. Increased style protrusion may hinder effective self-pollination and reduce fruit set, whereas elevated electrolyte leakage reflects membrane damage and reduces cellular stability under high-temperature stress. Therefore, lower values for these traits are desirable for maintaining productivity under adverse environmental conditions. Similar patterns of association were previously documented (34, 35). Fruit set percentage showed a positive association with pollen viability, indicating the importance of viable pollen in successful fertilisation and subsequent fruit development under heat stress conditions. These observations align well with early researchers, who emphasised the role of pollen viability in sustaining reproductive success under elevated temperatures (36).

Plant height demonstrated strong positive associations not only with fruit yield (0.873) but also with fruit set percentage (0.807), number of clusters per plant (0.626) and number of fruits per plant (0.649). These relationships suggest that robust vegetative growth supports reproductive development and ultimately enhances yield potential. Findings analogous to the present studies (31, 37, 38).

Furthermore, NFP was strongly and positively associated with no. of clusters per plant (0.762) and number of fruits per cluster (0.704), highlighting the complementary role of cluster production and fruit density in determining overall productivity. These findings corroborate those of early results (26, 29). Fruit weight was positively associated with the number of fruits per cluster (0.377). Comparable findings for the relationship between fruit number per plant and average fruit weight were also observed (24, 25, 39–41).

The quality traits total soluble solids (TSS) and ascorbic acid also showed positive associations with fruit yield, indicating the possibility of simultaneous improvement of yield and fruit quality. Similar results have been previously reported (40, 42).

Overall, the correlation analysis identified PH, FS, FW, NFC, NCP, NFP and key physiological traits such as relative water content, chlorophyll content and pollen viability as important contributors to fruit yield under heat stress conditions. Consequently, these characteristics could be employed as reliable criteria for identifying and developing high-yielding, heat-resilient tomato genotypes.

Path coefficient analysis

Path coefficient analysis revealed that FW made the largest positive direct contribution to FYP (0.450), emphasising its key role in enhancing yield under heat stress (Table 4). This is in concurrence with early results (43). Other traits exhibiting positive direct effects on fruit yield included NCP (0.224), NFC (0.194), FS (0.145), NFP (0.091),

SB (0.065), PH (0.07), titratable acidity (0.033), primary branches (0.028), relative water content (0.026), DFPF (0.014) and proline content (0.024). The positive direct effects of these traits suggest that they contribute substantially to yield improvement and may therefore serve as effective selection criteria in tomato breeding programmes. Similar observations highlighting the importance of FW and fruit number-related traits in yield determination have been previously reported (44, 45).

In contrast, DFF (-0.055) recorded a negative direct contribution to FYP, suggesting that delayed flowering may adversely affect productivity. A similar trend was previously documented. Negative direct effects on fruit yield were also observed for total phenols (-0.043), ascorbic acid (-0.03), chlorophyll content (-0.019), electrolyte leakage (-0.012) and pollen viability (-0.007) and the results were presented in Table 4. The negative direct influence of DFF indicates the potential advantage of earliness in improving yield performance under heat stress conditions, whereas the negative effects of certain quality and physiological traits suggest a complex relationship with yield expression (Fig. 3). Comparable findings for ascorbic acid were reported in previous studies (46).

Indirect effects

Besides the direct effects, several traits contributed to fruit yield through indirect effects mediated by other yield components. Plant height exerted a positive indirect effect on fruit yield through FW (0.284), followed by NCP (0.140), NFC (0.136) and FS (0.117), resulting in a strong positive correlation with fruit yield (0.873). Similarly, primary branches exerted a positive indirect effect through FW (0.267), NFC (0.099) and FS (0.085), explaining its high correlation with fruit yield (0.744) (47–49).

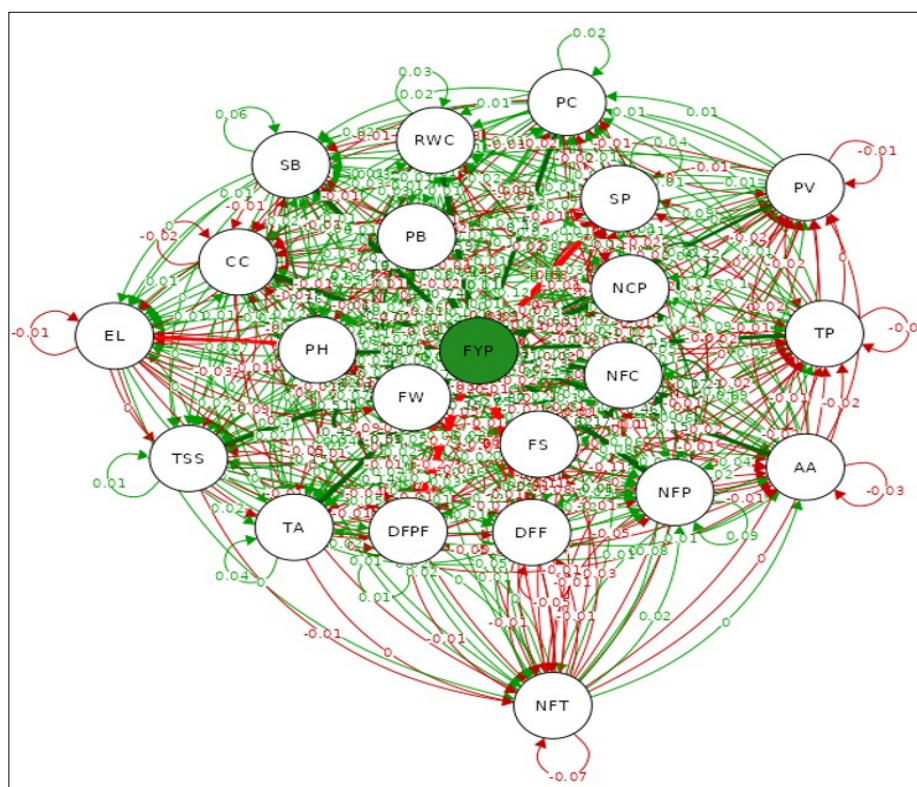


Fig. 3. Path diagram for yield-contributing traits and physiological characters of tomato. PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids (°Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (μg/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

Table 4. Genotypic path coefficient analysis for yield and its components in the F₁ population of PKM 1 × *Solanum pimpinellifolium*

	PH	DFF	PB	SB	DFPF	NFT	NFC	NCP	NFP	FW	FS	TSS	AA	TA	TP	PC	PV	SP	CC	RWC	EL	gen_corr with main variable
PH	0.07	0.038	0.019	0.035	-0.009	0.005	0.136	0.14	0.059	0.284	0.117	0.005	-0.014	0.018	-0.021	0.011	-0.003	-0.024	-0.012	0.014	0.005	0.873
DFF	-0.048	-0.055	-0.017	-0.029	0.013	-0.006	-0.098	-0.103	-0.045	-0.286	-0.089	-0.004	0.011	-0.011	0.017	-0.008	0.003	0.02	0.009	-0.012	-0.003	-0.743
PB	0.047	0.034	0.028	0.029	-0.008	0.004	0.099	0.12	0.051	0.267	0.085	0.004	-0.01	0.015	-0.014	0.008	-0.002	-0.018	-0.009	0.013	0.004	0.744
SB	0.037	0.024	0.012	0.065	-0.006	0.003	0.079	0.083	0.041	0.163	0.067	0.003	-0.01	0.014	-0.015	0.008	-0.001	-0.02	-0.006	0.009	0.003	0.553
DFPF	-0.046	-0.053	-0.016	-0.03	0.014	-0.005	-0.095	-0.099	-0.044	-0.269	-0.084	-0.003	0.011	-0.01	0.016	-0.008	0.002	0.02	0.008	-0.011	-0.003	-0.706
NFT	-0.007	-0.007	-0.002	-0.004	0.001	-0.051	0.075	-0.011	0.019	-0.144	-0.031	0.001	0.001	0.002	-0.001	-0.002	-0.001	0.001	-0.002	0.002	0.001	-0.158
NFC	0.049	0.028	0.014	0.026	-0.007	-0.02	0.194	0.102	0.064	0.169	0.118	0.004	-0.012	0.018	-0.019	0.009	-0.003	-0.019	-0.01	0.013	0.005	0.725
NCP	0.044	0.026	0.015	0.024	-0.006	0.003	0.088	0.224	0.069	0.082	0.076	0.003	-0.012	0.017	-0.019	0.008	-0.003	-0.019	-0.009	0.012	0.005	0.627
NFP	0.045	0.028	0.016	0.029	-0.007	-0.01	0.137	0.171	0.091	0.052	0.09	0.004	-0.012	0.017	-0.018	0.008	-0.003	-0.022	-0.01	0.012	0.005	0.623
FW	0.044	0.035	0.017	0.024	-0.008	0.016	0.073	0.041	0.011	0.448	0.088	0.003	-0.01	0.01	-0.013	0.009	-0.001	-0.016	-0.008	0.011	0.002	0.775
FS	0.056	0.034	0.016	0.03	-0.008	0.011	0.158	0.117	0.057	0.27	0.145	0.004	-0.013	0.018	-0.019	0.01	-0.002	-0.021	-0.01	0.013	0.005	0.871
TSS	0.037	0.023	0.012	0.024	-0.005	-0.006	0.092	0.081	0.041	0.153	0.065	0.009	-0.012	0.013	-0.013	0.01	-0.002	-0.018	-0.009	0.013	0.004	0.513
AA	0.032	0.021	0.01	0.023	-0.005	0.001	0.077	0.088	0.036	0.145	0.065	0.004	-0.03	0.013	-0.016	0.01	-0.002	-0.018	-0.009	0.013	0.006	0.464
TA	0.038	0.019	0.013	0.028	-0.004	-0.004	0.108	0.117	0.047	0.133	0.079	0.003	-0.012	0.033	-0.015	0.01	-0.002	-0.018	-0.008	0.013	0.005	0.581
TP	0.035	0.021	0.009	0.023	-0.005	-0.002	0.083	0.099	0.039	0.134	0.064	0.003	-0.011	0.011	-0.043	0.009	-0.003	-0.017	-0.009	0.011	0.005	0.455
PC	0.034	0.019	0.01	0.022	-0.005	0.003	0.071	0.072	0.031	0.17	0.063	0.004	-0.012	0.013	-0.016	0.024	-0.002	-0.021	-0.007	0.013	0.006	0.491
PV	0.03	0.02	0.009	0.012	-0.005	-0.006	0.07	0.095	0.04	0.088	0.047	0.002	-0.008	0.011	-0.018	0.007	-0.007	-0.012	-0.007	0.009	0.004	0.382
SP	-0.044	-0.03	-0.014	-0.035	0.007	-0.002	-0.099	-0.116	-0.053	-0.193	-0.082	-0.004	0.014	-0.016	0.02	-0.013	0.002	0.037	0.012	-0.017	-0.006	-0.632
CC	0.044	0.026	0.014	0.02	-0.006	-0.004	0.106	0.107	0.049	0.196	0.079	0.004	-0.014	0.014	-0.02	0.009	-0.003	-0.023	-0.019	0.015	0.005	0.598
RWC	0.037	0.025	0.013	0.023	-0.006	-0.004	0.098	0.1	0.044	0.192	0.074	0.004	-0.015	0.016	-0.018	0.012	-0.002	-0.024	-0.011	0.026	0.006	0.59
EL	-0.032	-0.015	-0.008	-0.017	0.004	0.004	-0.084	-0.087	-0.042	-0.089	-0.061	-0.003	0.014	-0.012	0.019	-0.011	0.002	0.019	0.009	-0.014	-0.012	-0.418

PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids (°Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (µg/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FVP: fruit yield per plant (g).

Similarly, FS exerted a considerable positive indirect effect through FW (0.270), NFC (0.158), while NFP influenced fruit yield indirectly through NCP (0.171) and the NFC (0.137). Relative water content also contributed positively through FW (0.192), indicating that maintenance of plant water status indirectly supports higher yield under heat stress. These findings demonstrate that several vegetative, reproductive and physiological traits improve fruit yield mainly through their influence on FW. Therefore, simultaneous selection for FW, FS, PH, primary branches, NCP and NFC would be more effective than selection based on individual traits alone for developing high-yielding, heat-tolerant tomato genotypes.

The low magnitude of the residual effect (0.0465) demonstrates that the selected traits collectively accounted for a considerable share of the variability in fruit yield. The inclusion of important yield determinants such as fruit set, fruit number, average FW and associated reproductive traits contributed to this result.

Principal component analysis

Principal component analysis was undertaken to identify the pattern of variation among the twenty-two yield, quality and physiological traits evaluated in the F₂ population under heat stress conditions. The scree plot and PCA biplot were presented in Fig. 4 respectively. The analysis generated eight principal components with eigenvalues greater than 0.60, accounting for 80.99 % of the total variation. Out of eight PCs, the initial three principal components, PC1, PC2 and PC3, possessed eigenvalues exceeding one and collectively contributed 62.51 % of the total variation (Table 5). The first three main components have eigenvalues greater than one, PC1 accounted for 48.12 % of the percentage of variance with the largest eigenvalue (10.59), whereas PC2 contributed 8.70 % with an eigenvalue of 1.91 and PC3 contributed 5.70 % with an eigenvalue of 1.25, indicating that these three components captured most of the variation present in the population (50, 51).

The first three principal components collectively explained 62.511 % of the total variance, indicating that these components effectively represented the major phenotypic differences among the population. Similar observations were previously reported (52, 53).

The major contributors to PC1 were FYP (7.933 %), PH (7.511 %), FS (6.607 %), NFC (5.625 %), style protrusion (5.746 %), DFF (5.495 %), NFP (5.384 %), primary branches (5.185 %), DFPF (5.101 %), chlorophyll content (4.965 %), relative water content (4.871 %), NCP (4.625 %) and titratable acidity (4.182 %). These traits were therefore the major factors influencing variability among the population.

The major contributors to this component were NFT (27.457 %), FW (18.842 %), DFF (7.583 %), DFPF (7.163 %), electrolyte leakage (6.557 %), NFP (6.401 %) and NFC (3.475 %). These findings were like those previously reported (54). Higher contributions of yield and reproductive traits in the first two principal components indicated their major role in generating variability among the F₂ population, suggesting that these traits could be effectively utilised for selection of superior heat-stress-tolerant genotypes (55, 56).

PC3 contributed 5.70 % of the total variation and was mainly influenced by proline content (18.708 %), electrolyte leakage (11.909 %), NFT (11.058 %), ascorbic acid (10.385 %), NFC (8.630 %) and NFP (7.997 %).

The biological interpretation of the principal components indicates that the FYP, FS, PH, NFC, NFP, chlorophyll content and relative water content all had a significant impact on PC1, which

primarily represents yield potential under heat stress. Together, these characteristics show how plants may sustain vegetative growth, reproductive growth and physiological stability at high temperatures. With significant contributions from fruit weight, number of flowers per truss and flowering characteristics, PC2 mainly indicates variation in fruit development and reproductive efficiency, indicating that this component distinguishes genotypes according to reproductive performance under heat stress. PC3 was primarily linked to physiological and biochemical adaptation, specifically ascorbic acid, proline content and electrolyte leakage, highlighting the significance of osmotic adjustment, membrane stability and antioxidant defence in heat stress tolerance. Thus, the three principal components collectively describe complementary mechanisms governing heat tolerance and productivity in the F₂ population.

A sharp decline in eigenvalues was observed after PC1 in the scree plot, indicating that the first principal component explained a substantial proportion of overall variability. The first principal component (48.12 %) contributed the largest proportion of variation, followed by PC2 (8.69 %), PC3 (5.70 %), PC4 (4.52 %), PC5 (4.21 %), PC6 (3.55 %), PC7 (3.17 %) and PC8 (3.03 %). Collectively, the first two principal components explained 56.81 % of the total variation, while the first three components accounted for 62.51 %. The gradual reduction in variance from PC4 onwards suggests that most of the phenotypic variability was captured by the first few components, confirming the existence of substantial genetic diversity within the population. The first three main components were sufficient to explain the major variability among the population. This is illustrated in Fig. 5.

The PCA biplot analysis of the F₂ tomato population revealed considerable phenotypic variability among the 200 plants under heat stress conditions (Fig. 4). The population was widely distributed across all quadrants, indicating broad genetic diversity. PC1 (48.1 %) and PC2 (8.7 %), together explained 56.8 % of the total variation.

Population 5, 17, 96, 101 and 117 were located on the positive side of PC1 and were associated with favourable yield attributes, whereas population 1, 2, 28, 40 and 181 exhibited contrasting phenotypes on the negative side. Traits such as NFP, NFC, NCP, FS, TSS, (PH and FYP showed positive association and contributed substantially to total variability. In contrast, DFF and DFPF were negatively associated with yield-related traits, indicating the importance of earliness under heat stress conditions. Fruit weight contributed independently to variability and was associated with the population in the lower right quadrant.

The variable plot showed that NFT, DFF, DFPF, PH, FYP, FW, NFP NCP exhibited longer vectors, indicating greater contribution towards total variability, whereas traits such as SB showed relatively lower influence. Overall, the PCA biplot confirmed the presence of wide genetic variability and identified promising populations with desirable combinations of yield and heat stress tolerance traits for further selection and breeding programmes.

By concurrently considering several agronomic, physiological and qualitative parameters, PCA offers an efficient method for discovering superior and genetically varied genotypes from a breeding perspective. Individuals positioned on the positive side of PC1 and associated with favourable yield and physiological traits represent promising candidates for advancement in subsequent generations. Conversely, genetically distant individuals occupying different quadrants of the PCA biplot may be selected as

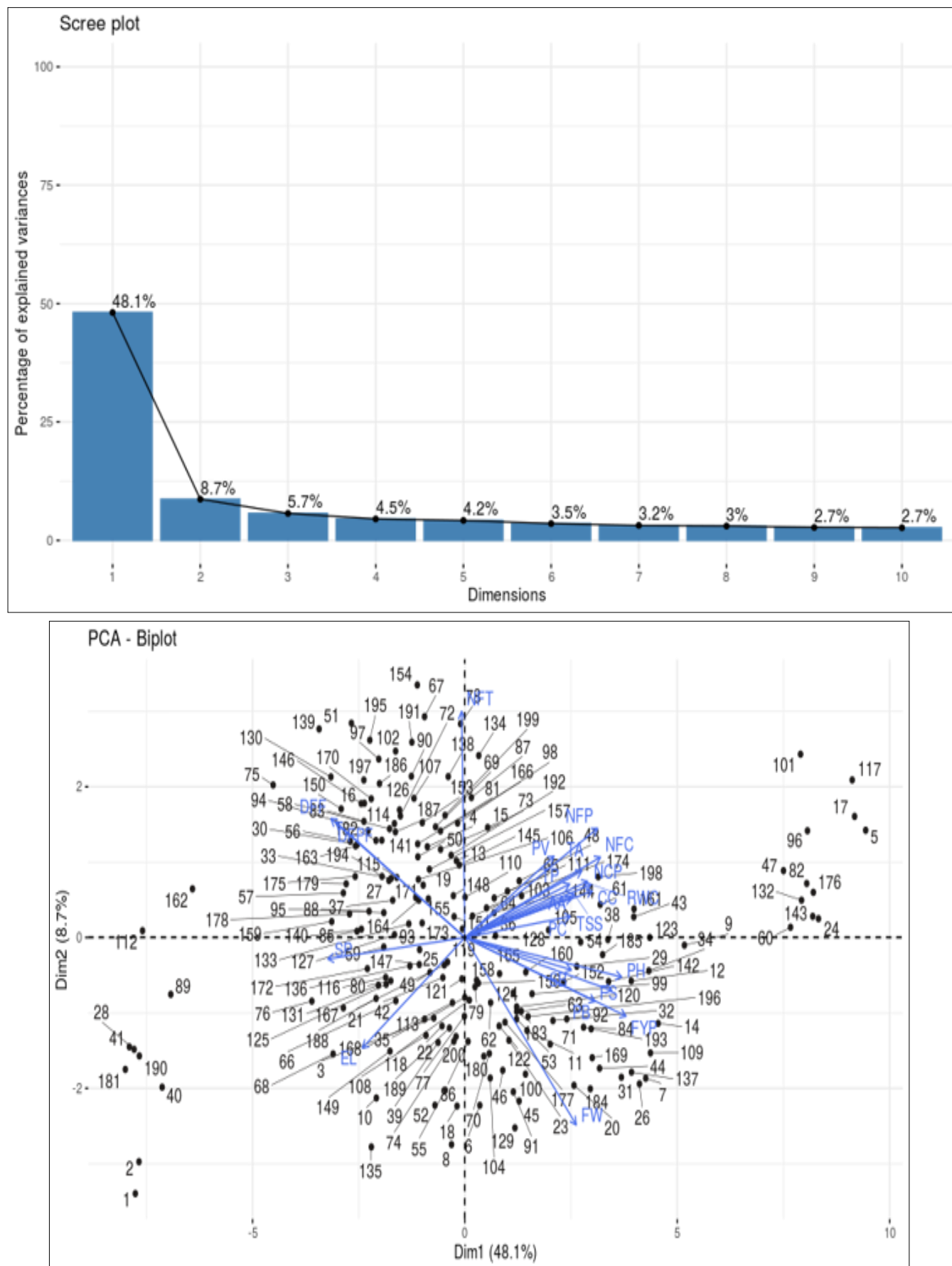


Fig. 4. Principal component analysis (PCA) of 200 tomato F_2 population. A: Scree plot showing the number of informative principal components; B: PCA biplot illustrating the grouping of similar individuals, with trait vectors indicating the relationships and relative importance of the variables. PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFP: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids ($^{\circ}$ Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (μ g/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

Table 5. Eigenvalues, percent variance, cumulative percent of variance, percent contribution of each variable to principal components

Principal components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8
Eigenvalue	10.586	1.913	1.254	0.995	0.926	0.78	0.696	0.667
percentage of variance	48.119	8.694	5.698	4.523	4.21	3.546	3.165	3.033
Cumulative percentage of variance	48.119	56.813	62.511	67.033	71.243	74.789	77.955	80.987
PH	7.511	0.836	0.822	0.072	0.315	1.761	0.224	0.029
DFF	5.495	7.583	3.886	0.083	9.803	6.798	0.456	0.145
PB	5.185	2.191	2.87	0.037	0.944	0.118	5.739	0.859
SB	3.468	0.564	0	0.006	10.942	29.613	21.458	1.171
DFFP	5.101	7.163	3.765	0.057	11.209	10.225	0.026	0.242
NFT	0.003	27.457	11.058	21.735	4.263	1.395	1.297	0.204
NFC	5.625	3.469	8.63	8.244	0.539	5.909	5.455	1.656
NCP	4.604	1.684	2.467	23.524	2.97	0.539	9.411	0.333
NFP	5.384	6.401	7.997	4.234	2.138	1.791	1.916	1.399
FW	3.789	18.842	0.986	5.979	1.542	6.213	0.573	0.725
FS	6.607	1.512	0.858	0.01	3.803	11.912	2.355	2.757
TSS	3.673	0.991	0.863	11.808	0.655	2.501	11.646	8.569
AA	3.459	0.832	10.385	0.025	0.092	0.813	2.47	11.292
TA	4.178	2.381	0.004	0.223	14.385	2.879	0.696	10.217
TP	3.353	1.53	1.147	6.343	8.769	0.022	26.301	2.439
PC	3.408	0.239	18.708	0.471	0.003	0.069	0.824	17.58
PV	2.426	3.538	0.691	12.225	22.278	3.081	0.005	28.619
SP	5.746	0.245	4.656	0.026	0.314	7.883	0.008	0.426
CC	4.965	1.156	0.61	0.831	2.811	2.375	4.347	6.187
RWC	4.871	1.512	6.802	3.185	0.334	0.056	3.835	0.375
EL	3.216	6.557	11.909	0.771	0.923	1.015	0.899	4.761
FYP	7.933	3.318	0.885	0.114	0.969	3.031	0.056	0.015

PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFFP: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: total soluble solids (°Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (µg/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

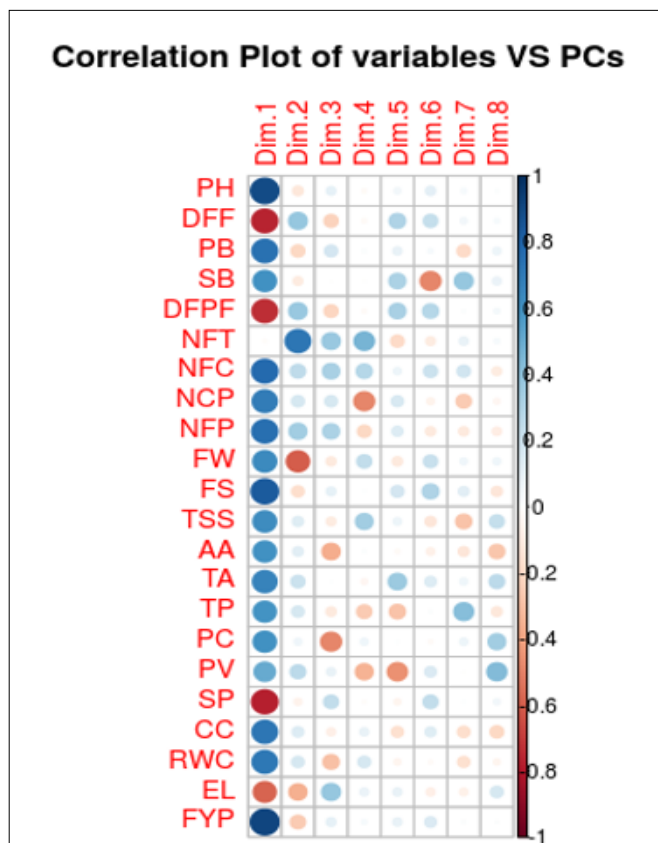


Fig. 5. Contribution on the individual trait in first 8 major principal components. PH: plant height (cm); DFF: days to first flowering; PB: primary branches; SB: secondary branches; DFPF: days to 50% flowering; NFT: number of flowers per truss; NFC: number of fruits per cluster; NCP: number of clusters per plant; NFP: number of fruits per plant; FW: fruit weight (g); FS: fruit set percentage; TSS: total soluble solids (°Brix); AA: ascorbic acid (mg/100 g); TA: titratable acidity; TP: total phenols (mg GAE/100 g); PC: proline content (µg/g); PV: pollen viability (%); SP: style protrusion (%); CC: chlorophyll content; RWC: relative water content (%); EL: electrolyte leakage (%); FYP: fruit yield per plant (g).

parents in future hybridisation programmes to maximise genetic recombination and combine complementary traits related to heat tolerance and yield. As a result, PCA is a useful multivariate tool for developing climate-resilient tomato cultivars, identifying superior breeding materials and choosing parents.

The superior F_2 segregants identified in the present study represent valuable early-generation breeding materials for improving heat tolerance in tomato. However, the present study was conducted at a single location during a single growing season under natural high-temperature conditions. Although significant genetic variability and promising heat-tolerant segregants were identified, genotype $\times$ environment interactions could not be evaluated. In addition, the F_2 population was evaluated under a single environment without replication, which is a common constraint in early-generation segregating populations because each plant represents a unique genotype. The h^2 and GA values should be regarded as preliminary indicators rather than definitive estimates of genetic control because environmental variance could not be measured independently. Confirmation of these genetic parameters will require evaluation of replicated F_3 and subsequent generations across multiple environments.

Since the F_2 generation is highly segregating, the selected individual plants will be advanced through selfing to develop F_3 families, where family-based evaluation and within-family selection will be undertaken for yield, physiological and reproductive traits associated with heat stress tolerance. Superior F_3 families will subsequently be advanced to F_4 and later generations to increase homozygosity and stabilise the desired allelic combinations. Therefore, to verify the stability of heat tolerance and yield-related traits, the chosen F_2 -derived segregants should be assessed over several locations, seasons and advanced generations before being used as stable breeding materials for varietal development.

Conclusion

The F_2 population derived from the cross between PKM 1 $\times$ *Solanum pimpinellifolium* showed wide genetic variability for yield and related traits under heat stress conditions, which indicates its potential for selection under heat stress. The high heritability coupled with high genetic advance (GA) for fruit yield (FY), fruit set percentage (FS), number of fruits per cluster (NFC) and number of flowers per truss (NFT) indicated that these characters are amenable to effective phenotypic selection. However, the gene action involved needs to be confirmed in advanced generations. Fruit yield per plant (FYP) was significantly and positively correlated with plant height (PH), secondary branching (SB), number of clusters per plant (NCP), number of fruits per plant (NFP), fruit weight (FW) and FS. The path coefficient analysis showed that FW and FS were the major direct contributors to yield.

Hence, these traits are reliable selection criteria for yield enhancement under high temperature conditions. The superior F_2 segregants identified in the present study can be advanced to the next generations for validation of trait stability and incorporated into tomato improvement programmes. Also, the incorporation of molecular markers, quantitative trait locus (QTL) mapping, marker-assisted selection and genomic selection with conventional breeding will help to verify the genomic regions responsible for heat tolerance and hasten the development of high-yielding, climate-resilient tomato varieties.

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Authors' contributions

AP conducted the research work. VSKS provided valuable guidance, critical suggestions and overall supervision throughout the preparation of manuscript. BA¹ made significant corrections and provided insights that enhanced the quality and accuracy of the manuscript. All co-authors MBN, BA², GK reviewed the manuscript. All authors have read and approved the final manuscript [BA¹ stands for Beaulah A and BA² stands for Bharathi A].

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References

- Food and Agriculture Organization of the United Nations. FAOSTAT: crops and livestock products. Rome: FAO; 2024. <https://www.fao.org/faostat/en/#data/QCL>
- Ministry of Agriculture and Farmers Welfare. Final estimates of 2022–23 and first advance estimates of 2023–24 of area and production of horticultural crops [Internet]. New Delhi: Press Information Bureau, Government of India; 2024. [Press Information Bureau](https://www.pib.gov.in)
- Khan Q, Wang Y, Xia G, Yang H, Luo Z, Zhang Y. Deleterious effects of heat stress on the tomato, its innate responses and potential preventive strategies in the realm of emerging technologies. *Metabolites*. 2024;15(5):283. <https://doi.org/10.3390/metabo14050283>
- Mohammed SP, Natarajan S, Eybshitz A, Jakkula D, Veerasamy R, Prasanthrajan M, et al. Heat stress in tomato plants: current challenges and future directions for sustainable agriculture. *N Z J Crop Hortic Sci*. 2025;53(5):1283–307. <https://doi.org/10.1080/01140671.2024.2432624>
- Bashary N, Miller G, Doitsch-Movshovits T, Beery A, Ouyang B, Lieberman-Lazarovich M. New population of *Solanum pimpinellifolium* backcross inbred lines as a resource for heat stress tolerance in tomato. *Front Plant Sci*. 2024;15:1386824. <https://doi.org/10.3389/fpls.2024.1386824>
- Du M, Sun C, Deng L, Zhou M, Li J, Du Y, et al. Molecular breeding of tomato: advances and challenges. *J Integr Plant Biol*. 2025;67(3):669–721. <https://doi.org/10.1111/jipb.13879>
- Burton GW, DeVane EH. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron J*. 1953;45:478–81. <https://doi.org/10.2134/agronj1953.00021962004500100005x>
- Subramanian SS, Madhava MP. Genotypic and phenotypic variability in rice. *Madras Agric J*. 1973;60:1093–6.
- Lush JL. Heritability of quantitative characters in farm animals. *Hereditas*. 1949;35:356–75. <https://doi.org/10.1111/j.1601-5223.1949.tb03347.x>
- Hanson CH, Robinson HF, Comstock RE. Biometrical studies of yield in segregating populations of Korean lespedeza. *Agron J*. 1956;48(6):268–72. <https://doi.org/10.2134/agronj1956.00021962004800060008x>
- Robinson HF, Comstock RE, Harvey PH. Genetic variances in open pollinated varieties of corn. *Genetics*. 1955;40(1):45. <https://doi.org/10.1093/genetics/40.1.45>
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J*. 1955;47:314–8. <https://doi.org/10.2134/agronj1955.00021962004700070009x>
- Weber CR, Moorthy BR. Heritable and nonheritable relationships and variability of oil content and agronomic characters in the F2 generation of soybean crosses. *Agron J*. 1952;44(4):202–9. <https://doi.org/10.2134/agronj1952.00021962004400040010x>
- Dewey DR, Lu K. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. *Agron J*. 1959;51(9):515–8. <https://doi.org/10.2134/agronj1959.00021962005100090002x>
- Akinwale MG, Gregorio G, Nwile F, Akinyele BO, Ogunbayo SA, Odiyi AC, et al. Comparative performance of lowland hybrids and inbred rice varieties in Nigeria. *Int J Plant Breed Genet*. 2011;5(3):224–34. <https://doi.org/10.3923/ijpb.2011.224.234>
- Kumar M, Yadav RK, Yadav RK, Behera TK, Talukdar A. Estimates of genetic variability, heritability and genetic advance for yield and yield component traits in thermo tolerant tomato (*Solanum lycopersicum* L.) genotypes. *Int J Agric Sci*. 2017;9(2):3640–2.
- Verma VK, Pandey A, Jha AK. Genetic parameters, diversity and population structure in tomato based on quantitative traits and microsatellite markers. *Indian J Plant Genet Resour*. 2021;34(3):437–46. <https://doi.org/10.5958/0976-1926.2021.00037.1>
- Saravanan KR, Vishnupriya V, Prakash M, Anandan R. Variability, heritability and genetic advance in tomato genotypes. *Indian J Agric Res*. 2019;53(1):92–5. <https://doi.org/10.18805/IJAReA-5030>
- Prajapati S, Tiwari A, Kadwey S, Jamkar T. Genetic variability, heritability and genetic advance in tomato (*Solanum lycopersicon* Mill.). *Int J Agric Environ Biotechnol*. 2015;8(2):245–51. <https://doi.org/10.5958/2230-732X.2015.00031.5>
- 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):1011–4.
- Kerketta A, Bahadur V, Rajesh J. Performance of different tomato genotypes (*Solanum lycopersicum* L.) for growth, yield and quality traits under Allahabad condition. *J Pharmacogn Phytochem*. 2018;7:1766–9.
- Rasheed A, Ilyas M, Khan TN, Mahmood A, Riaz U, Chattha MB, et al. Study of genetic variability, heritability and genetic advance for yield-related traits in tomato (*Solanum lycopersicon* Mill.). *Front Genet*. 2023;13:1030309. <https://doi.org/10.3389/fgene.2022.1030309>
- Zannat A, Hussain MA, Abdullah AH, Hossain MI, Saifullah M, Safhi FA, et al. Exploring genotypic variability and interrelationships among growth, yield and quality characteristics in diverse tomato genotypes. *Heliyon*. 2023;9(8):18958. <https://doi.org/10.1016/j.heliyon.2023.e18958>
- Sharma A, Pandey SK, Nair R. Correlation and path co-efficient analysis for yield and its contributing traits in tomato (*Solanum lycopersicum* L.). *J Pharm Innov*. 2021;10(3):616–22. <https://doi.org/10.22271/tpi.2021.v10.i3i.5837>
- Maurya RK, Singh AK, Sai A. Correlation and path analysis in tomato (*Solanum lycopersicum* L.) for yield and yield contributing traits. *J Pharmacogn Phytochem*. 2020;9(3):1684–7. <https://doi.org/10.22271/phyto.2020.v9.i3ab.11555>
- Uzair M, Kalsoom R, Attia KA, Ali I, Hussain T, Abushady AM, et al. Understanding the role of thermal stress in modulating growth, yield and quality attributes of tomato at two locations. *Turk J Agric For*. 2025;49(1):153–68. <https://doi.org/10.55730/1300-011X.3255>
- Ahmed EAY. Population parameters and path-coefficient analysis of tomato grown under heat stress. *Alex Sci Exch J*. 2017;38:600–12. <https://doi.org/10.21608/asejaicjsae.2017.4033>
- Vijayakumar A, Beena R. Characterizing tomato genotypes for high temperature stress adaptation in field conditions. *Vegetos*. 2026;39(1):397–409. <https://doi.org/10.1007/s42535-024-01109-6>
- Kumar SC, Jawadagi RS, Fakrudin B, Hanchinamani CN, Kulkarni MS, Lakshmidheevamma TN, et al. Assessment of growth and yield parameters in recombinant inbred line populations of tomato (*Solanum lycopersicum* L.) through correlation and path analysis. *J Hortic Sci*. 2023;18(2):295–300. <https://doi.org/10.24154/jhs.v18i2.1819>

30. Sharma S, Jindal SK, Patel SA, Sharma A, Chawla N. Genetic association analysis in advance tomato (*Solanum lycopersicum* L.) lines for horticultural and yield contributing traits. Trends Hortic. 2024;7(1). <https://doi.org/10.24294/th.v7i1.4090>
31. Das SB, Islam MS, Uddin MN, Goswami BK, Abedin SS, Baki MA. Evaluation of the performance of summer tomato lines in Bangladesh conditions. J Bio-Sci. 2023;31(2):13–23. <https://doi.org/10.3329/jbs.v31i2.741423>
32. Singh AK, Solankey SS, Akhtar S, Kumari P, Chaurasiya J. Correlation and path coefficient analysis in tomato (*Solanum lycopersicum* L.). Int J Curr Microbiol Appl Sci. 2018;7:4278–85.
33. Kadyan D, Srivastav P, Kumar J, Singh H. Genetic variability, correlation and path coefficient analysis in tomato (*Solanum lycopersicum* L.). Pharma Innov J. 2023;12(8):2325–9.
34. Ur Rahman S, Basit A, Ara N, Ullah I, Rehman AU. Morpho-physiological responses of tomato genotypes under saline conditions. Gesunde Pflanzen. 2021;73(4):541–53. <https://doi.org/10.1007/s10343-021-00576-0>
35. Bhattarai S, Harvey JT, Djidonou D, Leskovar DI. Exploring morpho-physiological variation for heat stress tolerance in tomato. Plants (Basel). 2021;10(2):347. <https://doi.org/10.3390/plants10020347>
36. Ghabileh M, Lotfi M, Aliniaefard S, Ramshini H. Variation in reproductive organ functionality among a population of tomato genotypes reveals the importance of pollen viability and fruit set in response to heat stress. Int J Veg Sci. 2024;30(6):717–31. <https://doi.org/10.1080/19315260.2024.2429118>
37. Vijaylaxmi SK, Rathod V, Evoor S, Kantharaju V, Tatagar MH, Laksmidevamma TN. Correlation and path coefficient analysis in cherry tomato (*Solanum lycopersicum* var. cerasiforme). J Pharmacogn Phytochem. 2021;10(2):1136–40.
38. Doddamani MB, Jagadeesha RC, Baby R, Prakash G. Correlation and path analysis for growth, yield and quality traits in F3 population of cherry tomato (*Solanum lycopersicum* L. var. cerasiforme). Int J Chem Stud. 2019;7(3):3712–6.
39. Sunilkumar MK, Vijeth S, Rathod V, Kaushik P. Genetic associations analysis in tomato (*Solanum lycopersicum* L.) involving improved germplasm lines for agronomic and yield contributing traits. Int J Curr Microbiol Appl Sci. 2019;8(10):2688–702. <https://doi.org/10.20546/ijcmas.2019.810.310>
40. Sushma K, Saidaiyah P, Reddy KR, Sudini H, Geetha A. Correlation and path coefficient analysis in tomato (*Solanum lycopersicum* L.). Int J Curr Microbiol Appl Sci. 2020;9(11):2569–75. <https://doi.org/10.20546/ijcmas.2020.911.311>
41. Nevani S, Sridevi O. Correlation and path coefficient analysis in tomato (*Solanum lycopersicum* L.). Pharma Innov J. 2021;10(7):1522–5.
42. Mishra A, Nandi A. Correlation and path coefficient analysis for quality traits in tomato (*Solanum lycopersicon* L.). J Pharmacogn Phytochem. 2018;7(1):1733–8.
43. Chernet S, Belew D, Abay F. Performance evaluation and path analysis studies in tomato (*Solanum lycopersicon* L.) genotypes under Humera, Northern Ethiopia condition. World J Agric Res. 2014;2(6):267–71. <https://doi.org/10.12691/wjar-2-6-3>
44. Reddy SB, Thomas B, Ankitha MO, Anand S, Jyothi BA. Association and path coefficient analysis among F2 segregating population of tomato (*Solanum lycopersicum* L.). Int J Plant Soil Sci. 2023;35(18):656–62. <https://doi.org/10.9734/ijpss/2023/v35i183330>
45. Akhter S, Najnine F. Variability of tomato (*Lycopersicon esculentum* L.) genotypes for higher yield and yield contributing traits. N Am Acad Res. 2022;5(2):48–64.
46. Patel P, Kumar U. Studies on correlation and path coefficient analysis for yield and quality traits in tomato. Pharma Innov J. 2021;10(9):1914–8.
47. Kumar R, Ram CN, Yadav GC, Deo C, Vimal SC, Bhartiya HD. Studies on correlation and path coefficient analysis in tomato (*Solanum lycopersicon* L.). Plant Archives. 2014;14(1):443–7.
48. Rajolli MG, Lingaiah HB, Malashetti IR, Bhat AS, Aravindkumar JS. Correlation and path co-efficient studies in tomato (*Solanum lycopersicum* L.). Int J Pure Appl Biosci. 2017;5(6):913–7. <https://doi.org/10.18782/2320-7051.6096>
49. Kumari S, Sharma MK. Genetic variability studies in tomato (*Solanum lycopersicum* L.). Vegetable Science. 2013;40(01):83–6.
50. Meena OP, Bahadur V. Genetic associations analysis for fruit yield and its contributing traits of indeterminate tomato (*Solanum lycopersicum* L.) germplasm under open field condition. J Agric Sci. 2015;7(3):148. <https://doi.org/10.5539/jas.v7n3p148>
51. Sharmin S, Hannan A, Tahjib-Ul-Arif M, Sagor GH. Genetic association and path coefficient analysis among yield and nutritional traits of tomato (*Lycopersicon esculentum* L.). J Bangladesh Agric Univ. 2019;17(2):187–93. <https://doi.org/10.3329/jbau.v17i2.41942>
52. Williams G, Anbuselvam Y. Assessment of genetic divergence through principal component analysis and clustering in tomato germplasm accessions. Environ Ecol. 2023;41(4D):3060–5. <https://doi.org/10.60151/envec/YLSS4838>
53. Sinha A, Singh P, Bhardwaj A, Verma RB. Principal component analysis approach for comprehensive screening of tomato germplasm for polyhouse condition. J Exp Agric Int. 2021;43(9):67–72. <https://doi.org/10.9734/jeai/2021/v43i930739>
54. Biradar G, Laxman RH, Shivashankara KS, Valiarambil Sebastin JS. Screening and selection of physio-biochemical traits to detect high temperature tolerance using multivariate analysis in tomato genotypes (*Lycopersicon esculentum* Mill). Acta Physiol Plant. 2022;44(8):79. <https://doi.org/10.1007/s11738-022-03414-6>
55. Haque MS, Husna MT, Uddin MN, Hossain MA, Sarwar AK, Ali OM, et al. Heat stress at early reproductive stage differentially alters several physiological and biochemical traits of three tomato cultivars. Horticulturae. 2021 S;7(10):330. <https://doi.org/10.3390/horticulturae7100330>
56. Dasgan HY, Dere S, Akhoundnejad Y, Arpaci BB. Effects of high-temperature stress during plant cultivation on tomato (*Solanum lycopersicum* L.) fruit nutrient content. J Food Qual. 2021;2021(1):7994417. <https://doi.org/10.1155/2021/7994417>

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