



OPEN ACCESS

EDITED BY

Sudip Kumar Dutta,
ICAR Research Complex For NEH Region,
India

REVIEWED BY

Wang Xiukang,
Yan'an University, China
Ehtisham Hussain,
University of Sargodha, Pakistan

*CORRESPONDENCE

Gmakouba Tighankoumi
✉ tgmakouba@wacci.ug.edu.gh

RECEIVED 12 March 2026

REVISED 05 May 2026

ACCEPTED 11 May 2026

PUBLISHED 15 June 2026

CITATION

Tighankoumi G, Léo DK, Kibalou PK,
Awovi AS, Some K, Dzidzienyo DK and
Atti T (2026) Morphotype-based
characterization of tomato (*Solanum
lycopersicum* L.) accessions cultivated in
Togo for conservation and genetic
improvement.
Front. Hortic. 5:1829079.
doi: 10.3389/fhort.2026.1829079

COPYRIGHT

© 2026 Tighankoumi, Léo, Kibalou,
Awovi, Some, Dzidzienyo and Atti. This is
an open-access article distributed under
the terms of the [Creative Commons
Attribution License \(CC BY\)](#). The use,
distribution or reproduction in other
forums is permitted, provided the
original author(s) and the copyright
owner(s) are credited and that the
original publication in this journal is
cited, in accordance with accepted
academic practice. No use, distribution
or reproduction is permitted which does
not comply with these terms.

Morphotype-based characterization of tomato (*Solanum lycopersicum* L.) accessions cultivated in Togo for conservation and genetic improvement

Gmakouba Tighankoumi ^{1,2,3*}, Djoyou Kibamalaki Léo¹,
Palanga Koffi Kibalou¹, Ahonon Selom Awovi², Koussao Some⁴,
Daniel Kwadjo Dzidzienyo^{3,5} and Tchabi Atti¹

¹Laboratory of Agronomic and Applied Biological Sciences (LaSABA), Higher Institute of Agricultural Professions (ISMA), University of Kara, Kara, Togo, ²Togolese Agricultural Research Institute (ITRA), Lomé, Togo, ³West Africa Centre for Crop Improvement (WACCI), University of Ghana (UG), Accra, Ghana, ⁴Institut de l'Environnement et de Recherches Agricoles (INERA), Ouagadougou, Burkina Faso, ⁵Biotechnology Centre, University of Ghana (UG), Accra, Ghana

Introduction: Tomato (*Solanum lycopersicum* L.) is one of the most important vegetable crops worldwide, yet its production is constrained by limited knowledge of locally cultivated varieties. Breeding of high-performing varieties requires a clear understanding of available genetic resources. This study aimed to characterize tomato accessions cultivated in Togo based on morphotype variation, with implications for conservation and genetic improvement.

Methods: A total of forty-five (45) accessions collected across the country were phenotyped under field conditions at the Coastal Agricultural Research Center (CRAL/Davié) station using a randomized complete block design with three replications. A total of eleven morphological traits were recorded according to the tomato crop ontology. Descriptive statistics, multiple correspondence analysis (MCA), and cluster analysis were carried out to assess the germplasm diversity and its structure.

Results and discussion: MCA revealed substantial variability among accessions in plant size, vigor, stem pubescence, foliage density, leaf shape, and severity of Tomato Yellow Leaf Curl Virus (TYLCV) and bacterial wilt. Field evaluation under natural infection conditions indicated that several accessions exhibited tolerance to bacterial wilt (91%) and TYLCV (76%), underscoring their value for genetic improvement programs. Cluster analysis revealed five distinct morphotypes, highlighting considerable diversity among the accessions. Morphotype 1 (6 accessions) comprised large, vigorous genotypes susceptible to TYLCV but tolerant to bacterial wilt, whereas morphotype 2 (18 accessions) included intermediate, vigorous genotypes with the inverse response. Morphotype 3 was represented by a single, distinct accession exhibiting tolerance to bacterial wilt. In contrast, morphotypes 4 (13 accessions) and 5 (7 accessions) grouped short-statured genotypes exhibiting dual field tolerance, differing in plant vigor and leaf

architecture. The identified polymorphic traits constitute robust phenotypic descriptors for preliminary varietal identification and offer practical entry points for targeted breeding strategies. Collectively, this germplasm provides a valuable genetic reservoir for the development of high-yielding, resilient tomato cultivars adapted to local agro-ecological conditions, with significant implications for enhancing food and nutritional security in Togo.

KEYWORDS

bacterial wilt, morphological characterization, morphotype, Togo, tomato, Tomato Yellow Leaf Curl Virus

Introduction

Tomato (*Solanum lycopersicum* L.) is one of the most widely cultivated vegetable crops worldwide, valued for its nutritional composition, particularly its high content of vitamin C, lycopene, and other bioactive compounds that contribute to human health and food security (Zannou et al., 2024). Beyond its dietary significance, tomato plays a crucial role in agricultural economies, serving as both a subsistence and commercial crop (Grozeva et al., 2021). In sub-Saharan Africa, and particularly in Togo, tomato production is a major source of income for smallholder farmers and an important component of local diets (Kanda et al., 2014; Akintayo et al., 2023).

Globally, tomato production reached approximately 186 million tons on 4.9 million hectares in 2024, with an average yield of 38 t ha⁻¹. In contrast, Togo cultivates about 20,000–25,000 hectares, producing 150,000–200,000 tons annually, with yields of only 7–10 t ha⁻¹, far below the global average (FAOSTAT, 2024). This pronounced productivity gap is largely driven by biotic stresses, notably Tomato Yellow Leaf Curl Virus (TYLCV) and bacterial wilt (Bamazi, 2021). Bacterial wilt, caused by *Ralstonia solanacearum*, is among the most destructive diseases in tropical and subtropical regions and is widespread across West Africa (Sikirou et al., 2022; Paudel et al., 2025). The pathogen is a highly aggressive soil-borne bacterium capable of infecting a wide range of host plants and persisting in soil for extended periods, making its management particularly challenging (Genin and Denny, 2012; Lowe-Power et al., 2018). In Togo, field surveys indicate that the disease is prevalent in most production areas, with incidence exceeding 40% at the plant level and, under severe conditions, leading to total crop failure (Bamazi et al., 2022). Globally, bacterial wilt can cause yield losses ranging from 35% to 90% in tomato, depending on environmental conditions and pathogen pressure (Paudel et al., 2025). Its persistence in soil, broad host range, and high genetic variability further complicate effective control strategies (Genin and Denny, 2012; Lowe-Power et al., 2018). Similarly, TYLCV, a whitefly-transmitted begomovirus, is highly prevalent in West Africa, including Togo, with reports of up to 100% field prevalence and substantial yield losses (Atassé et al., 2018). These combined disease pressures underscore the urgent need to identify and characterize tomato germplasm with enhanced resistance to both bacterial wilt and TYLCV to support the development of resilient, locally adapted varieties.

In addition to these biotic constraints, tomato production in Togo is further limited by restricted access to improved varieties,

suboptimal crop management practices, and inadequate knowledge of the genetic diversity of locally cultivated germplasm (Akintayo et al., 2023). Collectively, these factors reduce productivity, weaken system resilience, and pose significant challenges to the sustainability of tomato cultivation in the country (Bamazi et al., 2022).

Genetic variability is the cornerstone of crop improvement, providing the raw material for breeding programs aimed at enhancing yield, resilience, and adaptability (Rahman et al., 2018; Kumar and Lata, 2025). A comprehensive understanding of morphological diversity within cultivated germplasm is therefore essential for identifying promising genotypes and guiding the development of improved varieties (Badu-Apraku et al., 2015; Glato et al., 2017). Morphological descriptors, when systematically applied, offer a practical and cost-effective means of assessing genetic variation, particularly in resource-constrained settings where molecular tools may not be readily accessible (Rabbi et al., 2014; Kouassi et al., 2023). Such characterization not only facilitates varietal identification (Sattar et al., 2024) but also supports the conservation and sustainable utilization of genetic resources.

Studies across diverse agro-ecological contexts have consistently demonstrated that morphological characterization is a robust and informative approach for elucidating diversity patterns, discriminating morphotypes, and uncovering trait associations aligned with breeding objectives, particularly in settings where access to molecular tools remains constrained (Sinha et al., 2022; Alatawi et al., 2024). In Ghana, Osei et al. (2014) documented substantial phenotypic variability among cultivated tomato accessions, identifying plant vigor, leaf architecture, and fruit attributes as robust proxies for underlying genetic diversity. Consistent with this, Caramante and Rouphael (2024) demonstrated the discriminative power of morphological traits in resolving morphotypes and informing varietal improvement, thereby reinforcing their utility as cost-effective, field-applicable markers for enhancing yield potential, stress resilience, and environmental adaptability.

By contrast, in Togo, systematic germplasm characterization remains limited. Existing studies have largely prioritized agronomic performance and disease pressures; for instance, Akintayo et al. (2023) assessed a small set of tomato hybrids without a comprehensive evaluation of morphological diversity. This knowledge gap constrains the effective exploitation of local genetic resources for breeding. A rigorous documentation and analysis of morphological variation is therefore imperative to underpin tomato improvement programs and to support food security and rural livelihoods in the country.

Accordingly, the present study characterizes a panel of forty-five cultivated tomato accessions collected from diverse agro-ecological zones of Togo using standardized morphological descriptors. Variation in stem architecture, foliar traits, and disease responses was quantified, and multivariate approaches were employed to resolve diversity patterns and population structure. By generating an integrated phenotypic framework, this work provides actionable insights into the available genetic resources, facilitates the identification of superior and resilient genotypes, and informs evidence-based breeding strategies aimed at the sustainable intensification of tomato production in Togo.

Materials and methods

Plant material

A total of forty-five (45) cultivated tomato accessions, collected across the four agro-ecological zones of Togo by the Plant Genetic Resources Unit of the Togolese Institute of Agricultural Research (ITRA), were used as plant material. Detailed information on the accessions and their respective collection sites is presented in Table 1.

Experimental site

The experiment was conducted at the Agronomic Research Station of the Togolese Institute of Agricultural Research (ITRA) in Davié, located along National Road No. 1, approximately 30 km north of Lomé (6°23'5" N, 1°12'18" E; altitude: 76 m). Figure 1 presents maps depicting the location of Togo in West Africa, the country's principal tomato production zones, and the experimental site at the Coastal Agricultural Research Centre (CRAL/Davié).

The site experiences a subequatorial guinean-type climate characterized by two rainy and two dry seasons. The major rainy season extends from mid-March to late July, while the minor rainy season occurs from September to mid-November (Detchinli et al., 2017). Annual rainfall ranges from 1,000 to 1,400 mm, with temperatures varying between 24 °C and 34 °C and relative humidity ranging from 70% to 90%.

The soil at the experimental site is predominantly sandy loam, with coarse sand accounting for more than half of the particle size distribution (Table 2) (Ezui et al., 2016). It is characterized by low organic matter content (1.05%), limited nitrogen (0.41%), and low available phosphorus (10 ppm), indicating poor fertility. The cation exchange capacity is moderate (2.89 cmol·kg⁻¹), with a base saturation of 66%, reflecting a relatively balanced exchange complex dominated by calcium and magnesium. The soil is moderately acidic, with pH values of 5.5 (H₂O) and 4.4 (KCl), which may restrict nutrient availability. Overall, the soil is deep and well-drained but nutrient-deficient, requiring fertilizer inputs to support optimal tomato growth (Ezui et al., 2016).

Experimental design

A randomized complete block design (RCBD) with three replications was employed. Each block comprised 45 plots. Each

TABLE 1 Tomato accessions cultivated in Togo and their respective collection sites.

N°	Code	Vernacular name	Origin
1	TGTA001	Timati	Doufouli
2	TGTA002	Timati Guikoko	Doufouli
3	TGTA003	Timati	Kamina
4	TGTA004	Timati Egnedie	Akparé
5	TGTA005	Timati Lakoulakou	Akparé
6	TGTA006	Timati 4 Côtés	Akparé
7	TGTA007	Tohoun VI	Kouvé
8	TGTA008	Ouaga	Kouvé
9	TGTA009	Akiko	Kouvé
10	TGTA010	Djidji VI	Kpotomé
11	TGTA011	Lobolobouwe	Kpotomé
12	TGTA012	Tohoun VI	Kpotomé
13	TGTA013	Tohoun VI	Kouevi de Gblonkondji
14	TGTA014	Ginlenou	Kouevi de Gblonkondji
15	TGTA015	Koko Kou	Kouevi de Gblonkondji
16	TGTA016	Aliko Kokou	Kouevi de Gblonkondji
17	TGTA017	Lori Taya	Kouevi de Gblonkondji
18	TGTA018	Pagala	Akouvi Kondji
19	TGTA019	Akliko Akouko Kokou	Dzogbepimé
20	TGTA020	Akouko	Kpimé Tomégbé
21	TGTA021	Batrovi	Kpimé Tomégbé
22	TGTA022	Gbato	Kpimé Tomégbé
23	TGTA023	Tohouvi	Kpimé Tomégbé
24	TGTA024	Lori Taya	Kpimé Tomégbé
25	TGTA025	Mendarine	Kpimé Tomégbé
26	TGTA026	Tomato	Kpimé Tomégbé
27	TGTA027	Tomafaale	Bagre
28	TGTA028	Toma Kana	Bagre
29	TGTA029	Toma Kam	Bagre
30	TGTA030	Toma Agouda	Bagre
31	TGTA031	Toma Gnalga	Bagre
32	TGTA032	Timati Gbengbeng	Sabiebou
33	TGTA033	Timati Sonaf	Nandjessi
34	TGTA034	Timati Bobo	Nandjessi
35	TGTA035	Timati Kimoukou	Kolo
36	TGTA036	Timati Kibisou	Kolo
37	TGTA037	Inconnu 1	Agbazi
38	TGTA038	Kamantossi Watir	Natchamba
39	TGTA039	Kamantossi Kpaan	Natchamba
40	TGTA040	Tomakana	Nano Nassiégo
41	TGTA041	Inconnu 2	Davié
42	TGTA042	Tomati	Ebeva
43	TGTA043	Tomati obè	Okou omoutchi
44	TGTA044	Timati	Akpare
45	TGTA045	Yovogbo	Huilehoe

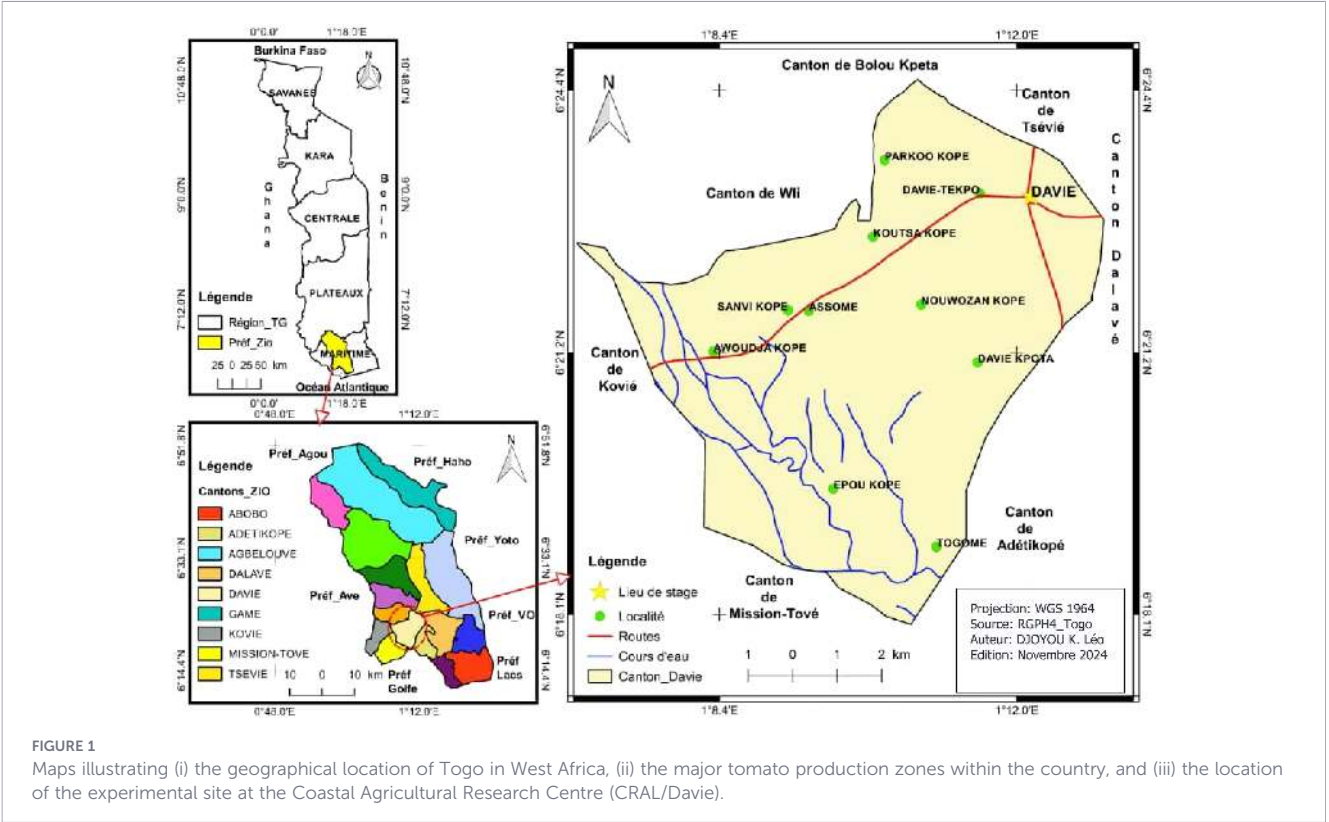


FIGURE 1 Maps illustrating (i) the geographical location of Togo in West Africa, (ii) the major tomato production zones within the country, and (iii) the location of the experimental site at the Coastal Agricultural Research Centre (CRAL/Davie).

plot measured 2.5 m × 1.25 m and contained two rows of five plants. Plots were separated by 0.5 m, while adjacent replications were spaced 2 m apart. Each replication covered an area of 25.75 m × 8.5 m (218.9 m²), resulting in a total experimental area of 759.6 m². The experimental layout and plot arrangement are illustrated in Figure 2.

TABLE 2 Physicochemical properties of experimental site soil.

Parameters	Values	Parameters	Values
Particle size distribution (%)		Exchange complex (%)	
Clay	8.1	Calcium	1.21
Silt	3.8	Magnesium	0.58
Very fine sand	9.3	Potassium	0.12
Fine sand	26.4	Nitrogen	0.01
Coarse sand	52.3	Sum of bases	1.92
Organic matter (%)		Cation exchange capacity	2.89
Organic matter	1.05	Base saturation (V)	66
Carbon	0.61	Acidity	
Total nitrogen	0.41	pH (H ₂ O)	5.5
C/N ratio	15	pH (KCl)	4.4
Phosphorus (ppm)			
Total P	226		
Available P	10		

Trial establishment and management protocol

The experiment was conducted during the rainy season, a period characterized by high rainfall, elevated humidity, and favorable conditions for the proliferation of pests and diseases, thereby providing a relevant context for evaluating tomato accessions under natural disease pressure (Sinha et al., 2022). The subsequent cultural practices included substrate preparation, nursery establishment and maintenance, field preparation, seedling transplanting, and crop management (Alatawi et al., 2024).

Substrate preparation

This involved the collection, sieving, and sterilization of the substrate. The substrate was sterilized by heat treatment (Figure 3) for one hour (Osei et al., 2014) in iron trays, one week prior to nursery establishment.

Nursery establishment and maintenance

The nursery was established in trays filled with sterilized substrate and placed inside a greenhouse to protect the seedlings from pests, heavy rainfall, and strong winds. The trays were thoroughly watered one day prior to sowing. Seeds were treated with Montaz 45 WS, a seed treatment formulation containing imidacloprid (250 g/kg) and thiram (200 g/kg), to provide early protection against insect vectors and seed-borne fungal pathogens. Sowing was done in rows, with inter-row spacing used to separate the accessions. Seedlings were irrigated once daily and remained in the nursery for twenty one (21) days. Figure 4 illustrates the sequential steps involved in nursery establishment.

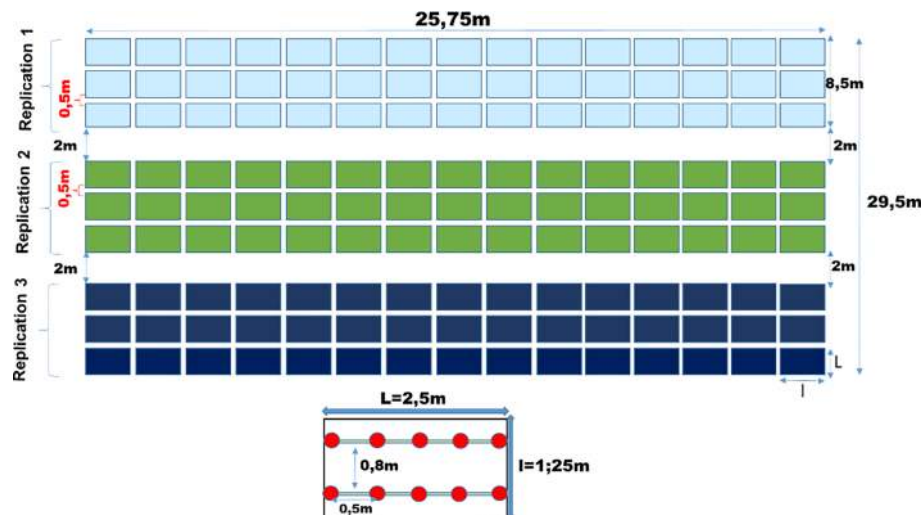


FIGURE 2
Experimental layout and unit design.

Experimental management

The experimental field was ploughed and harrowed to obtain a fine tilth. The field was then divided into three blocks, within which beds were raised manually using hoes. Raised beds were prepared according to the plot dimensions specified in the experimental design. Organic compost was applied at a rate of 20 tons per hectare during beds preparation. Compost was preferred over chemical fertilizer (NPK 15-15-15) to minimize the risk of plant burn under limited rainfall conditions.

Three weeks old healthy seedlings were transplanted in the plots at a plant spacing of 80 cm in between rows and 50 cm within the rows.

Crop maintenance primarily consisted of irrigation, weeding, fertilization, and phytosanitary treatments. Watering was carried out manually using watering cans to maintain adequate soil moisture, twice daily after transplanting, and once daily from the fifth day after transplanting (DAT), due to the low water-retention capacity of the soil (ferralitic soil). Basal fertilization was applied at

15 DAT using NPK (15-15-15), followed by top-dressing with urea at flowering and fruit set stages. Fertilizer rates were applied according to local agronomic recommendations. Weeds were controlled manually by hoeing at regular intervals to reduce competition and maintain field hygiene. The first weeding was performed at 15 DAT and subsequent ones as required. Plants were treated with BANKO PLUS® at a rate of 3 liters per hectare. This broad-spectrum fungicidal formulation, containing carbendazim (12% w/w) and mancozeb (63% w/w), was applied to protect against seed-borne and soil-borne fungal pathogens during early crop establishment and at the onset of flowering. One month after planting, the plants were staked with wooden sticks to support upright growth and minimize lodging.

Phenotypic data collection

Table 3 summarizes the traits recorded during field observations, including growth habit, plant height, main stem pubescence density, plant vigor, foliage density, leaf attitude, and leaf type, as



FIGURE 3
Seedbed preparation process: (a) collection and sieving of the substrate; (b) substrate sterilization; (c) tray filling.



FIGURE 4

Nursery establishment: (a) seeds of the different accessions; (b) stakes with Montaz[®] treatment; (c) row sowing; (d) seedling emergence at 6 days after sowing; (e, f) tomato seedlings at 15 days after sowing.

well as severity scores and percentage disease incidence for Tomato Yellow Leaf Curl Virus (TYLCV) and bacterial wilt. All traits were assessed for each plant within each plot at the vegetative stage (Osei et al., 2014; Dhyani et al., 2019).

TYLCV severity score was assessed at 30 days after transplanting under natural field conditions using a five-class visual scale (Segbefia et al., 2018; Zindović et al., 2025): 1 = no visible symptoms, 2 = mild infection, 3 = moderate infection, 4 = severe infection, and 5 = plant death. No artificial inoculation was performed; thus, the evaluation reflects field tolerance or symptom escape rather than confirmed genetic resistance. Bacterial wilt severity was assessed using the same scale (Kumar et al., 2025).

Disease incidence for both TYLCV and bacterial wilt was determined by recording the number of symptomatic plants per plot throughout the cropping period, based on characteristic symptoms. Percentage disease incidence (PDI) was calculated as (number of infected plants/total number of plants assessed) × 100, with final values recorded at peak disease expression and used for statistical analysis (Pandey et al., 2003).

Statistical analysis

All analyses were conducted in XLSTAT 2024. Raw data were screened for inconsistencies, outliers and missing values prior to analysis. Qualitative traits were encoded as categorical variables following the defined morphological descriptors.

The morphological diversity of the germplasm was assessed through two complementary approaches. First, descriptive analysis

was performed to provide an overview description of the germplasm variation (Caramante and Rouphael, 2024). Frequencies were calculated for categorical variables. Disease severity scores and incidence were analyzed descriptively to characterize accession responses under natural infection conditions.

Subsequently, Multiple Correspondence Analysis (MCA) was applied to identify the most relevant traits explaining variability within the germplasm (Yadav et al., 2025). MCA was chosen because it is the most appropriate multivariate technique for analyzing categorical morphological descriptors, allowing us to capture patterns of association among traits more effectively than alternative methods such as Principal Component Analysis (PCA), which is better suited for continuous variables (Husson et al., 2008). Dimensions were retained based on eigenvalues and the proportion of explained inertia (Greenacre, 2007). Interpretation of axes relied on variable contributions, squared cosine values ($\cos^2$), and v-test statistics. Categories with $v\text{-test} > 1.96$ were considered significantly associated with a given dimension (Lebart et al., 1995). Variables contributing above the average expected contribution and exhibiting high $\cos^2$ values were retained for downstream analyses to define morphotype (Alatawi et al., 2024). Hierarchical clustering was performed on MCA-derived accession coordinates using Ward's minimum variance method with Euclidean distance (Ward, 1963; Dhyani et al., 2019).

The optimal number of clusters (reflecting the intrinsic quality of the partition) was determined based on compactness (accessions within the same group being as similar as possible) and separability (accessions in different groups being as distinct as possible), using

TABLE 3 Plant trait assessment: parts, codes, methods, and rating scales.

N°	Trait	Code	Evaluation method	Rating scale
1	Growth habit	TyCrPlt	Observed across the entire plot after removal of off-type plants	1 = determinate; 2 = indeterminate
2	Plant height	TaiPlt	Visual estimation after observing plants across the plot	3 = short; 5 = intermediate; 7 = tall
3	Pubescence density of the main stem	DenPubTi	Observed across all plants in the plot after removal of off-types; most frequent phenotype recorded	3 = sparse; 5 = intermediate; 7 = dense
4	Plant vigor	VigPlt	Observed across the plot after removal of off-type plants	1 = slender; 2 = weak; 3 = moderately vigorous; 4 = vigorous; 5 = very vigorous
5	Foliage density	DenFeu	Observed across all plants in the plot after removal of off-types; most frequent phenotype recorded	3 = sparse; 5 = intermediate; 7 = dense
6	Leaf attitude	AtFeu	Observed across all plants in the plot after removal of off-types; most frequent phenotype recorded	3 = semi-erect; 5 = horizontal; 7 = drooping
7	Leaf type	TyFeu	Observed across all plants in the plot after removal of off-types; most frequent phenotype recorded	1 = dwarf; 2 = potato leaf type; 3 = standard; 4 = Peruvianum; 5 = Pimpinellifolium; 6 = Hirsutum; 7 = other
8	Severity score of Tomato Yellow Leaf Curl Virus (TYLCV)	Seveviro	Observation of symptom intensity across all plants in the plot	Highly tolerant ($1 \leq \text{score} < 2$); Tolerant ($2 \leq \text{score} < 3$); Susceptible ($3 \leq \text{score} < 4$); Highly susceptible ($4 \leq \text{score} \leq 5$)
9	Severity score of bacterial wilt	Sevbact	Observation of symptom intensity across all plants in the plot	Highly tolerant ($1 \leq \text{score} < 2$); Tolerant ($2 \leq \text{score} < 3$); Susceptible ($3 \leq \text{score} < 4$); Highly susceptible ($4 \leq \text{score} \leq 5$)
10	Percentage disease incidence of TYLCV	TYCLV_PDI	Assess under natural field conditions by recording the number of plants showing typical symptoms (leaf curling, chlorosis, and stunting). Percentage Disease Incidence (PDI) was calculated as: $\text{PDI} (\%) = (\text{Number of symptomatic plants} / \text{Total number of plants assessed}) \times 100$	0% = Highly tolerant 1%-25% = Tolerant 26%-50% = Susceptible 51%-100% = Highly susceptible
11	Percentage disease incidence of Bacterial wilt	BW_PDI	Assess under natural field conditions by recording the number of plants showing typical symptoms (leaf curling, chlorosis, and stunting). Percentage Disease Incidence (PDI) was calculated as: $\text{PDI} (\%) = (\text{Number of symptomatic plants} / \text{Total number of plants assessed}) \times 100$	0% = Highly tolerant 1%-25% = Tolerant 26%-50% = Susceptible 51%-100% = Highly susceptible

the Calinski-Harabasz index (Karna, 2021), which represents the ratio of between-group to within-group inertia. The appropriate number of clusters was selected by maximizing the Calinski-Harabasz criterion (Jain and Kumar, 2023). Finally, the morphological groups obtained were characterized by cross-referencing the typology with the variables included in the MCA factorial plan.

Results

Description of the germplasm based on morphological traits

The modalities of each trait observed are presented in Figure 5. All accessions (100%) exhibited a determinate growth type. With respect to plant height, nearly half of the accessions (47%) were of intermediate stature, while only 13% were tall. Plant vigor showed greater variability, with 29% of accessions classified as vigorous and 18% as weak (Figure 5).

Stem pubescence analysis revealed a balanced distribution, as 20% of accessions lacked pubescence, 60% displayed intermediate pubescence, and 20% exhibited dense pubescence. This variation may serve as a useful morphological marker for accession differentiation.

Leaf attitude was predominantly semi-erect (49%), followed by horizontal (42%) and drooping (9%), reflecting a tendency toward upright foliage architecture. Foliage density assessment indicated that most accessions (64%) had intermediate foliage, while fewer exhibited sparse (24%) or dense (11%) foliage, suggesting moderate canopy coverage as the prevailing trait. Regarding leaf type, the majority (76%) exhibited the standard type, whereas 20% displayed the potato-leaf type and 4% the Peruvianum type, underscoring the predominance of conventional leaf morphology (Figure 5).

Disease severity scoring demonstrated strong field tolerance within the germplasm. A substantial proportion of accessions (76%) were tolerant to TYLCV, while only 9% were highly susceptible. Similarly, 91% of accessions were tolerant to bacterial wilt, with 9% classified as susceptible (Figure 5).

Morphological variability of accessions

Table 4 summarizes detailed variable contributions derived from the Multiple Correspondence Analysis (MCA). The analysis identified five principal axes that together explained 80.86% of the total variability. Seven descriptors plant height, vigor, stem pubescence, foliage density, leaf type, and tolerance/susceptibility to TYLCV and bacterial wilt emerged as the most distinctive traits differentiating the accessions (Tables 5, 6).

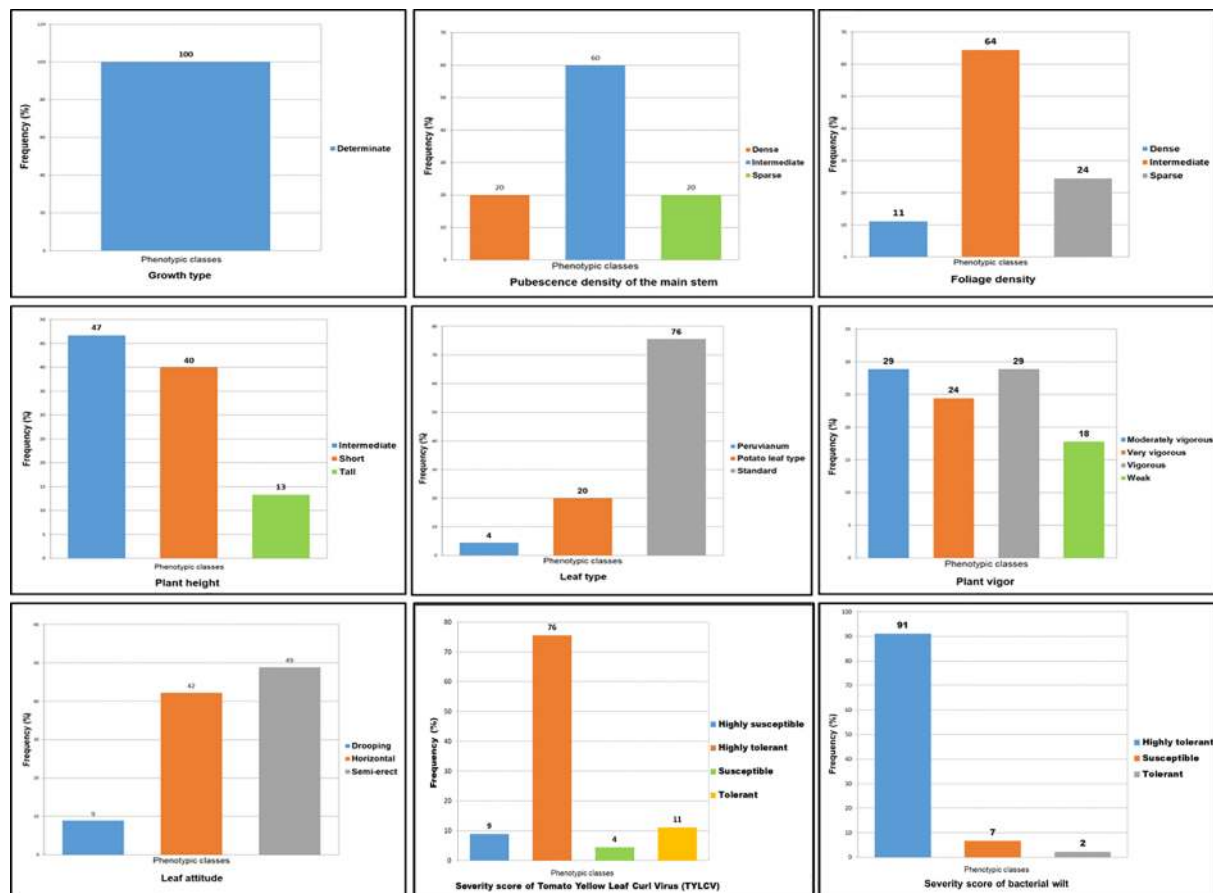


FIGURE 5
Distribution of morphological traits among tomato accessions.

Axis F1, accounting for 38.57% of the variability, was defined by plant height, vigor, stem pubescence, and foliage density, underscoring the dominant role of vegetative traits. Axis F2 (18.62%) further captured variation in stem pubescence and vigor, with smaller plant size negatively correlated, reinforcing the importance of vegetative development. Axis F3 (9.87%) was associated with bacterial wilt tolerance, effectively distinguishing tolerant from susceptible accessions. Axis F4 (8.48%) separated leaf types, highlighting morphological diversity across standard, potato-leaf, and peruvianum forms. Axis F5 (5.30%) was linked to TYLCV susceptibility, indicating viral tolerance as a secondary but relevant source of variability.

Identification and characterization of morphotypes

Hierarchical clustering, evaluated using the Calinski-Harabasz index (Table 7) as a measure of partition quality, revealed five morphotypes (Figures 6, 7). Each morphotype represents a group of accessions sharing similar morphological profiles. Morphotype 2 was the largest cluster, comprising 18 accessions, while morphotype 3 contained only a single accession (TGTA006), underscoring its distinct morphological profile. Morphotypes 1, 4, and 5 represented intermediate clusters with 6, 13, and 7 accessions, respectively (Figure 6). The distribution of variance and centroid distances confirmed the robustness of the five-class partition, with

morphotype 3 showing perfect homogeneity (variance = 0), highlighting its uniqueness within the germplasm (Table 8).

Integration of clustering results with the MCA factorial plan (Figure 8) enabled detailed characterization of these morphotypes. Morphotype 1 comprised large, vigorous accessions highly susceptible to TYLCV but tolerant to bacterial wilt (Figures 6, 8).

Morphotype 2 comprised intermediate-sized, vigorous accessions with sparse pubescence, intermediate foliage density, and standard leaf type, tolerant to TYLCV but susceptible to bacterial wilt. Morphotype 3, highly tolerant to bacterial wilt, was represented by a single accession, reflecting its unique profile. Morphotype 4 included short accessions with moderate vigor, sparse pubescence, sparse foliage density, potato-leaf type, and tolerance to both TYLCV and bacterial wilt. Morphotype 5 consisted of short, weak accessions with sparse pubescence, sparse foliage density, drooping leaf attitude, and tolerance to both TYLCV and bacterial wilt.

Discussion

Morphological diversity of the germplasm

Genetic variability constitutes the cornerstone of plant breeding, providing the essential raw material for selection, genetic

TABLE 4 Eigenvalues, explained variability, and contributions of variables to the first five multiple correspondence analysis (MCA) dimensions.

Variable	F1	F2	F3	F4	F5
Eigenvalue	4.147	2.071	2.038	1.032	1.020
Variability (%)	38.576	18.620	9.875	8.488	5.307
Cumulative (%)	38.576	57.196	67.071	75.559	80.866
Growth type-determinate growth	0,000	0,000	0,000	0,000	0,000
Plant height – Tall	8,965	5,088	0,071	0,097	11,424
Plant height – Intermediate	1,512	11,743	0,616	0,274	1,495
Plant height – Short	9,344	5,755	0,482	0,149	0,398
Stem pubescence – Dense	8,656	4,611	0,493	2,028	1,785
Stem pubescence – Sparse	5,177	1,779	4,825	12,134	0,080
Stem pubescence – Intermediate	0,148	4,039	0,744	8,027	0,370
Foliage density – Dense	12,879	8,265	1,526	0,684	1,443
Foliage density – Sparse	10,207	6,152	0,498	0,602	1,891
Foliage density – Intermediate	0,228	7,405	0,006	0,675	1,811
Plant vigor – Weak	6,738	5,741	11,518	5,472	0,004
Plant vigor – Moderately vigorous	1,795	0,036	11,774	3,213	2,705
Plant vigor – Very vigorous	13,080	3,296	0,003	0,161	0,030
Plant vigor – Vigorous	0,002	11,287	0,520	0,169	2,358
TYLCV severity – Highly tolerant	0,249	0,657	0,187	2,220	4,037
TYLCV severity – Susceptible	0,322	0,312	2,220	1,840	0,599
TYLCV severity – Tolerant	0,102	0,010	1,946	16,364	3,543
TYLCV severity – Highly susceptible	2,247	7,018	1,829	1,296	18,494
TYLCV_PDI – Highly tolerant	0,269	0,648	0,189	2,228	4,045
TYLCV_PDI – Susceptible	0,327	0,316	2,224	1,843	0,560
TYLCV_PDI – Tolerant	0,106	0,011	1,950	16,366	3,548
TYLCV_PDI– Highly susceptible	2,252	7,020	1,830	1,298	18,498
Bacterial wilt severity – Highly tolerant	0,043	0,290	2,431	0,153	0,839
Bacterial wilt severity – Susceptible	0,083	6,625	25,226	1,321	0,164
Bacterial wilt severity – Tolerant	3,312	1,017	1,648	0,263	43,101
Bacterial wilt_PDI – Highly tolerant	0,047	0,294	2,435	0,155	0,840
Bacterial wilt_PDI– Susceptible	0,086	6,630	25,230	1,325	0,168
Bacterial wilt_PDI– Tolerant	3,315	1,019	1,646	0,261	43,105
Leaf attitude – Horizontal	1,014	0,043	12,395	0,125	0,495
Leaf attitude – Semi-erect	2,424	0,555	8,311	0,004	0,987
Leaf attitude – Drooping	2,123	4,844	0,832	0,387	0,634
Leaf type – Peruvianum	0,879	0,779	5,246	35,852	1,045
Leaf type – Standard	2,274	0,326	1,960	0,021	0,168
Leaf type – Potato leaf type	6,197	2,326	2,694	6,471	0,099

Traits that contributed most to the variation of a particular component are in bold.

improvement, and adaptation (Yadav et al., 2025). Demonstrating diversity in agro-morphological traits is therefore a critical prerequisite for genetic enhancement programs (Caramante and Rouphael, 2024). Comprehensive knowledge of accession characteristics not only facilitates germplasm management and conservation but also enhances its effective utilization in varietal development (Alatawi et al., 2024).

The present study revealed substantial variability among accessions in traits such as plant height, vigor, stem pubescence, foliage density, leaf orientation, and disease severity scores. These polymorphic attributes serve as reliable descriptors for varietal identification and registration, thereby strengthening the genetic basis for breeding initiatives. Comparable findings have been reported in tomato germplasm from Burkina Faso, where agromorphological

TABLE 5 Squared cosine ($\cos^2$) values of variable categories on the first two dimensions of the MCA.

Variable	F1	F2	F3	F4	F5
Growth type-determinate growth	0,000	0,000	0,000	0,000	0,000
Plant height – Tall	0,618	0,169	0,001	0,001	0,108
Plant height – Intermediate	0,180	0,674	0,019	0,007	0,024
Plant height – Short	0,733	0,218	0,010	0,003	0,004
Stem pubescence – Dense	0,635	0,163	0,009	0,033	0,018
Stem pubescence – Sparse	0,438	0,073	0,105	0,226	0,001
Stem pubescence – Intermediate	0,030	0,389	0,038	0,352	0,010
Foliage density – Dense	0,700	0,217	0,021	0,008	0,011
Foliage density – Sparse	0,692	0,201	0,009	0,009	0,018
Foliage density – Intermediate	0,046	0,722	0,000	0,030	0,050
Plant vigor – Weak	0,470	0,193	0,206	0,084	0,000
Plant vigor – Moderately vigorous	0,220	0,002	0,369	0,087	0,046
Plant vigor – Very vigorous	0,833	0,101	0,000	0,002	0,000
Plant vigor – Vigorous	0,000	0,633	0,015	0,004	0,038
TYLCV severity – Highly tolerant	0,096	0,123	0,019	0,189	0,215
TYLCV severity – Susceptible	0,036	0,017	0,063	0,045	0,009
TYLCV severity – Tolerant	0,011	0,001	0,056	0,404	0,055
TYLCV severity – Highly susceptible	0,196	0,296	0,041	0,025	0,223
TYLCV_PDI – Highly tolerant	0,094	0,124	0,020	0,190	0,218
TYLCV_PDI – Susceptible	0,038	0,019	0,064	0,048	0,009
TYLCV_PDI – Tolerant	0,014	0,001	0,058	0,406	0,054
TYLCV_PDI– Highly susceptible	0,198	0,297	0,044	0,024	0,225
Bacterial wilt severity – Highly tolerant	0,039	0,130	0,577	0,031	0,107
Bacterial wilt severity – Susceptible	0,007	0,275	0,555	0,025	0,002
Bacterial wilt severity – Tolerant	0,286	0,042	0,036	0,005	0,511
Bacterial wilt_PDI – Highly tolerant	0,040	0,129	0,578	0,030	0,109
Bacterial wilt_PDI– Susceptible	0,008	0,272	0,556	0,024	0,002
Bacterial wilt_PDI– Tolerant	0,284	0,045	0,038	0,006	0,512
Leaf attitude – Horizontal	0,154	0,003	0,481	0,004	0,010
Leaf attitude – Semi-erect	0,368	0,041	0,323	0,000	0,021
Leaf attitude – Drooping	0,199	0,219	0,020	0,008	0,008
Leaf type – Peruvianum	0,074	0,032	0,114	0,668	0,012
Leaf type – Standard	0,580	0,040	0,128	0,001	0,006
Leaf type – Potato leaf type	0,500	0,091	0,056	0,115	0,001

$\cos^2$ values indicate the quality of representation of each category on the axes, with higher values reflecting better representation.

diversity was similarly pronounced (Sondo, 2017). Studies in Ghana revealed substantial genetic variability in tomato germplasm using morphological traits (Osei et al., 2014) and SSR markers (Gongolee, 2016), highlighting the importance of varietal identification for breeding and conservation. In Nigeria, evaluations of growth and yield diversity among local tomato germplasm demonstrated clear differentiation in phenotypic traits (Adeyemo and Olukanmi, 2014), supporting the role of morphotype classification in guiding selection strategies. Research in Asia has shown both inter and intra genetic diversity among tomato genotypes, integrating morpho-molecular and biochemical analyses (Alatawi et al., 2024). These

findings emphasize the versatility of tomato as a model species and confirm the global relevance of morphotype-based diversity studies.

Interestingly, all accessions evaluated in this study exhibited determinate growth, characterized by restricted vegetative development. This uniformity is particularly advantageous for agronomic evaluation across tomato production systems in Togo. In contrast, Sondo (2017) documented 69.7% indeterminate growth in Burkina Faso, underscoring differences in allelic richness and production practices between regions. Plant height variation was notable, with 47% of accessions classified as intermediate and 13% as tall. Such variation may be attributed to the genotype of accessions.

TABLE 6 V-test statistics of variable categories across the first two dimensions of the Multiple Correspondence Analysis (MCA).

Variable	F1	F2	F3	F4	F5
Growth type	0.000	0.000	0.000	0.000	0.000
Plant height – Tall	8.965	5.088	0.071	0.097	11.424
Plant height – Intermediate	1.282	-2.483	0.414	-0.256	0.473
Plant height – Short	-3.006	1.639	-0.345	0.178	0.230
Stem pubescence – Dense	2.506	1.271	-0.303	0.569	0.422
Stem pubescence – Sparse	-1.938	0.789	0.946	1.391	-0.089
Stem pubescence – Intermediate	-0.464	-1.682	-0.526	-1.601	-0.272
Foliage density – Dense	2.899	1.614	0.505	0.314	0.360
Foliage density – Sparse	-2.800	1.510	-0.313	0.319	0.447
Foliage density – Intermediate	0.610	-2.415	-0.050	-0.492	-0.638
Plant vigor – Weak	-2.180	1.398	1.442	-0.922	0.020
Plant vigor – Moderately vigorous	-1.210	-0.119	-1.568	0.759	0.551
Plant vigor – Very vigorous	3.169	1.105	0.023	-0.165	-0.057
Plant vigor – Vigorous	0.044	-2.108	0.330	0.174	-0.515
TYLCV severity – Highly tolerant	-0.769	-0.868	0.337	-1.077	1.148
TYLCV severity – Susceptible	-0.442	-0.302	-0.587	0.496	0.224
TYLCV severity – Tolerant	0.258	0.055	-0.570	1.533	-0.564
TYLCV severity – Highly susceptible	1.196	1.469	0.546	-0.426	-1.273
TYLCV_PDI – Highly tolerant	-0.759	-0.878	0.347	-1.067	1.158
TYLCV_PDI – Susceptible	-0.452	-0.309	-0.577	0.499	0.229
TYLCV_PDI – Tolerant	0.268	0.058	-0.581	1.543	-0.574
TYLCV_PDI – Highly susceptible	1.126	1.479	0.556	-0.439	-1.282
Bacterial wilt severity – Highly tolerant	-0.527	0.949	-2.015	-0.469	-0.868
Bacterial wilt severity – Susceptible	-0.227	-1.425	2.004	0.425	-0.118
Bacterial wilt severity – Tolerant	1.402	0.554	0.500	0.185	1.876
Bacterial wilt_PDI – Highly tolerant t	-0.525	0.955	-2.026	-0.471	-0.874
Bacterial wilt_PDI – Susceptible	-0.229	-1.435	2.009	0.429	-0.128
Bacterial wilt_PDI – Tolerant	1.407	0.558	0.502	0.198	1.869
Leaf attitude – Horizontal	-1.009	-0.145	-1.785	0.166	-0.262
Leaf attitude – Semi-erect	1.659	-0.551	1.554	-0.032	0.393
Leaf attitude – Drooping	-1.163	1.220	0.368	-0.233	-0.236
Leaf type – Peruvianum	-0.731	-0.478	0.903	2.189	-0.295
Leaf type – Standard	2.323	-0.611	-1.091	-0.104	0.234
Leaf type – Potato leaf type	-2.120	0.902	0.707	-1.016	-0.100

Values indicate the strength and direction of association between categories and axes; categories with $|v\text{-test}| > 1.96$ are significantly associated ($p < 0.05$). Bold values indicate statistical significance at $\alpha = 0.05$.

Variation in vigor was also evident, with 29% of accessions displaying high vigor and 18% exhibiting low vigor. Stem pubescence demonstrated polymorphism, with 20% of accessions lacking pubescence and another 20% exhibiting dense pubescence. These traits are of particular interest, as pubescence has been associated with pest resistance and microclimate regulation, thereby influencing adaptation to humidity and temperature fluctuations. This observation is consistent with previous reports linking pubescence to insect deterrence and enhanced resilience under variable climatic conditions (Dhyani et al., 2019).

Leaf orientation exhibited considerable diversity, with 49% semi-erect, 42% horizontal, and 9% drooping. Such variation may

directly influence photosynthetic efficiency and water-use dynamics. Foliage density was predominantly intermediate (64%), a desirable trait that optimizes photosynthesis, fruit productivity, weed suppression, and reduced evapotranspiration (Dhyani et al., 2019). Collectively, these morphological attributes highlight the adaptive potential of the germplasm under diverse agro-ecological conditions.

Tolerance levels against major biotic stresses were particularly promising. These results emphasize the overall resilience of the germplasm to major biotic stresses, reinforcing its potential value for breeding programs targeting disease resistance. A majority of

TABLE 7 Evolution of statistical indices assessing partition quality across cluster numbers (K).

Number of clusters (K)	2	3	4	5
Silhouette index	0.369	0.262	0.274	0.291
Hartigan index (H)	12.614	10.142	9.612	12.166
H (k–1) – H(k)	1.360	2.472	0.531	–2.554
Calinski–Harabasz index	13.975	15.182	15.705	16.656

Calinski–Harabasz index increased steadily with the number of classes, reaching its maximum at five, thereby supporting the selection of five morphotypes as the optimal partition. Although Silhouette index values remained relatively low, they were consistent across K, while the Hartigan index exhibited fluctuations. Taken together, these indices confirm that the five-class solution provides the most robust and biologically meaningful grouping of accessions.

accessions (91%) demonstrated field tolerance to bacterial wilt, while 76% exhibited tolerance to Tomato Yellow Leaf Curl Virus (TYLCV), a disease transmitted by whiteflies. These findings align with recent studies reporting genetic tolerance to TYLCV in tomato hybrids and improved lines (Alatawi et al., 2024). The early manifestation of bacterial wilt symptoms corroborates observations by Bamazi et al. (2022). Furthermore, genome-wide association studies have identified SNP markers linked to bacterial wilt resistance, confirming its heritable basis (Bhunchoth et al., 2025).

The observed variability underscores the immense potential of this germplasm for breeding programs aimed at enhancing agronomic performance and resilience to TYLCV and bacterial wilt. However, a limitation of this study is that agronomic data related to fruit yield and quality were not evaluated. As a result, while morphotype diversity and field tolerance to diseases were documented, the findings cannot be directly linked to productivity or market traits. To strengthen conservation and breeding programs, future studies should integrate comprehensive agronomic evaluations including yield, fruit quality, and post-harvest traits alongside morphotype characterization. This combined approach will provide a more holistic understanding of accession performance and ensure

that promising morphotypes also meet productivity and market demands. Future research should also prioritize controlled screening under artificial infestation, coupled with molecular characterization through marker-assisted selection. Such integrative approaches will be essential to validate resistance traits and accelerate their deployment in tomato improvement programs.

Identification and characterization of morphotypes

The morphotype-based classification of tomato accessions highlights substantial phenotypic and functional diversity within the germplasm, with important implications for both conservation and genetic improvement in Togo.

Morphotype 1 made of six accessions is characterized by large, highly vigorous plants, indicative of strong vegetative growth and potential for high biomass and yield. However, these genotypes were susceptible to Tomato Yellow Leaf Curl Virus while exhibiting tolerance to Bacterial wilt. This contrasting response suggests a possible trade-off between growth-related traits and viral resistance, a phenomenon often reported in crop improvement studies where resource allocation to rapid growth may compromise defense mechanisms against certain pathogens (Foolad, 2007). The tolerance to bacterial wilt may be associated with root system architecture or physiological adaptations that limit pathogen proliferation in vascular tissues (Scott et al., 2005). Consequently, Morphotype 1 represents a valuable genetic pool for improving yield potential and bacterial wilt tolerance, although the incorporation of TYLCV resistance genes remains necessary.

Morphotype 2 composed of 18 accessions, the most represented group, comprises genotypes with intermediate plant size but sustained vigor. These accessions exhibited tolerance to TYLCV but were susceptible to bacterial wilt, indicating an inverse disease response compared to Morphotype 1. The prevalence of this morphotype may reflect farmer-driven selection for TYLCV

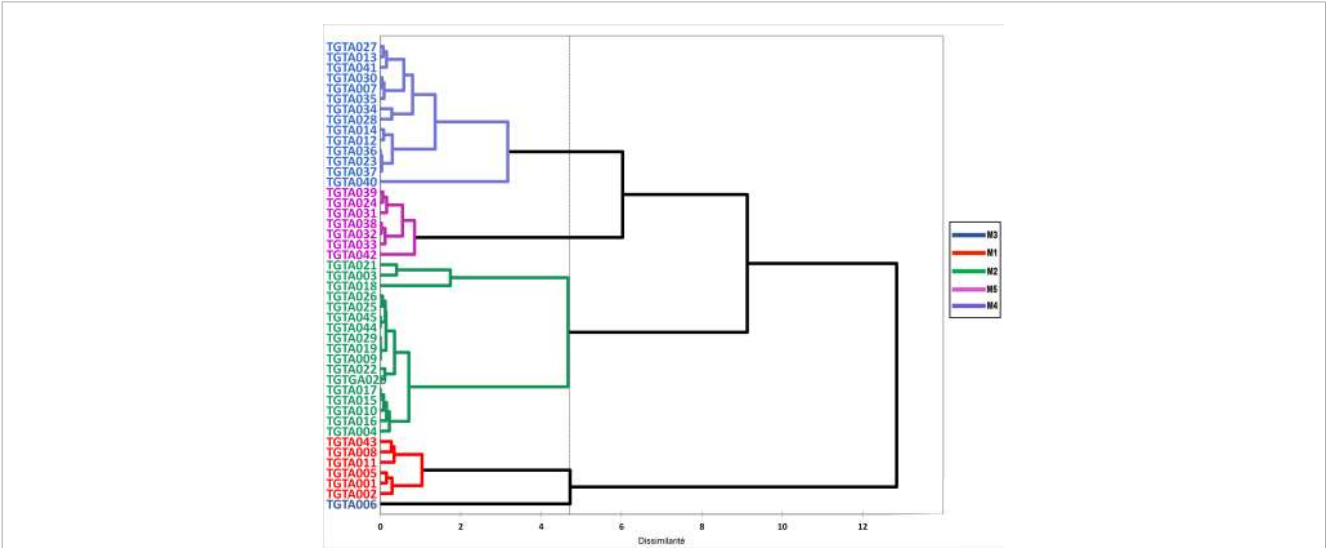
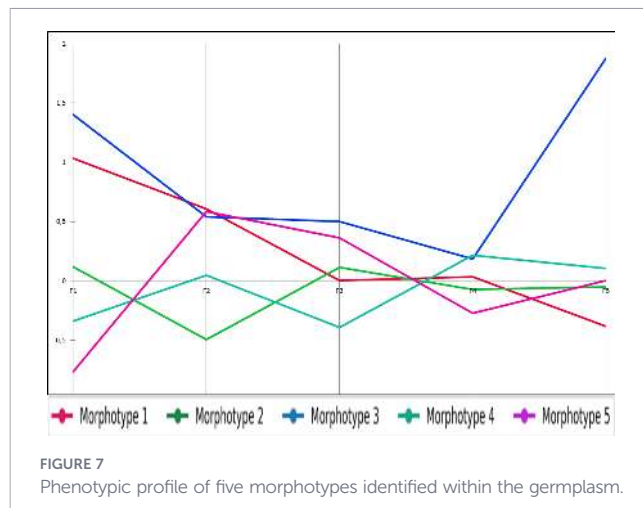


FIGURE 6 Cluster dendrogram of 45 tomato accessions showing five morphotypes. Branching structure highlights the relative similarity among accessions based on the most relevant morphological traits, with five major clusters identified as the optimal partition according to the Calinski-Harabasz index. M1: Morphotype 1, M2: Morphotype 2, M3: Morphotype 3, M4: Morphotype 4, M5: Morphotype 5.



tolerance, given the widespread and economically significant impact of this viral disease in tropical and subtropical regions (Hanssen et al., 2010). The observed TYLCV tolerance suggests the presence of resistance loci, such as *Ty* genes, which have been widely deployed in breeding programs (Prasanna et al., 2015). However, the susceptibility to bacterial wilt underscores the need to integrate resistance to soil-borne pathogens, which remain a major constraint to tomato production in humid environments.

Morphotype 3, represented by a single accession (TGTA006), exhibited a particularly high level of tolerance to bacterial wilt, distinguishing it from all other groups. This strong tolerance

suggests the presence of robust and potentially unique genetic factors conferring effective defense against *Ralstonia solanacearum*. Given that bacterial wilt is one of the most destructive soil-borne diseases affecting tomato in tropical environments, the identification of such a highly resistant genotype is of considerable importance for breeding programs.

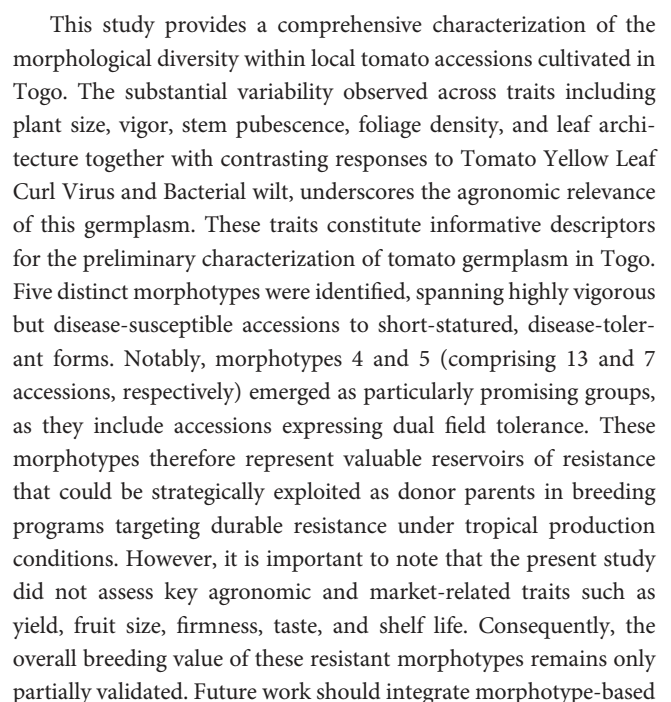
The singularity of morphotype 3 further indicates that this accession may harbor rare alleles or novel resistance mechanisms that are absent in the broader germplasm collection. Resistance to bacterial wilt is often quantitatively inherited and influenced by multiple genes, making the discovery of highly resistant sources particularly valuable for gene pyramiding strategies (Scott et al., 2005). Therefore, this morphotype should be prioritized for conservation and advanced characterization, including molecular analysis to identify resistance loci and validate its stability across environments. From a breeding perspective, morphotype 3 represents an elite donor parent for the introgression of bacterial wilt resistance into high-yielding but susceptible backgrounds. Its integration into crossing programs, particularly with morphotypes combining desirable agronomic traits or resistance to other diseases such as Tomato Yellow Leaf Curl Virus, could accelerate the development of improved tomato cultivars with durable, broad-spectrum resistance.

Morphotypes 4 (13 accessions) and 5 (seven accessions) consist of short-statured genotypes that exhibited combined resistance to both TYLCV and bacterial wilt. These morphotypes are particularly valuable for the development of resilient varieties adapted to low-input systems. Reduced plant height may confer agronomic

TABLE 8 Morphotypes composition derived from cluster analysis.

Morphotypes	Morphotype 1	Morphotype 2	Morphotype 3	Morphotype 4	Morphotype 5
Number of accessions	6	18	1	13	7
Sum of weights	6	18	1	13	7
Within-class variance	0.420	0.532	0.000	0.555	0.294
Minimum distance to centroid	0.452	0.235	0.000	0.366	0.307
Mean distance to centroid	0.582	0.584	0.000	0.636	0.471
Maximum distance to centroid	0.779	1.942	0.000	1.712	0.854
Accessions	TGTA001 TGTA002 TGTA005 TGTA008 TGTA011 TGTA043	TGTA003 TGTA004 TGTA009 TGTA010 TGTA013 TGTA015 TGTA016 TGTA017 TGTA018 TGTA019 TGTA020 TGTA021 TGTA022 TGTA025 TGTA026 TGTA029 TGTA044 TGTA045	TGTA006	TGTA007 TGTA012 TGTA014 TGTA023 TGTA027 TGTA028 TGTA030 TGTA034 TGTA035 TGTA036 TGTA037 TGTA040 TGTA041	TGTA024 TGTA031 TGTA032 TGTA033 TGTA038 TGTA039 TGTA042

Accessions in bold represent the central objects of each morphological group.



classification with comprehensive evaluations of yield components, fruit physicochemical quality, and market-preferred traits across multiple environments. Coupling these phenotypic assessments with high-resolution molecular characterization will enable the dissection of the genetic architecture underlying both adaptive and productivity-related traits, facilitate marker-assisted selection, and support the development of high-performing, climate-resilient tomato varieties adapted to the agro-ecological conditions of Togo.

Data availability statement

The original contributions presented in the study are included in the article/supplementary material. Further inquiries can be directed to the corresponding author.

Ethics statement

Written informed consent was obtained from the individual(s) for the publication of any potentially identifiable images or data included in this article.

Author contributions

GT: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Resources, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing. DL: Conceptualization, Data curation, Formal Analysis, Investigation, Methodology, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing. PK: Supervision, Visualization, Writing – review & editing. AA: Conceptualization, Data curation, Investigation, Methodology, Software, Supervision, Validation, Visualization, Writing – original draft, Writing – review & editing. KS: Methodology, Supervision, Validation, Visualization, Writing – review & editing. DD: Methodology, Supervision, Validation, Visualization, Writing – review & editing. TA: Conceptualization, Supervision, Validation, Visualization, Writing – review & editing.

References

- Adeyemo, O., and Olukanmi, B. (2014). Assessment of genetic diversity among selected tomato (*Solanum lycopersicum* L.) lines based on SSR markers. *Sci. Res. Dev.* 15, 54–59.
- Akintayo, T. O., Banito, A., Tchalla, P., Katagna, M., Donatien Kao, M., Kossi Dzinyefa Abotchi, L., et al. (2023). Agronomic characterization of six tomato genotypes in Togo. *Int. J. Advanced Res.* 11, 76–82. doi: 10.21474/ijar01/17364
- Alatawi, I., Xiong, H., Alkabkabi, H., Chiwina, K., Luo, Q., and Ling, K. (2024). Genetic diversity and population structure of tomato (*Solanum lycopersicum*) from the USDA-GRIN germplasm collection. *Agronomy* 15, 1–12. doi: 10.3390/agronomy15010022
- Atassé, K., Assion, S. M., Adjata, K. D., Duclercq, J., and Muller, E. (2018). Occurrence of tomato leaf curl virus on cassava (*Manihot esculenta* Crantz) in Togo. *Int. J. Agriculture Environ. Biores.* 3, 171–187. Available online at: <https://hal.science/hal-04426157v1>.
- Badu-Apraku, B., Fakorede, M. A. B., Gedil, M., Talabi, A. O., Annor, B., Oyekunle, M., et al. (2015). Heterotic responses among crosses of IITA and CIMMYT early white maize inbred lines under multiple stress environments. *Euphytica* 206. doi: 10.1007/s10681-015-1506-0
- Bai, Y., and Lindhout, P. (2007). Domestication and breeding of tomatoes: What have we gained and what can we gain in the future? *Ann. Bot.* 100, 1085–1094. doi: 10.1093/aob/mcm150
- Bamazi, B. (2021). Diagnostic des maladies fongiques et bactériennes de la tomate (*Solanum lycopersicum* L.) et approches de lutte dans la Région Centrale du Togo, Thèse de doctorat, Phytopathologie, Lomé, Université de Lomé: 169p.
- Bamazi, B., Banito, A., Ayisah, K. D., Sikirou, R., Paret, M. L., Kunwar, S., et al. (2022). Distribution and incidence of tomato bacterial wilt caused by *Ralstonia solanacearum*

Funding

The author(s) declared that financial support was not received for this work and/or its publication.

Acknowledgments

The authors gratefully acknowledge the support of local farmers and agricultural technicians in Togo for their assistance in collecting tomato accessions. Appreciation is also extended to colleagues and research staff who contributed to data collection and analysis.

Conflict of interest

The author(s) declared that this work was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Generative AI statement

The author(s) declared that generative AI was not used in the creation of this manuscript.

Any alternative text (alt text) provided alongside figures in this article has been generated by Frontiers with the support of artificial intelligence and reasonable efforts have been made to ensure accuracy, including review by the authors wherever possible. If you identify any issues, please contact us.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

- in the Central Region of Togo. *Plant Health Prog.* 23, 235–240. doi: 10.1094/PHP-09-21-0117-S
- Bhunchoth, A., Poncheewin, W., Yongsuwan, A., Chiangta, J., Thunnom, B., Aesomnuk, W., et al. (2025). Genome-wide association analysis and breeding-oriented SNP marker development for bacterial wilt resistance in tomato (*Solanum lycopersicum* L.). *Plants* 14, 3036. doi: 10.3390/plants14193036
- Caramante, M., and Roupheal, Y. (2024). Genetic diversity among and within tomato (*Solanum lycopersicum* L.) landraces grown in Southern Italy. *Genet. Resour. Crop Evol.* 71, 157–166. doi: 10.1007/s10722-023-01613-9
- Detchinli, K. S., Sogbedji, M. J., Atchoglo, R., and Bona, K. A. (2017). Modelisation des doses économiques optimales du fumier de ferme en culture du maïs (*Zea mays* L.) sur les sols ferrallitiques au Togo. *Rev. Ceres* 5, 52–58.
- Dhyani, S., Singh, D., and Singh, J. P. (2019). Genetic diversity studies in tomato (*Solanum lycopersicum* L.). *Int. J. Curr. Microbiol. App Sci.* 8, 2750–2755. doi: 10.20546/ijcmas.2019.802.322
- Ezui, K. S., Franke, A. C., Mando, A., Ahiabor, B. D. K., Tetteh, F. M., Sogbedji, J., et al. (2016). Fertiliser requirements for balanced nutrition of cassava across eight locations in West Africa. *Field Crops Res.* 185, 69–78. doi: 10.1016/j.fcr.2015.10.005
- FAOSTAT (2024). Crop production, yield, harvested area (Global - national - annual). Available online at: <https://www.fao.org/faostat/en/#data/QCL> (Accessed April 24, 2026).
- Foolad, M. R. (2007). Genome mapping and molecular breeding of tomato. *Int. J. Plant Genomics*, 64358. doi: 10.1155/2007/64358
- Genin, S., and Denny, T. P. (2012). Pathogenomics of the *Ralstonia solanacearum* species complex. *Annu. Rev. Phytopathol.* 50, 67–89. doi: 10.1146/annurev-phyto-081211-173000
- Glato, K., Aidam, A., Kane, N. A., Bassirou, D., Couderc, M., Zekraoui, L., et al. (2017). Structure of sweet potato (*Ipomoea batatas*) diversity in West Africa covaries with a climatic gradient. *PLoS One* 12, 1–17. doi: 10.1371/journal.pone.0177697
- Gongolee, G. A. K. (2016). Assessment of genetic variation among some introduced tomato (*Solanum lycopersicum* L.) varieties using SSR markers. *Agric. Food. Sci. J. Ghana* 9, 686–695.
- Greenacre, M. (2007). *Correspondence analysis in practice* (Boca Raton, FL, USA: Chapman & Hall/CRC).
- Grozeva, S., Nankar, A. N., Ganeva, D., Tringovska, I., and Pasev, G. (2021). Characterization of tomato accessions for morphological, agronomic, fruit quality, and virus resistance traits. *Can. J. Plant Sci.* 101, 476–489. doi: 10.1139/cjps-2020-0030
- Hanssen, I. M., Lapidot, M., and Thomma, B. P. H. J. (2010). Emerging viral diseases of tomato crops. *Mol. Plant-Microbe Interact.* 23, 539–548. doi: 10.1094/mpmi-23-5-0539
- Husson, F., Josse, J., Le, S., and Mazet, J. (2008). FactoMineR: An R package for multivariate analysis. *J. Stat. Software* 25, 1–18.
- Jain, K., and Kumar, M. (2023). Review on deciding optimal number of clusters in k-means clustering. *Int. J. Novel Res. Dev.* 8, 307–313.
- Kanda, M., Akpavi, S., Wala, K., Djaneye-Boundjou, G., and Akpagana, K. (2014). Diversité des espèces cultivées et contraintes à la production en agriculture maraîchère au Togo. *Int. J. Biol. Chem. Sci.* 8, 115. doi: 10.4314/ijbcs.v8i1.11
- Karna, A. (2021). Automatic identification of the number of clusters in hierarchical clustering. *Neural Comput. Appl.* 34, 119–134. doi: 10.1007/s00521-021-05873-3
- Kumar, H., and Lata, R. (2025). Scientific advances in tomato (*Solanum lycopersicum* L.) cultivation, agronomic innovation and genetic improvement: A comprehensive review. *J. Adv. Biol. Biotechnol.* 28, 781–803. doi: 10.9734/jabb/2025/v28i103103
- Kouassi, J. H. M., Boyé, M. A., Dibi, K. E. B., Essis, B. S., Kouakou, A. M., and Boni, N. (2023). Agronomic evaluation sweet potato (*Ipomoea batatas* (L.) Lam.) genotypes in two agro-ecological zones of Côte d'Ivoire. *World J. Advanced Res. Rev.* 17, 208–218. doi: 10.30574/wjarr.2023.17.2.0194
- Kumar, R., Verma, S. C., Sharma, R., Chauhan, A., and Yadav, A. (2025). Prevalence and transmission potential of tomato yellow leaf curl virus (TYLCV) by whitefly vectors on tomato (*Solanum lycopersicum* L.) in Himachal Pradesh, India. *Plant Sci. Today* 12, 1–11. doi: 10.14719/pst.9254
- Lebart, L., Morineau, A., and Piron, M. (1995). *Statistique exploratoire multidimensionnelle* (Paris, France: Dunod).
- Lowe-Power, T. M., Khokhani, D., and Allen, C. (2018). How *Ralstonia solanacearum* exploits and thrives in the flowing plant xylem environment. *Trends Microbiol.* 26, 929–942. doi: 10.1016/j.tim.2018.06.002
- Osei, M. K., Bonsu, K. O., Agyeman, A., and Choi, H. S. (2014). Genetic diversity of tomato germplasm in Ghana using morphological characters. *Int. J. Plant Soil Sci.* 3, 220–231. doi: 10.9734/IJPSS/2014/6466
- Pandey, K. K., Pandey, P. K., and Kalloo, G. (2003). Assessment of resistance to bacterial wilt in tomato. *Euphytica* 130, 197–205. doi: 10.1023/A:1023059123436
- Paudel, S., Dobhal, S., Alvarez, A. M., and Arif, M. (2025). Advances in understanding the biology and management of *Ralstonia solanacearum*. *Front. Microbiol.* doi: 10.3389/fmicb.2025.1559380
- Prasanna, H. C., Sinha, D. P., Rai, G. K., and Krishna, R. (2015). Pyramiding of resistance genes for tomato leaf curl virus. *Sci. Hortic.* 197, 677–684. doi: 10.1007/s12298-025-01548-8
- Rabbi, I. Y., Hamblin, M. T., Kumar, P. L., Gedil, M. A., Ikpan, A. S., Jannink, J.-L., et al. (2014). High-resolution mapping of resistance to cassava mosaic geminiviruses in cassava using genotyping-by-sequencing and its implications for breeding. *Virus Res.* 186, 87–96. doi: 10.1016/j.virusres.2013.12.028
- Rahman, M. M., Rashid, M. H., Hossain, M. M., and Zakaria, M. (2018). Morphological characterization of tomato (*Solanum lycopersicum* L.) genotypes. *J. Saudi Soc Agric. Sci.* 19. doi: 10.1016/j.jssas.2018.11.001
- Sattar, S., Iqbal, A., Parveen, A., Fatima, E., Samdani, A., Fatima, H., et al. (2024). Tomatoes unveiled: A comprehensive exploration from cultivation to culinary and nutritional significance. *Quies* 10, 1–14. doi: 10.32388/CP4Z4W.2
- Scott, J. W., Wang, J. F., and Hanson, P. (2005). Breeding tomatoes for resistance to bacterial wilt. *Plant Breed. Rev.* 26, 297–338. doi: 10.17660/actahortic.2005.695.18
- Segbefia, M. M., Amoatey, H. M., Ahiakpa, J. K., Quartey, E. K., and Appiah, A. S. (2018). Field evaluation of tomato varieties / breeding lines against tomato yellow leaf curl virus disease (TYLCV). *Agric. Food. Sci.* 41, 423–440.
- Sikirou, R., Zocli, B., and Zinsou, V. (2022). Distribution and impact of bacterial wilt on solanaceous crops in West Africa. *Crop Prot.* 158, 106012. doi: 10.1016/j.cropro.2022.106012
- Sinha, A., Singh, P., Kumar, R., and Bhardwaj, A. (2022). Assessment of genetic diversity for yield and its attributing traits in tomato (*Solanum lycopersicum* L.) genotypes for protected conditions 56, 480–484. doi: 10.18805/IJARE.A-5794
- Sondo, K. (2017). Caractérisation agro-morphologique des morphotypes de tomates issue d'accessions collectées au Burkina Faso. *Diplôme d'ingénieur du développement rural, agronomie, Université Nazi Boni (U.N.B)*, 72.
- Ward, J. H. (1963). Hierarchical grouping to optimize an objective function. *J. Am. Stat. Assoc.* 58, 236–244. doi: 10.2307/2282967
- Yadav, A., Singh, R., Yadav, V., Yadav, L. P., Mishra, D. S., Sahil, A., et al. (2025). Assessment of morphological and molecular diversity in tomato accessions using quantitative traits and RAPD markers. *Sci. Rep.* 15, 37151. doi: 10.1038/s41598-025-21062-x
- Zannou, O., Dedehou, E. S. C. A., Paul, B., Oscar, B., Maqsood, S., and Kayod, P. (2024). Tomato pomace as a source of valuable functional ingredients for improving physicochemical and sensory properties and extending the shelf life of foods: A review. *Heliyon* 10. doi: 10.1016/j.heliyon.2024.e25261
- Zindović, J., Grbin, D., Pul, P., Zwitter, Z. K., Kutnjak, D., and Vučurović, A. (2025). Tomato spotted wilt virus in tomato from Croatia, Montenegro and Slovenia: genetic diversity and evolution. *Front. Microbiol.* 16, 1–14. doi: 10.3389/fmicb.2025.1618327