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RESEARCH ARTICLE

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Deciphering phenotypic diversity within a tomato landrace: the 'Pomodoro di Sorrento' case study

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Abstract 'Pomodoro di Sorrento' – PS (*Solanum lycopersicum* L.) is a traditional Italian tomato landrace which is highly appreciated for its large multilocular pink fruits and distinctive organoleptic quality. In this study, a collection of 10 PS accessions was characterized for morphological, agronomic, and fruit quality traits and compared with three related Italian tomato landraces ('Cuore di Bue', 'Pera di Abruzzo', and 'Pera di Albenga'). The objectives were to (i) define the phenotypic identity of the PS landrace, (ii) assess intra-landrace variability, and (iii) identify key traits for germplasm management and valorization. Multivariate analyses revealed a clear phenotypic distinctiveness of PS compared to the reference landraces while highlighting substantial diversity within the PS collection. Fruit morphology and quality traits emerged as the main features defining the PS ideotype. PS accessions maintained distinct trait combinations and were grouped into three phenotypic clusters by hierarchical clustering. A stepwise discriminant analysis identified pH, a*/b* color ratio, soluble solids content, and glucose concentration as the most informative variables, capturing much of the phenotypic structure of the collection. These results demonstrate that a limited set of quality-related traits can effectively support the classification of newly collected materials and facilitate local germplasm management. Overall, the PS collection represents a coherent, diverse, and non-redundant reservoir of variability. The proposed phenotypic framework provides valuable tools for germplasm conservation, characterization, and valorization while offering a foundation for future breeding efforts aimed at combining varietal typicity, fruit quality, and agronomic performance.

Keywords Breeding · Distinguishability · Fruit quality · Genetic resources · Hierarchical cluster analysis · Intra-landrace variability · On farm conservation

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Introduction

Tomato (*Solanum lycopersicum* L.) stands as the foremost vegetable crop for its economic value worldwide, reaching 136 billion USD of Gross Production Value in 2024 (FAOSTAT 2024). Globally, nearly 5.1 million hectares are cultivated to produce over 188 million tons of fresh tomato (FAOSTAT 2024). This *Solanaceae*-belonging species was probably domesticated in Mexico or Peru and was then introduced in Southern Europe by Spanish explorers during the sixteenth century, being for long mostly used as an ornamental plant due to suspicions of alkaloids in the fruit (Bauchet et al. 2012). Starting from the eighteenth century, tomato was then introduced into the local cuisine of Spain and southern Italy, which are considered secondary centers of its diversification (García-Martínez et al. 2006).

In Italy, due to the highly diverse pedoclimatic, cultural, and political backgrounds, farmers selected several landraces differentiating for fruit morphology and use, some of which are still commonly cultivated in niche agricultural systems (Ercolano et al. 2008; Mazzucato et al. 2010; Sacco et al. 2015; Farinon et al. 2022). Landraces may represent an important asset for local farmers, by satisfying the needs and perspectives of niche agriculture and markets (Lázaro 2018; Asensio et al. 2019). These genetic materials are also very appreciated by consumers for their high organoleptic quality and represent an important source of healthy-related compounds in human diet (Cortés-Olmos et al. 2014; Sinesio et al. 2021; Casals et al. 2024). Furthermore, tomato landraces may be used as gene donors in breeding programs to improve taste and resilience to environmental stressors such as high temperatures and drought (Patanè et al. 2016; Olivieri et al. 2020; Gonzalo et al. 2021; Graci et al. 2025; Juan-Cabot et al. 2025). Several research performed in last 20 years examined the variability in agronomic, quality, and molecular traits among different European traditional tomatoes (Blanca et al. 2022; Pons et al. 2022, 2023), but few investigations focused on the analysis of phenotypic variation at intra-landrace level (Andreakis et al. 2004; Caramante et al. 2009; Mazzucato et al. 2010; Villena et al. 2023a, b; Rico Ferrer et al. 2026). This approach is crucial to unequivocally distinguish a landrace and to obtain the European labels (Protected Designation of Origin – PDO and Protected Geographical Indication – PGI) which guarantee the quality and the authenticity of food products to consumers.

The 'Pomodoro di Sorrento' (also called 'Sorrento', 'Sorrentino' or 'Rosa di Sorrento')–hereafter mentioned as PS–originating from Sorrento peninsula and traditionally also cultivated in the Vesuvian and Agro Sarnese-Nocerino areas (Southern Italy), represents an important multilocular tomato landrace for fresh market (*e.g.*, salad tomato) (Acciarri et al. 2007; Parisi et al. 2008; Pons et al. 2022). This landrace is characterized by large isodiametric fruits with a typical pinkish tone–due to the colorless epidermis (y) mutation (Parisi et al. 2008; Mazzucato et al. 2010)–and great organoleptic qualities that make it greatly appreciated by consumers, who are often willing to pay a premium than commercial modern cultivars (Sinesio et al. 2007; Ercolano et al. 2008; Lisanti et al. 2008). Few investigations have been published on the 'Pomodoro di Sorrento' landrace (Sinesio et al. 2007; Ercolano et al. 2008; Lisanti et al. 2008; García-Martínez et al. 2013), and its first wide description was reported by Parisi et al. (2016) that investigated its diversity focusing on molecular traits and morphological descriptors mainly related to fruit appearance. The analyses were able to discriminate 'Pomodoro di Sorrento' tomato from ten tomato landraces with similar fruit traits or reference saladtomato landraces. To date, the variation of agronomic performance and qualitative traits has not yet been extensively studied within the 'Pomodoro di Sorrento' landrace.

The present work aimed to improve knowledge of the diversity of 'Pomodoro di Sorrento' by assessing intra-landrace phenotypic variability through the analysis of morphological, agronomic, and quality traits. The specific objectives were to (i) establish the phenotypic identity of the landrace in comparison with reference landraces, (ii) investigate the structure of variation within the PS collection, and (iii) identify key traits, promising accessions and a discriminant model supporting its conservation, valorization, and future breeding.

Materials and methods

Crop management and experimental design

A randomized complete block design was carried out to compare ten 'Pomodoro di Sorrento' tomato accessions (PS01, PS02, PS04, PS05, PS06, PS07, PS08, PS09, PS10, and PS11; Table 1) with three reference Italian landraces chosen for their widespread diffusion in Italian market (Cuore di Bue – CBUE; Pera di Abruzzo ‘Red Pear sel. Gigante del Vomano’ – PABR; Pera d’Albenga ‘Sel. Cuore d’Albenga’ – PALB). Nine ‘Pomodoro di Sorrento’ accessions (PS) were collected from local farms, while PABR, PALB, and CBUE landraces and one accession of ‘Pomodoro di Sorrento’ tomato (PS05) were provided by seed companies (Table 1, Fig. 1). The trial was carried out in 2020 under a plastic-covered greenhouse located in Battipaglia, Italy (40°35′00.7"N 14°58′51.8"E; 45 m a.s.l.), where a temperature range from 10.2 to 32.7 °C (on average, 23.6 °C) and 71.2% of average relative humidity were recorded during the experiment. Physical and chemical soil properties were as follows: sand 28.3%, silt 38.3%, clay 33.4%, pH 7.6, O.M. 1.3%, total N 0.04%, and EC (1:5) 0.04 dS m^{-1}, while total and active limestone were absent.

The randomized complete block design had three block replicates and, within each block, one plot per genotype consisting of 10 plants. Seedlings were transplanted on March 29 with a crop density of 3.7 plants m^{-2} (0.30 m along the line and 0.92 m between lines) and a single shoot per plant was tied to a nylon string as support. Fertigation and pest management were carried out according to regional regulations and following local practices. A total of 284 kg ha^{-1} of N, 100 kg ha^{-1} of P_2O_5, and 227 kg ha^{-1} of K_2O was supplied by five drip fertigation events. Spinosad and spiromesifen were applied to control *Tuta absoluta* (Meyrick), *Trialeurodes vaporariorum* (Westwood), *Frankliniella occidentalis* (Pergande) and *Tetranychus urticae* (Koch), while treatments based on boscalid + pyraclostrobin, mandipropamid, copper oxychloride and wettable sulfur were performed against *Alternaria alternata* (Fr.) Keissler, *Phytophthora infestans* (Mont.) de Bary, *Botrytis cinerea* (Pers.) and *Leveillula taurica* (Lév.) G. Arnaud. Weed control was performed using black plastic mulch films. Ripe fruits were continuously reaped, and ten harvests took place between June 3 and August 4 (June 3, 6, 15, 22, and 30; July 7, 15, 21, and 29; August 4).

Plant morphological traits and yield

During the crop cycle, the number of fruits from the 1st to 4th truss was counted (NF1T, NF2T, NF3T, and NF4T), and plant and 1st truss height (PLH and TRSH, respectively, expressed in cm) at first harvest (June 3) were also measured. At each harvest, fruits were hand-picked and weighed to evaluate the total yield (TY) and then sorted as red-ripe (MY) and unmarketable fruits (UY) and expressed as g per plant. A summary and a classification of all acronyms is provided in Table 2.

Fruit morphological traits and external appearance

The average fruit weight (FRW, g) was assessed on 20 fruits from MY per plot. A selection of 15 fruits was used to evaluate some morphological and appearance-related traits, collected from the

Table 1 List of ‘Pomodoro di Sorrento’ tomato accessions and reference landraces assessed for agronomic, morphological and quality traits

Accession code	Landrace	Source	Original site
PS01	‘Pomodoro di Sorrento’	CREA(1)	Pontecagnano (SA, Italy)
PS02	‘Pomodoro di Sorrento’	CREA(1)	Sorrento (NA, Italy)
PS04	‘Pomodoro di Sorrento’	CREA(1)	Piano di Sorrento (NA, Italy)
PS05	‘Pomodoro di Sorrento’	La Semiorto(2)	Sorrento (NA, Italy)
PS06	‘Pomodoro di Sorrento’	CREA(1)	Piano di Sorrento (NA, Italy)
PS07	‘Pomodoro di Sorrento’	CREA(1)	Massa Lubrense (NA, Italy)
PS08	‘Pomodoro di Sorrento’	CREA(1)	Massa Lubrense (NA, Italy)
PS09	‘Pomodoro di Sorrento’	CREA(1)	Pagani (SA, Italy)
PS10	‘Pomodoro di Sorrento’	CREA(1)	Vico Equense (NA, Italy)
PS11	‘Pomodoro di Sorrento’	CREA(1)	Piano di Sorrento (NA, Italy)
CBUE	‘Cuore di Bue’	Sativa(2)	Cesena (FC, Italy)
PABR	‘Pera di Abruzzo’	Semencoop(2)	Cesena (FC, Italy)
PALB	‘Pera di Albenga’	Semencoop(2)	Cesena (FC, Italy)

(1) CREA = Consiglio per la ricerca in agricoltura e l’analisi dell’economia agraria, (2) Seed company

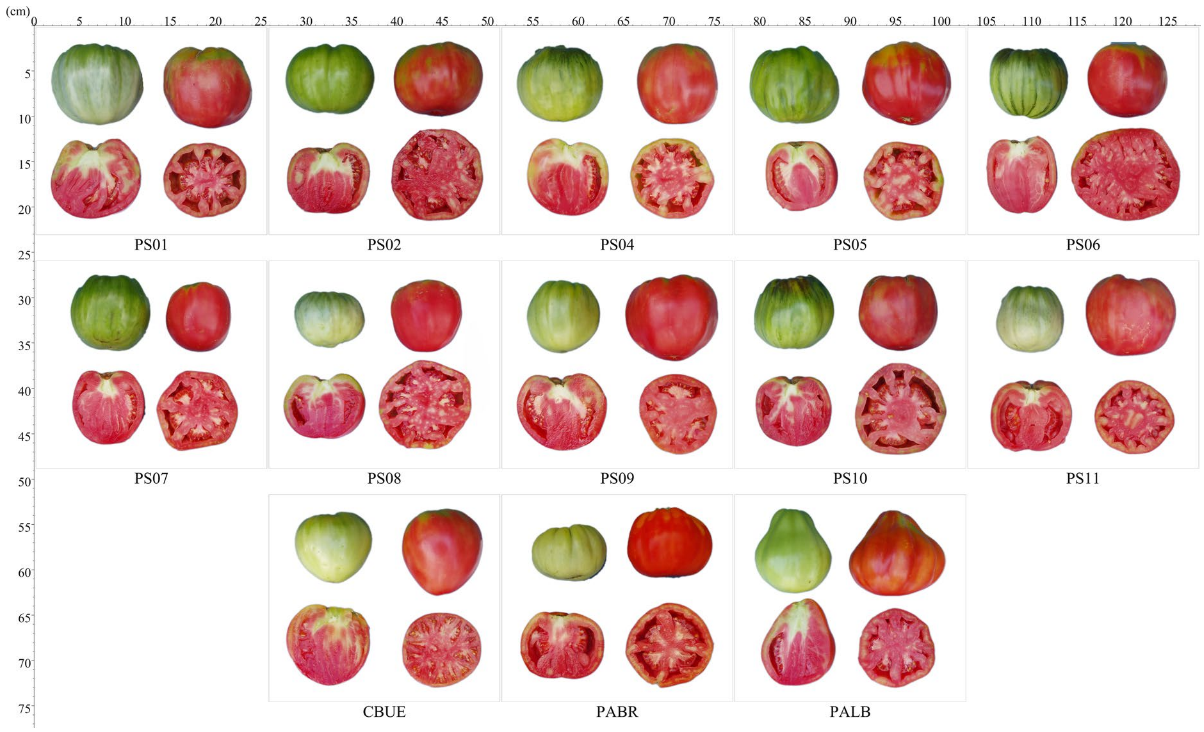


Fig. 1 External appearance (unripe and ripe), and longitudinal and cross sections of ripe ‘Pomodoro di Sorrento’ tomato accessions and reference landraces

most representative trusses (2nd and 3rd) for each plot. At each harvest, cross (FCSD) and longitudinal section diameters (FLSD) were measured and expressed in mm, and the percentage of cracking fruits on marketable fruits (CRAC, %) was assessed according to the IPGRI guidelines (International Plant Genetic Resources Institute 1996). The fruit axes ratio was then calculated as FCSD/FLSD. Afterwards, the fruits were cut on the equatorial axis to assess the number of locules (NLOC, n), fruit fleshiness (FLNS, calculated as the ratio of core diameter on equatorial diameter), and pericarp thickness (PER, mm).

Fruit quality traits and antioxidant activity

A sample of 3 kg of ripe fruits per plot was collected on July 7, as the most representative harvest, and selected for quality analyses. The color a*/b* ratio (-) was determined on the on the equatorial region of the fruits using a Minolta CR 300 Chroma portable colorimeter (Minolta Co., Osaka, Japan) with C illuminant (Parisi et al. 2022). Then, the fruits were washed and homogenized in a Waring blender (2 L capacity; Model HGB140, CA, USA) for 1 min. Dry matter content (DM, g on 100 g of fresh weight, or g % FW) was determined by drying 20 g of homogenized tomato sample in a stove at 72 °C until constant weight) (Mennella et al. 2018). Soluble solids content (SSC, °Brix on 100 g of FW, or °Bx) was measured using a digital refractometer (Refracto 30PX, Mettler-Toledo, Novate Milanese, IT). Titratable acidity (TTA, g of citric acid 100 g – 1 FW, or g % CA FW) and pH were assessed with a pH-Matic 23® titroprocessor model 5011 T, equipped with a pH electrode (Crison Instruments, Barcelona, Spain) (Mennella et al. 2018). Glucose – GLU and fructose – FRU (g % FW) contents were assessed according to HPLC methods reported by (Fusco et al. 2025). Three indices were then calculated: SSC-to-total titratable acidity ratio (SSC/TTA), total sweetness index (TSI, g % FW) calculated as $(0.76 \times GLU) + (1.5 + FRU)$ and total titratable acidity-to-fruit dry matter ratio (TTA/DM)

Table 2 Summary of the acronyms used for specific tomato traits, and classification into major groups

Group	Acronyms	Description
Plant morphological traits	NF1T, NF2T, NF3T, NF4T	Number of fruits on the 1st, 2nd, 3rd, and 4th truss
	PLH	Plant height at 1st harvest
	TRSH	Height of 1st truss at 1st harvest
Yield	TY, MY, UY	Total, marketable, and unmarketable yield
Fruit morphological traits and appearance	FRW	Average fruit weight
	FCSD	Cross section diameter
	FLSD	Longitudinal section diameter
	FCSD/FLSD	Cross-to-longitudinal section diameter ratio
	CRAC	Cracking fruits
	NLOC	Number of locules
	FLNS	Fruit fleshiness
	PER	Pericarp thickness
Fruit quality and antioxidant activity	a*/b*	CIELAB a*/b* ratio
	DM	Dry matter
	SSC	Soluble solids content
	TTA	Titratable acidity
	GLU	Glucose
	FRU	Fructose
	TSI	Total sweetness index
	SSC/TTA	Soluble solids content-to-titratable acidity ratio
	TTA/DM	Titratable acidity-to-dry matter ratio
	TEAC	Antioxidant capacity of lipophilic extracts
	DMPD	Antioxidant activity in the hydrophilic fraction

(di Cesare et al. 2003; Rosa-Martínez et al. 2021; Parisi et al. 2022). The antioxidant activity of the tomato extracts was determined using two well-known spectrophotometric assays. The antioxidant capacity of lipophilic extracts (Trolox Equivalent Antioxidant Capacity, TEAC) was assessed using the ABTS method as described by Pellegrini et al. (1999), whereas the antioxidant activity in the hydrophilic fraction was quantified using the N,N-dimethyl-p-phenylenediamine method (DMPD) according to Fogliano et al. (1999). Hydrophilic and lipophilic extracts were obtained as reported by Scalfi et al. (2000).

Statistical analysis

For statistical analysis and graphical visualization of results, IBM SPSS Statistics (Version 25) and R version 4.6.0 "Because it was There" were used (IBM Corp. 2017; R Core Team 2025). Distribution normality of standardized residuals in continuous variables was tested by Shapiro–Wilk test and variables lacking normality of residuals distribution underwent Box-Cox transformation for attempting normalization. Analysis of variance (one-way ANOVA) was applied on variables with normally distributed residuals or normalized residuals distribution, and a Duncan test was used to separate means when the F test of ANOVA for treatment was significant at $p < 0.05$. A Kruskal–Wallis one-way ANOVA test was applied to variables for which the normalization attempts were unsuccessful. Since results from Kruskal–Wallis multiple pairwise-comparison confirmed hypotheses tested with ANOVA and Duncan tests, only results from ANOVA parametric tests were reported. To compare genotypes based on all assessed variables, redundant variables were removed, and a Principal Component Analysis (PCA) was then performed to reduce the number of components. Hierarchical Cluster Analysis (HCA) was performed by Ward Cluster

Method, with squared Euclidean distance as the similarity measure, after z-score standardization of the variables. Finally, a stepwise discriminant analysis was carried out on the 'Pomodoro di Sorrento' groups identified by HCA, using Wilks' lambda as the selection criterion, to identify the canonical discriminant functions and the minimum set of variables useful for discriminating accessions according to their group membership and for supporting the classification of additional accessions. The robustness of the discriminant model was assessed by leave-one-out cross-validation (LOOCV), and the cross-validated classification accuracy is reported alongside the original grouped classification rate.

Results

To investigate the phenotypic variation within the 'Pomodoro di Sorrento' tomato and in comparison with three reference landraces, several morphological, yield, and quality traits were assessed on thirteen tomato accessions throughout the whole crop cycle. 'Pomodoro di Sorrento' accessions showed a considerable variability in terms of PLH, ranging from 126.25 (PS06) to 158.08 cm (PS01), and three of them (PS02, PS04, and PS06) were grouped together at Duncan post hoc test for a shorter mean PLH than reference landraces (127.86 *vs* 151.14 cm, on average) (Table 3, Supplementary Figure S1). As for TRSH, all the evaluated accessions shared at least one homogeneous subgroup (27.13 cm, on average) except for CBUE that highlighted a higher mean value (34.58 cm). As concerns the number of fruits per truss, NF2T, NF3T, and NF4T expressed a higher variability (CV equal to 36.70%, 42.80%, and 40.28%, respectively) than NF1T (21.88%). A general downward trend in fruit number was evident from the 1st to the 4th truss (4.56, 2.14, 2.00, and 1.63 fruits on 1st, 2nd, 3rd, and 4th truss, respectively). PS08,

Table 3 Plant morphological traits and yield variations among 10 'Pomodoro di Sorrento' (PS) accessions and three ('Cuore di Bue' – CBUE, 'Pera di Abruzzo' – PABR, 'Pera di Albenga' – PALB) reference tomato landraces

Accession	PLH cm	TRSH Cm	NF1T n	NF2T N	NF3T n	NF4T n	FRW g	TY g pt^{-1}	MY g pt^{-1}	UY g pt^{-1}
PS01	158.08 a	26.50 BC	4.67 b-d	2.08 b-e	1.25 c-e	1.33 b	213.87 e	3211.50 de	2817.77 cd	393.73 b-d
PS02	128.67 c	29.00 b	4.00 de	1.67 de	2.83 ab	0.92 b	365.53 a	4143.87 a	3526.40 ab	617.47 b
PS04	128.67 c	25.83 BC	5.42 a-c	1.83 c-e	2.92 ab	2.83 a	230.23 de	3982.93 ab	3636.03 a	346.93 b-d
PS05	133.42 BC	28.33 BC	3.83 de	2.17 b-e	1.83 b-e	1.08 b	333.13 ab	4157.23 a	3642.37 a	514.87 BC
PS06	126.25 c	25.33 BC	5.50 ab	2.08 b-e	1.17 de	1.00 b	245.00 c-e	3906.20 a-c	3551.47 ab	354.73 b-d
PS07	132.50 BC	25.33 BC	4.25 c-e	1.58 de	1.17 de	0.83 b	291.23 BC	2975.37 e	2688.87 d	286.57 cd
PS08	154.33 a	26.25 BC	5.58 ab	3.08 a-c	2.25 a-e	1.83 ab	212.10 e	3283.97 de	3009.63 b-d	274.30 d
PS09	154.58 a	26.58 BC	3.33 e	1.75 c-e	2.58 a-c	1.25 b	271.37 cd	2842.10 e	2586.60 d	255.47 d
PS10	131.50 BC	27.25 BC	3.33 e	0.92 e	3.50 a	1.83 ab	274.53 cd	3779.43 a-d	3343.23 a-c	436.13 b-d
PS11	138.08 BC	26.50 BC	4.83 b-d	3.58 a	2.50 a-d	1.58 ab	213.77 e	3344.87 c-e	2951.50 b-d	393.30 b-d
CBUE	155.33 a	34.58 a	6.42 a	3.33 ab	0.92 e	1.75 ab	206.03 e	3407.50 b-e	2998.67 b-d	408.77 b-d
PABR	144.00 ab	26.17 BC	3.25 e	1.33 de	0.92 e	2.17 ab	207.03 e	2988.63 e	1771.07 e	1217.57 a
PALB	154.08 a	25.00 c	4.83 b-d	2.42 a-d	2.17 a-e	2.75 a	214.80 e	3159.50 de	2861.90 cd	297.60 cd
sign	***	***	***	***	***	**	***	***	***	***
Mean	141.50	27.13	4.56	2.14	2.00	1.63	252.20	3475.62	3029.65	445.96
SD	12.20	2.52	1.00	0.79	0.86	0.66	52.00	462.16	527.37	252.95
CV (%)	8.62	9.28	21.88	36.70	42.80	40.28	20.62	13.30	17.41	56.72

PLH = plant height at 1st harvest, TRSH = 1st truss height at 1st harvest, NF1T, NF2T, NF3T, NF4T = total number of fruits on (1st, 2nd, 3rd, 4th) truss, FRW = average fruit fresh weight, TY = total yield per plant, MY = marketable yield per plant, UY = unmarketable yield per plant. **, ***:significant at $p \leq 0.01$, and 0.001, respectively, at one-way ANOVA test. The same letter within each column indicates no significant differences among accessions according to Duncan's multiple range test ($p \leq 0.05$), with hyphens summarizing letters comprised between the previous letter and the subsequent one. Means, standard deviations (SD) and global coefficients of variation (CV) are reported for each evaluated trait

PS11, and PALB recorded an above-average number of fruits on each truss, while an opposite behavior was detected in PS07. However, the average number of fruits per truss in PS08, PS11, and PALB accessions did not result in a higher total yield (TY), as comparable TY was recorded on these two accessions and PS07 (3283.97, 3344.87, 3159.50, and 2975.37 g pt^{-1}, respectively). Two accessions that performed higher yield, namely PS02 (TY = 4143.87 g pt^{-1}) and PS05 (TY = 4157.23 g pt^{-1}), reached the highest mean fruit weight (365.53 and 333.13 g, respectively) despite the low number of total fruits (9.63 and 10.93 fruits, respectively). The connection between FRW and TY was confirmed by a Spearman's correlation $\rho = 0.76$ ($p \leq 0.01$). Although FRW showed a high variability across genotypes (CV = 20.62%), especially among 'Pomodoro di Sorrento' accessions (CV = 19.97%, data not shown), PS tomatoes were generally characterized by a markedly greater fruit size when compared to reference landraces (265.08 *vs* 209.29 g, respectively). Overall, MY reached 87.17% of the total yield. Individually, the higher yielding accessions in terms of MY were PS02, PS04, PS05, PS06, and PS10 (3526.40, 3636.03, 3642.37, 3551.47, and 3343.23 g pt^{-1}, respectively), thus confirming the trend highlighted for TY. The unmarketable yield was highly variable among the evaluated genotypes (CV = 56.72%). Indeed, over 40% of total yield in PABR was considered as not marketable (1217.57 on 2988.63 g pt^{-1}), while the lowest values of UY were recorded on PS08 and PS09 (274.30 and 255.47 g pt^{-1}, respectively). The greatest percentage of fruits defects was represented by deformities and rotting.

Fruit morphological traits and appearance are shown in Table 4. While FCSD was slightly similar among CBUE, PABR, and PALB (78.49 mm, on average), it varied considerably within PS accessions, from 76.03 mm (PS09) to 93.63 mm (PS05). FLSD revealed a wider range of variations, from

Table 4 Variations in fruit morphological traits among 10 'Pomodoro di Sorrento' (PS) accessions and three ('Cuore di Bue' – CBUE, 'Pera di Abruzzo' – PABR, 'Pera di Albenga' – PALB) reference tomato landraces

Accession	FCSD	FLSD	FCSD/FLSD	CRAC	PER	FLNS	NLOC
	mm	Mm	-	%	mm	-	n
PS01	80.8 d–f	72.53 e–g	1.11 b–d	20.40 ab	6.85 c–e	0.43 cd	7.33 de
PS02	88.53 ab	80.70 BC	1.10 c–e	21.03 a	7.10 b–d	0.55 a	7.73 cd
PS04	79.50 d-f	77.90 cd	1.02 f	15.50 a-c	6.67 de	0.50 b	7.57 cd
PS05	93.63 a	80.17 BC	1.17 ab	18.57 ab	7.28 a–c	0.50 b	8.40 BC
PS06	83.50 b-d	80.03 BC	1.04 ef	22.00 a	6.38 e	0.52 ab	8.63 b
PS07	87.07 BC	82.83 ab	1.06 d–f	21.60 a	7.37 ab	0.49 b	7.20 de
PS08	82.60 c-e	74.63 de	1.11 b–d	18.73 ab	6.63 de	0.45 c	6.60 e
PS09	76.03 f	68.83 gh	1.12 b–d	21.00 a	6.70 de	0.43 cd	7.40 de
PS10	80.27 d-f	74.17 de	1.09 c–e	15.50 a-c	6.87 c–e	0.51 b	7.10 de
PS11	76.93 ef	73.57 d-f	1.05 d–f	20.53 ab	6.65 de	0.44 c	6.97 de
CBUE	78.83 d-f	69.60 e–h	1.14 a–c	11.53 b-d	4.25 f	0.55 a	11.03 a
PABR	77.90 d-f	66.17 h	1.18 a	9.53 cd	6.42 e	0.39 d	7.03 de
PALB	78.73 d-f	85.47 a	0.92 g	5.77 d	7.72 a	0.42 cd	7.00 de
Sign	***	***	***	**	***	***	***
Mean	81.87	75.89	1.09	17.05	6.68	0.47	7.69
SD	5.13	5.83	0.07	5.20	0.83	0.05	1.15
CV (%)	6.26	7.68	6.27	30.48	12.38	10.66	15.01

FCSD = fruit cross section diameter, FLSD = fruit longitudinal section diameter, FCSD/FLSD = fruit shape ratio, CRAC = percentage of cracking on marketable fruits, PER = pericarp thickness, FLNS = fruit fleshiness, NLOC = number of locules. **, ***: significant at $p \leq 0.01$, and 0.001, respectively, at one-way ANOVA test. The same letter within each column indicates no significant differences among accessions according to Duncan's multiple range test ($p \leq 0.05$), with hyphens summarizing letters comprised between the previous letter and the subsequent one. Means, standard deviations (SD) and global coefficients of variation (CV) are displayed for each evaluated trait

66.17 mm (PABR) to 85.47 mm (PALB). FCSD/FLSD ratio clearly distinguished the 'Pomodoro di Sorrento' accessions from PALB (0.92) and displayed substantial variability within PS landrace (from 1.02 for PS04 to 1.17 for PS05. The occurrence of fruit cracking was high and without significant differences within PS tomato type (19.49%, on average), while CRACK was less relevant in PALB (5.77%). PER had a low variation (CV = 4.56%) in PS accessions and showed mean values ranging from 6.38 mm in PS06 to 7.28 mm in PS05. CBUE combined the thinnest pericarp (4.52 mm) with the highest number of locules (11.03) and fleshiness (0.55). PS06 showed a higher NLOC (8.63) than the other PS accessions and two out of three reference landraces (PALB and PABR). An appreciable variation of FLNS trait was detected within 'Pomodoro di Sorrento' landrace (from 0.43 in PS01 and PS09 to 0.55 in PS02). The latter accession did not differ from CBUE tomato.

As for fruit quality traits, relevant differences were found within 'Pomodoro di Sorrento' tomato with respect to reference landraces (Table 5). Fruit external a*/b* ratio ranged from 2.03 (PS09) to 2.77 (PS02) among PS accessions, whereas PALB stood out among the reference landraces (2.63). DM and SSC were higher in PS01 (5.53 g and 5.19°Bx) and PS09 (5.57 g and 5.22°Bx), while the lowest values were observed in CBUE (4.91 g and 4.79°Bx), PABR (5.07 g and 4.66°Bx), PALB (5.09 g and 4.72°Bx), and PS08 (5.10 g and 4.69°Bx). TSI was averagely higher among PS tomatoes (3.78 g % FW) compared to the three reference landraces (3.45 g % FW). PS09 stood out for GLU (1.58 g % FW), whereas PS01 and PS09 showed considerable FRU content (1.85 g % FW). The lowest levels of GLU and FRU were detected in PALB and CBUE, while the latter genotype and PABR had a higher TTA (0.36 g % CA FW) and a lower pH (4.15 and 4.26) than the average 'Pomodoro di Sorrento' values (0.29 g CA 100 g FW^{-1} and pH of 4.36). Conversely, PALB showed the highest TTA amount (0.22 g CA 100 g FW^{-1}) and the lowest value of pH (4.54). These traits affected the SSC/TTA ratio, which was higher in PALB and PS10 (21.46 and 19.23, respectively) and lower in CBUE, PABR, and PS01 (13.49, 12.82, and 15.11, respectively). An opposite behavior was observed for TTA/DM, since CBUE, PABR, and PS01 recorded a significantly higher ratio (7.24, 7.19, and 6.25, respectively) compared to PALB, PS05, and PS10 (4.32, 4.95, and 4.93, respectively). In terms of antioxidant capacity, PABR was the only accession to record high values for both TEAC and DMPD. In more detail, a high variability was detected among the tested genotypes for TEAC (CV = 41.84%) (Supplementary Figure S1). PABR nearly doubled the average value of the 13 accessions (0.71 *vs* 0.35 mmol Trolox 100 g FW^{-1}), although PABR was not statistically different from PALB, PS06, PS07, PS08, and PS10. Conversely, PS01 and PS02 recorded the lowest antioxidant activity of lipophilic extract (0.15 and 0.17 mmol Trolox 100 g FW^{-1}). DMPD, which showed a more limited variation (CV = 13.10%), was higher in CBUE, PABR, PS04, and PS11 (1.49, 1.39, 1.41 and 1.40 mmol ascorbic acid 100 g FW^{-1}, respectively) compared to the other accessions.

Considering the whole set of traits used for the characterization, a Principal Component Analysis (PCA) was then run to reduce the dataset dimension, assess the impact of variables in discriminating the accessions and comprehensively compare the selected phenotypes. Two scatter biplots (Fig. 2A and Fig. 2B) were chosen to represent the four Principal Components (PC1 *vs* PC2 and PC3 *vs* PC4, respectively). Overall, the four rotated PCs accounted for 76.98% of the total variance (PC1 + PC2 = 44.36%; PC3 + PC4 = 32.62%) (Supplementary Tables S1 and S2).

The fruit morphology (FLSD, FCSD/FLSD, PER, NLOC), and quality traits (a*/b* ratio, TTA, pH, and DMPD) were grouped in the same PCA factor (PC1) and markedly discriminated the 'Pomodoro di Sorrento' accessions from the reference landraces on the Y axis (Supplementary Table S2). Conversely, SSC, GLU, FRU, TSI, TEAC, and CRACK differentiated the genotypes on X axis (PC2). 'Pomodoro di Sorrento' tomatoes showed higher sugar content and cracking aptitude, and lower TEAC values than the three reference landraces. Among these, PABR and CBUE had thinner pericarp, higher TTA, and DMPD, and lower pH and a*/b* ratio values than PALB. Some plant (PLH, TRSH) and fruit morphological (FRW), yield (TY and MY) and quality traits (a*/b*) were the main factors discriminating the phenotypes on the Y axis (PC3), whereas the FCSD/FLSD, FRW, UY, and NFT1, NFT2, and NFT4 mainly discriminated the analyzed accessions and reference landraces on X axis (PC4). Based on PC3 and PC4, only PABR was clearly separated from the PS accessions and the

Table 5 Variation in fruit quality and antioxidant activity traits among 10 'Pomodoro di Sorrento' (PS) accessions and three ('Cuore di Bue' – CBUE, 'Pera di Abruzzo' – PABR, 'Pera di Albenga' – PALB) reference tomato landraces

Accession	DM	SSC	TSI	GLU	FRU	pH	TTA	SSC/TTA	TTA/DM	a*/b*	DMPD	TEAC
	g% FW	°Bx	g% FW	g% FW	g% FW	-	g% CA FW	-	-	-	mmol asc. ac. 100 g FW^{-1}	mmol trolox 100 g FW^{-1}
PS01	5.53 a	5.19 ab	3.89 ab	1.47 c-e	1.85 a	4.30 e	0.35 a-c	15.11 de	6.25 b	2.24 e	1.21 bc	0.15 d
PS02	5.27 b-d	5.02 b-d	3.70 a-c	1.48 cd	1.72 a-d	4.43 bc	0.30 cd	16.83 b-d	5.68 bc	2.77 a	1.12 c	0.17 d
PS04	5.50 ab	5.05 a-d	3.92 ab	1.55 ab	1.83 ab	4.3 ef	0.31 b-d	16.35 cd	5.66 bc	2.69 ab	1.41 ab	0.23 b-d
PS05	5.35 a-c	4.92 c-e	3.88 ab	1.53 a-c	1.82 ab	4.46 bc	0.26 de	18.59 bc	4.95 cd	2.71 ab	1.24 bc	0.21 cd
PS06	5.42 ab	5.07 a-d	3.83 ab	1.51 b-d	1.79 ab	4.29 ef	0.31 b-d	16.36 cd	5.72 bc	2.74 ab	1.28 bc	0.42 a-c
PS07	5.26 b-d	4.86 d-f	3.79 ab	1.49 b-d	1.77 a-c	4.46 bc	0.28 d	17.5 b-d	5.33 c	2.29 e	1.23 bc	0.41 a-c
PS08	5.10 c-e	4.69 f	3.67 bc	1.40 f	1.74 a-d	4.28 ef	0.27 d	17.07 b-d	5.39 bc	2.32 de	1.30 bc	0.44 ab
PS09	5.57 a	5.22 a	3.97 a	1.58 a	1.85 a	4.35 d	0.28 d	18.34 bc	5.12 c	2.03 f	1.14 c	0.32 bc
PS10	5.39 ab	5.05 a-d	3.44 cd	1.25 g	1.66 b-d	4.41 c	0.27 de	19.23 ab	4.93 cd	2.50 cd	1.13 c	0.37 a-c
PS11	5.25 b-d	4.91 c-e	3.67 bc	1.40 f	1.74 a-d	4.31 e	0.27 de	18.71 bc	5.06 c	2.30 e	1.40 ab	0.42 bc
CBUE	4.91 e	4.79 ef	3.37 d	1.26 g	1.61 cd	4.15 g	0.36 ab	13.49 e	7.24 a	1.93 f	1.49 a	0.33 bc
PABR	5.07 de	4.66 f	3.52 cd	1.2 g	1.74 a-d	4.26 f	0.36 a	12.82 e	7.19 a	1.92 f	1.39 ab	0.71 a
PALB	5.09 de	4.72 ef	3.46 cd	1.42 ef	1.59 d	4.54 a	0.22 e	21.46 a	4.32 d	2.63 bc	0.87 d	0.45 ab
Sign	***	***	***	***	*	***	***	***	***	***	***	***
Mean	5.29	4.94	3.70	1.42	1.75	4.35	0.30	17.07	5.60	2.39	1.25	0.35
SD	0.20	0.18	0.20	0.12	0.09	0.11	0.04	2.35	0.86	0.31	0.16	0.15
CV (%)	3.77	3.74	5.45	8.52	4.89	2.48	13.96	13.80	15.28	12.84	13.10	41.84

DM = fruit dry matter, SSC = soluble solids content, TTA = titratable acidity, pH, SSC/TTA = soluble solids content to titratable acidity ratio, TTA/DM = titratable acidity to dry matter ratio, TSI = total sweetness index, GLU = glucose, FRU = fructose, a*/b* = a*/b* color ratio, DMPD = water antioxidant activity, TEAC = antioxidant activity of lipophilic extract. *, ***: significant at $p \leq 0.05$, and 0.001, respectively, at one-way ANOVA test. The same letter within each column indicates no significant differences among accessions according to Duncan's multiple range test ($p \leq 0.05$), with hyphens summarizing letters comprised between the previous letter and the subsequent one. Means, standard deviations (SD) and global coefficients of variation (CV) are reported for each evaluated trait

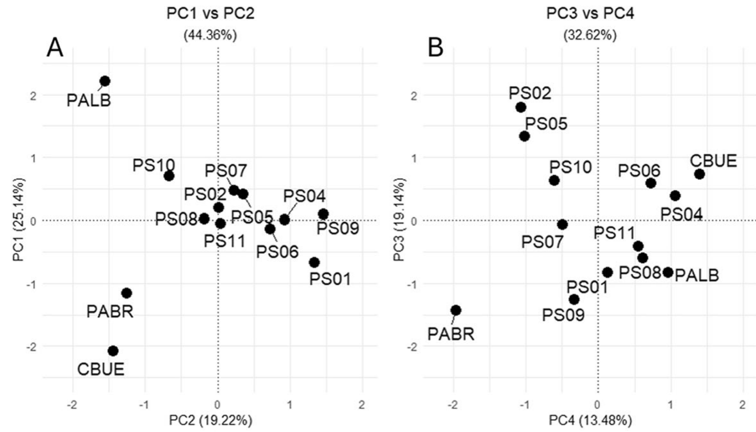


Fig. 2 Biplots of the four Principal Components. **A** Biplot of PC1 vs PC2, **B** Biplot of PC3 vs PC4. Loadings were obtained through a Principal Component Analysis using all assessed variables and carefully removing redundant variables

two remaining reference landraces. Overall, PABR appeared to be the most clearly differentiated landrace compared to the 'Pomodoro di Sorrento' type, as it differed from the PS accessions for a higher number of traits than the other reference landraces.

Hierarchical Cluster Analysis identified six clusters, highlighting an intra-group distance in the PS collection lower than the observed distances within the selected reference landraces (Fig. 3). Overall, biological replications consistently grouped within the identified clusters for most of accessions, although a few inconsistencies were observed for PS05 in cluster 3 and PS11 in the cluster 2.

The whole dataset of yield, plant, and fruit traits was used for discriminant analysis to identify the most informative discriminatory traits and to develop a classification and cataloguing system for new sources of variability within the collection. The discriminant analysis provided clear discrimination among the 'Pomodoro di Sorrento' accession groups previously defined by hierarchical cluster analysis (Fig. 4). Stepwise selection based on Wilks' lambda identified SSC, pH, a*/b*, and GLU as the variables with the greatest discriminatory power. The canonical discriminant analysis generated two functions with eigenvalues of 4.82 and 2.57 for functions 1 and 2, respectively, indicating good separation among groups. In addition, the Wilks' lambda tests associated with the two functions yielded significant chi-square values ($p<0.001$), supporting the robustness and statistical significance of the discriminant model. Function 1 was mainly related to pH, TSI, FRU, PER, GLU, TRSH, WY, and DMPD, whereas function 2 was mainly related to SSC, PLH, DM, TTA, TTA/DM, SSC/TTA, CRAC, FLNS, FLSD, a*/b*, CY, NF3T, TY, NF2T, FRW, FCSD/FLSD, NLOC, FCSD, TEAC, NF1T, and NF4T (Supplementary Table S3). Overall, leave-one-out cross-validation confirmed the stability of the model, with 100.0% of the original grouped cases correctly classified, confirming the strong discriminatory ability of the selected trait combination.

Discussion

The recovery and valorization of high-quality tomato landraces have attracted increasing attention (Andreakis et al. 2004; Caramante et al. 2009), particularly in the Mediterranean basin, a major center of tomato diversification. Among these resources, the Italian landrace 'Pomodoro di Sorrento' (PS) is especially appreciated for its multilocular pink fruits and excellent organoleptic quality. Nevertheless, the intra-varietal diversity of this landrace has so far been only partially explored, since previous research only explored small collections, a limited number of genetic loci, and a few fruit quality traits (Sinesio et al. 2007; Ercolano et al. 2008; Lisanti et al. 2008; Parisi et al. 2008). The present work builds upon and extends these previous efforts by focusing on PS tomato landrace and evaluating a larger collection of accessions through an extensive set of phenotypic descriptors. The combination of a broad genetic base and a comprehensive phenotypic characterization enabled a deeper assessment of intra-varietal diversity and a more robust classification of accessions according to their overall

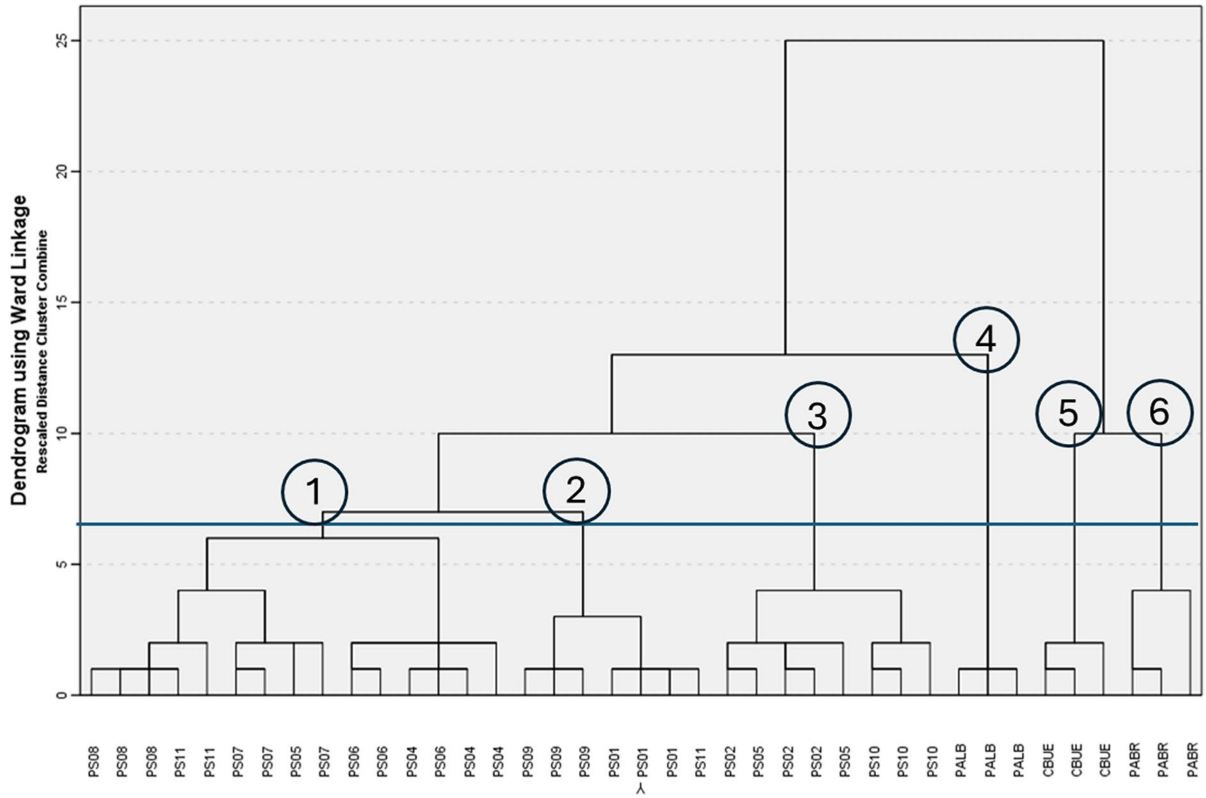
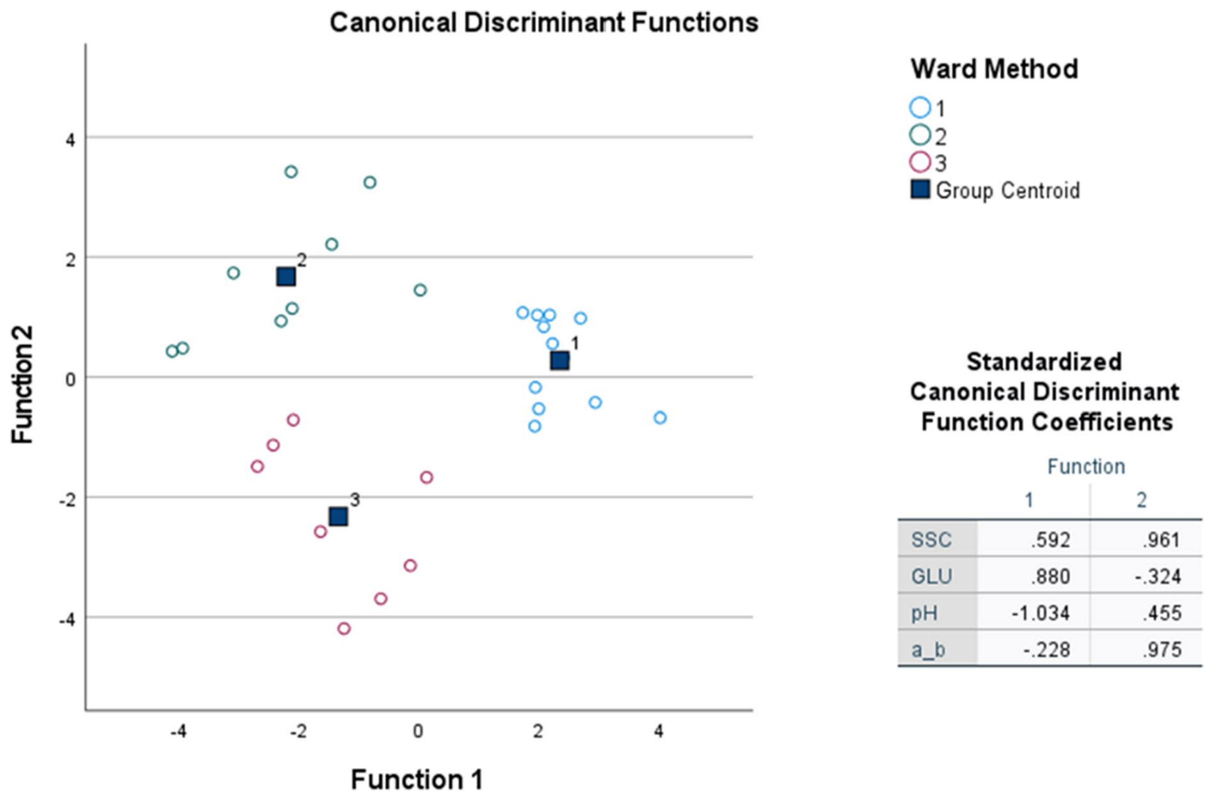


Fig. 3 Dendrogram computed through Hierarchical Cluster Analysis illustrating phenotypic relationship among 'Pomodoro di Sorrento' accessions and reference tomato cultivars. The whole set of analyzed variables was processed using the Wald Cluster Method, the Squared Euclidian distance as measure and a z-score transformation

phenotypic similarity. Furthermore, the identification of phenotypically distinct groups and of the traits that mainly contribute to their differentiation provides a clearer definition of phenotypic distinctiveness within the landrace. Such information is crucial for accessions conservation by reducing redundancy in collections, facilitating the classification of newly collected accessions, and enhancing the exploitation of this genetic resource through the identification of genotypes carrying desirable agronomic and quality attributes for breeding and valorization programs.

Our findings showed that most of the morphological variation was partitioned between the 'Pomodoro di Sorrento' tomato landrace and the reference landraces included in the study, confirming the existence of a well-defined landrace identity. Parisi et al. (2016) analyzed ten PS accessions through fruit morphological descriptors and genome-wide SNP markers, demonstrating the genetic distinctiveness of the landrace from reference multilocular tomato types. The authors also identified a SNP specifically associated with nearly all PS accessions, although some genotypes within the group displayed marked molecular similarity. The limited discriminating power of SNP markers was likewise highlighted by Mazzucato et al. (2010) who investigated the genetic diversity and distinctiveness of 'A pera Abruzzese' tomato type. Indeed, SNP markers explore only narrow portions of the whole tomato genome (Adedze et al. 2025), thus being suitable for unravelling landrace distinctiveness rather than for capturing the extent of intra-varietal diversity. However, Parisi et al. (2016) did not provide sufficient evidence of phenotypic structuring within the landrace, leaving open the question of whether clearly distinguishable intra-varietal groups that could support the selection of specific ideotypes or



	1	2
SSC	.592	.961
GLU	.880	-.324
pH	-1.034	.455
a_b	-.228	.975

Fig. 4 Discriminant analysis performed on yield, plant and fruit quality traits. 'Pomodoro di Sorrento' accessions are plotted according to a Discriminant Analysis based of Wilk's Lambda using a stepwise method. Significant variables entered are SSC, pH, a*/b* and GLU. Computed canonical discriminant functions showed eigenvalues of 4.82 for function 1 and 2.57 for function 2, respectively. Standardized Canonical Discriminant Function Coefficients are 0.592 (SSC), 0.880 (pH), − 1.034 (a*/b*) and − 0.228 (GLU) for function 1 and 0.961 (SSC), − 0.324 (pH), 0.455 (a*/b*) and 0.975 (GLU) for function 2. Function 1 was mainly associated with pH, TSI, FRU, PER, GLU, TRSH, WY, and DMPD, whereas Function 2 was mainly associated with SSC, PLH, DM, TTA, CGS, TTA/DM, SSC/TTA, CRAC, FLNS, FLSD, a*/b*, CY, NF3T, TY, NF2T, FRW, FCSD/FLSD, NLOC, FCSD, TEAC, NF1T, NF4T. 100.0% of original grouped cases were correctly classified by the model after leave-one-out cross validation. DM = fruit dry matter, SSC = soluble solids content, TTA = titratable acidity, SSC/TTA = soluble solids content to titratable acidity ratio, TTA/DM = titratable acidity to dry matter ratio, TSI = total sweetness index, GLU = glucose, a*/b* = a*/b* color ratio, DMPD = water antioxidant activity, TEAC = antioxidant activity of lipophilic extract, FRW = average fruit fresh weight, FCSD = fruit cross section diameter, FLSD = fruit longitudinal section diameter, FCSD/FLSD = fruit shape ratio, CRAC = percentage of cracking on marketable fruits, PER = pericarp thickness, FLNS = fruit fleshiness, NLOC = number of locules, PLH = plant height at 1st harvest, TRSH = 1st truss height at 1st harvest, NF1T, NF2T, NF3T, NF4T = total number of fruits on (1st, 2nd, 3rd, 4th) truss, TY = total yield per plant

the development of targeted valorization strategies. More recently, comprehensive investigations integrating plant and fruit morphology, agronomic, and quality-related traits have been carried out on reference collections of important landraces (Villena et al. 2023b; Rico Ferrer et al. 2026). These investigations demonstrated that a detailed phenotypic approach could reveal substantial diversity within landraces and identify key traits that effectively differentiate distinct phenotypic subtypes.

Overall, our results suggest that extensive phenotypic characterization remains a powerful and essential tool for dissecting diversity within tomato landraces, complementing molecular approaches and providing actionable information for both conservation and utilization of local germplasm. Specifically, PS accessions still retain an appreciable level of intra-landrace diversity, indicating that phenotypic differentiation persists within the population. Although this variation was markedly lower than that observed among landraces, it was sufficient to allow the identification of distinct phenotypic patterns among PS accessions. Plant architecture represents a source of high variability among Italian landraces (Pons et al. 2022). Plant height at first harvest (PLH) and first truss height at first harvest (TRSH) were relatively conserved among PS accessions as only limited variation was detected for these traits. However, on average, some PS accessions appeared less vigorous than the reference landraces, showing lower PLH and fertility. Given that a low fruit-setting had also been previously reported (Acciarri et al. 2007; Parisi et al. 2016), this trait appears to be a promising target for breeding within PS germplasm, especially considering the substantial variability observed in the collection for the number of fruits per truss. Indeed, the marked intra-landrace phenotypic variation observed in the second, third, and fourth truss reflects the poor and highly variable fruit set that typically characterizes multilocular tomato landraces (Parisi et al. 2016). This may have been further exacerbated by the absence of pollinating insects in the greenhouse, which were deliberately excluded to preserve seed reproduction and assess genotype performance under natural self-pollination. Consequently, the differences observed among trusses and accessions may, at least in part, be attributable to genetic factors governing fruit-set efficiency (Paupière et al. 2017).

Achieving a combination of fruit size and quality uniformity together with high yield throughout the entire crop cycle should be a major breeding objective, as this would help farmers stabilize economic returns (Villena et al. 2023a) and support the intensification of cultivation, since tomato landraces are often strongly affected by yield fluctuations (Cebolla-Cornejo et al. 2013; Donoso et al. 2023). In this regard, our results revealed considerable variability among PS accessions for yield-related traits, particularly for the unmarketable yield component. Epicarp cracking is common in round- and flat-shaped tomato landraces such as PS (Acciarri et al. 2007; Farinon et al. 2022), and are to some extent tolerated in local markets. However, fruit cracking increases susceptibility to fungal infections and may consequently lead to fruit rot (Farinon et al. 2022; Chen et al. 2025). In this context, increasing pericarp thickness may represent a viable strategy to reduce cracking susceptibility, as supported by the negative Spearman correlation observed between PER and CRAC ($r = -0.52$, $p \leq 0.01$). Therefore, the identification and introgression of favorable alleles controlling fruit set, pericarp thickness, and fruit regularity may represent key breeding strategies to improve the agronomic value of PS landrace and enhance its appreciated quality attributes (Villena et al. 2023a). In this regard, PS02 and PS04 emerged as the most promising accessions for breeding purposes, combining high yield performance with membership in two distinct phenotypic clusters (Fig. 3), a combination that would help preserve genetic variability within the breeding pool while selecting for improved PS cultivars.

Fruit morphology exhibited a considerable variability among the examined Italian accessions, with the most pronounced differences involving fruit size and shape rather than fruit color (Pons et al. 2022). In a previous study, PS accessions were yet profiled by Parisi et al. (2016), and two morphotypes were identified differing in puffiness at maturity and extent green shoulder color at unripe stage.

Conversely, fruit shape traits (FCSD, FLSD, and FCSD/FLSD) were found to be highly conserved within 'Pomodoro di Sorrento' type, together with FLNS, PER, and NLOC, showing a clear distinctiveness compared with reference landraces and possibly confirming that farmers have traditionally selected this material mainly based on fruit shape. Villena et al. (2023b) conducted a farmers' survey focusing on the 'Moruno' tomato landrace and reported appreciable variation for shape, fleshiness and pericarp width, suggesting that each farmer applied different selection criteria. Similarly, Rico Ferrer et al. (2026) reported a high degree of phenotypic diversity at intra-landrace level when dissecting the 'Tomata Valenciana' landrace, enabling the differentiation of three clear subtypes ('Blanca', 'Intermitja', and 'Masclet'). Traits subjected to recurrent selection pressure are expected to be more stable, whereas those not directly targeted during selection are likely to remain more variable. Consistent with this hypothesis, our findings suggest that plant morphological traits, such as PLH and TRSH, together with fruit shape-related traits have been major drivers of the farmer-led selection process. From a practical perspective, a lower first truss height is primarily associated with earlier flowering and fruit set, resulting in earlier harvests (i.e., increased early yield). Earlier production is of particular importance for this landrace, as it allows growers to enter the market sooner, when fruit generally command higher prices, thereby increasing their economic value. In addition, a lower first truss height facilitates manual harvesting by improving fruit accessibility and harvesting efficiency. In contrast, yield, fruit weight, and internal fruit morphology traits, combined with the number of fruits per truss and fruit cracking, appear to have been less considered during selection. These results partially disagreed with those reported for 'Tomata Valenciana' which showed high variability in several traits related to plant architecture (Rico Ferrer et al. 2026). This discrepancy may reflect differences in the selection objectives pursued by local farming communities, which have likely shaped the evolutionary trajectories of these landraces in distinct ways.

On average, PS accessions were characterized by higher DM, SSC, TSI, and reducing sugar contents (GLU and FRU) and exhibited a more intense perceived color than CBUE and PABR accessions. Pink-fruited multilocular landraces are uncommon within the Italian tomato germplasm. To the best of our knowledge, besides PS, only two other pink-fruited tomato ecotypes have been described in the scientific literature: 'Pomodoro Rosa di Rotonda', which shows a fruit shape similar to PS but has only been characterized morphologically (Acciarri et al. 2007), and 'Pomodoro di Belmonte Calabro', a heart-shaped tomato landrace with considerably larger fruits (800–1000 g), for which a molecular characterization is available (Parisi et al. 2016). However, no fruit quality data has been published for both landraces, preventing a direct comparison with the qualitative traits characterized in the present study for PS. The SSC/TTA and TTA/DM ratios, together with the volatile compound profile, are key parameters affecting tomato palatability and consumer acceptance (Seymour et al. 1993). Compared with CBUE and PABR, 'Pomodoro di Sorrento' accessions showed higher SSC/TTA ratios and lower TTA/DM ratios, suggesting a more favorable balance between sweetness and acidity and, consequently, greater consumer acceptability. This preference is consistent with local market trends in southern Italy, where PS fruits are almost exclusively destined for the fresh market and are traditionally used to prepare 'Caprese salad', in combination with basil and mozzarella or fiordilatte cheese, a use that strongly contributes to the commercial value and popularity of this landrace (Grandillo et al. 2004). These findings are consistent with previous research (Sinesio et al. 2007) which reported that the 'Pomodoro di Sorrento' type outperformed CBUE in terms of overall flavor and perceived sweetness.

The studied collection of PS accessions highlighted a highly significant variability in antioxidant capacity. As for DMPD, PS accessions were mostly distributed around intermediate values, with PS04 and PS11 emerging as the best-performing genotypes within the group, although CBUE showed the highest values overall. By contrast, TEAC revealed a broader variability, with PABR clearly outperforming all other accessions and several PS genotypes, namely PS06, PS08, and PS11, showing relatively high values. The much higher coefficient of variation associated with TEAC suggests that this parameter was more sensitive in discriminating genotypes than DMPD. The different ranking of genotypes obtained with DMPD and TEAC confirms that these assays captured partly different spectra of antioxidant activity components (Munteanu and Apetrei 2021). In particular, DMPD may be more closely associated with fast-acting hydrophilic reducing compounds, such as ascorbic acid, whereas TEAC is generally considered to provide a broader estimate of total antioxidant capacity, including the contribution of both hydrophilic and, to some extent, lipophilic antioxidants (Fogliano et al. 1999; Pellegrini et al. 1999). Therefore, the lack of full correspondence between the two assays likely reflects differences in the qualitative composition of the antioxidant pool among genotypes. Overall, the PS accessions did not consistently exceed the reference landraces. However, the presence of some promising genotypes supports their potential value as sources of antioxidant-related traits for future breeding and conservation efforts (Casals et al. 2024). Additionally, the observed variation in quality-related traits and metabolites suggests the potential existence of distinctive biochemical features. Future metabolomic investigations involving a broader set of accessions and environmental conditions could help identify a characteristic metabolic signature of the landrace. Such a fingerprint could contribute to a more objective definition of its typicity, while supporting authenticity assessment, traceability, quality stabilization, product valorization, and commercial recognition (Siracusa et al. 2012).

The PCA highlighted a clear phenotypic structure of the studied germplasm and described both the distinctiveness of the 'Pomodoro di Sorrento' type and the variability retained within the PS collection. The first four principal components captured most of the information provided by the evaluated variables. The first two components mainly separated the PS accessions from the reference landraces based on fruit morphology, acidity-related traits, color, sugar content, DMPD, TEAC, and cracking susceptibility, confirming that fruit quality and morphology are the main factors underlying the recognition of the 'Pomodoro di Sorrento' ideotype. However, the PS accessions were distributed across the PCA space and did not collapse into a single compact cluster, revealing an appreciable degree of intra-collection variability. This pattern suggests that the accessions share a common phenotypic background while maintaining distinct trait combinations. Landraces are generally expected to retain substantial intra- and inter-population variability because of the frequent occurrence of seed mixing and spontaneous cross-pollination in traditional cultivation systems (Cortés-Olmos et al. 2015). Under these conditions, farmers tend to apply selection mainly to a limited number of visually evident traits, a pattern that is well supported by our findings (Villena et al. 2023b). This suggests that the current phenotypic structure of the materials studied largely reflects farmers' seed-saving practices.

The multivariate distribution of the PS genotypes also points to a low level of redundancy within the collection. Indeed, no substantial overlap was observed among accessions across the first four PCs, and additional discrimination emerged when PC3 and PC4 were considered, especially for traits related to fruit morphology, fruit weight, and yield components. This indicates that the collection is substantially purged of phenotypically duplicated materials and includes differentiated accessions that complementary contribute to the overall variation. Such a result is particularly relevant for germplasm conservation, as it supports the maintenance of the entire PS collection. Furthermore, it highlights the availability of diverse phenotypic profiles that could be targeted by selection strategies for quality improvement and local varietal valorization (Villena et al. 2023b; Rico Ferrer et al. 2026). Comprehensively, the PCA underlined that the 'Pomodoro di Sorrento' collection represents a coherent, non-redundant, PS-type germplasm collection, characterized by both identity and internal diversity. The absence of phenotypic redundance among the ten PS accessions thus prospects the creation of a core collection, which could be populated by integrating new genotypes. Expanding the present collection is pivotal to exploit the maximum 'Pomodoro di Sorrento' genetic diversity and, thus, to breed new genotypes providing typical morphological and sensorial characteristics, resistance traits, and a high and stable yield (Parisi et al. 2008, 2016; Donoso et al. 2023; Villena et al. 2023a). The genetic variability, that is often found in regional landraces of tomato (Andreakis et al. 2004; Terzopoulos and Bebeli 2008; Mazzucato et al. 2010; Pons et al. 2022; Rico Ferrer et al. 2026) paves the way for selecting, within landraces, genotypes harboring more desired trait combinations. Hierarchical cluster analysis was used to identify repeatable phenotypic signatures that could distinguish the PS accessions from the selected reference cultivars, while also providing a synthetic representation of diversity within the 'Pomodoro di Sorrento' landrace. The six clusters identified a clear structure in the phenotypic variation of the studied germplasm. As expected, the lower intra-group distances observed within the PS collection, like those recorded among the reference cultivars, confirmed that the PS-type germplasm share a relatively cohesive phenotypic background. At the same time, their distribution into multiple clusters confirms that this collection is not phenotypically uniform and is organized into distinguishable subgroups. Thus, cluster analysis supports the view that the PS collection combines a recognizable common identity with an appreciable level of intra-landrace diversification.

Additionally, the consistency with which biological replicates were grouped within the same clusters for most accessions further strengthens the reliability of the phenotypic signatures identified. This result suggests that the clustering pattern largely reflects stable accession-specific traits rather than random experimental noise. However, few inconsistencies were expected because of residual heterogeneity in materials that have not been subjected to formal breeding. Among the Pomodoro di Sorrento accessions, PS05 did not group consistently with the other PS genotypes in the hierarchical cluster analysis, revealing an appreciable degree of phenotypic divergence. Notably, this was the only accession provided by a seed company rather than being directly collected from local farms. While the present study does not allow us to identify the underlying cause, several non-mutually exclusive explanations may account for this observation. These include the intrinsic heterogeneity of the landrace, differences in seed multiplication and maintenance practices over time, or the possibility that the commercial seed lot originated from a selection history different from that of the farmer-maintained populations included in this study. This finding further highlights the importance of comprehensive phenotypic characterization when evaluating and conserving traditional landraces, irrespective of the source from which the seed material is obtained. Indeed, some degree of within-accession variability is biologically plausible and should be interpreted as an inherent feature of the material rather than as a weakness of the analytical approach. Similarly, a low level of intrapopulation variability was reported in collections of two Spanish tomato landraces and is related to way farmers perform the selection for the next generation (Villena et al. 2023b; Rico Ferrer et al. 2026). Beyond its classificatory value, the hierarchical clustering also provided a useful framework for describing intra-landrace diversity. This is particularly relevant for germplasm management, because it allows the collection to be interpreted not merely as a set of individual accessions, but as a reservoir of related yet differentiated phenotypic entities. Such a perspective may be especially valuable when planning future sampling activities, as it facilitates the identification of materials that are truly complementary rather than potentially redundant. Implementing the collection with new accessions that may be identified in the future within the cultivation area of the PS-type would benefit from a simplified procedure for the classification of accessions based on trait performances. Toward this objective, discriminant analysis was applied to identify a limited set of highly informative variables capable of reproducing the group structure previously defined by hierarchical clustering. In particular, the stepwise procedure based on Wilks' lambda selected SSC, pH, a*/b* colorimetric ratio, and glucose content as the variables with the highest discriminatory power, indicating that a relatively restricted set of quality-related traits may be sufficient to capture much of the phenotypic structure of the collection. The discriminant model proved to be highly robust, as indicated by the high eigenvalues of the canonical functions and by the highly significant Wilks' lambda tests. The correct classification of all original grouped cases further confirms the strong discriminatory ability of the selected variable combination. Although this result should be interpreted cautiously until tested on independent materials, it nonetheless highlights the potential of this approach for the practical management of local germplasm. In particular, it suggests that the classification and cataloguing of newly collected PS-type materials may not require the full set of variables initially used for characterization but could instead rely on a reduced number of carefully selected variables without substantial loss of discriminatory efficiency. Taking together, these results outline a coherent strategy for the study and management of PS-type diversity.

Conclusion

This study provides a comprehensive phenotypic characterization of the 'Pomodoro di Sorrento' germplasm and offers new insights into the structure of diversity within this valuable Italian tomato landrace. Although the PS accessions shared a clear and recognizable varietal identity, they also retained an appreciable degree of intra-landrace variability involving fruit morphology, compositional quality, antioxidant capacity, and yield-related traits. This combination of phenotypic coherence and internal diversification confirms that the 'Pomodoro di Sorrento' type should not be considered as a uniform material, but rather as a structured and dynamic germplasm resource.

The results further showed that the main distinctive features of the landrace are associated with fruit-related traits, especially shape, fleshiness, and quality attributes, which are likely to have been maintained through repeated farmer selection. At the same time, traits related to plant performance and productivity appeared more variable, highlighting potentially useful targets for future breeding efforts aimed at improving yield stability and marketable production without compromising the typical identity of the landrace.

On the one hand, broad multivariate approaches such as PCA and hierarchical clustering were essential to capture the overall structure of variation and to reveal the existence of distinct phenotypic groups within the landrace. On the other hand, discriminant analysis makes it possible to translate this complexity into a simplified operational framework based on a limited number of key traits. This dual approach is particularly valuable in the case of traditional germplasm, where diversity must be both accurately documented and practically manageable.

Overall, the present work demonstrates that the studied 'Pomodoro di Sorrento' collection represents a coherent, diverse, and non-redundant reservoir of local tomato variability. These findings provide a stronger basis for the conservation and valorization of the landrace and offer useful tools for its future management. Expanding the collection with additional accessions from the cultivation area, and integrating phenotypic information with genomic approaches, will be important next steps to further capture the breadth of diversity within the 'Pomodoro di Sorrento' type and to support breeding strategies aimed at combining typicity, fruit quality, resilience, and yield stability.

Further metabolomic investigations could contribute to the identification of a characteristic chemical signature of the landrace, enabling the development of a metabolic fingerprint to strengthen its varietal identity. Such an approach could support product quality standardization, enhance traceability and authenticity, and promote the valorization and commercial recognition of this traditional genetic resource.

Overall, considering the observed phenotypic variability, the main agronomic constraints limiting productivity in the cultivation area, and consumer demand for a traditional product with a well-recognized identity, future breeding efforts for Pomodoro di Sorrento should primarily focus on (i) improving fruit fleshiness, fruit set uniformity across successive trusses, and pericarp thickness, and (ii) reducing fruit cracking. In addition, selection for higher SSC/TTA and TTA/DM ratios, together with enhanced antioxidant activity, would contribute to preserving and further strengthening the distinctive organoleptic and nutritional attributes that make this landrace highly appreciated by consumers.

To achieve these objectives while safeguarding the identity of the landrace, future breeding programs should adopt a conservative within-landrace improvement strategy aimed at enhancing quantitative agronomic traits without compromising the morphological, sensory, and adaptive characteristics that define the typicity, authenticity, and market value of Pomodoro di Sorrento. Preserving these attributes is essential, as they constitute the basis of consumer recognition and preference for this traditional tomato. Such a strategy could rely, among others, on within-landrace recurrent selection, family-based selection, and multi-trait selection indices, complemented by participatory evaluation under local growing conditions to ensure that selection remains aligned with farmers' preferences and the traditional ideotype.

Beyond genetic improvement, the long-term conservation of Pomodoro di Sorrento will also depend on strengthening the economic sustainability of the farming systems responsible for its on-farm maintenance. In this regard, the adoption of a European quality scheme, such as Protected Geographical Indication (PGI) or Protected Designation of Origin (PDO), could represent an effective tool for enhancing its market value. Given its strong territorial identity and long-standing association with the Sorrento Peninsula, PGI recognition appears to be the most appropriate pathway for this landrace. The potential benefits of such recognition are exemplified by two other traditional tomato landraces from the Campania region, Pomodorino del Piennolo del Vesuvio and Pomodoro San Marzano dell'Agro Sarnese-Nocerino, both of which experienced substantial commercial growth following PDO registration. A similar quality designation for Pomodoro di Sorrento could increase its market visibility, reinforce its economic value for local farmers, and ultimately promote its continued cultivation and in situ conservation.

Author contributions M.P. and G.G. carried out the investigation. M.P., A.B., and A.D.M. prepared the data. A.B. and A.D.M. carried out the statistical analysis and prepared the tables and figures. M.P., A.B., and A.D.M. carried out the formal analysis and wrote the main manuscript text. M.P., G.G., and A.D.M. validated the methodological process. M.P. conceptualized and supervised the whole experiment. All authors reviewed the manuscript.

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Declarations

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References

Acciarri N, Rotino G, Voltattorni S et al (2007) Recupero, caratterizzazione e valorizzazione di varietà locali di pomodoro da mensa. Italus Hortus 14:74–84

Adedze YMN, Xu Y, Liu S et al (2025) An advanced 10K SNP panel for genotyping tomato (*Solanum lycopersicum* L.) via targeted genome sequencing. Front Plant Sci. https://doi.org/10.3389/fpls.2025.1582241

Andreakis N, Giordano I, Pentangelo A et al (2004) DNA fingerprinting and quality traits of Corbarino cherry-like tomato landraces. J Agric Food Chem 52:3366–3371. https://doi.org/10.1021/jf049963y

Asensio E, Sanvicente I, Mallor C, Menal-Puey S (2019) Spanish traditional tomato. Effects of genotype, location and agronomic conditions on the nutritional quality and evaluation of consumer preferences. Food Chem 270:452–458. https://doi.org/10.1016/J.FOODCHEM.2018.07.131

Bauchet G, Causse M, Bauchet G, Causse M (2012) Genetic diversity in tomato (*Solanum lycopersicum*) and Its wild relatives. Genet Divers Plant. https://doi.org/10.5772/33073

Blanca J, Pons C, Montero-Pau J et al (2022) European traditional tomatoes galore: a result of farmers' selection of a few diversity-rich loci. J Exp Bot 73:3431–3445. https://doi.org/10.1093/jxb/erac072

Caramante M, Rao R, Monti LM, Corrado G (2009) Discrimination of 'San Marzano' accessions: a comparison of minisatellite, CAPS and SSR markers in relation to morphological traits. Sci Hortic 120:560–564. https://doi.org/10.1016/j.scienta.2008.12.004

Casals J, Romero del Castillo R, Pons C et al (2024) European fresh-market tomato sensory ideotypes based on consumer preferences. Sci Hortic 335:113351. https://doi.org/10.1016/j.scienta.2024.113351

Cebolla-Cornejo J, Roselló S, Nuez F (2013) Phenotypic and genetic diversity of Spanish tomato landraces. Sci Hortic 162:150–164. https://doi.org/10.1016/j.scienta.2013.07.044

Chen Y, Zhao J, He J et al (2025) Prediction of fruit cracking behavior in tomatoes due to irrigation using the extended finite element method. Smart Agric Technol 12:101393. https://doi.org/10.1016/j.atech.2025.101393

Cortés-Olmos C, Leiva-Brondo M, Roselló J et al (2014) The role of traditional varieties of tomato as sources of functional compounds. J Sci Food Agric 94:2888–2904. https://doi.org/10.1002/JSFA.6629

Cortés-Olmos C, Valcárcel JV, Roselló J et al (2015) Traditional eastern Spanish varieties of tomato. Sci Agric 72:420–431. https://doi.org/10.1590/0103-9016-2014-0322

di Cesare LF, Forni E, Viscardi D, Ferrari V (2003) Valutazione della composizione aromatica e chimico-fisica di alcune cultivar di pomodoro da impiegare per il consumo diretto o per la trasformazione. Industria Conserve 78:195–206

Donoso A, Carrasco B, Araya C, Salazar E (2023) Genetic diversity and distinctiveness of Chilean Limachino tomato (*Solanum lycopersicum* L.) reveal an in situ conservation during the 20th century. Front Conserv Sci 4:1156786. https://doi.org/10.3389/fcosc.2023.1156786

Ercolano MR, Carli P, Soria A et al (2008) Biochemical, sensorial and genomic profiling of traditional Italian tomato varieties. Euphytica 164:571–582. https://doi.org/10.1007/s10681-008-9768-4

FAOSTAT (2024) FAOSTAT. https://www.fao.org/faostat/en/#data/QCL

Farinon B, Picarella ME, Siligato F et al (2022) Phenotypic and genotypic diversity of the tomato germplasm from the Lazio region in central Italy, with a focus on landrace distinctiveness. Front Plant Sci. https://doi.org/10.3389/fpls.2022.931233

Fogliano V, Verde V, Randazzo G, Ritieni A (1999) Method for measuring antioxidant activity and its application to monitoring the antioxidant capacity of wines. J Agric Food Chem 47:1035–1040. https://doi.org/10.1021/jf980496s

Fusco GM, Burato A, Pentangelo A et al (2025) Processing tomato responses to plant-based biostimulants are modulated by environmental conditions. Physiol Plant 177:e70450. https://doi.org/10.1111/ppl.70450

García-Martínez S, Andreani L, Garcia-Gusano M et al (2006) Evaluation of amplified fragment length polymorphism and simple sequence repeats for tomato germplasm fingerprinting: utility for grouping closely related traditional cultivars. Genome 49:648–656. https://doi.org/10.1139/G06-016

García-Martínez S, Corrado G, Ruiz JJ, Rao R (2013) Diversity and structure of a sample of traditional Italian and Spanish tomato accessions. Genet Resour Crop Evol 60:789–798. https://doi.org/10.1007/s10722-012-9876-9

Gonzalo MJ, Nájera I, Baixauli C et al (2021) Identification of tomato accessions as source of new genes for improving heat tolerance: from controlled experiments to field. BMC Plant Biol 21:1–28. https://doi.org/10.1186/s12870-021-03104-4

Graci S, Francesca S, Addonizio M et al (2025) Identification of superior thermotolerant tomato hybrids through a multi-selection phenotypic and genotypic approach. Sci Hortic 350:114358. https://doi.org/10.1016/j.scienta.2025.114358

Grandillo S, Mustilli AC, Parisi M et al (2004) Tecniche avanzate per la valutazione qualitativa del pomodoro: Il caso Campania. Agroindustria 3:151–159

IBM Corp. (2017) IBM SPSS statistics for Windows

Juan-Cabot A, Carrillo L, Fullana-Pericàs M, et al (2025) Mediterranean tomato landraces exhibit genotype-specific transcriptomic responses to water stress 177 6 e70696
Lázaro A (2018) Tomato landraces: an analysis of diversity and preferences. Plant Genet Resour 16:315–324. https://doi.org/10.1017/S1479262117000351
Lisanti M, Piombino P, Genovese A, et al (2008) Traditional Italian tomato (*Lycopersicon esculentum* mill.) Cultivars and their commercial homologues: differences in volatile composition. Ital J Food Sci, 20, 333–350
Mazzucato A, Ficcadenti N, Caioni M et al (2010) Genetic diversity and distinctiveness in tomato (*Solanum lycopersicum* L.) landraces: the Italian case study of 'A pera Abruzzese.' Sci Hortic 125:55–62. https://doi.org/10.1016/j.scienta.2010.02.021
Mennella G, D'alessandro A, Francese G et al (2018) Occurrence of variable levels of health-promoting fruit compounds in horn-shaped Italian sweet pepper varieties assessed by a comprehensive approach. J Sci Food Agric 98:3280–3289. https://doi.org/10.1002/jsfa.8831
Munteanu IG, Apetrei C (2021) Analytical methods used in determining antioxidant activity: a review. Int J Mol Sci 22:3380. https://doi.org/10.3390/ijms22073380
Olivieri F, Calafiore R, Francesca S et al (2020) High-throughput genotyping of resilient tomato landraces to detect candidate genes involved in the response to high temperatures. Genes 11:626. https://doi.org/10.3390/genes11060626
Parisi M, Aversano R, Graziani G et al (2016) Phenotypic and molecular diversity in a collection of 'Pomodoro di Sorrento' Italian tomato landrace. Sci Hortic 203:143–151. https://doi.org/10.1016/j.scienta.2016.02.038
Parisi M, Burato A, Pentangelo A, Ronga D (2022) Towards the optimal mineral N fertilization for improving peeled tomato quality grown in Southern Italy. Horticulturae 8:697. https://doi.org/10.3390/horticulturae8080697
Parisi M, D'onofrio B, Pentangelo A, et al, (2008), Morphology, productivity and qualitative characterization of the traditional tomato ecotype pomodoro di sorrento originating from the campania region Southern Italy. Acta Hortic. https://doi.org/10.17660/actahortic.2008.789.28
Patanè C, Scordia D, Testa G, Cosentino SL (2016) Physiological screening for drought tolerance in Mediterranean long-storage tomato. Plant Sci 249:25–34. https://doi.org/10.1016/j.plantsci.2016.05.006
Paupière MJ, van Haperen P, Rieu I et al (2017) Screening for pollen tolerance to high temperatures in tomato. Euphytica 213:130. https://doi.org/10.1007/s10681-017-1927-z
Pellegrini N, Re R, Yang M, Rice-Evans C (1999) Screening of dietary carotenoids and carotenoid-rich fruit extracts for antioxidant activities applying 2,2′-azinobis(3-ethylenebenzothiazoline-6-sulfonic acid radical cation decolorization assay. Methods Enzymol 299:279–389
Pons C, Casals J, Palombieri S et al (2022) Atlas of phenotypic, genotypic and geographical diversity present in the European traditional tomato. Hortic Res. https://doi.org/10.1093/hr/uhac112
Pons C, Casals J, Brower M et al (2023) Diversity and genetic architecture of agro-morphological traits in a core collection of European traditional tomato. J Exp Bot 74:5896–5916. https://doi.org/10.1093/jxb/erad306
R Core Team (2025) R: A language and environment for statistical. Computing.
Rico Ferrer RG, Figàs MdelR, Arroyo N et al (2026) Morpho-agronomic and biochemical diversity of the Tomata Valenciana landrace reveal key traits for its revalorisation and subtype differentiation. J Agric Food Res 26:102717. https://doi.org/10.1016/j.jafr.2026.102717
Rosa-Martínez E, Adalid AM, Alvarado LE et al (2021) Variation for composition and quality in a collection of the resilient Mediterranean 'de penjar' long shelf-life tomato under high and low N fertilization levels. Front Plant Sci. https://doi.org/10.3389/fpls.2021.633957
Sacco A, Ruggieri V, Parisi M et al (2015) Exploring a tomato landraces collection for fruit-related traits by the aid of a high-throughput genomic platform. PLoS ONE 10:e0137139. https://doi.org/10.1371/journal.pone.0137139
Scalfi L, Fogliano V, Pentangelo A et al (2000) Antioxidant activity and general fruit characteristics in different ecotypes of Corbarini small tomatoes. J Agric Food Chem 48:1363–1366. https://doi.org/10.1021/jf990883h
Seymour GB, Taylor JE, Tucker GA (1993) Biochemistry of fruit ripening. Springer Netherlands, Dordrecht
Sinesio F, Moneta E, Peparaio M (2007) Sensory characteristics of traditional field grown tomato genotypes in Southern Italy. J Food Qual 30:878–895. https://doi.org/10.1111/j.1745-4557.2007.00161.x
Sinesio F, Cammareri M, Cottet V et al (2021) Sensory traits and consumer's perceived quality of traditional and modern fresh market tomato varieties: a study in three european countries. Foods 10:2521. https://doi.org/10.3390/FOODS10112521/S1
Siracusa L, Patanè C, Avola G, Ruberto G (2012) Polyphenols as chemotaxonomic markers in Italian "long-storage" tomato genotypes. J Agric Food Chem 60:309–314. https://doi.org/10.1021/jf203858y
Terzopoulos P, Bebeli P (2008) DNA and morphological diversity of selected Greek tomato (*Solanum lycopersicum* L.) landraces. Sci Hortic 116:354–361. https://doi.org/10.1016/j.scienta.2008.02.010
Villena J, Moreno C, Roselló S et al (2023a) Breeding tomato flavor: modeling consumer preferences of tomato landraces. Sci Hortic 308:111597. https://doi.org/10.1016/j.scienta.2022.111597
Villena J, Moreno C, Roselló S et al (2023b) Dissecting a vegetable landrace: components of variation in Spanish 'Moruno' tomatoes as a case studio. Sci Hortic 318:112128. https://doi.org/10.1016/j.scienta.2023.112128