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Phenotypic diversity of a wild Solanum population from the Ecuadorian Andes: morphological characterization and preliminary genomic DNA assessment

Angélica Tigre-León
Universidad Estatal de Bolívar
Favian Bayas-Morejón
fbayas@ueb.edu.ec

Universidad Estatal de Bolívar
Fernando Riveliño Ramón Espinoza
Universidad Estatal de Bolívar
Alex Barrionuevo Remache
Universidad Estatal de Bolívar

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Abstract

The genetic resources of wild *Solanum* plants constitute reservoirs of variability of interest for the conservation and improvement of Andean crops. In this study, a wild population of Solanum sp., "tomatillo," located in Cascarillas, Bolívar, Ecuador, was characterized. Twenty independent individuals were evaluated using vegetative, fruit, and seed characteristics, complemented by principal component analysis (PCA) and cluster analysis. The plants reached a height of 245.90 ± 29.72 cm and produced rough, predominantly conical fruits (4.17 × 2.61 cm; 76.94 g), with 251.60 seeds per fruit. The first three principal components explained 67.03% of the variability, identifying three phenotypic groups. Detectable genomic DNA (22.6 ng/µL) was obtained, although of limited purity. These results reveal intrapopulation phenotypic variability and support the conservation interest of this material as a potential plant genetic resource; however, its taxonomic identity requires confirmation through molecular and phylogenetic analyses.

1. INTRODUCTION

The tree tomato (*Solanum betaceum* Cav.) is one of the most economically and nutritionally important Andean fruits in South America due to its high content of vitamins, phenolic compounds, carotenoids and other bioactive metabolites of interest to the food and pharmaceutical industries (Zambrano-Moreno et al., 2025; INIAP, 2008)

Its cultivation is mainly distributed in Ecuador, Colombia, Peru and Bolivia, where it represents an important source of income for small and medium producers (Moreno-Miranda et al., 2020). In addition to its commercial value, this species has considerable potential for genetic improvement programs aimed at increasing productivity, disease resistance, and adaptation to climate change. Crop wild relatives (CWRs) constitute natural reservoirs of genetic diversity and represent a strategic source of agronomic traits of interest, including tolerance to biotic and abiotic stress, resistance to pests and diseases, nutrient use efficiency, and adaptation to extreme environmental conditions. Consequently, the characterization, conservation, and utilization of these plant genetic resources are considered priorities for strengthening food security and the development of sustainable agricultural systems (Flores-Hernández et al., 2017).

Within the genus *Solanum*, the identification and taxonomic delimitation of wild populations remain challenging due to high phenotypic variability, influenced by environmental factors, and the existence of shared morphological characteristics among populations. Traditionally, taxonomic classification has been based on morphological descriptors related to leaves, flowers, fruits, plant architecture, and reproductive characteristics; however, these traits can exhibit considerable phenotypic plasticity, hindering the precise delimitation of taxonomic units and the identification of materials with potential for conservation and genetic improvement programs (Poulsen, 2020).

In recent years, the integration of morphological, ecological, and molecular studies has significantly improved the taxonomic resolution of numerous plant species (Olabamiji, 2025). Obtaining high-quality

genomic DNA is the first step in applying tools such as polymerase chain reaction (PCR), DNA barcoding, molecular marker analysis, and genomic sequencing—methodologies that allow us to confirm phylogenetic relationships, estimate genetic variability, and more accurately identify species and ecotypes (Rey Bentos & Capdevielle Sosa, 2020; Bayas Morejón & Tigre León, 2025). In this context, DNA extraction, quantification, and integrity assessment represent critical steps to ensure the reliability of future molecular analyses.

Ecuador harbors considerable diversity of cultivated and locally occurring tree tomato germplasms (Vilanova et al., 2012; Pazmiño Gaibor, 2025). However, scientific knowledge about these resources remains limited, especially regarding their ecological distribution, morphological variability, agronomic potential, and genetic characterization. In Bolívar province, the available information on wild ecotypes is scarce, which restricts their incorporation into conservation, sustainable management, and plant breeding programs.

During prospecting activities conducted in the Cascarillas sector, San Miguel canton, Bolívar province, a naturally occurring *Solanum* population locally known as “tomatillo” was identified. Preliminary field observations indicated distinctive vegetative and fruit characteristics and persistence under local high-Andean environmental conditions. Previous observations associated with this material also suggested a possible differential response to root-knot nematodes (*Meloidogyne* spp.); however, this characteristic has not yet been experimentally evaluated.

Therefore, this study aimed to characterize the phenotypic diversity of a naturally occurring *Solanum* sp. population from the Ecuadorian Andes through morphological and ecological assessment and to conduct a preliminary evaluation of genomic DNA recovery as a basis for subsequent molecular and taxonomic studies.

2. MATERIALS AND METHODS

2.1. Study Area

The research was conducted in the Cascarillas sector, San Pablo de Atenas parish, San Miguel canton, Bolívar province, Ecuador. The site is located at approximately 2750 meters above sea level in an Andean montane forest environment. Environmental references for the area included an average temperature of approximately 12°C, relative humidity between 70 and 90%, and an approximate annual rainfall of 904 mm. These conditions were used to ecologically contextualize the occurrence and phenotypic characteristics of the plant material.

2.2. Plant material and prospecting

Surveys were conducted in the Bolívar province to locate wild populations of *Solanum* morphologically related to the tree tomato (*Solanum betaceum* Cav.). In the Cascarillas sector, a wild population locally

called “tomatillo” was identified, characterized by its hardiness, vegetative vigor, conspicuous foliar pubescence, and fruits with a rough surface and a conical shape.

Twenty adult individuals distributed throughout the naturally occurring population were selected for morphological characterization. Sampling was carried out during the months of May to July 2025, when the plants had mature vegetative structures and fruits. Each plant was identified by a consecutive code (P01–P20) and considered an independent observation unit. The individuals were photographed, and vegetative and reproductive structures, including leaves, flowers, fruits, and seeds, were collected. Additionally, young, healthy leaf tissue was collected for preliminary genomic DNA extraction.

The history of possible tolerance of the material to root-knot nematodes of the genus Meloidogyne was considered only as prior information of phytosanitary interest and not as a characteristic experimentally evaluated in the present study.

2.3. Cultivated *Solanum betaceum* reference material

For comparative morphological purposes, two cultivated tree tomato (*Solanum betaceum* Cav.) plants growing in the experimental plantations of the Faculty of Agricultural Sciences, Natural Resources and Environment, Universidad Estatal de Bolívar, were evaluated as local reference material.

These plants were assessed using the same qualitative morphological criteria applied to the wild Solanum population from Cascarillas, including growth habit, leaf pubescence, fruit shape and surface, fruit coloration during ripening, and general seed characteristics.

Because only two cultivated plants were available, this material was used exclusively as a local morphological reference and was not considered an experimental comparison group for inferential statistical analyses. Therefore, the observed differences were interpreted descriptively and should not be considered sufficient evidence of taxonomic differentiation.

2.4. Morphological characterization

The morphological characterization included vegetative and reproductive characters of the 20 selected individuals. The size and architecture of the plant, branching, shape of the leaf blade, apex, base, margin, pubescence, characteristics of flowers and inflorescences, shape and surface of the fruit, coloration during maturation and general characteristics of the seeds were qualitatively recorded.

The quantitative variables considered for the statistical analysis were: plant height (cm), leaf length (cm), leaf width (cm), fruit length (cm), fruit diameter (cm), fruit weight (g), number of seeds per fruit, seed length (mm) and seed width (mm). The measurements corresponding to each individual were recorded in an independent data matrix.

For each quantitative variable, the mean, standard deviation, minimum value and maximum value were calculated. The observed characters were subsequently contrasted with the morphological descriptions

available for *S. betaceum* and related wild materials, with the purpose of identifying phenotypic similarities and differences.

2.5. Ecological characterization

The ecological characterization considered the environmental conditions of the collection site, including altitude, temperature, relative humidity, and precipitation, supplemented by direct observations of habitat conditions.

Environmental information was used as a contextual element to interpret the expression of the observed phenotypic traits. Because plant morphological characteristics can be influenced by both genetic and environmental factors, the recorded phenotypic differences were not considered, on their own, as evidence of genetic or taxonomic divergence.

2.6. Genomic DNA extraction

Young, healthy leaves of the Cascarillas *Solanum* sp. population were used to obtain genomic DNA. These leaves had been previously preserved under conditions that minimized the degradation of the plant material. A preliminary molecular evaluation of a representative sample was also performed.

The leaf tissue was subjected to cryogenic maceration using liquid nitrogen until a fine powder was obtained. Extraction was then carried out using a commercial silica-column kit (HiBind® DNA Mini Column, IBI Scientific, USA), following the manufacturer's recommendations. These recommendations included successive steps of cell lysis, protein precipitation, purification, washing, and final DNA elution. The purified DNA was stored at − 20°C until analysis.

2.7. Quantification and evaluation of DNA quality

The concentration and purity of the genomic DNA were determined by spectrophotometry using a NanoDrop One™ instrument (Thermo Scientific®, USA). DNA concentration was recorded in ng/µL, and the A260/A280 and A260/A230 absorbance ratios were used as indicators of DNA purity and the possible presence of proteins, salts, and other residual compounds from the extraction process.

DNA integrity was assessed by electrophoresis on a 2% agarose gel, using a molecular weight marker as a reference. The presence and definition of the DNA band were considered for a qualitative assessment of its integrity.

2.8. Statistical analysis

Statistical analyses were performed using InfoStat Libre version 4.0. The morphological data corresponding to the 20 independent individuals were organized into a data matrix and initially subjected to descriptive statistical analysis. For each quantitative variable, the mean, standard deviation, minimum, and maximum values were calculated to characterize the magnitude of phenotypic variability within the studied population.

To explore the relationships among morphological traits and summarize the main sources of variation, principal component analysis (PCA) was performed. Before analysis, quantitative variables were standardized to account for differences in measurement units and scales. Seed width was excluded from the multivariate analysis because it showed zero variance, with a constant value of 1.00 mm across all 20 individuals. Consequently, the PCA was conducted using the remaining eight quantitative variables.

For each principal component, the percentage of explained variance, cumulative variance, and variable loadings were determined to identify the traits contributing most strongly to the morphological differentiation among individuals.

In addition, hierarchical cluster analysis was performed using the same standardized morphological variables. Clustering was conducted using Ward's method to explore patterns of phenotypic similarity among individuals and to identify groups within the studied population. The resulting grouping pattern was represented by a dendrogram.

Analysis of variance (ANOVA) and Tukey's multiple comparison test were not performed because the 20 individuals represented independent observations from a single naturally occurring population, and no replicated experimental structure involving different populations or treatments was available for formal comparison of group means. The two cultivated Solanum betaceum plants evaluated in this study were used exclusively as local morphological reference material and were therefore not included as a comparison group in inferential statistical analyses.

2.9. Taxonomic considerations

The preliminary taxonomic identification of the plant material was performed by comparing its vegetative and reproductive characteristics with available taxonomic descriptions for *Solanum betaceum* Cav. and other related materials of the genus *Solanum*. We particularly considered characteristics associated with leaf morphology, pubescence, floral characteristics, and fruit and seed morphology.

Because taxonomic delimitation based solely on morphological characteristics can be affected by phenotypic plasticity and environmental conditions, the studied material was kept under the provisional designation of *Solanum* sp., avoiding the assignment of a definitive taxonomic category.

The extraction and preliminary evaluation of genomic DNA was performed as an initial step for future molecular studies. Confirming taxonomic identity will require subsequent application of molecular markers, PCR amplification, sequencing, and phylogenetic analyses, which will allow establishment of the relationships of the wild material from Cascarillas with *S. betaceum* and related species.

3. RESULTS AND DISCUSSION

3.1. Morphological characterization and phenotypic variability

The survey conducted in the Cascarillas sector identified a naturally occurring population of *Solanum* locally known as “tomatillo.” The plants exhibited a robust growth habit, high vegetative vigor, conspicuous leaf pubescence, and predominantly conical fruits with a rugose surface. Although these characteristics differentiated the Cascarillas material phenotypically from the cultivated tree tomato plants used as local reference material, they were not considered sufficient for definitive taxonomic identification. Consequently, the studied material was maintained under the provisional designation *Solanum* sp. pending molecular and phylogenetic confirmation.

Morphological characterization of the 20 individuals revealed variation in both vegetative and reproductive traits. The leaves were simple, alternate, predominantly cordate, with entire margins and conspicuous pubescence, particularly on the abaxial surface. Flowers were small, approximately 1 cm in diameter, pink to white, pentamerous, and arranged in axillary or supra-axillary racemes. The fruits were predominantly conical, with a rough surface, and changed from dark green to orange when fully ripe. (Fig. 1). Table 1 summarizes the main qualitative morphological descriptors observed in the Cascarillas population.

Table 1
Main qualitative morphological characteristics observed in the wild *Solanum* sp. Population from Cascarillas.

Plant organ	**Character**	**Observed phenotype**
Plant	Growth habit	Robust and vigorous
Leaves	Arrangement	Alternate
Leaves	Shape	Predominantly cordate
Leaves	Margin	Entire
Leaves	Pubescence	Conspicuous, particularly on abaxial surface
Flowers	Color	Pink to white
Flowers	Floral structure	Pentamerous
Flowers	Inflorescence	Axillary or supra-axillary racemes
Fruits	Shape	Predominantly conical
Fruits	Surface	Rugose
Fruits	Ripening color	Dark green to orange when fully ripe
Seeds	General morphology	Are grayish in color, with a size 1.00 ± 0.00 mm of diameter and 2.0 mm in length.

Quantitative characterization confirmed intrapopulation phenotypic variability (Table 2). Plant height averaged 245.90 ± 29.72 cm and ranged from 200 to 300 cm. Mean leaf length and width were 5.49 ± 0.34 cm and 3.04 ± 0.28 cm, respectively. Fruit length averaged 4.17 ± 0.12 cm, whereas fruit diameter showed comparatively greater variation, with a mean of 2.61 ± 0.49 cm and a range of 2.00–4.00 cm. Mean fruit weight was 76.94 ± 4.68 g, ranging from 71.00 to 90.00 g.

Table 2
Descriptive statistics of quantitative morphological variables evaluated in 20 individuals of the Cascarillas *Solanum* sp. population.

Variable	Mean	SD	Minimum	Maximum
Plant height (cm)	245.90	29.72	200.00	300.00
Leaf length (cm)	5.49	0.34	5.00	6.00
Leaf width (cm)	3.04	0.28	2.30	3.50
Fruit length (cm)	4.17	0.12	4.00	4.50
Fruit diameter (cm)	2.61	0.49	2.00	4.00
Fruit weight (g)	76.94	4.68	71.00	90.00
Number of seeds/fruit	251.60	37.53	201	321
Seed length (mm)	2.08	0.10	2.00	2.30
Seed width (mm)	1.00	0.00	1.00	1.00
SD: standard deviation; n = 20 individuals.				

Reproductive traits also showed variation among individuals. The number of seeds per fruit averaged 251.60 ± 37.53 and ranged from 201 to 321, representing one of the most variable reproductive characteristics. Seed length showed comparatively limited variation (2.08 ± 0.10 mm; range: 2.00–2.30 mm), whereas seed width remained constant at 1.00 mm in all evaluated individuals.

The simultaneous occurrence of variation in plant architecture, leaf dimensions, fruit morphology, fruit weight, and seed number indicates that phenotypic heterogeneity within the Cascarillas population is multidimensional rather than restricted to a single morphological character. Fruit traits, in particular, exhibited substantial differentiation among individuals and therefore appear to represent informative descriptors for subsequent characterization of this material.

Morphological variation within *Solanum* may result from the combined effects of genetic differentiation, developmental processes, and environmental influences (Knapp, 2013; Spooner et al., 2014). Therefore, although the observed variation is relevant for germplasm characterization, it should not be interpreted independently as evidence of genetic or taxonomic divergence. Common-garden evaluations and molecular analyses would be required to distinguish genetically determined variation from phenotypic plasticity.

3.2. Multivariate morphological differentiation

To further explore the structure of the morphological variability observed among the 20 individuals, standardized quantitative data were subjected to principal component analysis (PCA) and hierarchical cluster analysis. Seed width was excluded from these analyses because it showed zero variance. Consequently, eight quantitative variables were included in the multivariate analyses.

The first principal component (PC1) explained 29.03% of the total morphological variation, whereas PC2 explained 21.31%. Together, the first two components accounted for 50.34% of the total variance. PC3 explained an additional 16.69%, increasing the cumulative variance explained by the first three components to 67.03%. When the first five components were considered, cumulative explained variance reached 88.98% (Table 3).

Table 3
Variance explained by the principal components of quantitative morphological characteristics of the Cascarillas *Solanum* sp. population.

Component	Variance explained (%)	Cumulative variance (%)
PC1	29.03	29.03
PC2	21.31	50.34
PC3	16.69	67.03
PC4	12.75	79.78
PC5	9.19	88.98

Analysis of component loadings showed that PC1 was primarily associated with fruit weight (0.540), leaf length (-0.481), and fruit diameter (0.441), indicating a contrast mainly between fruit-related and foliar characteristics. PC2 was predominantly associated with fruit length (0.525), plant height (0.499), and seed length (0.433), whereas PC3 was mainly characterized by the number of seeds per fruit (0.564) and leaf width (0.440) (Table 4).

Table 4
Morphological variable loadings on the first three principal components.

Variable	PC1	PC2	PC3
Plant height	-0.163	**0.499**	-0.235
Leaf length	**-0.481**	-0.324	-0.211
Leaf width	-0.393	0.170	**0.440**
Fruit length	0.026	**0.525**	-0.476
Fruit diameter	**0.441**	0.003	-0.299
Fruit weight	**0.540**	-0.328	0.040
Number of seeds	0.139	0.215	**0.564**
Seed length	0.287	**0.433**	0.268

These results indicate that morphological differentiation among individuals was not driven by a single descriptor. Instead, vegetative, fruit, and seed traits contributed jointly to the observed phenotypic structure. PC1 predominantly represented variation associated with fruit size and weight in relation to leaf dimensions, whereas PC2 reflected variation in plant height, fruit length, and seed size. PC3 captured an additional reproductive dimension primarily associated with seed number.

Because the PCA was conducted on 20 individuals and eight variables, the results should be interpreted as an exploratory description of morphological structure rather than as definitive evidence of population differentiation. Nevertheless, the analysis provides a useful basis for identifying the morphological traits that contribute most strongly to intrapopulation variation and that could therefore be prioritized in future germplasm characterization.

Hierarchical cluster analysis using the standardized morphological variables and Ward's method further supported the existence of phenotypic heterogeneity among the evaluated individuals. Based on visual inspection of the main separation pattern in the dendrogram, three exploratory phenotypic clusters were retained for descriptive interpretation (Table 5). Group 1 comprised ten individuals (P01, P05, P07, P09, P10, P11, P15, P16, P17, and P18), Group 2 included eight individuals (P02, P04, P08, P12, P13, P14, P19, and P20), and Group 3 consisted of P03 and P06.

Table 5
Exploratory phenotypic grouping of *Solanum* sp. individuals based on hierarchical cluster analysis.

Cluster	Individuals	n
Group 1	P01, P05, P07, P09, P10, P11, P15, P16, P17, P18	10
Group 2	P02, P04, P08, P12, P13, P14, P19, P20	8
Group 3	P03, P06	2

Table 6
Descriptive morphological comparison between the wild *Solanum* sp. population from Cascarillas and two cultivated *Solanum betaceum* plants used as local reference material.

Character	Wild Material from Cascarillas	Cultivated *S. betaceum*
Growth habit and vigor	Robust growth habit and high vegetative vigor	Cultivated growth habit
Leaf pubescence	More pronounced	Generally less conspicuous
Fruit	Rugose surface, conical tendency, and smaller size	Smooth surface, ellipsoid or ovoid shape, and larger commercial size
Ripening	dark green to orange when fully ripe	Yellow, orange, or red depending on the cultivar
Note: Cultivated *S. betaceum* was represented by two plants; therefore, the comparison is descriptive and should not be interpreted as a population-level statistical comparison.		

In Fig. 2, Groups 1 and 2 contained most of the individuals, whereas P03 and P06 formed a smaller and more differentiated third group. This separation was largely associated with fruit characteristics. P03 exhibited the largest fruit diameter (4.00 cm) and the highest fruit weight (90.00 g) recorded in the population, whereas P06 exhibited the greatest fruit length (4.50 cm) and a relatively large fruit diameter (3.20 cm). These distinctive values likely contributed substantially to their separation in the multivariate space.

The importance of fruit-related traits in both PCA and cluster analysis suggests that fruit morphology represents one of the principal sources of phenotypic differentiation within the Cascarillas population. This observation is consistent with previous tree tomato germplasm studies in which fruit morphological and agronomic characteristics contributed substantially to differentiation among accessions. Considerable genetic diversity among tree tomato accessions from different origins has also been documented in Ecuador (Vilanova et al., 2012).

However, the three clusters identified here should be interpreted as exploratory phenotypic groups rather than genetically distinct lineages. Confirmation of whether these morphological groups reflect underlying genetic structure will require analysis using molecular markers and broader population sampling.

3.3. Comparison with local cultivated *Solanum betaceum* reference plants

To provide a local phenotypic reference, the Cascarillas population was descriptively compared with two cultivated *Solanum betaceum* Cav. plants growing in the experimental plantations of the Faculty of Agricultural Sciences, Natural Resources and Environment, Universidad Estatal de Bolívar. Because only two cultivated plants were available, they were considered reference material rather than a statistically comparable population, and no inferential statistical comparison was performed.

Several qualitative differences were observed between the Cascarillas material and the cultivated reference plants. The Cascarillas plants showed a robust growth habit, greater apparent vegetative vigor, and more conspicuous leaf pubescence. Their fruits were predominantly conical and had a rugose surface, whereas the fruits of the cultivated reference plants were smoother and predominantly ellipsoid or ovoid. Differences in fruit coloration during ripening were also observed.

These observations provide a local morphological reference supporting the phenotypic distinctiveness of the Cascarillas population. However, because the cultivated reference consisted of only two plants, the observed differences cannot be generalized to cultivated *S. betaceum* as a whole and should not be interpreted as evidence of taxonomic divergence.

This distinction is particularly important because morphological characteristics in *Solanum* may be influenced by genotype, developmental stage, cultivation conditions, and environmental factors. Therefore, broader comparative sampling involving multiple cultivated accessions and related wild *Solanum* populations would be necessary to determine the consistency and taxonomic significance of the observed differences.

3.4. Ecological context and conservation relevance

The Cascarillas population was found at approximately 2750 m above sea level in a high-Andean environment characterized by an average temperature of approximately 12°C, relative humidity of 70–90%, and annual precipitation of approximately 904 mm. The plants occurred spontaneously and without conventional agronomic management, indicating their capacity to persist under the local environmental conditions.

The occurrence of this population under relatively cool and humid high-Andean conditions, together with its robust growth and vegetative vigor, suggests potential local adaptation. Nevertheless, the present study did not experimentally evaluate environmental adaptation. Consequently, these observations should be regarded as ecological context rather than direct evidence of adaptive differentiation.

This distinction is relevant because phenotypic expression may result from both genetic variation and environmental plasticity. Common-garden or reciprocal-transplant experiments, combined with molecular characterization, would therefore be necessary to determine whether the distinctive

characteristics observed in the Cascarillas population are genetically determined or represent environmentally induced phenotypic responses.

Wild relatives and locally adapted populations of cultivated species constitute important reservoirs of genetic diversity and may contain alleles associated with tolerance to biotic and abiotic stresses (Dempewolf et al., 2017; Khoury et al., 2022). In this context, the morphological heterogeneity observed in the Cascarillas population, particularly in fruit-related traits, supports its potential relevance as a plant genetic resource and provides justification for its conservation and further characterization.

Previous field observations associated with this material suggested a possible differential response to root-knot nematodes (*Meloidogyne* spp.); however, this response has not yet been experimentally evaluated. This observation should be considered only as a hypothesis for future phytosanitary evaluation. Controlled inoculation experiments incorporating galling index, egg production, final nematode population density, and reproduction factor would be necessary to determine whether the Cascarillas material possesses resistance or tolerance to *Meloidogyne* spp.

From a conservation perspective, the Cascarillas population may represent locally relevant germplasm suitable for inclusion in both *in situ* and *ex situ* conservation strategies. Collection of seeds, establishment of germplasm accessions, and maintenance of living material would facilitate subsequent studies of phenotypic stability, reproductive biology, phytosanitary response, and potential use as breeding material or rootstock.

Nevertheless, these potential applications should remain conditional on confirmation of the taxonomic identity and genetic diversity of the material. At the current stage, the evidence supports recognition of the Cascarillas population as phenotypically distinctive germplasm of potential conservation interest rather than as a distinct taxonomic entity.

3.5. Preliminary genomic DNA assessment and perspectives for molecular validation

Genomic DNA was successfully recovered from young leaf tissue of the Cascarillas material using cryogenic maceration followed by silica-column purification. Spectrophotometric analysis of the representative sample yielded a DNA concentration of 22.6 ng/µL. However, the A260/A280 and A260/A230 ratios were 1.21 and 0.46, respectively, indicating limited purity. Agarose gel electrophoresis confirmed the presence of genomic DNA, although its integrity was qualitatively classified as moderate (Table 7).

Table 7
Preliminary genomic DNA quality parameters obtained from the Cascarillas *Solanum* sp. material.

Sample	Concentration (ng/µL)	A260/A280	A260/A230
Wild tomato	22.6	1.21	0.46

These results demonstrate that genomic DNA could be recovered from the plant material but also indicate that the extraction procedure requires optimization before downstream molecular applications. The low absorbance ratios suggest the presence of residual contaminants that could interfere with PCR amplification, sequencing, or molecular marker analyses. Additional purification steps or optimization of the extraction protocol should therefore be considered.

Importantly, the DNA assessment performed in this study represents a preliminary technical evaluation rather than molecular characterization of the population. No molecular markers, PCR-based identification, DNA barcoding, sequencing, or phylogenetic analyses were conducted. Consequently, the DNA results cannot currently provide evidence regarding the genetic diversity or taxonomic identity of the Cascarillas population.

The next stage should include DNA extraction from a broader representation of the sampled individuals, followed by amplification and sequencing of appropriate molecular regions and comparison with authenticated *Solanum* reference material. Integrating these molecular data with the morphological and ecological information generated in the present study would allow assessment of whether the observed phenotypic differences represent intrapopulation variability, differentiation within *S. betaceum*, or a more distinct taxonomic relationship.

Overall, the present study establishes a morphological and ecological baseline for the Cascarillas *Solanum* population. The combination of measurable intrapopulation phenotypic variability, distinctive fruit and vegetative characteristics, persistence under high-Andean environmental conditions, and successful preliminary recovery of genomic DNA supports the value of this material for continued germplasm characterization and conservation. However, broader comparative sampling and molecular and phylogenetic evidence are required before definitive conclusions regarding its taxonomic status or breeding potential can be established.

Conclusions

The wild *Solanum* sp. population from Cascarillas exhibited measurable intrapopulation phenotypic variability among the 20 individuals evaluated, particularly in vegetative, fruit, and seed-related traits. Exploratory principal component analysis showed that the first three components explained 67.03% of the total morphological variation, with fruit weight and diameter, leaf dimensions, plant height, fruit length, seed length, and number of seeds contributing substantially to the observed differentiation. Hierarchical cluster analysis further identified three phenotypic groups, with individuals P03 and P06 showing the greatest differentiation, mainly associated with fruit characteristics.

Descriptive comparison with two locally cultivated *S. betaceum* plants provided a preliminary reference for distinguishing the Cascarillas material based on characteristics such as vegetative vigor, leaf pubescence, and fruit morphology. However, because the cultivated reference was limited to two plants, these differences cannot be generalized to cultivated *S. betaceum* or interpreted as evidence of taxonomic divergence. The spontaneous occurrence of the Cascarillas population under high-Andean

environmental conditions supports its interest as locally occurring germplasm, but adaptive differentiation was not experimentally evaluated.

Genomic DNA was successfully recovered, although the low purity values indicate that the extraction and purification procedure should be optimized before PCR, sequencing, or molecular marker analyses. Overall, the morphological diversity observed supports the conservation and further characterization of the Cascarillas population as a potentially valuable plant genetic resource. Broader comparative sampling, molecular characterization, and phylogenetic analyses are required to confirm its taxonomic identity, assess its genetic diversity, and determine its potential value for future tree tomato breeding programs.

Declarations

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Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Ethics approval

No ethical approval was needed for this study.

Author Contribution

Author ContributionsAngélica Tigre-León: Investigation, Methodology, Data curation, Formal analysis, Visualization, and Writing – original draft.Favian Bayas-Morejón: Conceptualization, Methodology, Formal analysis, Supervision, Validation, Writing – original draft, and Writing – review & editing.Fernando Riveliño Ramón Espinoza: Investigation, Methodology, Laboratory analysis, Data curation, and Writing – review & editing.Alex Barrionuevo Remache: Investigation, Resources, Validation, Visualization, and Writing – review & editing.All authors contributed to the interpretation of the results, critically reviewed the manuscript, and approved the final version for submission.

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Figures

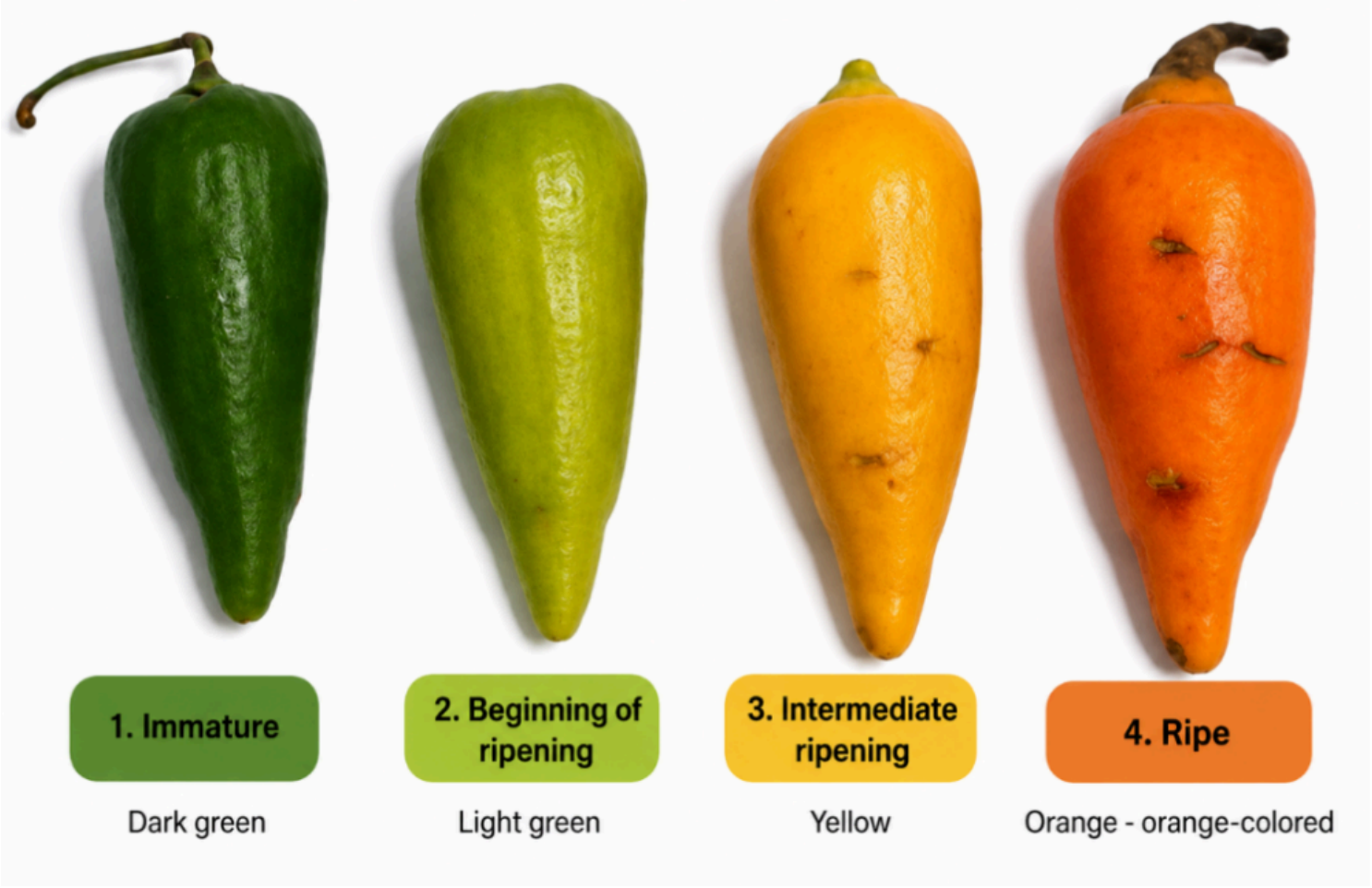
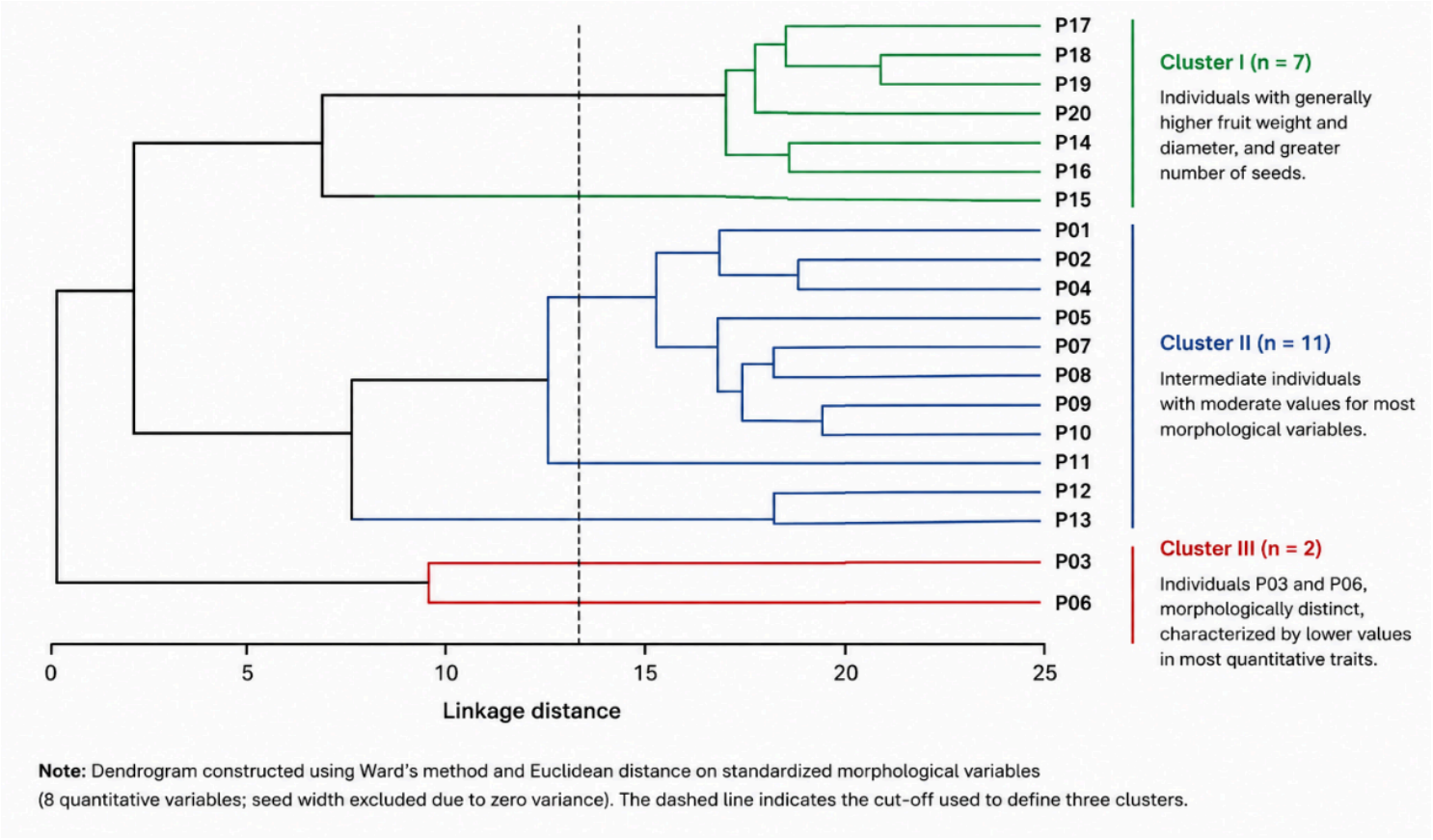


Figure 1

Fruit of the Cascarillas *Solanum* sp. population at different stages of ripening.



Note: Dendrogram constructed using Ward's method and Euclidean distance on standardized morphological variables (8 quantitative variables; seed width excluded due to zero variance). The dashed line indicates the cut-off used to define three clusters.

Figure 2

Dendrogram of hierarchical cluster analysis of 20 individuals from the Cascarillas *Solanum* sp. population based on standardized quantitative morphological traits using Euclidean distance and Ward's method.