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Analysis of passport data of *Sechium* spp. from the Mexican chayote genebank in Huatusco, Veracruz

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Abstract: Chayote (*Sechium* spp.) (Cucurbitaceae) is a Mesoamerican genus, with Mexico being the primary centre of biodiversity for four species: *Sechium compositum*, *S. chinantlense*, *S. hintonii* and *S. edule*. Mexico also hosts the only chayote genebank in the world, which follows a taxonomic arrangement for its intraspecific variants. Descriptive and multivariate techniques were used to analyze the passport data of the accessions conserved *ex situ* aiming to identify associations and similarity patterns to allow efficient management and origin traceability, stakeholder engagement, consumer preferences, destination, use and conservation practices. Results showed that 23% of the accessions belong to *S. edule* var. *virens levis,* 62.8% come from backyards, and 58.9% of the *S. edule* variants are kept and preserved by women. Interestingly, about 70.8% of the accessions are used for trading, and the rest for self-consumption. Multiple correspondence analyses showed that 27.24% of the first two components variation and the variables with the greatest phenotypic contribution were fruit flavour (sweet and bitter), condition of the populations (forest, ruderal-wild, orchard), fruit colour (yellow, light green), small size and flattened shape. The morphological boundaries of *S. edule*, *S. compositum* and *S. chinantlense* variants are defined by the fruit morphology. These findings from passport data analysis support the development of strategies for replacement, regeneration, distinction, genetic improvement, conservation and bioprospective studies.

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Introduction

Plant genetic resources for food and agriculture are the basis of human nutrition, industrial inputs and pharmacologically active ingredients. Cereals, fruits, roots and vegetables contribute significantly to agrobiodiversity (Bellon *et al*, 2009). The *ex situ* conservation of underutilized landraces and wild relatives has become a relevant source of unexplored genes, enriching germplasm banks and their use in breeding. Mexico is a megadiverse country, and rural communities manage a wide range of domesticated and semi-domesticated biological variants, cultivated and wild relatives which significantly increase agrobiodiversity (Casas and Vallejo, 2019). Field collections of species with recalcitrant seeds, such as chayotes (genus *Sechium* P. Br.), are among the strategies for *ex situ* conservation of agrobiodiversity. Chayote is an increasingly important vegetable in international markets, and morphotypes of the

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Mexican clade have gradually been collected (Barrera-Guzmán *et al*, 2021a).

In Mexico, *Sechium compositum* (Donn. Sm.) C. Jeffrey, *S. chinantlense* Lira & F. Chiang, *S. hintonii* (Paul G. Wilson) C. Jeffrey and *S. edule* (Jacq.) Sw have been recorded as endemic species. Among these, only *S. edule* is edible since the other three species have bitter-tasting fruits. *S. edule*, particularly the smooth green var. *virens levis* variant, is distributed on all continents (Cadena-Iñiguez, 2005). Its success as a vegetable has transcended local markets, becoming an export product (Cadena-Iñiguez and Arévalo-Galarza, 2011). Different studies highlight *S. edule* as a species with notable intraspecific diversity, contributing to the feeding and rural local economy (Aguirre-Medina *et al*, 2021). However, most published research only mentions *S. edule* without specifying the biological variant. For example, Dire *et al* (2003), Setzer and Setzer (2003), Ordoñez *et al* (2006), Loizzo *et al* (2016), Vieira *et al* (2019), among others, do not specify the variants studied, making it challenging to reproduce their findings. Lira *et al* (1999) performed a grouping analysis of edible morphotypes of *S. edule* and another for a wild type, without distinguishing or specifying the variation. This makes conservation actions difficult since morphotypes must be identified by some taxonomic method to be included in genebanks. In this case, the popular common name is not appropriate.

Morphological, anatomical, biochemical and genetic studies, carried out by various authors (Donato *et al*, 1994; Cadena-Iñiguez, 2005; Cadena-Iñiguez and Arévalo-Galarza, 2011; Iñiguez *et al*, 2011; Avendaño-Arrazate *et al*, 2012; Machida-Hirano *et al*, 2015; Barrera-Guzmán *et al*, 2021a,b; Iñiguez-Luna *et al*, 2021), have shown that there are stability, heritability and uniformity traits that allow the distinction of *S. edule* variants, which facilitate their conservation, management and research. These traits confer different and desirable characteristics for its use as food (Cadena-Iñiguez *et al*, 2013a; Aguiñiga-Sánchez *et al*, 2015, 2017; Salazar-Aguilar *et al*, 2017). Genebanks are crucial to avoiding diversity loss and maintaining this agrobiodiversity. In 2005, the National Germplasm Bank for *Sechium edule* (BANGESe) was founded to preserve endemic species and biological variants. To achieve this, fruits were collected from 12 Mexican states, as well as from Guatemala and Costa Rica. Currently, the BANGESe safeguards more than 300 accessions in a field collection since *Sechium* seeds are recalcitrant and do not respond to traditional conservation methods (Ramírez-Rodas *et al*, 2021).

The accessions are conserved in a taxonomic arrangement following the principles by (Stace, 1986) and adapted for *S. edule*. It integrates morphotypes as varietal groups that possess stable, heritable characteristics and fertile offspring. These varietal groups are *albus minor, a. levis, a. dulcis* and *a. spinosum* for plants with yellow, smooth and prickly fruits. For fruits with dark green epidermis with and without thorns are *nigrum minor, n. conus, n. levis, n. xalapensis, n. spinosum* and *n. maxima*. The morphotype *virens levis*, the most widely distributed in the world, reports light green fruit without spines, while the only representative with bitter fruits of *S. edule* is the *amarus sylvestris* morphotype. The above taxonomic nomenclature has facilitated the handling, distribution and distinction of accessions, allowing research, bioprospecting, breeding and preservation activities.

As in many germplasm collections, BANGESe accessions come from direct collection from the areas of origin, distribution and domestication, as well as from donations by rural inhabitants who have locally safeguarded agrobiodiversity for a particular interest. This raises several important questions related to the management, design and regeneration strategies of these resources. For example: Which of the *Sechium* varietal groups have the broadest geographical distribution? Which biological variants (morphotypes) are the most important in terms of consumer preferences and what characteristics drive this? What is the origin of the accessions, and what implications does this have for their conservation? Which stakeholders are most engaged with conservation efforts? What are the primary uses of the fruits? How does the distribution of varietal groups vary with altitude? Finally, what are the morphological traits of the fruits that facilitate their visual distinction?

Genebanks are long-term conservation centres of genetic resources, especially to preserve agrobiodiversity. However, without thorough characterization and documentation of the accessions, making informed decisions about conservation, research, genetic improvement and potential use is challenging (Weise *et al*, 2020). Since *Sechium* is a cross-pollinated plant, asexual methods of multiplication are used to preserve the genetic identity of the accessions. The most successful are grafting, rooting of cuttings, and in vitro multiplication (Figure 1).

Materials and methods

Location of the genebank and passport data

The National Germplasm Bank of *Sechium edule* (BANGESe) is located in Huatusco, Veracruz, Mexico (19° 08’ 48” N, and 97° 57’ 00” W). The vegetation type is mountain cloud forest (altitude of 1,340 masl), with a mean annual temperature of 19–22°C, 85–90% relative humidity, and 2,250mm mean annual precipitation. The soils are vitric luvisol, rich in organic matter, low calcium and high iron, manganese and zinc nutrients, with moderate fertility, coarse texture and volcanic glass fragments (pH 4.3–6.5). The current area of the genebank covers 3ha. Because chayote is a climbing plant, accessions are kept in a metal net-like support structure at a 2.2m height. The accessions are introduced into the genebank as ±20cm plants, obtained by direct sampling, donation or purchase from rural inhabitants. *Sechium* plants are cross-pollinated. To maintain the genetic identity of each accession, asexual

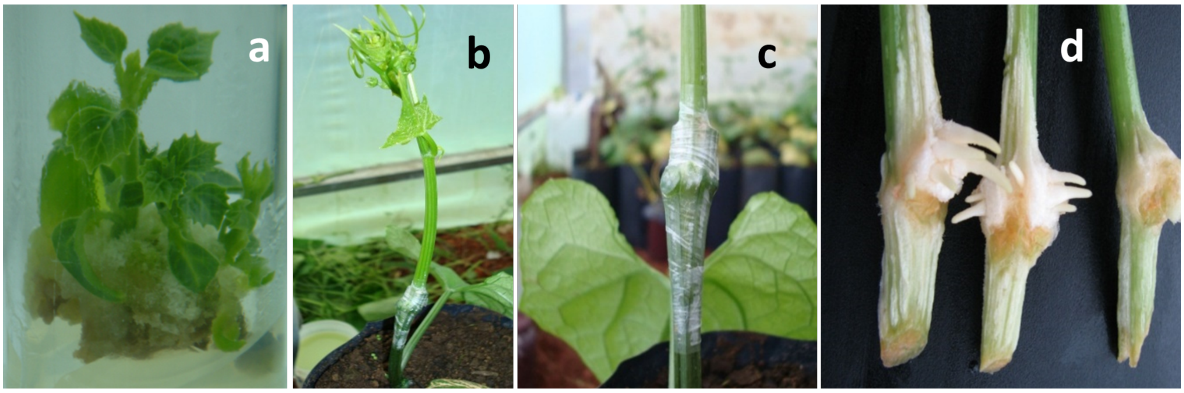

Figure 1. Methods of regeneration and asexual multiplication of *Sechium* spp. accessions. a) *In vitro* multiplication, b-c) grafting and c) callus emission, training sites and emission of roots from the use of regulators of growth.

multiplication techniques such as grafting, rooting of three-node cuttings, and in vitro multiplication are employed.

Statistical analysis

The passport data in BANGESe include georeferenced and taxonomic data, origin, morphological characteristics of fruits and seeds, biological status and ethnobotanical information, following the descriptor guide for *S. edule* varieties (Cadena-Iñiguez *et al*, 2017). Passport details can be found at Bangermex (https://bangermex.snics.gob.mx/bancos). The information was analyzed with the Rstudio software (R Core Team, 2023). Out of a total of 309 accessions, only 231 were analyzed, since 78 were excluded being genetic segregants from the hybridization programme. Graphic analysis was performed with tidyverse (Wickham *et al*, 2019) to assess the proportion of varietal complexes regarding their origin, type of establishment (orchard, backyard, ruderal) and owner/donor. Additionally, the central tendency and dispersion statistics of the altitude variable were evaluated to know any pattern related to the distribution ranges at which *Sechium* varietal complexes develop. Qualitative variables were studied by multiple correspondence analysis (MCA) with FactoMineR (Lê *et al*, 2008) and factoextra (Kassambara and Mundt, 2020). To calculate the eigenvectors, eigenvalues and the graph of each variable's contribution to the components, the same statistics used for the MCA were employed.

Results

Descriptive analysis

BANGESe contains 231 accessions representing the intraspecific variability of *S. edule* in 12 varietal complexes: *albus dulcis*, *albus levis*, *albus minor*, *albus spinosum*, *amarus sylvestris*, *nigrum conus*, *nigrum levis*, *nigrum maxima*, *nigrum minor*, *nigrum spinosum*, *nigrum xalapensis* and *virens levis*. Also, there are four accessions of *S. chinantlense*, 12 of *S. compositum* and two of *S. hintonii* (the latter was not analyzed). The *virens levis*, *n. spinosum* and *n. xalapensis* varietal complexes are the most represented in the collection (Figure 2a). The major diversity of *S. edule* in Mexico is found in the state of Veracruz, with 110 accessions (47.6% of the total) (Figure 2b). Of the 231 accessions, 62.8% were collected from backyards and 23.3% from commercial orchards, while *S. compositum*, *S. chinantlense* and *S. edule* var. *amarus sylvestris* came from ruderal and forest areas (Figure 2c). Some accessions of *virens levis*, *n. spinosum* and *n. xalapensis* were from Costa Rica (CR) and Guatemala (Guat) (Figure 3).

It is well known that women play a key role in vegetable cultivation and plant breeding in domestic orchards. Our data showed that women managed 58.9% of the *S. edule* accessions, all of which are edible. Wild accessions are outside the interest of men and women; however, their conservation in genebanks is important due to their phytochemical potential for pharmacological use and as sources of genes for genetic improvement in the face of new challenges. The varietal complexes *virens levis, nigrum xalapensis, n. spinosum, n. levis* and *albus dulcis* were identified as man-enterprise, due to their large-scale commercialization. The 70.8% of the varietal complexes are cultivated for commercial purposes, while 29.2% are used for self-consumption, mainly focusing on fruit. This is especially relevant for the lesser-known variants, highlighting their potential to open new markets. The *virens* and *nigrum* groups are mainly used for commercialization, while *albus* is used for self-consumption. Bitter-flavoured varieties are generally not used by rural stakeholders (Figure 4).

Sechium sp. can be found at altitudes from 1,200–3,376m, due to its plasticity, which allows it to adapt to conditions different from its original habitat in mesophyll forests (Cadena-Iñiguez *et al*, 2008). The highest average altitude for *nigrum spinosum* was 1,993m. Outliers' presence affects some central tendency measures such as the mean, and some populations of the varietal complexes appear far from their optimal ranges for each specific variety.

Multiple correspondence analysis (MCA)

For this analysis, the phenotypic variables of fruits were included (colour, presence/absence of thorns, size,

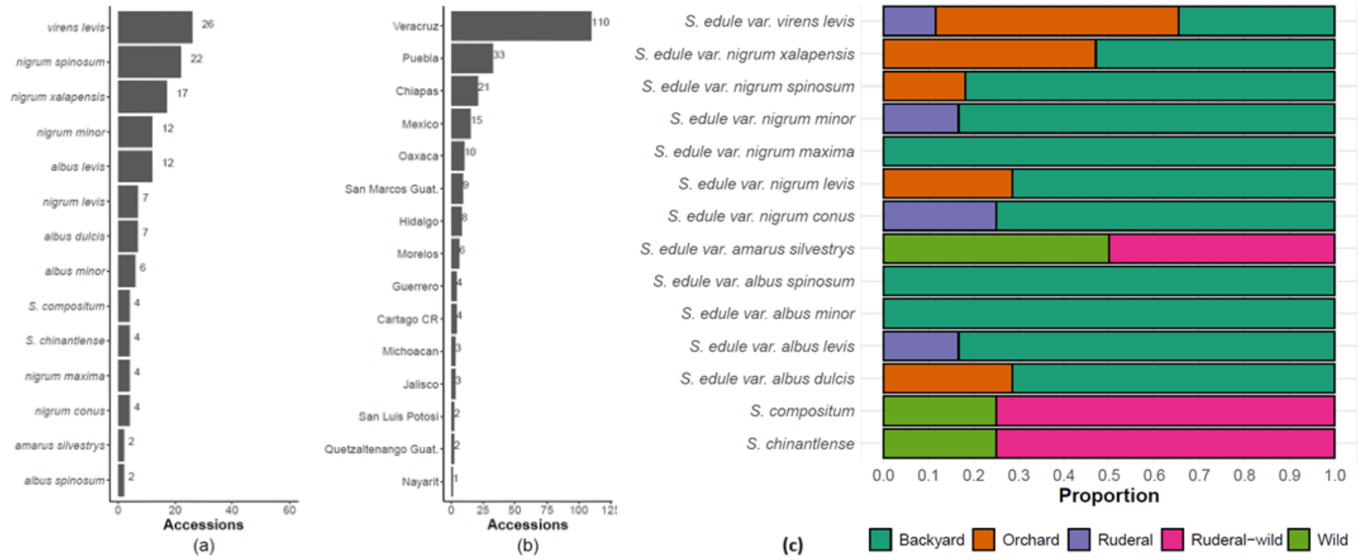

Figure 2. Composition of the *Sechium* collection at BANGESe. (a) Number of accessions per varietal group of *S. edule*, *S. compositum* and *S. chinantlense*; (b) Geographical origin of the accessions; (c) Sampling locations.

flavour and shape). The first two principal components explained 27.24% of the total obtained variation. Table 1 shows the eigenvalues and eigenvectors, respectively. For principal components 1 and 2 (PC1 and PC2), the variables contributing the most were fruit flavour, populations condition (forest, ruderal-wild and orchard), fruit colour (yellow and light green), small fruit size and flattened shape.

The distribution of the accessions depended on the environmental conditions. Accessions of *S. compositum*, *S. chinantlense* and *S. edule* var. *amarus sylvestris* were distributed in wild and ruderal-wild forms. The *virens levis* complex was primarily found in orchard conditions and is the most commercially important variety of S. edule. The yellow-fruited varietal complexes were generally found in backyards. Ownership patterns indicate that the *virens levis* varietal group was more often associated with male farmers, while female tended to maintain the *albus* and *nigrum* groups.

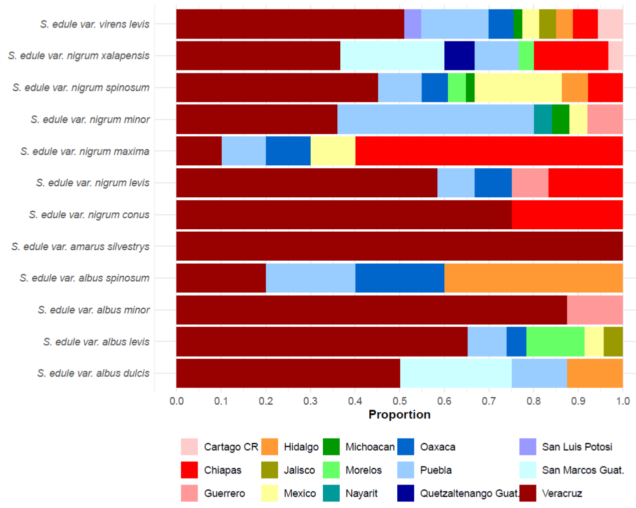

Figure 3. Proportion and distribution of *Sechium edule* varietal groups in the BANGESe collection according to place of origin of *Sechium* germplasm. CR, Costa Rica; Guat, Guatemala.

Regarding fruit colour, most accessions exhibited various shades of green, except for the *albus* group, which had yellow fruits (Figure 5a). Figure 5b shows that all accessions of *amarus sylvestris* (AW), *nigrum spinosum* (NS) and *albus spinosum* (AS) had thorns on their fruits. This is relevant, considering that the wild ancestor *S. edule* (wild type) is dark green, bitter and densely spiny, suggesting that consumer preference is for smooth fruits and neutral or sweet flavour.

The fruit size of the chayote is highly variable, ranging from very large (15–22cm), medium (6–10cm), and small (3–4cm) (Figure 6a). Regarding flavour, the ellipses show a very noticeable separation, revealing that the fruits of *S. chinantlense*, *S. compositum* and *amarus sylvestris* are bitter, a trait attributed to their tetracyclic triterpenes content, mainly cucurbitacins (Aguiñiga-Sánchez *et al*, 2015, 2017; Salazar-Aguilar *et al*, 2017). Fruits of the *albus* group have a slightly sweet flavour (7.6–8.1°Brix), while *nigrum* (4.9–6.4°Brix) and *virens* groups have a neutral flavour (5.1°Brix) (Figure 6b) (Cadena-Iñiguez *et al*, 2007; Cadena-Iñiguez and Arévalo-Galarza, 2011).

Cucurbitacins are secondary metabolites of triterpene origin that give a bitter taste to plants (root, guides, leaves, and fruits) and have been recorded in all *Sechium* species in the BANGESe, although with notable differences in concentration and type of compound (aglycones and glycosides). For instance, the *albus* group contains one-hundredth of the triterpenes levels found in wild species, and ten times less than nigrum (Uriostegui, 2014; Iñiguez-Luna *et al*, 2021).

Fruit shape is highly variable and it is difficult to establish a clear grouping pattern (Figure 7); however, the commercially preferred shape is pyriform, which is the shape of *virens levis* and is the basis of the international standard Codex-Stan-83-993 (pyriform

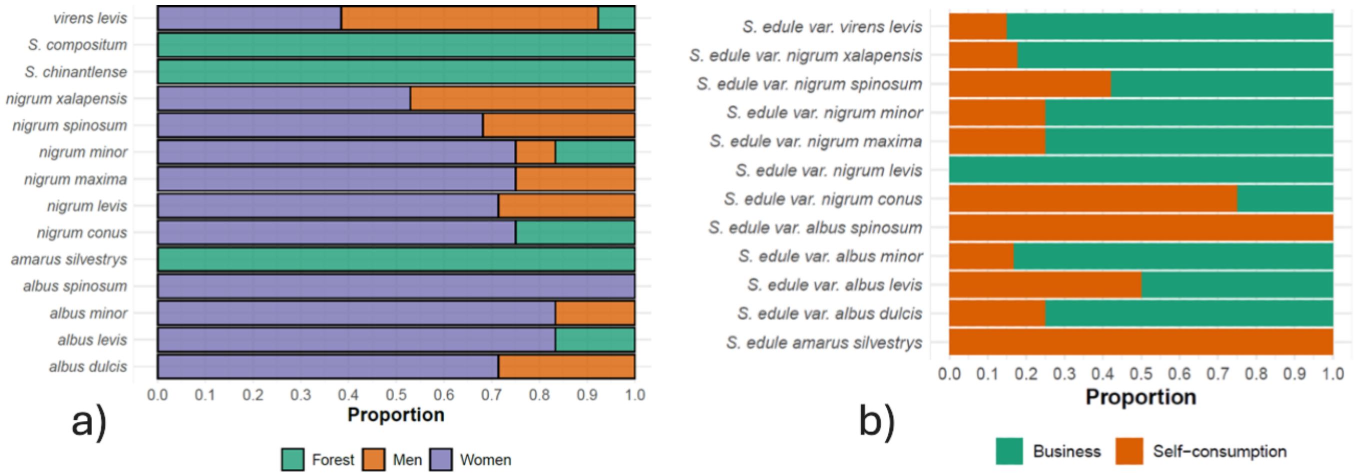

Figure 4. Relationship between stakeholders and conservation of *Sechium edule*, *S. chinantlense* and *S. compositum* of the *Sechium* germplasm collection at BANGESe; a) the conservation methods/users and b) the use of the accessions.

Table 1. Eigenvalues and variance are explained for the first ten components of the MCA. PC, principal component.

Component	Eigenvalue	Variance (%)	Cumulative variance (%)
PC 1	0.49	15.50	15.50
PC 2	0.42	13.48	28.98
PC 3	0.30	9.48	38.46
PC 4	0.24	7.79	46.24
PC 5	0.20	6.49	52.74
PC 6	0.19	6.16	58.90
PC 7	0.18	5.82	64.72
PC 8	0.16	5.20	69.92
PC 9	0.15	4.82	74.73
PC 10	0.15	4.70	79.44

fruits, light green colour, smooth without thorns and grooves, 12–15cm long, 8–10cm equatorial width, 270–310g, neutral flavour, and free of pathogens). The pyriform shape may be a derivation of continued selection by cultivars, as the *S. edule* fruits of the wild type (ancestor) are small and ovate (Figure 8).

Morphological boundaries

Establishing morphological limits in intraspecific complexes is relatively difficult, since it requires to determine whether distinctive traits are stable and heritable. Variation in plants may be continuous (clinal) or discontinuous, consisting of distinct morphotypes or races (Styles, 1986). In *Sechium*, variation is clinal since it shows a gradient that allows any character to take values between two extremes (Cadena-Iñiguez, 2005). Environmental factors, including numerous physical, chemical and biological sub-variables, induce this variation by exerting extra pressure on the differentiation process, enabling organisms to express a sufficiently satisfactory plasticity response for survival. For example, in *S. edule* and *S. compositum*, fruit shape and size vary according to altitude, with accessions from lower elevations (60m) producing round and small fruits, while those from higher elevations (200m) produce medium pyriform fruits in evergreen forests. Figure 9 shows the morphological limits based on fruit shape, which helps to distinguish the varietal complexes of *S. edule*, *S. chinantlense* and *S. compositum*, based on the colour of the epidermis, spines, shape and size.

Discussion

The preference in the consumption of chayote varietal groups is based on the physical and chemical characteristics of its fruits. In Mexico, the most present in the markets are *virens levis*, *nigrum xalapensis* and *nigrum spinosum*, the latter recently introduced in the United States. For these markets, fruits are harvested at horticultural maturity (Aung *et al*, 1990) and have a watery consistency, neutral flavour and little fibre content. In regional markets, fruit with higher starch content in the endocarp, such as *albus*, or physiologically mature green fruits, are preferred. This promotes unconscious conservation actions in backyards by women, who determine the type of chayote to be used in the diet. Their decision to either conserve a single morphotype or diversify indirectly leads to reproductive isolation and inbreeding selection, which helps to fix characters and make them stable and heritable or may induce spontaneous crosses (Cadena-Iñiguez *et al*, 2010).

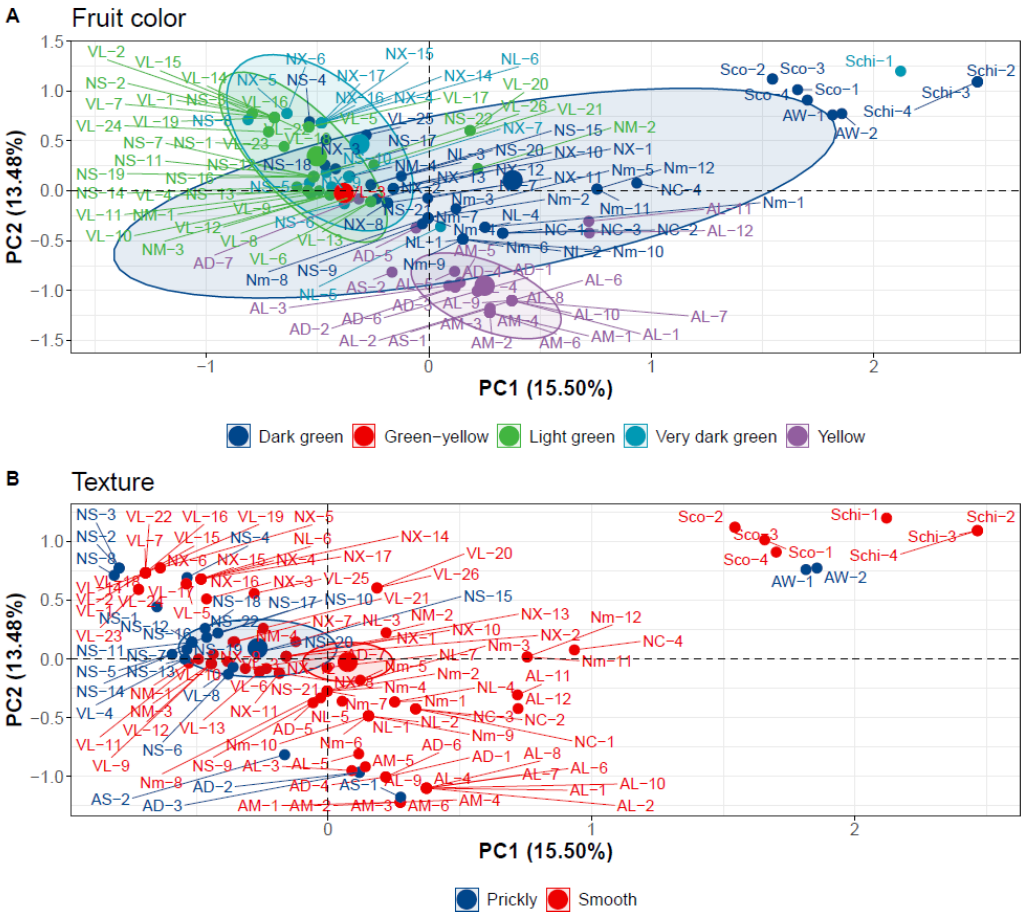

Figure 5. Multiple correspondence analysis for A) Fruit colour, and B) Fruit texture variables on *Sechium* germplasm. AL, *albus levis*; AS, *albus spinosum*; AW, *S. edule* var. *amarus sylvestris*; NC, *nigrum conus*; NM, *nigrum maxima*; Nm, *nigrum minor*; NS, *nigrum spinosum*; NX, *nigrum xalapensis*; Sci, *S. chinantlense*; Sco, *S. compositum*; VL, *virens levis*. PC, principal component.

Women play a key role in the conservation of plant genetic resources mainly through the management of family orchards, where these resources are used for food and sometimes for local sale. Local marketing or exchange of backyard surpluses allows genetic diversity to flow at the regional level (Watson and Eyzaguirre, 2002). When phytogenetic resources are used for human consumption, strong selection pressures arise. For chayote, the preference tends to converge on green fruits with neutral or sweet flavour and low fibre, although preferences for fruits with starchy consistency (*albus* group) have also been identified (Cadena-Iñiguez *et al*, 2010).

The first wild populations of *S. edule* evolved in mesophyll forests, producing dark green, spiny and bitter fruits (Lira, 1996). This type of vegetation is conducive to intraspecific variation in *S. edule* (Iñiguez *et al*, 2011). Mesophilic forests, distributed across the highlands of the Sierra Madre Oriental, Sierra Norte de Chiapas and Sierra Madre del Sur, range from 600–3,100m in altitude, with annual precipitation of 1,000-3,000mm, and temperatures ranging between 12–23°C (Ruiz-Jiménez *et al*, 2012).

Along with natural and artificial selections, migratory routes also cause variations in fruit colour and flavour. When wild populations of *S. edule* spread to low sub-evergreen forests, greater irradiance led to a change in chlorophyll content (Iñiguez *et al*, 2011), giving rise to some varietal complexes such as *virens levis* and those of the *nigrum* group. In the high plateaus and high valleys, it is common to find thorny green varietal complexes. In medium evergreen and low deciduous forest vegetation types, leaves and fruits began to change in colour and shape, later giving rise to varietal complexes of the *albus* group, where the fruits have low chlorophyll and cucurbitacin content but high carotenoid and ascorbic acid content (Iñiguez *et al*, 2011), presumably for photoprotection, since these fruits have high stomata density (Ramírez-Rodas *et al*, 2021). Also, the derivation of yellow fruits is strongly influenced by selection pressures. Valenta *et al* (2018) indicate that fruit colour plays an important role in seed dispersal and can be considered an evolutionary signal in plants. A contrast between leaf and fruit colour is important for zoochory success. In this regard, Iñiguez *et al* (2011) mention that yellow chayotes are considered the most evolved in terms of their environmental adaptation.

MCA of the fruit size shows that this variable tends to be dynamic. Wild populations of *S. edule*, *S. chinantlense* and *S. compositum* have relatively small fruits (Figure 9) and bitter taste. The latter is related to bi-1 and Bt-1 genes, which confer bitter taste to leaves and

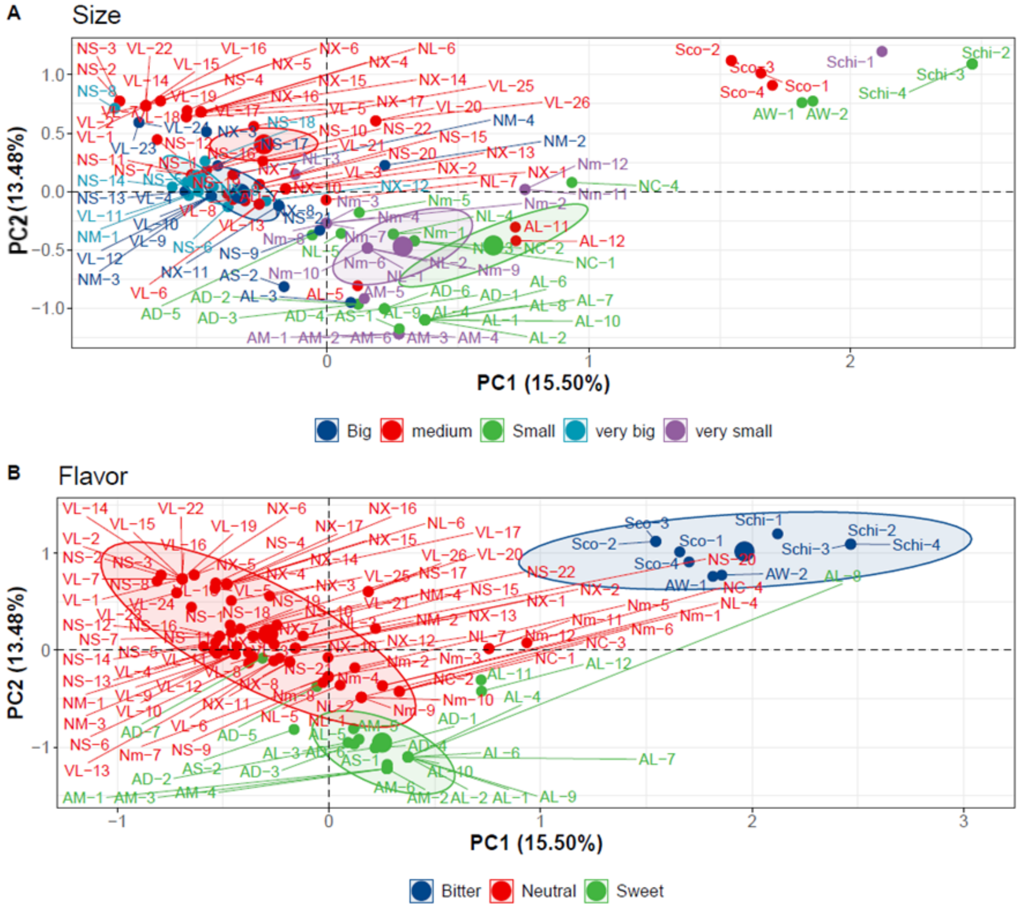

Figure 6. Multiple correspondence analysis for the variables A) Size, and B) Flavour of fruit on *Sechium* germplasm. Sco, *S. compositum*; Sci, *S. chinantlense*; AW, *S. edule* var. *amarus sylvestris*; VL, *virens levis*; NM, *nigrum maxima*; Nm, *nigrum minor*; NX, *nigrum xalapensis*; NC, *nigrum conus*; NS, *nigrum spinosum*; AL, *albus levis*; AS, *albus spinosum*, PC, principal component.

fruits (Valenta *et al*, 2018). Subsequently, with recurrent selection, this characteristic is reduced. In *Sechium* spp., the bitter taste is influenced by the concentration of cucurbitacins, higher in wild populations, and has applications in pharmacology particularly in cancer treatment (Cadena-Iñiguez *et al*, 2013b; Rosado-Pérez *et al*, 2019).

Numerous examples illustrate the role of rural women in conserving plant diversity in home gardens for family food, which in turn supports broader biodiversity. In Indonesia, Elfrida *et al* (2020) recorded the conservation of 39 fruit plant species of 23 genera and 17 botanical families by women. Other studies such as Tefera and Kim (2019) demonstrated the diversity of medicinal plants conserved by rural families in Ethiopia (52 families and 96 genera). Rural women are critical to conserving local knowledge, encompassing beliefs, medicine, food and economic livelihood. Conservation behaviour often arises from culture rather than formal education. Ondiba and Matsui (2021) mention that, from a sample of rural women surveyed, 98% expressed motivation to obtain economic income through acts of conservation, and 88% expressed a commitment to environmental conservation.

George and Christopher (2020) recorded the high species diversity in home orchards in Kerala, India; others, such as Zhang *et al* (2020) documented the plants and their local function, highlighting that altitude could be the most important variable that determines the composition of home gardens in China. Galluzzi *et al* (2010) reported the importance of home orchards in safeguarding agrobiodiversity, which reflects a complex structure.

According to the passport data, the variability of *Sechium* accessions in BANGESe is mainly attributed to the actions of rural women in home gardens or backyards, despite conservation not being their conscious objective. However, and for the reasons documented in the passport data, aspects such as self-consumption, local trade, medicinal and ancestry uses, have fostered a wide agrobiodiversity, mainly determined by these plants' value as food.

An important aspect that interacts with conservation, agrobiodiversity, bioprospective research, new applications, industry, rural players, home orchards and genebanks, are international treaties. The Nagoya Protocol (CBD, 2011) addresses several of these aspects and seeks, as far as possible, a fair and equitable distribution of benefits to the stakeholders that have safeguarded agrobiodiversity or have enriched collections in genebanks. In this regard, the analysis of passport data is a useful tool for identifying potential beneficiaries for bioprospective research and products over the

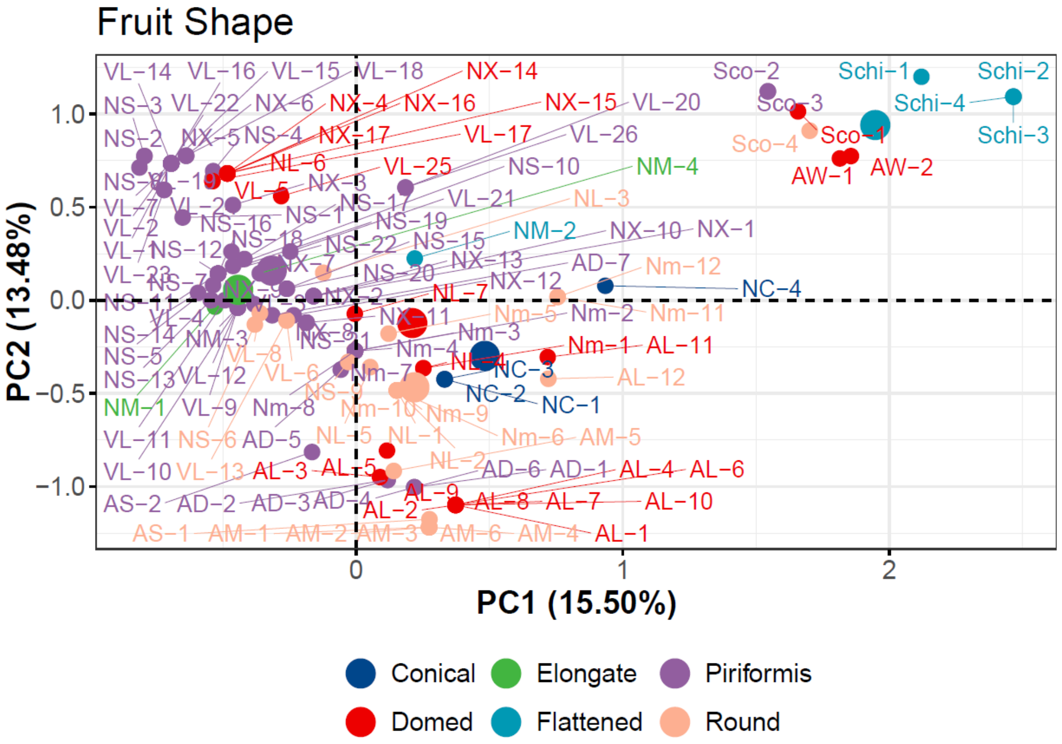

Figure 7. Multiple correspondence analysis for the fruit shape variable of *Sechium* germplasm in the BANGESe collection. Sco, *S. compositum*, Sci, *S. chinantlense*; AW, *S. edule* var. *amarus sylvestris*; VL, *virens levis*; NM, *nigrum maxima*; Nm, *nigrum minor*; NX, *nigrum xalapensis*; NC, *nigrum conus*; NS, *nigrum spinosum*; AL, *albus levis*; AS, *albus spinosum*, PC, principal component.

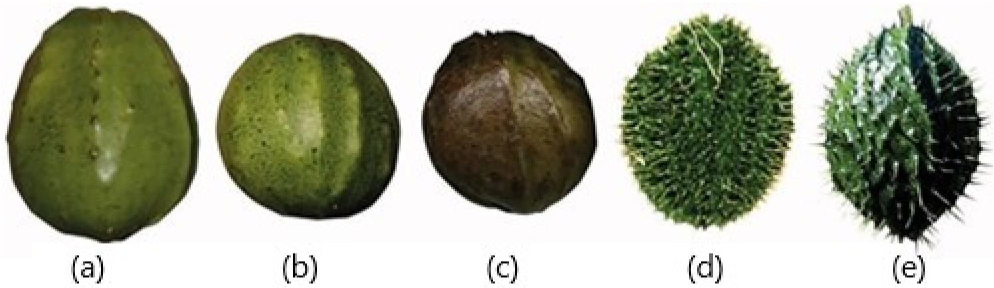

Figure 8. Colour, shape and fruit size variation in *Sechium compositum* (a and b, 6.0–8.0cm), *S. chinantlense* (c, 5.0–6.0cm), *S. edule* (wild type: d, 5.0–6.0cm) and *S. edule* var. *amarus sylvestris* (e, 6.5–7.0cm).

medium or long term. Varshney *et al* (2020) proposed a 5G approach to conserved agrobiodiversity: Genome of each crop species, Genomically and agronomically characterized germplasm, Gene function identification, Genomic breeding methodologies, and finally Gene editing.

This approach is a desirable strategy for germplasm collections; however, it does not consider the participation of rural stakeholders, whose ancestral knowledge and practices have helped maintain high agrobiodiversity. Therefore, analyzing passport information is key to designing strategies for replacing and regenerating genotypes in *ex situ* collections, as well as for designing shared conservation models with rural stakeholders. Such models could include morpho-anatomical, phytochemical, genomic and agronomic characterization lines, as well as bioprospective studies to explore new applications and benefits. These efforts could also support descriptor guides for legal registration of new plant varieties or facilitate compliance with international treaties and material transfer agreements.

Wild populations with small, dark green fruits, thorns and bitter taste were the promoters of the morphological diversity that is currently known of *S. edule*. However, there is also evidence of introgression and hybridization with the species *S. compositum* and *S. chinantlense* (Barrera-Guzmán *et al*, 2021a). Conserving this valuable resource begins with evaluating and characterizing genetic variability through morphological and molecular markers, as well as establishing evolutionary relationships among wild, cultivated populations and related species (Cadena-Iñiguez *et al*, 2007). Ecology studies in conjunction with ecological niche models also provide information on species adaptability, highlighting

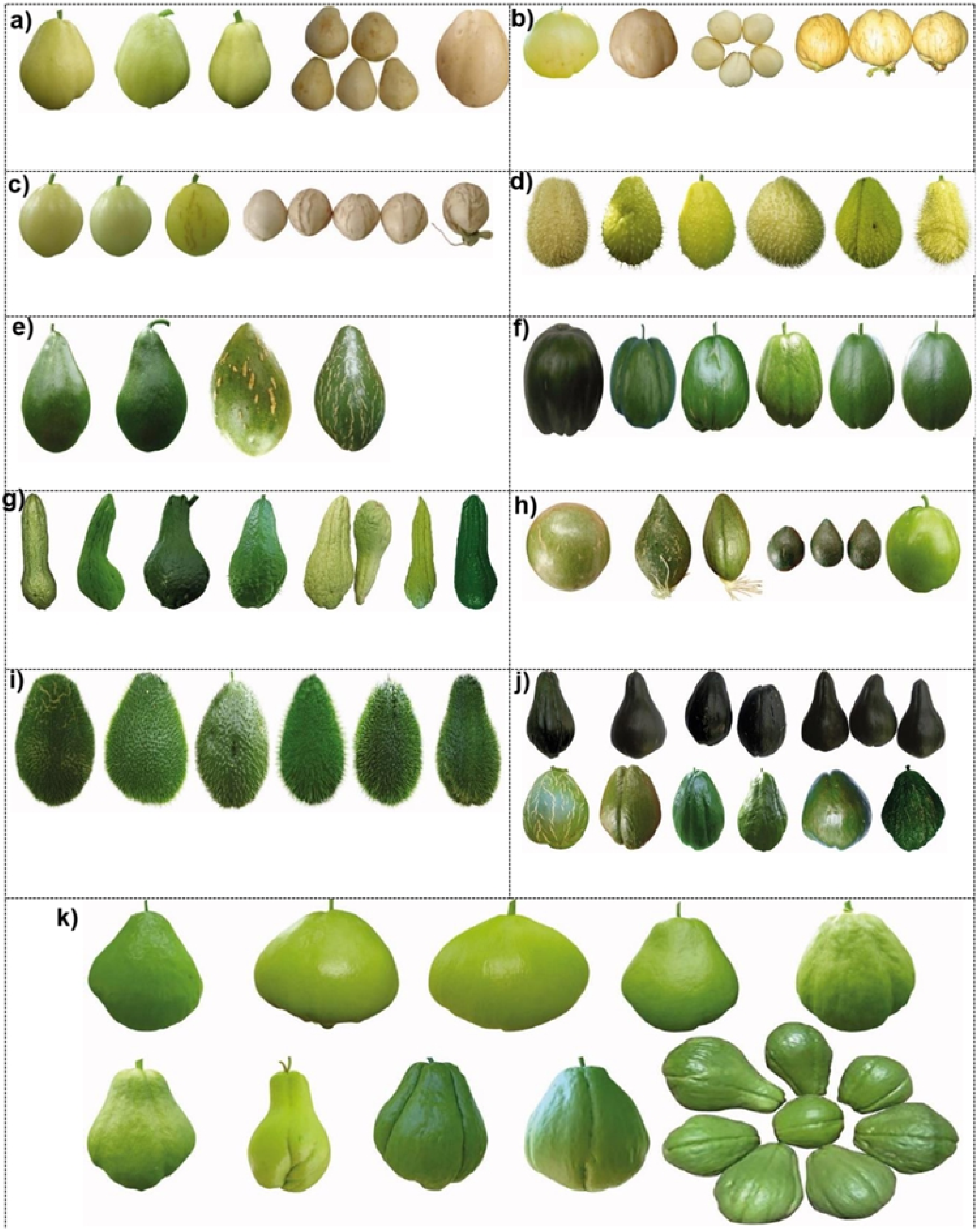

Figure 9. Colour, shape and fruit size variation in varietal complex of *Sechium edule*; a) *albus dulcis* (6.2–7.0cm), b) *albus levis* (6.0–7.0cm), c) *albus minor* (3.0–3.5cm), d) *albus spinosum* (13–16cm), e) *nigrum conus* (5.5–7.5cm), f) *nigrum levis* (5.7–7.0cm), g) *nigrum maxima* (16–22cm), h) *nigrum minor* (3.0–3.5cm), i) *nigrum spinosum* (10–16.5cm), j) *nigrum xalapensis* (15–17.5cm) and k) *virens levis* (13–16cm).

potential areas for conservation and zones threatened by climate change.

The study of biodiversity is also an incentive for participatory genetic improvement programmes of chayote, fostering collaboration and knowledge exchange between researchers and farmers. This encourages the continuous planting of native varieties or populations in traditional plots, and economic support and public policies are essential to maximize these efforts. Additionally, awareness campaigns are needed to inform the population about the importance of chayote as a plant genetic resource (Aguiñiga-Sánchez *et al*, 2017).

It is important to highlight that cytological information is missing or scarce in many accessions both in chromosome number and ploidy level as well as nuclear amount. The chromosomal level variegation such as translocation or inversion could explain species incompatibility (Olvera-Vazquez *et al*, 2019).

Conclusion

The morphological diversity of *S. edule* lies mainly in fruit characters, where traits such as bitterness, the presence of thorns and a dark green colour are representative of wild populations. Geographical and cultural richness also influence crop diversification, and the mountainous areas of Veracruz offer the ideal habitat for growth and development of new varieties. Women play a vital role in the conservation of native chayote populations through backyard cultivation. *S. chinantlense* and *S. compositum* are species related to *S. edule*, and from which important advances are being made in the production of cucurbitacins for the pharmaceutical sector.

Data availability statement

To facilitate access to the data from our chayote germplasm collection, information on how interested researchers can get full access is provided below. The data is hosted in our online database, which is accessible upon request. Researchers interested in accessing the full dataset can do so by contacting the corresponding author and providing a brief description of the intended use of the data. In addition, access requests will be reviewed to ensure proper use in accordance with established ethical guidelines for the conservation and research of plant genetic resources. Our goal is to support collaborative research efforts and encourage studies that expand the knowledge and utilization of this important collection of germplasm.

Authors contribution

Jorge Cadena-Iñiguez y Luis A. Barrera-Guzmán wrote the article and performed the statistical analysis of the database; Víctor M. Cisneros-Solano, the curator of the genebank, provided the information on the morphological aspects of the collection; Carlos H. Avendaño-Arrazate, Ma. de Lourdes C. Arévalo-Galarza, Kazuo N. Watanabe and Jorge D. Cadena-Zamudio, who have been developing the database over the years, also contributed to the discussion of this research.

Conflict of interest statement

The authors have no conflicts of interest to report.

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