American Journal of Plant Sciences, 2019, 10, 1261-1279
http://www.scirp.org/journal/ajps
ISSN Online: 2158-2750
ISSN Print: 2158-2742

The Cytological Studies on Neglected and Underutilized Cucurbit Species with Special Reference to Chayote, an Under-Exploited Species

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How to cite this paper: Olvera-Vazquez, S.G., Cadena-Iñiguez, J., Gilani, S.A. and Watanabe, K.N. (2019) The Cytological Studies on Neglected and Underutilized Cucurbit Species with Special Reference to Chayote, an Under-Exploited Species. *American Journal of Plant Sciences*, **10**, 1261-1279.
https://doi.org/10.4236/ajps.2019.108091

Received: July 2, 2019
Accepted: August 9, 2019
Published: August 12, 2019

Abstract

Cucurbitaceae family contains important economic and medical crops, they can be divided into two categories according to the worldwide consumption, use, and production. The Cucurbit Popular Crops (CuPoC) are comprised of cucumber, the *Cucurbita* group (pumpkin and squash), melon and watermelon. On the other hand, Neglected and Underutilized Cucurbit Species (NUCuS) group has been used as food sources, medicinal properties and elements in the elaboration of different types of items. The NUCuS is represented in this review work by bitter gourd, bottle gourd, chayote, ridge gourd, and snake gourd, which are recognized mainly in Asia. The center of origin of the majority of NUCuS was proposed to be in the Old World. In contrast, the origin of chayote or *Sechiumedule* (Jacq.) Sw. was suggested in the New World, precisely in Mesoamerican region based on linguistic uses and distribution of wild relatives. The environmental factors along with artificial selection, production systems and traditional knowledge have been influenced the evolutionary history of NUCuS, Infraspecific variation of chayote has been reported in Mexico over-described varietal groups. These descriptors were determined based on biochemical and morpho-structural traits; however, cytogenetic analyses are scarce. Specifically, chromosome and nuclear content analyses are important to support botanical groups, analyze artificial selection history, developing breeding and conservation programs. The present review paper discusses agronomic and evolutionary importance based on cytological evidence in NUCuS, mainly in the prominent chayote; with the perspective to prompt breeding, conservation, cytology, structural and functional genomics research for its sustainable utilization.

Keywords

Chayote, *Sechiumedule,* NUS, Nuclear Content, Chromosome Number, Cucurbit Species

1. Introduction

Plant Genetic Resources (PGR) hold potential traits to be used in cultivated plant improvement [1]. Neglected and Underutilized Species (NUS) are included within these resources. These are crops that under different conditions had economic and ethnobotanic value, being an important food resource in agriculture of indigenous people, communities and small towns [2]. Nowadays, it is necessary to use these resources to face current world challenges. The United Nations in coalition with different organisms like the Food and Agricultural Organization of the United Nations developed the Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources comprises of 17 goals [3]. The main objectives were ensuring food security, facing undernourishment, famine and poverty based on cultivars that front current environmental stress and marginal areas, encouraging sustainable crop production through input-output balance, and creating new target production areas among others [4] [5]. Through human history approximately 80,000 plant species have been identified as edible, only 7000 taxa are used as food supply [6] [7] [8]. About 30 species have been considered as main world food source crops; from these, ten species cover the 75% of worldwide calorie requirement: out of them, three species (maize, rice and wheat) provide almost 50% of the human needs, while 7 species (pearl millet, potato, sorghum, soybean, sugarcane, sugar beet, and sweet potato) sustain the remaining half [9] [10]. The restricted number of crop species has replaced traditional landraces that along to increment in crop production transforms cropping systems, inducing genetic erosion [11] [12]. The utilization of NUS is proposed in order to mitigate genetic erosion, risky agricultural production systems, rural poverty, and undernourishment to achieve food security [13] [14]. Species of the most global economy important plant families contain prominent NUS. Cucurbitaceae family contains important members utilized in food processing industries and fresh vegetable species [15]. Utilization of Cucurbitaceae family in human history has been documented since over 10,000 to 15,000 year B.P. approximately [16] [17]. According to FAOSTAT [18], the highest production of cucurbits has been reported in Asia in 2013 with an approximate production of 191,431,365 tons, more than the reported for Africa (11,406,859 ton), Europe (16,231,783 ton), North America (8,731,854 ton), and South America (1,355,075 ton). Vast proportion of this data relies mainly on few crops belonging to three genera: *Citrullus* Schrad. (watermelon), *Cucumis* L. (cucumber and melon) and *Cucurbita* L. (pumpkin and squash). They are the most economic important crops in the family and will be treated as cucurbit popular crops (CuPoC) in the present work. *E.g.*: watermelon is one of cash crops, positioned in the top five fresh fruits consumed, occupying around 7% of the world area appointed for vegetable production, and reaching an annual world production of 90 million tons [19]. Alternately, Behera [20] reported an annual production of 20,889,375 ton of gourds, pumpkins, squashes and the neglected or underutilized cucurbit species (NUCuS) discussed in the present review. For example, *Cucumis* genera that included over 32 species, two of them, gherkin (*C. anguria* L.) and African horned cucumber (*C. metuliferus* E. Mey) were utilized as a food and medicinal properties [21] [22]. Nevertheless, present paper focuses on different genera from the most economic important entities, in order to boost up research and utilization of under-exploited Cucurbitaceae member species. The CuPoC and NUCuS members are used for human uses, mainly as food sources, but also for cosmetics, indigenous culture items, jewelry, medicine, storage containers, sponges, ornamental purposes, among others [22] [23]. The CuPoC is comprised of a limit number of over-utilized species [24] included *Citrullus lanatus* (Thunb.) Matsum. & Nakai (watermelon), *Cucumis sativus* L. (cucumber), *Cucumis melo* L. (melon), and *Cucurbita* ssp. L. (pumpkin and squash). On the other hand, the NUCuS includes *Beninca sahispida* (Tunb.) (ash gourd), *Lagenaria siceraria* (Molina.) Standley (bottle gourd), *Luffa acutangula* (L.) Roxb. (ridge sponge), *Momordica charantia* L. (bitter gourd), *Sechiumedule* (Jacq.) Sw. (chayote) and *Trichosanthes cucumerina* L. (snake gourd). The taxonomy category, common name, main utilization, sexual system, life cycle, number of species and cultivars of the proposed NUCuS from the present review are described in **Table 1**. Even though that Cucurbitaceae is represented by many species, a limited number of members are globally used, among them, NUCuS are crucial to establish new economy sources and mitigate undernourishment based on rational conservation and breeding programs [14]. For example, the chayote has presence over the five continents and manipulated mainly for agriculture purposes for the last twenty years (**Table 1**) [25]. Even though this species has been commercial, ignored in a vast part of the world, is a staple food some regions; yet is crucial to identify chayote's limitations and propose innovative utilizations, detect gaps in conservation, breeding and crop improvement programs through the analysis of genetic diversity and cytological analysis [26]. For these reasons, the objective of this review paper is described current utilization and importance of NUCuS from six genera, discussing present cytology information available and highlighting the importance of research in this approach of the prominent chayote.

2. Medical Properties of Domesticated Cucurbit

The Cucurbitaceae family contains species that are important mainly in the Asian traditional system of medicine. The leaves, buds, fruit, and seeds of NUCuS members are consumed as treatment of different diseases. *Lagenariasiceraria* was used in the treatment colitis, diabetes, diuretic, hypertension,

Table 1. Common name, number of cultivated species, number of species inside of genus, scientific name and more frequent utilization of neglected and underutilized cucurbits (NUCuS).

Genera	Species	Common name	Utilization	Sexual System	Life Cycle	Species	Cultivated
Benincasa Savi.	*hispida* (Thunb. ex Murray) Cogn.	Ash gourd	Food source (flowers, fruit, leaves, seed, and stem) industrial, medicinal	M	An	1	1
Lagenaria Ser.	*Siceraria* (Molina) Stand	Bottle gourd	Food source (fruit, seeds and stem), industrial (containers, musical instruments, decoration), medicinal	M	An	5 - 6	1
Luffa Mill.	*Acutangula* (L.) Roxb	Angled/ridge gourd	Food source (fruit), medicinal	M, D	An	5 - 9	2
	Cylindrica (L.) M. Roem	Sponge gourd	Food source (fruit and leaves), industrial (filters, sponge) medicinal	M	An		
Momordica L.	*Charantia* L	Bitter gourd	Food source (flowers, fruit, leaves, and young shoots), industrial, medicinal, ornamental	M	An	40 - 150	~6
Trichosanthes L.	*Anguina*/ *Cucumerina* L.	Snake gourd	Food source (fruit, leaves, roots, seeds and young shoots), medicinal	M	An	91 - 100	~15
	Dioica Roxb.	Pointed gourd	Food source (fruit, leaves and young shoots)	D	An		
Sechium P. Brownie	*Edule* (Jaqc.) Sw	Chayote	Food source (fruit, leaves, root, stem and young shoots), medicinal	M	P	11 - 15	2

Acronym description: M = monoecious, D = dioecious, A = andromonoecious, H = hermaphroditic, G = gynoecious, An = annual, P = perennial [32] [33] [39] [57] [79] [112] [113] [114] [115].

among other [27] [28]. *Luffa acutangula* and *L. cylindrical* analgesic, antioxidant, antimicrobial, hypoglycemic activities were reported [19] [29] [30] [31]. Among the NUCuS, *Momordica charantia* has been more analyzed for its pharmacological compounds because of its abortifacient, antidiabetic, anthelmintic, contraceptive, laxative effects [32] [33]. Alternatively, *Trichosan thesdioica* and *T. cucumerina* represent the most analyzed because of its antidiabetic, cardiotonic, diuretic, antiulcer, gastro protective activity [34] [35] [36]. Recently, *Sechiumedule* has been analyzed for its antimicrobial, anti-inflammatory, cardiotonic, cytotoxic and antitumor action [37] [38] [39] [40] [41]. NUCuS contain important pharmacological compounds that would be a key to face important diseases. Hence, phytochemical studies on NUCuS group, with the aim to identify compounds and their functions are essential.

3. Taxonomy of Domesticated Cucurbit

The Cucurbitaceae family contains between 96 to 118 genera and 825 to 1000 species [42] [43] [44]. The main morphological characteristics that represents most of the cucurbits are: hairy climbers' habit, long root system, branched stem, simple 3 - 5 lobed leaves, palmate form being most common, tendrils (simple, bifid or absent), unisexual flowers (yellow and whitish), inferior ovary with parental placentation, high number of large seeds, and the cucurbitacin presence [44] [45]. Related with the sexual system dioecy was proposed to be the ancestral condition of this group, an example of this situation was described on *Bryona* genus has been analyzed [46]. NUCuS from present work has different number of domesticated species (**Table 1**). *Benincasa* Savi. genus is represented by only one domesticated *B. hispida* (ash gourd) [47]. *Lagenaria* Ser. is represented by five wild species and the cultivated *L. Siceraria* or bottled gourd [48]. *Luffa* Mill. genus is composed of approximately five to nine species, being ridge gourd and sponge gourd the domesticated [49] [50]. *Momordica* L. is a difficult taxonomic group which widespread common names delayed the exact species identification [51] [52]. Around 40 to 150 species have been described, seven of them are the most analyzed: *M. balsamina* L., *M. cochinchinensis* (Lour.) Spreng., *M. charantia* L., *M. cymbalaria* Fnzl., *M. dioica* Roxb., *M. foetida* Schumach., and *M. sahyadrica* Joseph John and Antony [20] [53]. Among these six members *M. charantia* has been widely cultivated, two botanical varieties were recognized: the wild type *M. charantia* var. *muricata* (syn. var. *abbreviate*) and domesticated var. *charantia* [52]. The genus *Sechium* P. Brownie has over eleven species, from which *S. edule* and *S. tacaco* (Pittier) C. Jeffrey are the cultivated form [26] [54] [55]. Finally, *Trichosanthes* genus is one of the largest inside Cucurbitaceae family around 91 species have been described, being *T. acuminate* and *T. cucumerina* the most utilized [35].

4. Proposed Origin of Neglected and Underutilized Cucurbit Species

Cucurbits have tropical and subtropical distribution through the Old and New World [56]. Phylogenetic analysis proposed Asia as the center of origin of this group [57]. Early studies of the cucurbits subdivided them into two subfamilies, Zanonoideae and Cucurbitoideae, the last contained most of the human-interest species [58]. Different studies have been made to elucidate the phylogenetic relationship of cucurbits, but the absence of key species hampered the results [59]. Genomic, chloroplast and mitochondrial loci analysis, allowed to recognize order Cucurbitales (including the Cucurbitaceae family) asmonophyletic, result complemented by their morphology and sexual system [60]. Most of CuPoC and NUCuS members have either African or Asian origin (**Figure 1**) [58]. The annual and monoecious *B. hispida*or ash gourd was proposed to have Indo-Chinese origin and domestication center, but it has not been supported by archeological records [22] [61] [62]; however, some Japanese and Javanese origins are also suggested [23]. Bottle gourd or *L. siceraria*is distributed in the tropic and subtropic regions; Africa is considered the center of origin of this species, being supported by the presence of five wild congeners and archeological remains [23] [63] [64] [65] [66]. Additionally, archeological records suggested that the bottle gourd arrived in America around 7000 - 10,000 years ago, migration through sea has been analyzed as an explanation of its wide distribution, this information identifies as one of the fist domesticated crops in the human history [25] [28] [67] [68]. The worldwide presence and high morphological variation among the *Luffa* cultivars hindered the center of origin and domestication

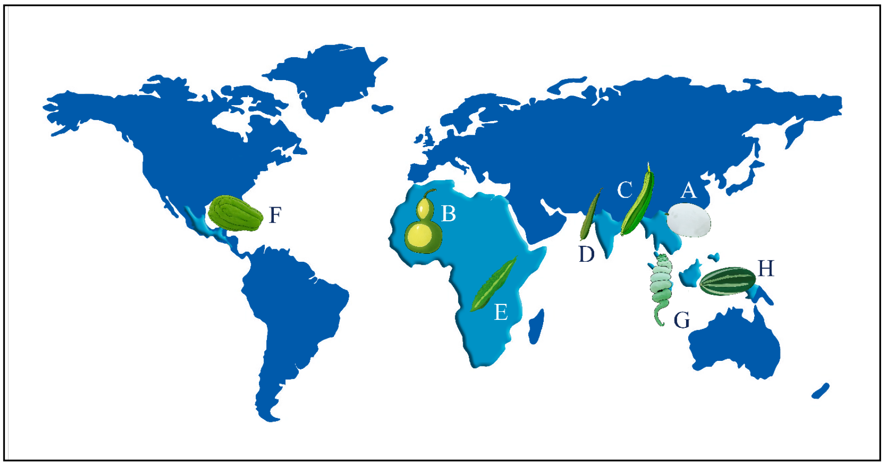

Figure 1. Proposed center of origin of NUCuS. (A) *Benincasa hispida* (ash gourd) Indo/China region [22] [61] [62] [71]; (B) *Lagena riasiceraria* (bottle gourd) Africa [22], [48] [49]; (C) *Luffa acutangula* (sponge gourd) India [22] [49] [56] [69]; (D) *Luffa cylindrica* (ridge gourd) India [22] [49] [56] [69]; (E) *Momordica charantia* (bitter gourd) Tropical Africa [72]; (F) *Sechium edule* (chayote) Mesoamerican region [22] [55] [68] [101] [102]; (G) *Trichosan thescumerina* (snake gourd) South East Asia [77] [78] [79], and (H) *Trichosanthes dioica* (pointed gourd) South East Asia [77] [78] [79].

of these species, but the presence of their wild relatives suggested India as the region of these events [22] [49] [56] [69]. Bitter gourd or *M. charantia* is an Indigenous-Old-World species present currently in all over the subtropics and tropic [70]. Its origin has been widely analyzed. Primarily, the identification of the domesticated and putative wild bitter gourd progenitors was described in the tropical Africa, Asia, and Indian flora postulating this crop as native to the tropic of India or Southeast Asia [61] [71]. Recent phylogenetic analysis suggests that this crop arose in tropical Africa and Asian members appeared from a dispersal event about 19 million years ago [72]. Easter India was considered a primary center of diversity of bitter gourd, based on the presence of its wild form *M. charantia* var. *muricata* in this area, literature studies, and molecular analysis [73] [74] [75] [76]. The domestication center is not clear due to lack of reliable archeological records, still, China, Eastern India and South-Western India were proposed [22] [71] [73]. The *Trichosanthes* cultivated species' center of origin and diversification was suggested to be Southeast Asia, and their distribution has been documented from tropical and subtropical Asia: Australia, Fiji, Japan, and New Guinea [77] [78] [79]. Finally, Chayote or *S. edule* is the only species which center of origin is proposed to be in the New World. More detailed, the center of origin, diversification and domestication of chayote has been proposed to be Mesoamerican [55], based on findings described below.

5. Chromosome Number Situation of Domesticated Cucurbits

Cucurbitaceae primitive base number is highly discussed, n = 12 is suggested based on its high frequency, followed by n = 7 and 11, as well as 3 and 5 are proposed as primary basic number, while 6 and 10 as secondary [22] [23] [45] [80] [81]. According to several studies autoploidy, alloploidy, aneuploidy, and secondary polyploidy events were presented in the cucurbits' speciation history [42] [45] [81] [82]. Vast number of papers have discussed the NUCuS' chromosomal number, determining a constant value for most species with some exceptions (**Table 2**). Reports in diploid CuPoC and NUCuS have postulated n = 11 and 2n = 22 how the most frequent value followed by n = 12 and 13, 2n = 24 and 26 while the less occurrence were n = 7, 14 and 20, 2n = 14, 28 and 40 (**Table 2**). The minor chromosome number described was n = 7 in the CuPoC cucumber (*C. sativus*). Number 11 was reported in high frequency in NUCuS bottle gourd (*L. siceraria*), bitter gourd (*M. charantia*), snake gourd (*T. cucumerina*), and pointed gourd (*T. dioica*), as well in the CuPoC watermelon (*C. lanatus*).The value of n = 12 was discussed in ash gourd (*B. hispida*) and melon (*C. melo*); while n = 13 was debated in species of ridge gourd (*L. acutangula*) and sponge gourd (*L. cylindrica*). Higher number of chromosome number was n = 20 identified in different species of *Cucurbita* spp. (**Table 2**). Finally, several values have been discussing for chayote (*S. edule*), n = 11, 12, 13 and 14, proposing a new cytological analysis to elucidate these differences.

6. Nuclear Content of Domesticated Cucurbits

Contrary to chromosomal number, nuclear content studies in CuPoC and NUCuS are limited (**Table 3**). Nowadays, early cucurbit nuclear content analyses continue being fundamental toper form and understand different methodologies, Ingle *et al.* [83], Arumuganathan and Earle [84], and Bennett *et al.* [85]. *E. g.* these values are base for genome size calculation that are available in The Herbarium Catalogue, Royal Botanical Garden, Kewdatabase [85] and reported in some papers, those values are described in **Table 3**. Even though that CuPoC has been intensively analyzed due to its higher economic importance, lack of nuclear content research has been proposed, in order to encourage conservation and sustainable utilization of the presented cucurbits crops it is imperative to contrast and confirm the results with up-to-date methodologies complementing and contrasting current information. **Table 3** highlights the estimation of nuclear content of the different domesticated cucurbits, allowing the recognition of contrasting values owing to the diverse of material and methodology utilized, following described. First discussions about nuclear content were mainly focused in CuPoC [83]-[87]. Only the NUCuS bitter gourd, bottle gourd and sponge gourd were analyzed for Ingle *et al.* [83]. Notwithstanding, bottle gourd and sponge gourd dissimilar values were identified in subsequent analysis [47] [88]. The nuclear content of cultivated pointed gourd was initially studied by Chattopadhyay and Sharma [89], opposite values were obtained in female and male pointed gourd population in a research by Bhowmik and Jha [47]. The biological significance of nuclear content and genome size variation among families, genera, species and cultivars is still not clear, this disparity is independent of

Table 2. Summary of cucurbit popular crops (CuPoC) and neglected and underutilized cucurbit species (NuCuS) Cucurbits Crops chromosomal number reports.

Species	n	2n	Source
		NUCuS	
B. hispida	12	24	[20] [22] [45] [47] [62] [71] [81].
L. siceraria	11	22	[20] [22] [45] [68] [81] [109].
L. acutangula.	13	26	[20] [45] [81] [109].
L. cylindrica	13	26	[20] [22] [45] [37] [81] [109].
M. charantia	11	22	[20] [22] [45] [52] [53] [80] [81] [109].
T. cucumerina	11	22	[20] [22] [45] [47] [79] [115].
T. dioica	11	22	[20] [22] [45] [47] [79] [81] [109] [115].
S. edule	11, 12, 13, 14	22, 24, 26, 28	[20] [22] [26] [37] [54] [56] [68] [81] [109] [116].
		CuPoC	
C. lanatus	11	22	[22] [24] [45] [68] [81] [97] [109].
C. melo	12	24	[22] [24] [45] [68] [81] [97] [109].
C. sativus	7	14	[22] [24] [45] [68] [81] [97] [109].
Cucurbita spp.	20	40	[22] [45] [68] [81] [97] [109] [117].

Table 3. Summary of cucurbit popular crops (CuPoC) and neglected and underutilized cucurbit species (NUCuS) nuclear content reports.

Species	Nuclear content 2C/pg	Genome size 2C/Mbp	Source
		NUCuS Crops	
B. hispida	1.97, 1.98	1926	[47].
L. siceraria	0.73, 1.4	688, 1369	[83] [85] [88].
L. cylindrica	1.70, 1.56, 3.0	1663	[47] [83] [85].
M. charantia	4.1	4010	[83].
T. dioica	2.27, 2.28, 2.30, 5.65	5526	[47] [85] [89].
		CuPoC	
C. lanatus	0.90	880	[84] [85].
C. sativus	0.76 - 2.1	1760	[83] [84] [87] [118].
C. melo	1.9 - 2.48	1858	[83] [84] [85] [118].
Cucurbita spp.	0.74 - 2.6	671 - 1076	[83] [85] [86] [87] [119] [120].

the complexity of organism, the C-value paradox [90] [91] [92]. However, diverse studies performed correlating between genome size with cell cycle, life cycle, phenotypic traits (subcellular and organismal level), plant development phases, phenology and ecology interactions [92] [93] [94] [95] [96]. Nowadays, the genome size reported for popular cucurbits has been identified as small compared with important crops like corn (5330 Mbp), onion (32,763 Mbp), wheat (33,888 Mbp), among others [97] [98]. The present discussion remarked the scarce number of NUCuS nuclear content research reports, *e.g.* bitter gourd information is limited, and it was not possible to find meither chayote nor ridge gourd estimations reports. Moreover, the majority of reports belong to CuPoC, reflecting their economic importance. NUCuS is comprised of prominent crops to mitigate with current problems and has potential to become a staple food for low- and middle-income country (LMIC). This situation was discussed in the following section through chayote.

7. *Sechiumedule* a Prominent NuCuS

The genus *Sechium* P. Brownie has been grouped in the Sycioeae Tribe Schrad. along with the NUCuS *Luffa* Miller and *Trichosanthes* L. [99]. *Sechium* has at least eleven species, from which the chayote and *S. tacaco* (Pittier) C. Jeffrey, are the cultivated form (**Table 1**). The reported wild types were *S. chinantlense* Lira & F. Chiang, *S. compositum* (Donn. Sm.) C. Jeffrey, *S. hintonii* (Paul G. Wilson) C. Jeffrey, *S. talamacense* (Wunderlin) C. Jeffrey, *S. mexicanum* Lira & M. Nee, *S. panamense* (Wunderlin) Lira & F. Chiang, *S. pittieri* (Cogn.) C. Jeffrey, *S. venosum* (L.D. Gómez) Lira & F. Chiang and *S. vilosum* (Wunderlin) C. Jeffrey [26] [54] [55] [99]. Intraspecific morphological variation has been reported in chayote highly perceptible in fruit anatomy, color, form, flavor and size [84] [86] (**Table 4**). The center of origin, diversification and domestication of chayote has been proposed to be Mesoamerican [55]. Due to its fleshy fruit there is a lack of archaeological records, pollen grains and plant structures [26]; Yet, historical and linguistic records, in addition of the presence of its wild relatives pointed Mexico as origin site [22] [68] [100] [101] [102]. Furthermore, the highest level of chayote diversity was identified in Mexico, particularly in Chiapas, Oaxaca and Veracruz, maximum intraspecific variation were identified in the central area of Veracruz [100] [103]. In order to classify this variation, a taxonomic arrangement was proposed; morphology and chromosomal number in subspecies *S. edule* ssp. *edule* and *S. edule* spp. *Silvestrys* [99], nonetheless this did not include cultivars and infraspecific hybrids [104]. Nowadays, ten varietal descriptors were created on morpho-structural, biochemical, physiological and genetic diversity of chayote accessions from the *Sechiumedule* National Germplasm Bank (*BANGESe*)—Autonomously University of Chapingo (UaCh) [105]. Chayote production has raised, but it has been focused on the smooth green (*virenslevis*) varietal group, parallel situation with other cucurbit species [106]. Nowadays, it is imperative to promote chayote varietal groups to avoid the overexploitation of one group and marginalizing others, moreover, the wild type populations are decreasing due to cultivar production practices affecting the surrounding wild groups, e.g. avoid crossed pollination and they are eradicated to establish organic coffee plantations [104]. The improvement of different varieties that replaced old landraces produced genetic erosion, increased the incidence of pests and diseases due to the lack of genetic diversity within the cucurbit gene pool and abiotic stress [107] [108]. The genetic erosion of chayote is

Table 4. Description of fruit characteristics of ten varietal groups of chayote.

Variety	Fruit morphology	Peduncle	Mesocarp	Fruit Color	Shape	Size	Flavor
albusminor	Glabrous, absence of furrows	Slightly pubescence, light green	White	White-yellow (Pantone 1205c)	Piriform	S	Neutro
albus levis	Glabrous, shallow furrows	Light green with yellow striae and slightly pubescence	White	White-yellow (Pantone 1205c)	Piriform	M	Sweet
albusdulcis	Five furrows	Glabrous light green with yellow striae	White	White-yellow (Pantone 1205c)	Piriform-round	M	Sweet
nigrum conus	Absence of furrows	Slightly pubescence, dark green	Dark green	Green (Pantone 371c and 574c)	Conic	M	Sweet
nigrum levis	Absence of furrows	Pubescent, dark green	Light green	Green (Pantone 575c and 576c)	Piriform	M	Neutro
nigrum maxima	Five slightly furrows	Slightly pubescence	Light green	Green Pantone 373c and 7492c)	Piriform-elongate	B	Neutro
nigrum minor	Absence of furrows	Light green slightly pubescence	Dark green	Dark green (Pantone 374c and 586c)	Round-piriform	M	Neutro
nigrum spinosum	Five slightly furrows	Slightly pubescence	Green	Green (Pantone 350c and 1205c)	Piriform	M/B	Neutro
nigrum xalapensis	Five furrows	Slightly pubescence	Dark	Dark green (Pantone 575c and 5065c)	Piriform-elongate	B	Neutro
virens levis	Five shallow furrows	Light green low pubescence	Light green	Light green (Pantone 373c)	Piriform-elongate	B	Neutro

Acronym description: B = big size (10.5 - 15 cm), M = medium size (5.7 - 8.2 cm), S = (<8.2 cm), [24] [89] [90].

boosted through the inbreeding and usage of cloned plants in orchids increasing the incidence of viruses and fungal plants infected [101]. The chayote holds high nutritional value with high antioxidant activity, rich in important amino acids (particularly: arginine, aspartic acid, leucine, proline among others), recently it has been pharmacologically analyzed for antimicrobial, anti-inflammatory, cardiotonic, cytotoxic and antitumor action [37]-[41]. In order to take advantage of nutritional and pharmacological properties cytogenetic analyses are proposed. There are a plenty of reports about the Chayote chromosomal number, yet the nuclear content and genome size information is restricted. Initially, research focused on chromosomal description had conflicting results. Singh [109] made a description of the cytogenetics and evolution in the Cucurbitaceae family, describing a karyotypic analysis on 22 large somatic chromosomes in chayote, discussing that three pairs have a secondary constriction and the remaining pairs sub-median constrictions. The different reports identified a diploid state in chayote, but a wide range of chromosomal number. The chromosomal number reported are 2n = 22, 2n = 24, 2n = 26, and 2n = 28 (**Table 2**). These variations in chayote would be result of isolation mechanism, aneuploid events, structural rearrangements (fusion or unequal translocation, non-disjunctions of chromosomes, among others) that provided adaptative genes [109] [110]. Different reports found an invariably small chromosome, dying problems, and clustering chromosomes because of secondary metabolites contain [37] [111]. Alternately to the wide chromosome number information available, the nuclear content and genome size of cucurbits are scarce, in the case of chayote null.

8. Conclusion

Cucurbitaceae family consists of many species, however, human uses rely basically on four of CuPoC, increasing the agriculture vulnerability. NUCuS was postulated as crucial to face poverty, undernourishment and the protection of cucurbit genetic resources. Present review was mainly focused on the need to develop research and encourage utilization of *S. edule* or chayote. Chayote is a prominent Mesoamerican NUCuS resource, that contains high nutritional value and medicinal properties that could be used for food security purposes. Even though chayote has different varietal groups, the commercial and economical value has been focused only on *virenslevis* or smooth green. Infraspecific chayote variation research is fundamental for rational exploitation and new economic source establishment through *ex situ* and *in situ* conservation and breeding programs based on cytological information. However, limited cytogenetic information was identified through the present discussion, this information is a key to analyze the effect of artificial selection in the chayote varietal groups' genome. Chayote is a first insight for the NUCuS utilization based on rational and responsible agricultural management as well as to establish diplomatic networking to face current and future challenges.

Acknowledgements

SGOV thanks the Japanese Government (Monbukagakusho) Scholarship. Authors thank Science and Technology Research Partnership for Sustainable Development (SATREPS) and the University of Tsukuba that allowed the development of present research product.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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