Research Article

Ekin
Journal of Crop Breeding and Genetics

7(2):86-105, 2021

www.ekinjournal.com

Ekin International biannual peer-reviewed journal

Determination of Morphological Variation by Principal Component Analysis and Characterization of the *Capsicum chinense* Genetic Resources

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Citation:
Tas K., Balkaya A., 2021. Determination of Morphological Variation by Principal Component Analysis and Characterization of the *Capsicum chinense* Genetic Resources. Ekin J. 7(2):86-105.

Received: 21.04.2021 ***Accepted: 07.06.2021*** ***Published Online: 29.07.2021*** ***Printed: 30.07.2021***

ABSTRACT

The characterization of plant genetic resources and genetic diversity levels are determined with the morphological descriptors and molecular analysis methods. *Capsicum chinense* populations show a high level of variation in terms of fruit size, fruit width, fruit shape, fruit colour and bitterness. This study aimed to define the plant characteristics of the *C. chinense* genetic resources collected from different locations of the world according to the UPOV (International Union for the Protection of New Varieties of Plants) criteria and to determine the morphological variation levels in the current population within the species. In the first stage of this study, a gene pool consisting of 75 genotypes of the *C. chinense*s pecies was created. It was found that genotypes belonging to the *C. chinense* species show a high level of phenotypic diversity in terms of morphological identification criteria. Cluster and principal component analysis (PCA) were performed to determine relationships among populations. A dendrogram clustered into seven groups was prepared to evaluate morphological differences among *C. chinense* genotypes. In addition, the principal component (PC) analysis showed that the first six PC axes explained 70.99% of the total multivariate variation. It revealed high morphological variation among the *C. chinense* genotypes. In conclusion, this identified *C. chinense* genetic resources to be evaluated as qualified breeding materials for developing new variety candidates in the near future.

Keywords*: Capsicum chinense*, population, characterization, classification, variation

Introduction

The pepper (*Capsicum annuum* L.) belongs to the genus *Capsicum*, which is one of the 98 genera in the Solanaceae family (Greenleaf 1986; Eshbaugh 2012). The number of species within the *Capsicum* genus, which was 38, has been systematically updated to 43 species with the determination of 5 new species as a result of the botanical classification made by taxonomists (Barboza et al. 2019). Today, only 5 of these species (*C. annuum* L., *C. baccatum* L. var *pendulum*, *C. chinense* Jacq., *C. frutescens* L. and *C. pubescens* Ruiz & Pav.) have been cultivated (Eshbaugh 2012; Barboza et al. 2019). In the literature, the primary gene center of *C. annuum* is stated as Mexico and the secondary gene center as Guatemala. The primary gene center of the *C. chinense* and *C. frutescens* is accepted as the Amazon Basin (Ramchiary et al. 2014). Otherwise, the primary gene center of *C. baccatum* and *C. pubescens* species is Peru and Bolivia.

The origin of the pepper is known as Central America. However, studies conducted on the pepper species have revealed that the different origin according to the *Capsicum* species. In the literature, especially hot peppers have been reported to originate from South Brazil and Bolivia (McLeod et al. 1983; Pickersgill 1984). *C. chinense* is the most grown and consumed hot pepper in Brazil. It is also widely spread in the Central and South American countries (Eshbaugh 2012). Today, there are also transitional forms along with the forms that are cultivated. Therefore, *C. chinense* species; shows high phenotypic diversity in terms of fruit shape, fruit colour, fruit size, and bitterness levels.

The chromosome number of *C. chinense* was determined as 2n=24 (Moscone et al. 2007). *Capsicum* species are classified into three main groups according to their flower colours. Accordingly, peppers with white flowers were defined as the *C. annuum* complex, with yellow flowers as the *C. baccatum* group, and purple flowers as the *Capsicum eximium* complex. *C. chinense* species are included in the *C. annuum* complex in terms of flower characteristics (Ince et al. 2009).

Genetic resources are the greatest help to breeders in developing new varieties with high yield and superior qualities in agricultural production and the creation of breeding programs (Balkaya and Yanmaz 2001; Karaağaç and Balkaya 2017). In addition, they are unique resources for breeding programmes due to their adaptability to different ecologies, the resistance ability to diseases and pests, and many desired quality characteristics (Hawkes, 1983). Genetic resources also include both cultivated plants and their wild relatives (Engels et al. 1995). Ortiz and Delgado (1990) searched the morphological characteristics of five different cultured from the *Capsicum* genus found in different seed gene banks (UNA, Peru; CATIE, Costa Rica; INIA, Mexico and CIRF, Mexico), and they grouped genotypes belonging to *C. annuum* L., *C. chinense* Jacq., *C. frutescens* L., *C. pubescens* and C. *baccatum* species based on their plant characteristics to be used in breeding programmes.

Breeders carry out interspecific hybridization studies to benefit from the superior properties of interspecific crosses in the plant breeding programs. The information and data to be obtained from interspecific crosses are very important to increase yield, high resistance to abiotic and biotic stress factors, to develop varieties that can be used as rootstocks and to improve the quality of the cultivars, especially root rot disease (Mavi 2020). The success rate in interspecific hybridization studies changes depending on the genetic relationships between the species (Kurt 2001). It was stated in the literature that *Capsicum* species in wild form carry characters that constitute many resistance properties, especially resistance/tolerance to biotic and abiotic stress factors (Grubben 1977; Pickersgill 1980). The first known interspecific hybridization studies were done between *C. annuum* and *C. frutescens* in *Capsicum* species (Halstead 1912). Nowadays, *C. annuum* and *C. chinense* interspecific hybrids are utilized in F_1 hybrid variety breeding and rootstock breeding programs due to their resistance to low temperatures and viruses for grafted pepper seedlings (Balkaya 2013).

Over time, a high level of genetic diversity has emerged in countries where pepper is cultivated commonly, and as a result, traditional landraces with many different qualities have been formed. The local populations are genotypes of remarkable functional value. Introduction materials arriving in a region by various means adapt to their location. During the time they spend there, genetic diversity arises in its existing genetic structure with environmental factors (Karaağaç 2006). The cross-pollination rate varies between 9-32% in peppers (Bayraktar 1970). If plant isolation techniques are not followed in pepper seed production, a high level of genetic diversity may occur between genotypes (Karaağaç and Balkaya 2010).

Morphological variations have great importance in plant breeding studies. Determination of variation shown by available genetic resources for quantitative and qualitative traits is important for vegetable breeding programmes (Bliss 1981; Gil and Ron 1992; Escribano et al. 1998). Phenotypic diversity within landraces and populations of *Capsicum* is high, including variations in fruit shape, fruit weight, fruit size (length, diameter), fruit flavors, bitterness, fruit colour, and the number of seeds/fruit (García-Neria and Rivera-Bustamante 2011). The number of studies on the *C. chinense* species that demonstrate the level of variation in current populations is quite a few. Vasconcelos et al. (2012) reported the presence of a high level of variation and genetic diversity in terms of flower characteristics. Knowledge of the extent of genetic diversity, identification, differentiation, and characterisation of genotypes and populations, respectively, provides an information tool for detecting duplicates in the collection, their effective extension, and better characterisation and use in breeding (Hornakova et al. 2003). A morphological characterization is the first step in describing and classifying of local genetic resources (Smith and Smith 1989). There was a need to characterize the pepper populations collected so that they could then be used as lines for the development of new varieties (Balkaya and Yanmaz 2001; Karaağaç 2006; Karaağaç and Balkaya 2010). Objective descriptors based on morpho-agronomic characters are considered reliable traits to verify or assess genetic distance or conformity among populations (Hunter 1993). Further, successful results could have been obtained by using DNA markers and molecular techniques determine genetic traits for pepper improvement in recent years (Geleta et al. 2005). *Capsicum* species have been studied using morphological descriptors, cytogenetic data, and molecular markers by many researchers (Conicella et al. 1990; Lefebvre et al. 1993; Zewdie and Zeven 1997; Lefebvre et al. 2001, Geleta et al. 2005; Moscone et al. 2007; Ince et al. 2009; Karaağaç and Balkaya, 2010; Villota-Cerón et al. 2012; Ramchiary et al. 2014;

Barboza et al. 2019). According to the literature, there are similarities and differences regarding morphological variations and molecular markers in pepper (mostly of *C. annuum*) genetic resources. To date, characterization and the determination of morphological variation in *C. chinense* populations are less than other *Capsicum* species. Therefore, this research aimed to define plant characteristics of C. *chinense* genotypes and determine similarities and differences in the morphological variation of *C. chinense* genetic resources collected from the different eco-geographical regions of the world.

Materials and Methods

The study was carried out in the experimental field of Ondokuz Mayıs University Faculty of Agriculture in the year 2018. Seventy-five genotypes belonging to the *Capsicum chinense* obtained from the USDA-ARS National Germplasm Bank; these genetic materials were collected from different parts of the world (Table 1).

The seeds of all genotypes were sown into plug trays containing peat and perlite (in the ratio 2:1) on March 05, 2018. Seedlings were grown in a controlled greenhouse unit at 25°C ± 2 temperature until they reached four true leaves. It was planted on April 25, 2018. The distance between rows of *C. chinense* plants was 0.5 m and with 0.5 m between plants in the row. Soil tests were done before and after planting. After the seedling planting, all cultural processes were applied regularly. The harvest period started at the end of July and lasted until the end of October because the investigated populations have different harvest periods.

Morphological analyses were carried out on 20 plants harvested from each genotype. The morphological characters measured and their scales are presented in Table 2. All characters were measured in the field and at the normal harvest time. The characters are included in the description form developed for *Capsicum* spp. by UPOV with reference TG/76/8 (UPOV 2006). Fruit characteristic analyses were carried out on 10 fruits from each of the accessions. These characters are expressed according to the principles of numerical taxonomy (Sneath and Sokal 1973), so that similarity or dissimilarity coefficients between cultivars can be estimated. The diversity present in a group of populations can be displayed by means of Cluster analysis (Balkaya et al. 2005). Statistical analysis of the data was conducted using the statistical programme SPSS (15.0 for Windows). Principal Component Analysis (PCA) was used for revealing the general differences between genotypes as numerical values, which indicate the traits that could be used to differentiate between genotypes (Balkaya et al. 2010). In the Principal Component Analysis (PCA) and the load coefficient values which relate the values, those principal components with eigenvalues >1.0 were selected, and those characters with load coefficient values >0.3 were considered highly relevant characters cores for principal components (Brown 1991). For a better overview of diversity in the *C. chinense* genotypes, Cluster analysis was also used according to Ward's method. The results of cluster analysis are presented in the form of a dendrogram. The dendrogram obtained in the study represents "similarities among the groups" (Rohlf 1993; Balkaya et al. 2005; Balkaya and Ergün 2008; Balkaya et al. 2010).

Results and Discussion

The results of the plant characteristics examined in genotypes belonging to the *C. chinense* species are given in Table 3. In terms of plant growth types of genotypes, it was determined that 29.3% had vertical, 53.4% semi-upright, and 17.3% horizontal. It was determined that the majority of *C. chinense* genotypes developed in semi-upright growth form. The longest plant height was measured respectively in CC40-3 (106.0 cm), CC40-4 (93.0 cm), CC40-2 (88.0 cm) genotypes and the shortest plant height were found in CC29-1 (34.0 cm), CC11 (36.0 cm), and CC72 (37.5 cm) genotypes (Table 3). It was determined that there is approximately a 3-fold difference between *C. chinense* genotypes in terms of plant height. Cherian and Indira (2003) reported that the average plant height ranged 29.0-52.0 cm in 25 genotypes belonging to the *C. chinense* species. Deonton and Vakinde (1993) determined that the average plant height varied 35.0-95.0 cm in the local pepper genotypes from Nigeria. Otulaj and Makine (1994) measured the average plant height as 30.9 cm-47.8 cm in bell pepper and long pepper genotypes. In another study, Alegbejo and Orakwue (2002) reported that the average plant height ranged from 42.2 cm to 83.62 cm in different pepper varieties. The thickest stem diameter was measured in the CC52 (26.3 mm) genotype, and the thinnest stem diameter was found in the CC61 (8.4 mm) genotype (Table 4). Karaağaç (2006) reported that the stem thickness showed a distribution between 7.6-15.5 mm in red pepper genotypes in Samsun location. The differences between the mentioned literatures may be due to the effect of the species and genotype. This study determined that 85.3% of the *C. chinense* genotypes did not have anthocyanin coloration in the plant stem (Table 4).

Leaf characteristics of *C. chinense* genotypes are given in Table 5. It has been determined that there are significant differences between genotypes in terms of

leaf length values. The highest leaf height was measured as 9.3 cm in the CC5 genotype. The CC11 (2.2 cm) was determined as the shortest genotype in terms of leaf length. The widest leaf width was determined respectively, CC5 (17.0 cm), CC22 (13.1 cm) and CC3 (12.9 cm) genotypes. The narrowest leaf width (3.7 cm) was measured in the CC11 genotype. The leaf colours are visually identified as light green, green, and dark green in *C. chinense* populations (Table 5). It was determined that 18.6% of the leaves of the detailed genotypes were light green, 49.4% green, and 32.0% dark green tonnes.

When the genotypes of *C. chinense* species were examined in terms of flower colour, it was determined that they had white (21.4% of the genotypes) and yellowish flower colours 78.6% of the genotypes). Vasconcelos et al. (2012) reported a high level of variation and genetic diversity in terms of flower characteristics in *C. chinense* genotypes. Ortiz et al. (2010) mentioned that the flower colour is mostly white in genotypes belonging to the *C. chinense* species. The difference with the mentioned literature has arisen from the different genotypes within the species.

Average fruit length values varied between 14.5-123.3 mm in Table 6. The longest fruit length was measured in the CC40-3 genotype with 123.3 mm, and the shortest fruit length was 14.5 mm in the CC13 genotype. It was determined that there is an 8.5-fold difference between genotypes in terms of fruit lengths. This result shows that the population is very heterogeneous in terms of fruit length. It was determined that the average fruit width values varied between 8.4 mm and 49.7 mm (Table 6). The widest fruit width was measured at 49.7 mm in CC76 genotype, and the narrowest fruit width was determined as the CC61 genotype with a width of 8.4 mm. There was a significant difference of approximately 6.0 times between *C. chinense* genotypes in terms of fruit width values. Deonton and Vakinde (1993) reported that the average fruit length was 2.5-14.0 cm and the fruit width was 2.0-10.5 cm in the local pepper genotypes from Nigeria. Otulaj and Makine (1994) measured the average fruit length as 4.0- 9.2 cm and the fruit width as 2.0-4.5 cm in pepper genotypes. Hallidri and Tome (2000) reported that the average fruit length ranged from 7.6 cm to 12.5 cm in sweet pepper genotypes. Alegbejo and Orakwue (2002) found that the fruit length in pepper genotypes is between 1.93-12.03 cm and the fruit width is between 0.81-2.33 cm. Cherian and Indira (2003) determined that the average fruit length in genotypes belonging to the *C. chinense* species is between 3.0-7.7 cm and the fruit width is between 0.9-6.2 cm. Akıncı and Akıncı (2004) reported that the average fruit length varied between 10.4-13.6 cm and the fruit diameter varied between 1.8-2.6 cm in 22 pepper varieties from different countries. It was determined that the CC40-3 genotype has the highest fruit shape index (7.2) (Table 6). The lowest fruit shape index was found to be the CC47 genotype (0.6). The significant difference in fruit sizes caused the high variation in the *C. chinense* genetic resources.

The genotypes in terms of fruit shape; have been determined as flat, round, heart-shaped, square, isosceles trapezoid, triangular, narrow triangle, and horn-shaped. Of the investigated genotypes, 10.7% had flat, 5.4% had round, 14.6% had heart-shaped, 6.6% had square, 8% had isosceles trapezoid triangle, 32% had triangular, 10.7% had a narrow triangle, and 6.6% had horn-shaped fruits. The fruit colours of the *C. chinense* genotypes were determined visually. In the visual examination, it was determined that there were significant differences in terms of colour tones. The fruits were detected to be in dark green, green, light green, yellow, and light-yellow colour tones (Table 7; Figure 1). In this work, of the genotypes belonging to the *C. chinense* species, 25.4% were determined to have dark green, 40.0% green, 24.0% light green, 8.0% yellow, and 2.6% light yellow fruit colour. The fruit stalk lengths varied between 19.9-61.9 mm in *C. chinense* genotypes (Table 7). The shortest fruit stalk length value was measured in the genotype CC11 (19.9 mm). The longest fruit stalk length was determined in the CC5 genotype with 61.9 mm. It was found that there is approximately a 3-fold difference between genotypes in terms of fruit stalk lengths.

The study determined that *C. chinense* populations show a rich genetic variability in terms of fruit yield components (Table 8). The average number of fruits in *C. chinense* genotypes ranged between 54-2100. The highest fruit number was found as 2100 in the CC52 genotype. This was followed, respectively, the CC50 genotype (1913) and the CC61 genotype (1555). The lowest number of fruits was determined to be in the CC40-4 genotype as 54 units. Deonton and Vakinde (1993) reported that the number of fruits per plant in local pepper genotypes ranged between 16-273 units. In another study, Otulaj and Makine (1994) mentioned that there were between 60-123 unit/plants in bell pepper and long pepper genotypes. Cherian and Indira (2003) stated that the average number of fruits per plant in the *C. chinense* genotypes changed between 4.0 and 63.5. The results of the present study were higher than Cherian and Indira's (2003) findings. This difference occurred due to genotypes and environmental factors. The average fruit weight varied between 0.5 g and 14.1 gin *C. chinense* genotypes (Table 8). The highest

average fruit weight values were determined in the CC40-4 (14.1 g), CC37 (13.0 g), and CC55 (11.6 g) genotypes, respectively. Otherwise, the lowest fruit weights were found in the genotypes CC34 (0.4 g), CC11 (0.5 g) and CC52 (0.5 g). Cherian and Indira (2003) stated that the average fruit weight in *C. chinense* genotypes changed varied between 0.9-7.2 g. The results of this research showed the average fruit weights to be higher compared to the mentioned literature. The highest total yield per plant values were found in the CC56 (6548.6 g), CC60 (5374.7 g), and CC79 (4955.3 g) genotypes (Table 8). The lowest yield value was determined respectively, CC25 (216.0 g) and CC39-2 (217.0 g) genotypes. Cherian and Indira (2003) reported that the yield value per plant in *C. chinense* genotypes was between 12.0 g and 185.0 g. The results of this study in respect to the fruit yield values were very high compared to the mentioned literature.

Determination of variation shown by available genetic resources for quantitative and qualitative traits is important for vegetable breeding programmes (Escribano et al. 1998). The number of studies revealing the level of variation in existing populations in *C. chinense* species is quite low (Cherian and Indira 2003; Manju and Sreelathakumary 2004; Fonseca et al. 2008). The existence of morphological variation in *C. chinense* populations collected from different parts of the world has been demonstrated with this study. Principal Component Analysis (PCA) was used for revealing the general differences between genotypes as numerical values, which indicate the traits that could be used to differentiate between genotypes (Balkaya et al. 2010). In this study, the principal components of *C. chinense* populations were performed in Table 9. The total variance ratios and cumulative variance values of the principal axes were also determined in detail. The fact that eigenvalues are greater than 1 in the principal component analysis indicates that the principal component axes values considered are quite reliable (Mohammadi and Prasanna 2003; Balkaya et al. 2010). This study found that the eigenvalues of the first six principal axes ranged from 1.02 to 4.18. The principal component analysis showed that the first six principal component axes explained 70.99% of the total multivariate variation. The first principal component axis accounted for 26.18% of the variation, whereas the second and third axes accounted for 12.45% and 10.49%, respectively (Table 9). The first three principal component axes explained 49.13% of the total variation. Mohammadi and Prasanna (2003) reported that the total variation of the first three axes should be over 25%. In this study, traits with high coefficients in the first, second, and third principal components should be considered more important since these axes explain the biggest share of the total variation. Though clear guidelines do not exist to determine the significance of a character coefficient, one rule of thumb is to treat coefficients>0.3 as having a large enough effect of being considered important (Brown 1991). Characteristics with high coefficients are: leaf width (0.38), leaf length (0.37), fruit stalk length (0.34) and plant height (0.32) for principal component 1; fruit length 0.40), average fruit weight (0.37), and anthocyanin coloration on the stem (0.31) for the second principal component, and fruit width (-0.45), leaf colour (0.41) and the number of fruits per plant (0.37) for the third principal component. On the PC4 axis, which represents 8.65% of the total variation, the characteristics of stem diameter (0.41), fruit attitude (0.38), and plant attitude (-0.32) were found to be important. Characters such as flower colour (-0.60) and pre-maturity fruit colour (0.35) were found to be important in the PC5 axis. Finally, principal component 6 was mainly related to fruit shape (0.61). Obtained results indicated that the *C. chinense* populations could be distinguished by leaf length, fruit stalk length, and plant height, which had the highest coefficients on the first principal component axis.

Duman and Düzyaman (2004) reported that the total variation was 81.77% as a result of the principal component analysis among 25 pepper genotypes. Karaağaç and Balkaya (2010) determined that the total variation was 74.3% according to the PCA results in 56 red pepper genotypes. Binbir and Baş (2010) reported that according to the results of the PCA performed nine principal component axes representing 85.35% of the total multiple variations in 29 pepper genotypes. Villota-Cerón et al. (2012) determined that the total variation was 70.8% as a result of the principal component analysis among 68 pepper genotypes. It has been found that the results of this study are generally compatible with the mentioned literatures.

To better understand the overall diversity of the *C. chinense* populations, the data were analysed by Cluster analysis that revealed the distribution of genetic diversity. The resultant groups and their subgroups are shown in Table 10, and the related dendrogram is shown in Figure 2. *C. chinense* genotypes clustered within 7 groups and 16 subgroups in the dendrogram. The seven groups and sixteen subgroups can be considered to be distinct germplasm pools in this study. General plant and fruit characteristics of the investigated *C. chinense* populations are as follows:

Group A: There were a total of 12 genotypes in group A. This group consisted of five subgroups (Table 10; Figure 2). It was determined that they varied as horizontal and semi-vertical forms in terms of plant

growth type of genotypes. The average stem diameter in this group was 23.4 mm, higher than all the other groups.

Group B: This group consisted of 12 genotypes. Genotypes in this group were clustered into four subgroups. The average fruit width was 30.5 mm. The fruit width of this group was the greatest of all the groups.

Group C: This group, which consists of twelve genotypes in the dendrogram, was classified into four subgroups. It was found that the average leaf length (6.2 cm) had the longest among all groups. The flower colour was yellowish tonnes. The average plant height was 70.1 cm. This value was the second rank after Group F among all groups.

Group D: There were a total of 15 genotypes in group D. This group had the biggest cluster of genetic groups (Table 10). The average fruit length in these populations was 38.2 mm. Fruit shapes changed according to the genotypes. Fruit shapes; rectangular, isosceles trapezoid, square, heart shape, narrow triangle, and triangle are defined in this group.

Group E: This group consists of 10 *C. chinense* genotypes. The average leaf length was 2.4 cm. This value was the shortest among all groups. The average fruit weight was 4.8 g. The average fruit stalk length was measured as 19.4 mm. The formation of anthocyanin in the stem of the plants was determined in this group.

Group F: There were a total of seven genotypes in this group. This group was clustered into two subgroups. It was determined that the genotypes in group F had the longest average plant height (81.6 cm) among all groups. The average leaf width was 11.1 cm. The leaf width of this group was the greatest of all the groups. Group F has the longest fruits (93.5 mm) in terms of fruit length. The fruits were horn-shaped or narrow triangular-shaped. The average fruit weight was 9.2 g. The fruit weight of this group was determined to rank firstly among all groups.

Group G: This group consisted of seven *C. chinense* genotypes and clustered into two subgroups (Table 10). Group G had the narrowest fruits in terms of average fruit width (11.5 mm). Genotypes in this group ranked first among all groups in terms of the number of fruits per plant (1570 units). The average fruit weight was 1.1 g. Its fruits were the smallest of all groups. It was ranked last among all groups in terms of fruit weight. This finding showed that the fruits were maximum in number but very small size than the other groups.

This study shows that there is considerable genetic diversity between *C. chinense* populations in terms of all morphological characteristics. Cluster groups were not associated with the geographical origins of *C. chinense* genotypes collected from different countries. The clustering of *C. chinense* genetic resources on the dendrogram in seven separate groups resulted from their different morphological structure and special fruit characteristics. Morphological differences between genotypes may have resulted from the influence of the origin from which they were collected and the environmental conditions.

Conclusions

C. chinense is one of the most important cultivated species in the genus *Capsicum*. Today, there are wild and transitional forms along with the forms that are cultivated. *C. chinense* species is an important genetic resource in terms of resistance to biotic and abiotic stress conditions. The genotypes in *C. chinense* show a high level of genetic diversity in terms of fruit shape, fruit colour, fruit size, and bitterness levels. In this study, the components of the plant characteristics of *C. chinense* were demonstrated by applying multivariate techniques to the morphological data sets. At the end of this study, we have found that genetic diversity within populations of *C. chinense* is high, including variations in leaf length, fruit stalk length, and plant height. Reliable information on morphological variability within *C. chinense* germplasm collections is very useful for breeders in planning variety improvement programs.

Acknowledgements

This study is a small part of a master thesis by Kübra Taş. We gratefully acknowledge the support of the Agriculture Faculty of Ondokuz Mayıs University and the Graduate School of Sciences Institute of Ondokuz Mayıs University.

Figure 1. The view of the diversity fruit size, shape and colour for detailed *C. chinense* populations. (Original)

Table 1. Genotype code, accession number and geographical origins of 75 *C. chinense* genotypes studied.

Genotype Code	Accession Number	Origin	Genotype Code	Accession Number	Origin
CC1	PI 159223 01	USA	CC39-2	PI 281430 01	Bolivia
CC2	PI 213916 01	Bolivia	CC39-3	PI 281430 01	Bolivia
CC3	PI 215736 01	Peru	CC39-4	PI 281430 01	Bolivia
CC4	PI 244667 01	India	CC40-1	PI 315013 01	Peru
CC5	PI 257085 01	Colombia	CC40-2	PI 315013 01	Peru
CC6	PI 257129 01	Colombia	CC40-3	PI 315013 01	Peru
CC7	PI 257145 01	Peru	CC40-4	PI 315013 01	Peru
CC8	PI 260470 01	Peru	CC47	PI 238053 01	Mexica
CC9	PI 260485 02	Bolivia	CC50	PI 497976 01	Philippines
CC10	PI 260486 01	Bolivia	CC51	PI 241669 01	USA
CC11	PI 260508 01	Peru	CC51-3	PI 241669 01	USA
CC13	PI 281393 01	Mexica	CC52	PI 653747 01	Venezuela
CC14	PI 281417 01	Philippines	CC54	PI 653677 02	Peru
CC16	PI 281435 01	USA	CC55	PI 653676 02	Peru
CC17	PI 281440 01	Venezuela	CC56	PI 645487 03	India
CC18	PI 315019 01	Peru	CC57	PI 257068 01	Costa Rica
CC19	PI 315023 02	Peru	CC59	PI 639655 02	Costa Rica
CC20	PI 322721 01	India	CC60	PI 645555 01	Mexica
CC21	PI 406725 01	Costa Rica	CC61	PI 593925 02	Bolivia
CC22	PI 438532 01	Belize	CC62	PI 585253 04	South Korea
CC23	PI 438636 02	Mexica	CC63	PI 241668 01	Equator
CC24	PI 439416 01	Bolivia	CC65	PI 257064 01	Spain
CC25	PI 439432 01	South Korea	CC66	Grif 9261 01	Costa Rica
CC26	PI 585278 02	Equator	CC68	PI 439419 01	Mexica
CC27	PI 257158 01	Peru	CC69-1	PI 257126 01	Colombia
CC28	PI 666562 01	Mexica	CC69-2	PI 257126 01	Colombia
CC-29	PI 260491 01	USA	CC69-3	PI 257126 01	Colombia
CC29-1	PI 260491 01	USA	CC69-4	PI 257126 01	Colombia
CC-30	PI 666561 01	Bolivia	CC72	PI 441635 01	Brazil
CC31	PI 438635 01	Peru	CC72-4	PI 441635 01	Brazil
CC33	PI 439467 01	India	CC76	PI 260465 02	Argentina
CC34	PI 653746 02	Colombia	CC78	Grif 9193 02	Colombia
CC35	Grif 9308 01	Colombia	CC79	PI 666547 01	Guatemala
CC36	PI 639657 04	Peru	CC82-1	PI 260477 01	Peru
CC37	PI 485593 01	Peru	CC82-2	PI 260477 01	Peru
CC38	PI 209028 01	Bolivia	CC82-3	PI 260477 01	Peru
CC38-2	PI 209028 01	Bolivia	CC82-4	PI 260477 01	Peru
CC39-1	PI 281430 01	Bolivia			

Table 2. List of morphological characters used in the characterisation of *C. chinense* populations.

1.	Plant attitude (1.prostrate, 2. semi-upright, 3. upright)
2.	Plant height (cm)
3.	Anthocyanin coloration (1. absent, 2. present)
4.	Stem diameter (mm)
5.	Leaf length (cm)
6.	Leaf width (cm)
7.	Leaf colour (1. light green, 2. green, 3.dark green)
8.	Leaf shape (1. ovate, 2 lanceolate, 3. deltoid)
9.	Flower colour (1.white, 2. yellow)
10.	Fruit attitude
11.	Fruit length (mm)
12.	Fruit width (mm)
13.	Fruit shape index (fruit length/fruit width)
14.	Fruit stalk length (mm)
15.	Fruit shape (1. flat, 2. round, 3. heart shape, 4. square, 5. isosceles, 6. trapezoid, 7. triangle)
16.	Fruit colour (before maturity) (1. dark green, 2. green, 3. light green, 4. yellow)
17.	Fruit number/plant
18.	Total fruit weight (g / plant)
19.	Average fruit weight (g)

Table 3. Distribution of *C. chinense* genotypes in terms of plant height values.

Genotype Code	Plant Height (cm)	Genotype Code	Plant Height (cm)	Genotype Code	Plant Height (cm)	Genotype Code	Plant Height (cm)
CC1	61.0	CC22	65.4	CC39-2	34.0	CC62	50.0
CC2	58.7	CC23	51.0	CC39-3	65.0	CC63	77.5
CC3	48.3	CC24	48.5	CC39-4	57.0	CC65	84.5
CC4	63.5	CC25	40.0	CC40-1	87.0	CC66	63.0
CC5	67.0	CC26	60.0	CC40-2	88.0	CC68	62.0
CC6	71.0	CC27	71.5	CC40-3	106.0	CC69-1	60.0
CC7	85.5	CC28	31.0	CC40-4	93.0	CC69-2	73.0
CC8	68.5	CC29	30.5	CC47	55.0	CC69-3	48.0
CC9	50.0	CC29-1	34.0	CC50	63.0	CC69-4	52.0
CC10	58.3	CC30	52.4	CC51	58.6	CC72	37.5
CC11	36.0	CC31	47.3	CC51-3	38.0	CC72-4	56.0
CC13	63.5	CC33	47.0	CC52	59.0	CC76	63.0
CC14	43.0	CC34	45.7	CC54	48.4	CC78	71.3
CC16	61.5	CC35	44.5	CC55	51.0	CC79	56.8
CC17	61.0	CC36	46.5	CC56	78.8	CC82-1	51.0
CC18	54.5	CC37	56.5	CC57	55.8	CC82-2	42.0
CC19	57.0	CC38	49.5	CC59	73.5	CC82-3	63.0
CC20	63.0	CC38-2	58.0	CC60	49.6	CC82-4	59.0
CC21	83.4	CC39-1	76.0	CC61	44.0		

Table 4. Distribution of *C. chinense* genotypes in terms of stem diameter and anthocyanin coloration characters.

Genotype Code	Stem Diameter (mm)	Anthocyanin Coloration	Genotype Code	Stem Diameter (mm)	Anthocyanin Coloration
CC1	21.8	Absent	CC39-2	13.0	Absent
CC2	20.6	Absent	CC39-3	25.9	Absent
CC3	21.5	Present	CC39-4	14.1	Absent
CC4	24.4	Absent	CC40-1	16.3	Absent
CC5	20.9	Absent	CC40-2	11.9	Absent
CC6	23.9	Absent	CC40-3	19.9	Absent
CC7	24.9	Absent	CC40-4	15.2	Absent
CC8	27.5	Absent	CC47	20.3	Absent
CC9	25.6	Absent	CC50	21.1	Absent
CC10	23.5	Absent	CC51	16.8	Absent
CC11	11.2	Absent	CC51-3	12.8	Absent
CC13	21.5	Absent	CC52	26.3	Absent
CC14	16.8	Absent	CC54	19.9	Present
CC16	27.3	Absent	CC55	24.1	Present
CC17	22.2	Absent	CC56	25.8	Absent
CC18	29.5	Absent	CC57	16.0	Present
CC19	19.0	Present	CC59	19.0	Absent
CC20	20.4	Absent	CC60	23.0	Absent
CC21	22.9	Absent	CC61	8.4	Present
CC22	25.5	Absent	CC62	13.7	Absent
CC23	19.6	Absent	CC63	16.7	Absent
CC24	18.1	Absent	CC65	22.0	Present
CC25	18.2	Absent	CC66	13.5	Absent
CC26	18.1	Absent	CC68	22.2	Present
CC27	20.8	Absent	CC69-1	19.5	Absent
CC28	10.4	Absent	CC69-2	21.3	Present
CC29	13.5	Absent	CC69-3	13.8	Absent
CC29-1	17.5	Absent	CC69-4	15.1	Absent
CC30	20.3	Absent	CC72	13.3	Present
CC31	20.2	Absent	CC72-4	15.9	Present
CC33	23.2	Absent	CC76	17.3	Absent
CC34	18.9	Absent	CC78	14.1	Absent
CC35	13.4	Absent	CC79	23.5	Absent
CC36	21.9	Absent	CC82-1	17.1	Absent
CC37	13.0	Absent	CC82-2	16.6	Absent
CC38	17.5	Absent	CC82-3	20.1	Absent
CC38-2	18.9	Absent	CC82-4	14.5	Absent
CC39-1	21.3	Absent			

Table 5. Leaf characteristics of genotypes belonging to the *C. chinense* species.

Genotype Code	Leaf Length (cm)	Leaf Width (cm)	Leaf Colour	Leaf Shape
CC1	6.0±1.7	8.9±2.5	Dark green	Ovate
CC2	5.3±2.6	11.2±2.1	Green	Ovate
CC3	6.7±1.3	12.9±0.4	Green	Ovate
CC4	5.7±0.8	11.0±0.5	Dark green	Lanceolate
CC5	9.3±2.1	17.0±1.1	Dark green	Deltoid
CC6	6.3±1.1	11.5±1.5	Green	Deltoid
CC7	5.8±1.4	12.1±0.6	Green	Ovate
CC8	6.0±1.0	10.6±0.7	Dark green	Deltoid
CC9	6.0±1.3	10.6±0.6	Light green	Deltoid
CC10	6.2±1.6	11.5±0.7	Dark green	Ovate
CC11	2.2±0.7	3.7±2.2	Dark green	Deltoid
CC13	5.0±0.9	9.7±0.6	Dark green	Ovate
CC14	4.2±1.1	5.6±0.7	Green	Ovate
CC16	6.3±1.1	11.8±0.6	Green	Ovate
CC17	8.4±1.3	12.0±0.8	Light green	Deltoid
CC18	7.3±1.7	13.0±0.8	Green	Deltoid
CC19	4.7±0.7	9.2±0.4	Green	Ovate
CC20	6.7±1.1	11.5±0.8	Light green	Ovate
CC21	8.2±1.3	10.0±1.3	Light green	Lanceolate
CC22	7.9±1.8	13.1±0.9	Dark green	Deltoid
CC23	6.9±1.4	11.4±0.9	Dark green	Deltoid
CC24	6.1±1.7	11.7±0.6	Dark green	Deltoid
CC25	6.4±0.9	10.2±0.8	Green	Deltoid
CC26	5.8±1.0	12.4±0.9	Green	Deltoid
CC27	6.1±2.1	9.6±1.1	Green	Deltoid
CC28	2.6±0.5	4.9±0.2	Dark green	Ovate
CC29	2.7±0.8	6.2±0.4	Green	Lanceolate
CC29-1	4.7±0.8	8.7±0.7	Green	Lanceolate
CC-30	5.7±1.1	9.8±0.7	Light green	Ovate
CC31	4.1±0.7	7.9±0.4	Light green	Lanceolate
CC33	4.8±0.8	8.8±0.5	Green	Deltoid
CC34	3.6±0.5	6.2±0.4	Green	Lanceolate
CC35	6.2±1.2	11.4±0.7	Light green	Ovate
CC36	6.2±1.3	10.8±0.6	Light green	Lanceolate
CC37	4.1±0.8	8.1±0.9	Green	Lanceolate
CC38	5.5±0.9	9.7±0.9	Green	Ovate
CC38-2	5.5±0.4	9.8±0.4	Green	Ovate

Continuing Table 5

Genotype Code	Leaf Length (cm)	Leaf Width (cm)	Leaf Colour	Leaf Shape
CC39-1	5.8±0.7	10.9±0.2	Light green	Lanceolate
CC39-2	3.9±0.5	8.0±0.2	Green	Lanceolate
CC39-3	4.1±1.1	7.4±0.2	Light green	Lanceolate
CC39-4	4.1±1.0	8.6±0.8	Light green	Lanceolate
CC40-1	6.7±0.8	10.8±0.4	Dark green	Ovate
CC40-2	4.9±2.4	8.8±1.2	Dark green	Ovate
CC40-3	6.9±0.5	12.8±0.4	Dark green	Ovate
CC40-4	5.8±1.1	10.1±0.6	Dark green	Ovate
CC47	6.2±0.4	10.2±0.3	Green	Deltoid
CC50	3.8±0.4	6.6±0.6	Dark green	Deltoid
CC51	4.3±0.6	8.6±0.5	Green	Lanceolate
CC51-3	4.5±0.6	8.0±0.5	Green	Lanceolate
CC52	3.2±0.8	7.1±0.6	Dark green	Lanceolate
CC54	5.7±1.0	14.7±0.6	Dark green	Deltoid
CC55	4.1±1.0	8.9±0.5	Dark green	Ovate
CC56	4.7±0.9	8.3±0.5	Green	Ovate
CC57	3.5±1.2	8.0±0.5	Dark green	Lanceolate
CC59	5.3±1.2	10.1±0.8	Dark green	Deltoid
CC60	3.0±0.7	6.2±0.4	Green	Ovate
CC61	2.3±0.9	4.8±0.4	Dark green	Lanceolate
CC62	3.4±0.9	6.7±0.4	Light green	Lanceolate
CC63	4.4±1.0	7.9±0.6	Light green	Ovate
CC65	4.8±1.3	10.9±0.5	Green	Ovate
CC66	4.9±1.3	9.9±0.6	Light green	Ovate
CC68	4.5±2.0	9.9±0.7	Dark green	Lanceolate
CC69-1	3.0±0.4	6.5±0.2	Green	Ovate
CC69-2	4.5±1.4	8.2±0.8	Green	Ovate
CC69-3	4.3±1.4	9.1±0.4	Green	Ovate
CC69-4	3.8±0.7	8.0±0.5	Green	Ovate
CC72	3.6±0.9	7.2±0.3	Green	Ovate
CC72-4	4.1±0.4	8.2±0.2	Green	Ovate
CC76	3.9±1.0	10.9±0.5	Green	Lanceolate
CC78	6.7±0.9	8.9±0.6	Green	Ovate
CC79	5.7±1.9	9.4±0.8	Dark green	Ovate
CC82-1	3.9±1.0	7.2±0.7	Green	Ovate
CC82-2	3.9±0.4	6.8±0.8	Green	Ovate
CC82-3	4.7±1.0	7.6±0.8	Green	Ovate
CC82-4	4.2±0.6	7.4±0.5	Green	Ovate

Table 6. Fruit dimensions results of *C. chinense* genotypes.

Genotype Code	Fruit Length (mm)	Fruit Width (mm)	Fruit Shape Index	Genotype Code	Fruit Length (mm)	Fruit Width (mm)	Fruit Shape Index
CC1	74.3±6.6	23.6±4.7	3.1	CC39-2	46.7±6.3	10.7±1.9	4.3
CC2	45.6±6.1	18.8±2.9	2.4	CC39-3	41.1±8.9	19.6±3.1	2.0
CC3	52.8±6.7	22.2±4.0	2.3	CC39-4	28.6±5.7	24.8±8.1	1.1
CC4	46.9±9.8	18.0±5.4	2.6	CC40-1	90.5±12.7	21.6±1.7	4.1
CC5	71.7±11.7	18.8±4.0	3.8	CC40-2	67.0±13.3	12.1±1.8	5.5
CC6	39.8±8.2	17.6±3.0	2.2	CC40-3	123.3±18.5	17.0±2.2	7.2
CC7	26.1±3.4	22.4±2.6	1.1	CC40-4	113.2±14.9	18.3±2.3	6.1
CC8	40.1±5.6	23.8±3.5	1.6	CC47	21.5±3.6	33.3±4.3	0.6
CC9	51.5±7.5	21.3±4.3	2.4	CC50	31.7±6.0	14.1±4.1	2.2
CC10	36.2±8.0	26.5±9.3	1.3	CC51	63.0±11.9	19.3±3.3	3.2
CC11	21.3±6.1	10.2±2.1	2.0	CC51-3	48.8±5.0	19.4±1.7	2.5
CC13	14.5±2.3	18.0±3.6	0.8	CC52	16.9±12.3	13.2±4.6	1.2
CC14	43.8±5.2	19.8±2.1	2.2	CC54	49.5±7.0	25.8±3.3	1.9
CC16	41.3±4.2	14.6±1.4	2.8	CC55	49.8±9.4	23.7±3.8	2.1
CC17	28.1±3.5	24.3±3.7	1.1	CC56	41.7±5.3	35.2±4.1	1.1
CC18	28.2±5.4	23.1±2.7	1.2	CC57	47.9±6.9	17.9±2.5	2.6
CC19	28.1±5.6	21.3±1.9	1.3	CC59	86.6±16.2	19.3±2.6	4.4
CC20	22.6±2.0	20.7±1.6	1.0	CC60	36.0±7.6	22.5±2.5	1.6
CC21	27.4±2.3	22.5±2.5	1.2	CC61	16.9±1.9	8.4±0.7	2.0
CC22	28.4±4.6	27.9±0.8	1.0	CC62	55.1±7.8	21.6±2.8	2.5
CC23	38.3±4.0	27.1±4.7	1.4	CC63	55.7±10.9	15.8±2.0	3.5
CC24	26.5±3.1	28.1±3.4	0.9	CC65	46.1±8.1	18.1±2.5	2.5
CC25	15.3±2.9	17.9±1.2	0.8	CC66	52.4±6.1	14.3±2.4	3.6
CC26	42.3±5.6	13.4±2.3	3.1	CC68	63.8±8.8	10.1±2.1	6.3
CC27	77.3±12.2	17.1±3.7	4.5	CC69-1	40.1±5.1	15.3±1.5	2.6
CC28	19.4±2.5	10.3±1.5	1.8	CC69-2	65.5±8.7	13.2±4.9	4.9
CC29	32.1±5.2	24.8±2.5	1.2	CC69-3	28.7±3.5	18.0±1.6	1.5
CC29-1	49.5±8.0	25.3±3.2	1.9	CC69-4	22.1±3.5	16.8±1.4	1.3
CC-30	29.3±5.3	31.6±3.8	0.9	CC72	37.6±9.5	21.3±1.9	1.7
CC31	42.2±7.5	26.7±3.9	1.5	CC72-4	24.3±2.4	20.2±1.3	1.2
CC33	39.7±5.1	26.6±5.0	1.5	CC76	54.5±8.5	49.7±2.5	1.0
CC34	10.3±1.4	9.3±0.8	1.1	CC78	47.2±4.2	21.3±2.9	2.2
CC35	50.2±7.5	18.5±2.1	2.7	CC79	32.4±4.4	34.6±3.2	0.9
CC36	42.1±6.5	26.7±5.4	1.5	CC82-1	60.8±7.9	21.3±1.8	2.8
CC37	102.3±18.4	39.7±3.7	2.5	CC82-2	40.3±5.7	25.5±2.4	1.5
CC38	26.1±6.3	31.4±5.3	0.8	CC82-3	44.3±4.1	24.2±6.0	1.8
CC38-2	41.7±5.9	28.7±3.8	1.4	CC82-4	50.8±4.1	24.0±2.7	2.1
CC39-1	50.1±8.7	17.3±1.5	2.8				

Table 7. Results of fruit colour and fruit stalk length traits of *C. chinense* genotypes.

Genotype Code	Fruit Colour	Fruit Stalk Length (mm)	Genotype Code	Fruit Colour	Fruit Stalk Length (mm)
CC1	Green	37.1±7.4	CC39-2	Green	32.1±3.1
CC2	Green	30.5±5.3	CC39-3	Green	28.1±5.1
CC3	Dark green	34.4±5.0	CC39-4	Green	34.1±4.6
CC4	Light green	40.7±7.5	CC40-1	Green	49.1±4.4
CC5	Yellow	61.9±8.2	CC40-2	Dark green	34.9±2.6
CC6	Green	37.3±6.4	CC40-3	Dark green	48.6±3.9
CC7	Light green	44.8±13.7	CC40-4	Green	42.8±6.1
CC8	Green	26.9±4.2	CC47	Light green	26.3±3.2
CC9	Dark green	33.7±4.9	CC50	Yellow	25.4±4.6
CC10	Green	29.3±5.0	CC51	Light green	35.8±5.9
CC11	Light yellow	19.9±3.2	CC51-3	Yellow	32.0±4.1
CC13	Dark green	26.8±5.5	CC52	Light green	23.5±5.8
CC14	Green	32.6±5.6	CC54	Light green	39.8±4.8
CC16	Dark green	30.3±5.9	CC55	Dark green	35.6±4.8
CC17	Light green	29.9±3.4	CC56	Green	34.2±5.2
CC18	Dark green	27.4±4.1	CC57	Green	34.3±4.6
CC19	Dark green	28.1±3.3	CC59	Dark green	41.5±7.0
CC20	Green	27.2±4.2	CC60	Yellow	26.4±5.3
CC21	Light green	32.4±6.5	CC61	Dark green	24.7±4.6
CC22	Dark green	27.9±4.8	CC62	Green	35.1±6.7
CC23	Green	31.3±3.8	CC63	Light green	38.9±7.1
CC24	Green	25.7±3.7	CC65	Green	35.3±5.0
CC25	Light green	23.0±2.5	CC66	Yellow	35.3±54
CC26	Green	34.0±5.4	CC68	Dark green	35.0±6.8
CC27	Green	35.0±6.2	CC69-1	Dark green	44.5±6.6
CC28	Light green	21.6±3.5	CC69-2	Green	39.7±6.0
CC29	Green	25.6±3.1	CC69-3	Yellow	34.0±4.5
CC29-1	Light green	28.9±3.5	CC69-4	Light green	30.0±4.2
CC-30	Light green	32.9±5.6	CC72	Dark green	31.6±4.9
CC31	Dark green	30.6±5.0	CC72-4	Green	27.1±3.3
CC33	Light yellow	35.2±5.3	CC76	Dark green	34.5±5.1
CC34	Dark green	22.2±3.5	CC78	Green	38.6±6.0
CC35	Green	32.9±4.6	CC79	Green	33.5±4.5
CC36	Green	35.4±7.1	CC82-1	Green	23.7±4.9
CC37	Green	28.2±5.0	CC82-2	Light green	29.3±5.7
CC38	Light green	30.1±5.5	CC82-3	Dark green	30.3±3.3
CC38-2	Light green	30.5±5.5	CC82-4	Light green	28.8±4.0
CC39-1	Green	31.9±3.8			

Table 8. Results of fruit yield components of *C. chinense* genotypes.

Genotype Code	Fruit Number/Plant	Average Fruit Weight (g)	Total Fruit Weight/Plant (g)	Genotype Code	Fruit Number/Plant	Average Fruit Weight (g)	Total Fruit Weight/Plant (g)
CC1	217	6.0	1321.5	CC39-2	128	1.6	217.0
CC2	120	2.2	270.2	CC39-3	310	3.7	256.0
CC3	335	3.9	1333.3	CC39-4	184	3.0	564.5
CC4	440	3.1	1372.8	CC40-1	81	8.5	747.9
CC5	550	6.3	3514.5	CC40-2	95	3.8	380.2
CC6	120	2.5	300.0	CC40-3	160	13.2	1781.9
CC7	298	2.5	736.6	CC40-4	54	14.1	560.3
CC8	692	4.2	2920.2	CC47	917	3.6	4250.4
CC9	426	8.0	3433.5	CC50	1913	1.9	3740.0
CC10	110	7.5	834.9	CC51	479	3.5	2499.4
CC11	1280	0.5	640.0	CC51-3	231	2.6	918.9
CC13	63	3.0	192.1	CC52	2100	0.5	1570.2
CC14	626	4.3	2691.8	CC54	556	9.9	4737.8
CC16	216	2.2	483.8	CC55	551	11.6	4427.1
CC17	302	2.7	830.5	CC56	975	6.4	6548.6
CC18	481	2.8	1351.6	CC57	679	6.6	2281.7
CC19	190	2.3	446.5	CC59	148	5.4	1392.1
CC20	128	2.7	352.0	CC60	1382	3.4	5374.7
CC21	1469	2.8	4171.9	CC61	1555	0.7	1010.5
CC22	592	3.5	2107.5	CC62	246	5.3	1444.0
CC23	228	3.4	793.4	CC63	892	3.1	3156.7
CC24	126	4.3	544.3	CC65	658	2.8	2407.4
CC25	100	2.1	216.0	CC66	663	2.5	1547.8
CC26	856	3.3	2824.8	CC68	1235	3.6	2368.2
CC27	397	4.8	1944.4	CC69-1	1469	1.6	327.6
CC28	1239	1.0	1264.6	CC69-2	592	1.5	1111.3
CC29	355	4.8	1715.6	CC69-3	227	2.2	636.6
CC29-1	128	7.1	910.2	CC69-4	692	1.7	972.4
CC30	294	5.3	1576.4	CC72	708	3.6	2904.6
CC31	441	4.5	1992.5	CC72-4	355	1.8	1957.4
CC33	377	5.4	2057.5	CC76	544	3.5	2458.8
CC34	1434	0.4	600.0	CC78	558	4.1	2458.8
CC35	433	3.7	1634.7	CC79	956	4.3	4955.3
CC36	207	5.3	1098.6	CC82-1	394	3.0	1603.1
CC37	262	13.0	3395.8	CC82-2	166	4.0	843.1
CC38	617	4.0	2514.9	CC82-3	231	4.9	1776.1
CC38-2	165	4.7	783.1	CC82-4	222	3.9	1039.5
CC39-1	190	3.5	680.2				

Table 9. Principal component (PC) analysis of characters associated with 75 *C. chinense* populations. Proportions of variations are associated with first six PC axes, which correspond to Eigenvalues greater than 1.

	PC Axis					
Eigenvalues	4.18	1.99	1.67	1.38	1.15	1.02
Variation, %	26.18	12.45	10.49	8.65	7.19	6.00
Cumulative variation, %	26.18	38.64	49.13	57.79	64.99	70.99
	Eigen Vectors					
Trait	**PC 1**	**PC 2**	**PC 3**	**PC 4**	**PC 5**	**PC 6**
Stem diameter (mm)	0.19	-0.27	0.13	0.41	0.23	-0.32
Plant height (cm)	0.32	-0.02	0.34	-0.22	0.06	-0.09
Plant attitude	0.29	-0.19	0.26	-0.32	0.03	0.14
Leaf length (cm)	0.37	-0.30	0.04	0.15	-0.07	-0.09
Leaf width (cm)	0.38	-0.20	0.07	0.28	-0.10	-0.08
Leaf colour	0.02	0.24	0.41	0.22	0.26	0.41
Flower colour	-0.15	0.08	0.17	0.19	-0.60	0.12
Fruit attitude	0.21	0.19	-0.14	0.38	-0.29	0.27
Fruit stalk length (mm)	0.34	0.17	0.18	-0.11	-0.28	-0.04
Fruit width (mm)	0.15	-0.07	-0.45	0.26	0.27	0.30
Fruit length (mm)	0.28	0.40	0.01	-0.24	-0.01	0.14
Fruit colour (before maturity)	-0.11	0.25	0.24	0.20	0.35	-0.08
Fruit shape	-0.10	-0.37	0.20	0.06	-0.03	0.61
Anthocyanin coloration	-0.08	0.31	0.21	0.37	-0.12	-0.27
Number of fruits per plant	-0.25	-0.07	0.37	0.03	0.17	0.02
Average fruit weight (g)	0.30	0.37	-0.16	0.00	0.26	0.10

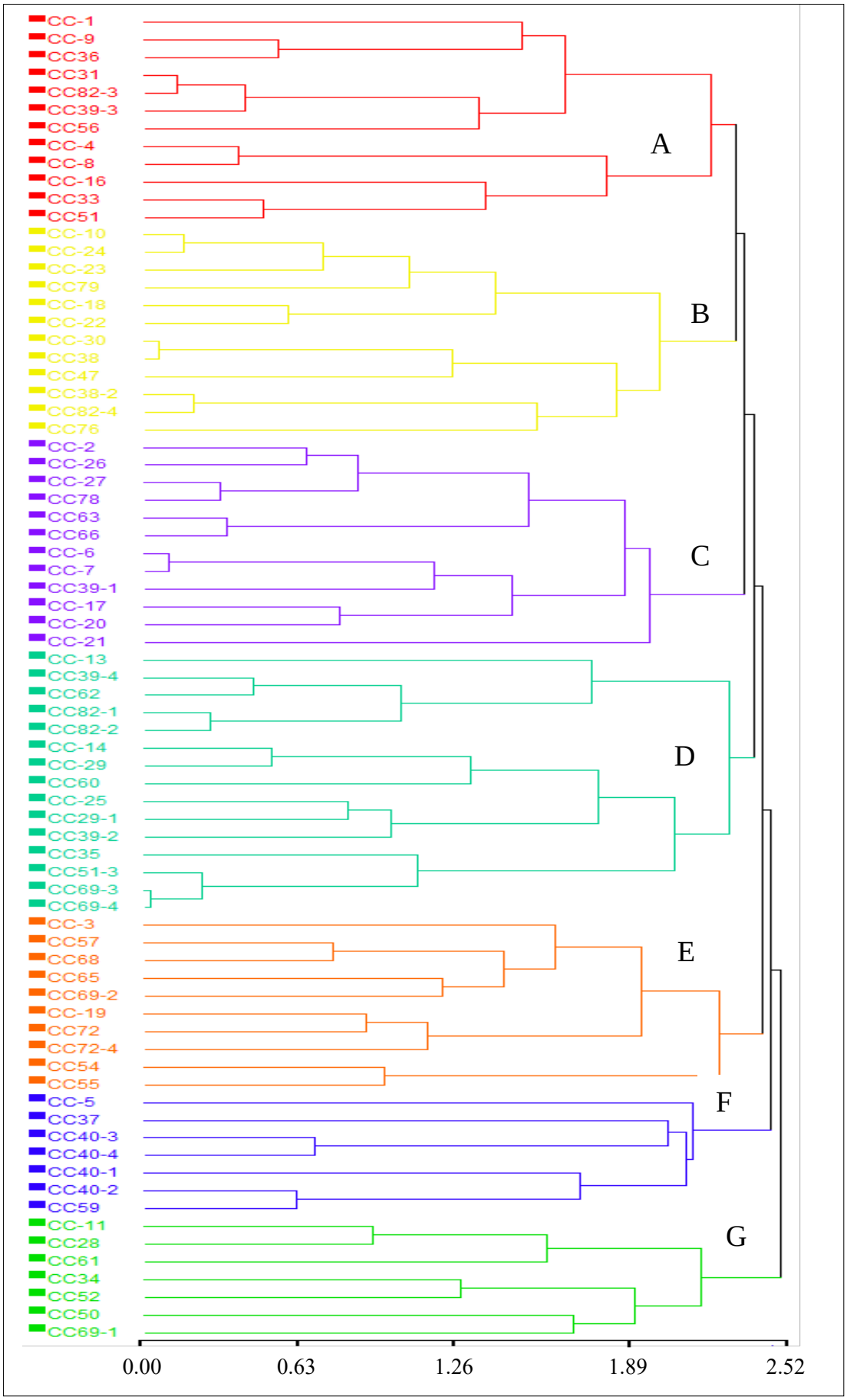

Figure 2. Genetic groupings of *C. chinense* genotypes according to cluster analysis.

Table 10. *C. chinense* genotype groups and subgroups obtained by Cluster analysis.

Groups	Subgroups	Genotypes	Total Genotype Number
A	5	CC1, CC9, CC36, CC31, CC82-3, CC56, CC39-3, CC4, CC8, CC16, CC33, CC51	12
B	4	CC10, CC24, CC23, CC79, CC18, CC22, CC30, CC38, CC47, CC38-2, CC82-4, CC76	12
C	4	CC2, CC26, CC27, CC78, CC63, CC66, CC6, CC7, CC39-1, CC17, CC20, CC21	12
D	5	CC13, CC39-4, CC62, CC82-1, CC14, CC82-2, CC29, CC60, CC25, CC29-1, CC39-2, CC35, CC51-3, CC69-3 CC69-4	15
E	4	CC3, CC57, CC68, CC65, CC69-2, CC19, CC72, CC72-4, CC54, CC55	10
F	2	CC5, CC37, CC40-3, CC40-4, CC40-1, CC40-2, CC59	7
G	2	CC11, CC28, CC61, CC34, CC52, CC50, CC69-1	7
Total	**16**		**75**

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