



## **Developing a Core collection of Brazilian arracacha (*Arracacia xanthorrhiza* Banc.) based on morphological and agronomic descriptors character of Brazil.**

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### **ABSTRACT**

Genetic diversity of 63 entries of Arracacha was studied by estimating 25 morphological and agronomical descriptors during 2007 and 2008. The selected entries were classified into

twelve groups based on the identical and correlated morphological and agronomical traits. The selected traits were 19 main characters. Five characteristics were excluded as they did not show much variability. Morphological characteristics did not show much variation. Some characteristics like root yield, number of roots and number of shoots showed more. A sampling intensity of 30% was found to represent the core collection since it showed 87.09% determination coefficient ( $R^2$ ) and 96.67% coincidence rate (CR). Entries BHG-4551 and BHG-7628 were duplicated.

### **Introduction**

Arracacha (*Arracacia xanthorrhiza* Bancroft) belongs to family Umbelliferae (Apiaceae) and gender *Arracacia*. The specie *A. xanthorrhiza* was mainly found in Andean region that comprised of Venezuela, Ecuador, Peru, Bolivia and Colombia. Where, intensive and extensive farming were found. Moreover, a great diversity of these species massively prevails in this district of South America.

The edible roots contain 10-25% starch and have a high content of calcium and vitamin A. Besides; roots are considered a source of starch used in other food stuffs. For that reason, the crop has a common usage as a staple food in some parts of South America as it is very palatable and easily digested also. Moreover, the stems are sometimes blanched and used like celery in salads. From the fact that, it has a wide range of culinary uses, is free of undesirable substances for human consumption, its agro industrial potentials and adaptability to a wide range of mesothermic and tropical highland environments and variable day length regimes as well, it will meet a great expansion worldwide (Hermann 1997).

Seeds are not used for commercial production since germination is often poor, less than 50%. The plant forms a clump of tubers around a central root; each tuber can be used to grow a

new plant. Traditionally the base of the tuber is repeatedly slashed to stimulate shoots to form and encourage a uniform arrangement of lateral roots. They are then left for a few days to heal before planting them out. The plant has some favorable conditions, where grows best in a sandy loam with a pH in the range of 5 to 6, requiring a minimum rainfall of about 600mm. Plants take about 120 - 240 days from planting to produce a crop and 300 - 400 days to produce a crop of mature tubers. One plant can yield 2 - 3 kg of edible roots. Total yield of 40 tons per hectare is possible. Plants might be sensitive to day length, possibly requiring short days to initiate tuber production, and so may not be suitable for temperate climates.

A core collection is a set of collection represents the genetic diversity of the entire collection (Frankel 1984). Frankel and Brown (1984a) have highlighted a general approach for selecting a core set by stratifying the collection and selecting representative random samples from each of the classified groups. Some bases of the stratification may be geographical origin of entries, qualitative descriptors, quantitative traits, molecular and biochemical markers and appropriate multivariate methods. Sampling strategies for obtaining a core collection are mainly focused on grouping entries into initial homogenous clusters then selecting sub-samples from each cluster to obtain a pooled core set. However, the variation is usually not random by distributed, and various stratification strategies are therefore applied, depending on the available information of the accessions (Logozzo et al., 2007). The sampling intensity varies from 0.3% in the international Barley Core Collection (Knupffer and van Hintum 1995) to 20% in cotton (Xu et al. 2006) and 15-20% in eggplant (Mao et al. 2008). Higher percentages, 20–30%, may sometimes be needed (Noirot et al. 1996) depending on the species (Yonezawa et al. 1995), the objective of the core collection (Miklas et al. 1999), the strategy adopted (Diwan et al. 1995) and, most often, the size of the collection to be sampled (van Hintum et al. 2000).

The genetic diversity of *Arracacia* genus has been studied mainly in Central and North America by Mathias and Constance where they have carried out various investigations in 1944, 1968, and 1973. Besides, Constance and Affolter (1995). However, In South America, Knudsen (2003) mentioned 10 *Arracacia* species distributed in the mountainous Andean region of Venezuela, Colombia, Ecuador, Peru and Bolivia. The crop was introduced to Brazil century ago. Furthermore, Brazil was the greatest commercial producer and had a respective number of studies on its reproductive biology, seed physiology and yield breeding (Hermann 1997). This work was aimed at studying the genetic diversity of 63 entries of *arracacia* with a view to establish a core collection.

## MATERIALS AND METHODS

Cormels of 63 entries of *aracacha*, belonging to the Viçosa Public University Germplasm Bank (BGH-UFV), were used into the current investigation. For each entry, 15 cormels were used. The experimental design was randomized block design with two replications. The plot area was 9 m<sup>2</sup> and contained three lines. Plant spacing was 0.6 m between plants and 1 m between rows. Three plants were randomly selected for evaluation from each entry. Entries were characterized and evaluated for the selected traits (Table 1) using IPGRI (2004) and RHS Color Chart (The Royal Horticultural Society 2001). The entries were then grouped by maximum dissimilarity using Tocher method with inverse gathering criterion (Vasconcelos et al. 2007), by which the most dissimilar pair of individuals formed the initial group. To include an entry, distances were calculated between the original group and the other genotypes. The entry, which presented greatest distance to this group, was included. The evaluation and characterization was

continued until we attained the required number of entries to develop the core collection. The obtained values were then statistically analyzed as described by Cruz and Carneiro (2003)

A homogeneity *F*-test for variances and *t*-test for means were performed to determine the differences between the core and the initial collection. Core collections properties were tested by estimating four parameters. Significant difference percent between core and initial collections was estimated for the mean difference percentage (*MD%*) and the variance difference percentage (*VD%*) of traits. The coincidence rate was used to evaluate how appropriate was the core collection to the initial collection.

$$CR\% = \left[ \frac{1}{m} \sum_{j=1}^m \frac{R_C}{R_I} \right] 100$$

where *m* is the number of traits ; *R<sub>c</sub>* is the difference between the maximum and the minimum of each variable observed in the core collection; *R<sub>I</sub>* is the difference between maximum number and minimum of each variable observed in the initial collection. Determination Coefficient (*R<sup>2</sup>*) was estimated by the ratio between the sum of squares of deviations of core collection and total sum of squares of deviations of the initial collection

$$R^2\% = \left[ \frac{1}{m} \sum_{j=1}^m \frac{(SD_C)^2}{(SD_I)^2} \right] 100$$

where *SD<sub>C</sub>* is the standard deviation of the core collection, *SD* is the standard deviation of the initial collection, *m* is the number of traits (Cruz 1997). The core collection is considered to be representative of the initial collection under the following conditions: (1) no more than 20% of the traits have different means in the core collection from the initial collection; and (2) the *CR%* retained by the core collection is no less than 80%. (Hu et al., 2000)

## RESULTS AND DISCUSSION

Five botanical traits, shoots disposition on the crown, pulp shoot pigment, leaflet term form; pigment insertion leaflet and pigment leaflets edge did not show sufficient variability so they were excluded from the statistical analysis.

Multicollinearity analysis showed a high correlation ( $>0.80$ ) between the traits chimeras and disposition on crown. Therefore, the first one was abolished from the analysis and trait disposition on crown was maintained. The three primary principle components of analysis did not explain the existing variability among entries (Table 2). The minimum limit that could be explained by three primary components is 80 % of the total variation (Cruz and Carneiro 2003). Entries were grouped into 12 groups (Table 3).

Morphological variation in the cultivated genepool of arracacha appeared to be minimal. Plant roots tubers are the most variable parts. Three horticultural root forms are widely recognized: yellow-roots , white-roots and additional purplish pigmentation. Arracacha root characteristics are the subject of regional or even local preferences.

In the cluster analysis grouped, the entries which mainly have yellow root color together (table 3). While, the other root color cultivars were found in different groups (5 to 12). The only known segregating population resulted from (self-pollinated) seed progenies of the most popular Brazilian clone BGH5746. This progeny showed a wide range of white to intensely yellow root color. However, purple genotypes also occurred at low frequency.

Determination coefficient, ( $R^2$ ) of the first sample intensity 10%, was 70.14% and the maximum value of 87.09 % was obtained with the 30% sample intensity (Table 4). Similarly, the coincidence rate, (CR%) it was 70.55 and 96.67 for 10 and 30% of sample intensity. The VD% of significant difference between core collection and initial collection for variance of traits

was equal in both the sample intensities of 20 and 30%. While, the highest variation in case of 10% sample intensity was 15.8%. Core collections are considered representative of initial collection when no more than 20% of the traits have different means between both core and initial collection. The sample intensity, (30%), could be considered a core collection that represents the initial collection. Clustering 63 entries with 19 selected descriptors showed three main groups.

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