Acta Scientiarum

http://www.periodicos.uem.br/ojs/
ISSN on-line: 1807-8621
Doi: 10.4025/actasciagron.v46i1.68484

On farm conservation of cassava in traditional communities of Jangada, Mato Grosso State, Brazil: ethnobotany and genetic diversity

Juliana Larrosa Rodrigues Oler[1], Elizabeth Ann Veasey[2], Joyce Mendes Andrade Pinto[3] and Eulália Soler Sobreira Hoogerheide[4*]

[1]Instituto de Desenvolvimento Sustentável Mamirauá, Tefé, Amazonas, Brazil. [2]Escola Superior de Agricultura "Luiz de Queiroz", Universidade de São Paulo, Piracicaba, São Paulo, Brazil. [3]Empresa Brasileira de Pesquisa Agropecuária, Embrapa Agrossilvipastoril, Sinop, Mato Grosso, Brazil. [4]Empresa Brasileira de Pesquisa Agropecuária, Embrapa Agropecuária Oeste, Rodovia BR-163, km 253, Zona Rural, Dourados, Mato Grosso do Sul, Brazil. *Author for correspondence. E-mail: eulalia.hoogerheide@embrapa.br

ABSTRACT. Jangada is a municipality in the Baixada Cuiabana region, State of Mato Grosso, Brazil. This study aimed to evaluate the collection of local cassava conserved by four traditional communities of Jangada in terms of ethnobotanical/socioeconomic and genetic aspects. Socioeconomic and ethnobotanical analyses were carried out with 40 farmers using qualitative techniques and descriptive statistics. Seven microsatellite markers were used for genetic analysis. A total of 182 cassava citations were verified, 31 of which were different. The Broto Branco variety was the most frequent (94.3%), followed by Vermelha Gaiadeira and Liberata (82.9 and 77.1%, respectively). The calculated median age for farmers was 56 years. Spearman's coefficient indicated a positive correlation between the increase in farmer's age and the number of cultivated local varieties. Few varieties are planted by many farmers, and most are planted by few farmers. High genetic diversity was observed, and most of the variability occurred within communities (88%). Two groups were formed in the cluster analysis, with two communities in each group. The propagule circulation network helped to understand the genetic similarity of communities with the closest geographic location. Cassava cultivation plays an important role in the studied communities, which maintain a high ethnobotanical and genetic diversity and relevant knowledge about the cultivated varieties.

Keywords: *Manihot esculenta*; Baixada Cuiabana; circulation network; microsatellites; socioeconomic analysis; traditional agriculture.

Received on June 6, 2023.
Accepted on November 21, 2023.

Introduction

On-farm conservation strategies are essential for the effective maintenance of agrobiodiversity, considering the accelerated process of genetic erosion after the Green Revolution (Bellon & Risoupolos, 2001). The traditional farmer, a protagonist of this conservation process, holds relevant knowledge about the species and the environment in which it is cultivated, contributing to the conservation of existing genetic resources, which can represent a relevant source of resistance to biotic and abiotic stresses (Sunwar, Thornstro, Subedi, & Bystrom, 2006). In this context, ethnobotany is an important tool for understanding farmers' local knowledge concerning the agroecosystem (Bittencourt, 2020).

The region known as Baixada Cuiabana, located in the State of Mato Grosso, Brazil, made up of 11 municipalities around Cuiabá, stands out for preserving characteristics and traditional knowledge in agriculture, which are passed down from generation to generation (Amorozo, 2010). Despite the dominance of modern large-scale agriculture in the State, the region is home to family communities that practice traditional agriculture, mainly for subsistence, maintaining significant agricultural diversity, with emphasis on the local varieties of cassava (*Manihot esculenta* Crantz.) (Amaral, Souza, Ritter, Loboruk, & Melo, 2017). The municipality of Jangada, located in this region, has 28 rural communities, 20 of which are traditional and eight come from government projects of agrarian reform settlements (Amaral, Coelho-de-Souza, Schuch, & Souza, 2016).

Traditionally managed cassava fields have high genetic diversity due to the possibility of incorporating new germplasm via sexual reproduction, as well as the circulation of genetic material and knowledge via circulation networks of propagation material (Martins & Oliveira, 2009; Oler et al., 2019; Santos, Zárate-

Salazar, Carvalho, & Albuquerque, 2020). Studies that reconcile ethnobotany and population genetics enrich the understanding of the maintenance of agricultural diversity, valuing local knowledge, being able to indicate priority areas for conservation, and mainly promoting a dialogue between scientific and local knowledge. The use of molecular tools proves to be effective in mapping population genetic diversity. Simple sequence repeat (SSR) markers have been widely used for analyzing the genetic diversity of cassava populations (Mühlen et al., 2019; Tiago et al., 2019; Pedri et al., 2019; Oler et al., 2019).

This study aimed to prepare an ethnobotanical inventory of cassava, evaluate the socioeconomic aspects of farmers, and characterize the genetic diversity of cassava grown in four traditional communities in the municipality of Jangada, Mato Grosso State, Brazil. The results are important to support the on-farm conservation of genetic diversity in these communities and municipalities.

Material and methods

Study location

This study was conducted at the communities Mutum (Mt), Vaquejador (Vq), Ribeirão das Pedras Acima (Ra), and Quilombo (Qb), located in Jangada, State of Mato Grosso, Brazil (15°14′09″ S; 56°29′20″ W) (Figure 1). These communities are contiguous and located approximately 25 km from the municipal headquarters. They are basically dependent on small-scale agriculture for self-consumption, with the sale of surpluses in some cases, and cassava consisting of the main crop. Cassava flour production is also important for the studied communities (Amaral et al., 2017). This project is registered in Sisgen under the number A3DF14E.

Figure 1. Location of the communities evaluated in this study (Green – Vq; Red – Ra; Purple – Mt; Yellow – Qb) in the municipality of Jangada, included in the region of Baixada Cuiabana, State of Mato Grosso, Brazil.

Ethnobotanical characterization

This research was approved by the Ethics Committee of the Biosciences Institute of UNESP – Rio Claro (DECISION CEP No. 096/2013), which included the Written Informed Consent Form that was prepared to document the residents' authorization to carry out the interviews and sample collection. The family units were visited in 2014 and the heads of families (men and/or women) were interviewed i) to characterize the farmer, the infrastructure in the community, and identify the number of children who left rural communities and live in the urban area; and ii) to collect information regarding the management, techniques, and spaces for growing cassava and the production and trade of cassava flour.

A non-probabilistic sample was selected (Albuquerque, Lucena, & Neto, 2010) using the judgment method and free listing (Amorozo, 2010) for the ethnobotanical inventory of cassava varieties. All informants mentioned the main farmers growing cassava in the community, according to the following criteria: having knowledge about cassava, its management and cultivation techniques; practicing subsistence agriculture and/or flour production; and presenting a history of life in agriculture. The ten most cited farmers in the Mt, Vq, and Ra communities (with more than 15 informants), and the five most cited in the Qb community, with less than 15 informants, were selected. Therefore, a total of 35 family units were visited and data on local varieties (name, origin, time of planting, source of propagating material, and form of identification) were obtained through semi-structured interviews during a guided tour to their cultivation space (Albuquerque et al., 2010). Information was also collected on the dissemination of the propagation through the social network of circulation.

Molecular genetic diversity

Young leaves of each local variety identified by the farmers were collected and stored in NaCl-CTAB solution (6.0 M NaCl and 1.5% CTAB) for seven days at 10°C. The leaves were macerated in 1.5 mL of STE buffer (0.25 M sucrose, 0.03 M Tris, 1.00 M HCl, and 0.05 M EDTA), and DNA extraction was performed according to the protocol by Doyle and Doyle (1990) with modifications by Siqueira et al. (2010). The genetic material was quantified using electrophoresis in a 1% agarose gel with GelRed dye (Biotium, Hayward, USA) to visualize the bands under UV light.

The accessions were evaluated with seven SSR loci (SSRY 28, SSRY 35, SSRY 43, GA 12, GA 131, GA 136, and GA 140) (Chavarriaga-Aguirre et al., 1998; Mba et al., 2001). Amplifications were performed following the protocol by Schuelke (2000) with the addition of an M13 tail at the 5' end of the forward primer and the fluorescence chosen for the label primers (HEX, FAM, or NED). Reactions contained 10-50 ng genomic DNA, 0.6 or 0.7 mM $MgCl_2$, 10X buffer, 0.2 mM each dNTP, 1.25 pmol forward primer, 5 pmol reverse primer, 0.25 pmol M13 universal tail primer, and 1.25 U of Taq DNA polymerase (Invitrogen, Carlsbad, California). Thermocycler amplification was programmed at 94°C for 1 minute, followed by 30 cycles at 94°C for 30 seconds, 45°C or 56°C according to the specific annealing temperature for each primer for 45 seconds, and 72°C for 45 seconds, plus 8 cycles at 94°C for 30 seconds, 53°C for 45 seconds, and 72°C for 45 seconds, ending with a final extension phase at 72°C for 10 minutes. The reactions were submitted to an automatic sequencer model ABI3730. The electropherograms were analyzed using the GeneMarker® v. 1.95 (Softgenetics).

Data analysis

Socioeconomic and ethnobotanical knowledge analyses were performed using qualitative techniques and descriptive statistics (Huberman & Miles, 1994). The correlation between farmer age and the number of local cassava varieties was determined by calculating Spearman's correlation coefficient. The Shannon-Wiener (H′) and Simpson (1-D) indices were used for the analysis of ethnobotanical diversity. The PAST v. 2.17c software (Hammer, Harper, & Ryan, 2001) was used for the Shannon-Wiener equity index. The cluster analysis was constructed using the UPGMA method and the Sorensen similarity coefficient was obtained from the matrix of presence and absence of citation of each local cassava variety per respondent. The analyses and graphs were generated using the R software (R Development Core Team, 2016). The graphical representation of the circulation networks was built using the Pajek software (Program for Large Network Analysis) (Batagelj & Mrvar, 2013).

Genetic diversity indices, such as average number of alleles per locus ($\bar{A}$), percentage of polymorphic loci (*P%*), average observed (H_O), and expected (H_E) heterozygosity, and Wright's coefficient index (f), were estimated for the molecular analysis. Clustering analyses were carried out among communities with the UPGMA method and Nei's genetic distance (Nei, 1972), using the UPGMA method (Miller, 1997). Considering the cultivation spaces, a dendrogram was generated using the Unweighted Neighbor-Joining method and Nei's distance (Nei, 1972). Molecular analysis of variance (AMOVA) was obtained to compare intra- and inter-community diversity, using the GenAlEx 6.5 program (Peakall & Smouse, 2006). The Bayesian analysis was conducted using the Structure 2.3X program (Falush, Stephens, & Pritchard, 2007), with ten independent simulations for each K number of groupings (K ranging from 1 to 5, considering the number of probable populations), with 500,000 MCMC interactions after initial discard of 200,000, also applying the mixed ancestry and correlated allele frequency models. The most likely number of clusters was estimated using the ad hoc method of Evanno, Regnaut, and Goudet (2005).

Results and discussion

Ethnobotanical aspects

There were 182 mentions of varieties made by farmers in the four communities, with 31 different varieties identified. Similar numbers were observed in a traditional community (n = 30) and a rural settlement (n = 39) in Porto Estrela, Mato Grosso State, Brazil (Oler & Amorozo, 2017). The median age calculated for the farmers was 56 years, and Spearman's coefficient indicated a positive correlation between the increase in the informant's age and the number of cultivated local varieties (0.92; $p < 0.05$). The pattern of positive correlation between cultivated diversity and farmers' age may be a consequence of the accumulation of varieties throughout life and/or changes in the agricultural scenario, with the abandonment of traditional activities by younger people (Santos et al., 2020). This situation is cause for concern, as the existence of younger farmers who are engaged in diversifying the collection is crucial for maintaining diversity. A community that concentrates its collection only among older farmers is liable to lose important resources due to the decrease in agricultural activities and the failure to transmit knowledge to the next generations.

The structure for the frequency of local varieties per community was similar in the four studied communities, with few very common varieties and most with only one occurrence (Figure 2). The variety Broto Branco was the most frequent (94.3%), followed by Vermelha Gaiadeira and Liberata (82.9 and 77.1%, respectively). Twelve varieties were found in the group of varieties with intermediate frequency. The others (n = 16) were registered in only one family unit. This structure of collections of the studied communities is similar to that found in other traditional communities, with few varieties planted by many farmers and most being planted by just a few farmers (Marchetti, Massaro Jr., Amorozo, & Butturi-Gomes, 2013; Amaral et al., 2016; Silva, Cordeiro, Tiago, Pedri, & Rossi, 2022).

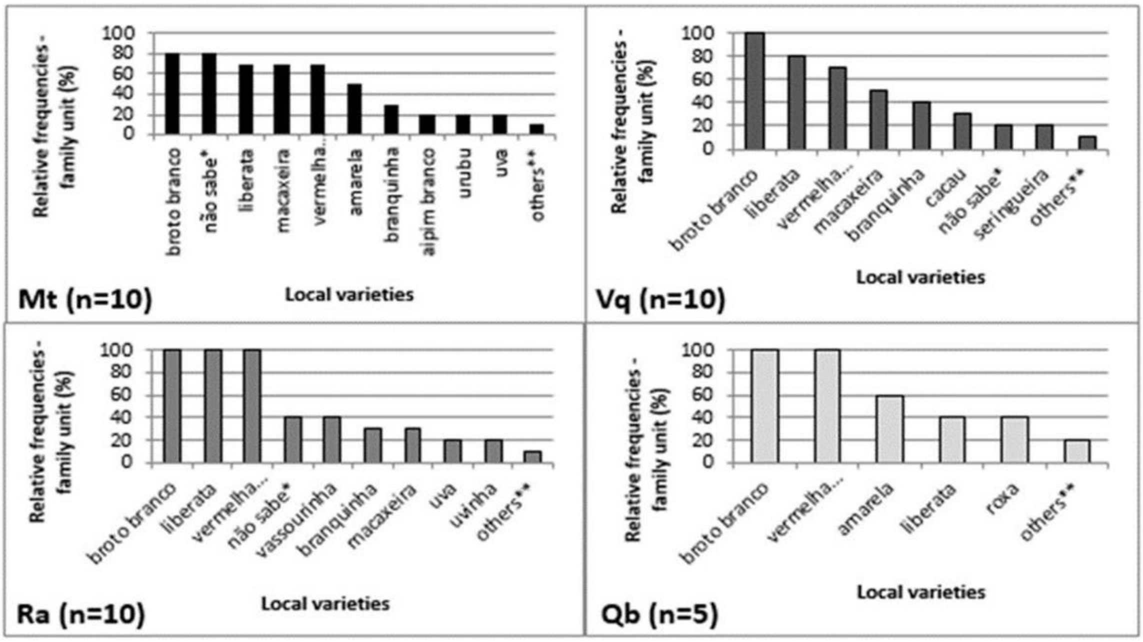

Figure 2. Relative frequencies of local varieties in family units for each community (Mt: Mutum; Vq: Vaquejador: Ra: Ribeirão das Pedras Acima; Qb: Quilombo) in the municipality of Jangada, Mato Grosso State, Brazil. *Do not know (Mt: set of eight unidentified varieties; Vq: set of two unidentified varieties; Ra: set of four unidentified varieties); **Other (Mt: 11 local varieties with 10% frequency; Vq: three local varieties with 10% frequency; Ra: eight local varieties with 10% frequency; Qb: three local varieties with 20% frequency).

The most cited motivation for selecting varieties was the profitability of flour production in the four communities (57.7%), followed by palatability and ease of cooking (47.2%). In general, the most common varieties are the most important for subsistence. In the case of communities more connected to markets, the most frequent varieties are those that have the characteristics required for greater commercialization (Souza, Hoogerheide, Reis, Duarte, & Silva, 2016). The most common variety (Broto Branco) was planted almost exclusively to produce flour, as it has a higher yield due to the lower water concentration, according to the farmers. However, as reported, its fresh form is not indicated for consumption and is consumed only when it is very young. The variety Vermelha Gaiadeira was planted both for flour and for table consumption, with good acceptance in the market and a satisfactory average yield in obtaining flour, being considered a "joker" local variety. The Liberata, also used for table and flour, was planted mainly for its palatability and acceptance in the market despite the low yield for flour manufacture.

Some changes in the composition of the collection of varieties, intended mainly to respond to the needs of the consumer market, can lead to a homogenization of the swiddens and simplification of agroecosystems, putting at risk the maintenance of diversity, as well as the autonomy of the farmer (Ribeiro & Ribeiro, 2017; Bittencourt, 2022). Communities that direct their collections to a few more productive varieties are subject to the disappearance of rare local varieties, thus restricting the farmer's ability to deal with the biotic and abiotic adversities that may arise (Elias, Rival, & McKey, 2000). The reduction in diversity in the studied communities may be driven mainly by specialization in varieties for flour production.

All local varieties were classified by farmers as sweet varieties. They stated that bitter cassava was not present in the region. The classification of bitter cassava occurs when the variety has a high concentration of cyanogenic glycosides. Varieties with less than 50 mg kg^{-1} on a fresh weight basis are considered sweet, while those with up to 400 mg kg^{-1} are classified as bitter (Peprah et al., 2020). This absence can be summarized as a process of replacement of the collection over time, prioritizing more versatile local varieties in a view to reducing cultivated areas and the workforce available for managing the swiddens.

Regarding the diversity measured by the Shannon index, the communities with the highest and lowest diversity were, respectively, Mt (H′ = 2.64) and Qb (H′ = 1.88) (Table 1). The values of this index in the four communities are lower than those observed in other communities in the State of Mato Grosso, Brazil (Marchetti et al., 2013; Oler & Amorozo, 2017). The emptying of communities, with young people leaving in search of better living conditions, may be related to this lower-managed diversity. The values for Simpson's index (1-D) corroborate with the H′ pattern, with greater diversity in Mt (0.91) and lower in Qb (0.82).

The similarity of the variety collections was observed in a cluster analysis, with a cophenetic coefficient of 0.81 (Figure 3). The clustering analysis showed a division into two groups (A and B), with low similarity between farmers, including those from the same community. The division of groups was characterized by the absence (A) or presence (B) of the variety Macaxeira. This variety of relatively old introduction, previously the most cultivated to produce flour, was replaced by Broto Branco, as it is more profitable to produce flour, which may explain the absence of Macaxeira in swiddens of the Ra community, the most dependent on this product. Due to the strong focus on flour manufacturing, 40% of Ra farmers (Ir, Fr, Dr, and Cr) showed maximum similarity, growing only three local varieties (Figure 3). Farmer Hv (community Vq) also had maximum similarity with this group, and like them, destined most of the production to the manufacture of cassava flour. Although the Ra community chose its collection according to the need to produce cassava flour, this community did not present the least diversity (H′ = 2.34), refuting the hypothesis that the communities that are most influenced by the market handle less diversity.

Table 1. Diversity indices of the studied communities* in the municipality of Jangada, Mato Grosso State, Brazil.

Diversity index	Mt	Vq	Ra	Qb	Total
Shannon-Wiener (H′)					
Diversity	2.64	2.03	2.34	1.88	2.62
Equity	0.88	0.88	0.84	0.91	0.76
Simpson (1-D)					
Diversity	0.91	0.85	0.87	0.82	0.88

*Mt: Mutum; Vq: Vaquejador; Ra: Ribeirão das Pedras Acima; Qb: Quilombo.

The informants who showed almost maximum dissimilarity between the two groups (Hm, Gm, and Fm), all from the Mt community, were distinguished by the absence of cultivation of at least one of the most frequent local varieties (Broto Branco, Liberata, or Vermelha Gaiadeira) (Figure 3). The presence of the variety Macaxeira, mainly among Mt farmers, can be explained by the lower dependence on cassava cultivation and flour production as a source of income. In addition, these farmers had in common the cultivation in home gardens (only Hm cultivated in both swiddens and home gardens). These farmers were older and practiced agriculture only to complement their diet and maintained considerable diversity in their home gardens motivated by criteria such as palatability. The importance of home gardens for the conservation of domesticated plant resources is highlighted by other authors in traditional communities (Oler et al., 2019) and rural settlements (Carrasco et al., 2016) and peri-urban family farmers (Figueredo, Hoogerheide, Rondon, Barcelos, & Zanetti, 2023). Informant Er differed from the other cassava growers in the group, as he had several local varieties considered rare (Figure 3).

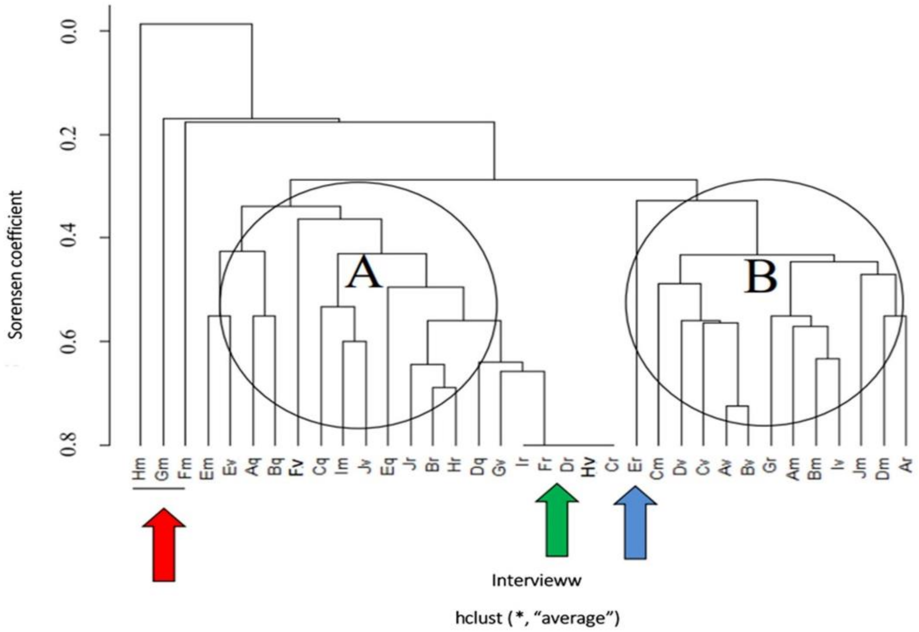

Figure 3. Grouping based on the Sorensen coefficient and the UPGMA method for farmers in the studied communities. The codes on the x-axis correspond to the identification of each interviewee, with the uppercase letter being the initial name of the interviewees and the lowercase letter the initial of the community to which the farmer belongs (m: Mutum; v: Vaquejador; r: Ribeirão das Pedras Acima; q: Quilombo). The red arrow indicates the greater dissimilarity between the two formed large groups, the blue arrow indicates the farmer who presented the highest cultivated wealth, and the green arrow the informants with 100% similarity.

The causes of similarity were explored by examining the origin of the propagating material for the 2014/2015 season. Most of the interviewed farmers used stem cuttings from their own fields (50.5%), which was more expressive in Mt (71.0%) and less in Ra (21.4%). Most farmers in the Ra community did not yet have swiddens, seeking possible sources of propagation material in neighboring communities to start their plantings. These exchanges can be observed with the analysis of the circulation network (Figure 4), which indicates a grouping of communities, standing out the Vq and Ra communities, which appear in the central area. The geographic position of these two communities is strategic, enabling exchanges with all the study communities (Figure 1). No exchanges were observed between the Mt and Qb communities, probably due to the longer distance between them (approximately 15 km). Farmer Er stood out for being the link between the studied communities, receiving and donating material to several farmers and showing the greatest wealth in his swidden (S = 16). Informant Ar received stem cuttings from different communities in the region and could be considered an introducer of new local varieties. Some surrounding communities and farmers from the studied communities who were not interviewed were also cited as introducing material into the communities. Similarly, Santos et al. (2020) found that farmers share a nucleus of ethnovarieties most used among communities, including those with the highest subsistence levels. Furthermore, the authors showed that farmers who opt for rare varieties manage high diversity on their properties, representing central figures in circulation networks.

Better planning of conservation policies requires knowledge of the key elements of circulation networks and the main forces that shape exchange relations (Thomas, Dawson, Goldringer, & Bonneuil, 2011). In this regard, the analysis of the circulation network of propagules in this study showed that farmers in the Mt community mainly used their own stem cuttings, which may be motivated by planting mainly for self-consumption, disregarding high production. The Ra community mainly used material from other areas. Farmers belonging to this community, when asked about the external source of propagation material, stated that the local variety "gets used" to the soil and loses productivity. Thus, changes in the set of local varieties or even in the source of origin of propagation material cultivated in a given area are quite common. This practice was also reported in a study on traditional indigenous agriculture (Elias, Lenoir, & McKey, 2007).

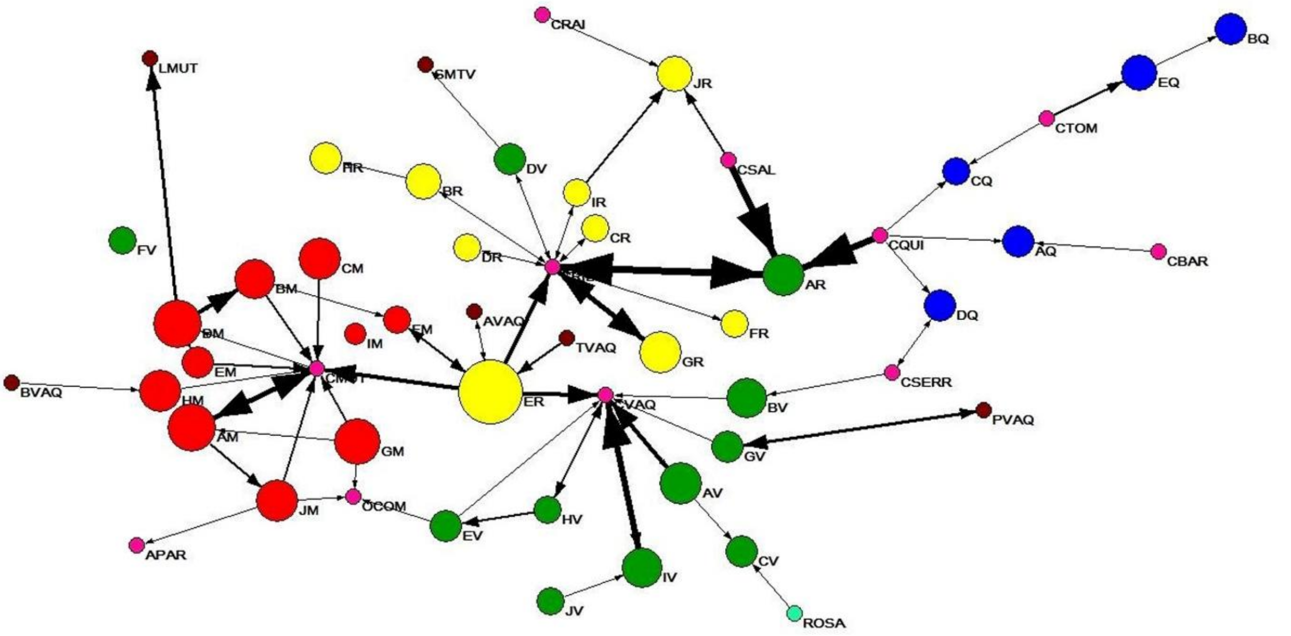

Figure 4. Graphical representation of the circulation networks of stem cuttings in the studied communities (2014/2015 harvest), such as Mt (red), Vq (green), Ra (yellow), and Qb (blue), in the municipality of Jangada, Mato Grosso State, Brazil. The circle size represents the number of local varieties cultivated by each farmer. Layout: Kamada-Kawai. Pink: communities in the region, including those studied; wine: people from different communities not interviewed in the study; and light blue: municipality of Rosário do Oeste, State of Mato Grosso, Brazil. Thin arrow: one to two local varieties exchanged; intermediate arrow: three to four local varieties exchanged; thick arrow: five or more local varieties exchanged. End of arrows indicates the location that received the local varieties.

Another important source of diversity for the cassava varieties was sexual reproduction, even though cassava is vegetatively propagated among farmers. In the four studied communities, 90% of the interviewed farmers had already seen cassava flowers and fruits. When questioned about the "cassava seed", approximately half of the farmers had already observed them in the gardens (48.8%). Farmers reported identifying "cassava seed" mainly due to the presence of a taproot. One of the farmers also identified these cassavas by the presence of differentiated leaves, probably referring to the cotyledons, absent in vegetatively originated plants. This classification system was found in other traditional communities dependent on cassava cultivation (Marchetti et al., 2013). Three farmers belonging to the Mt, Ra, and Qb communities, all over 60 years of age, reported that "cassava seed" was more commonly observed when they did not harrow the land but planted it in the slash-and-burn system, with a fallow period. The management techniques applied in this type of agriculture combined with the dormancy capacity of the species favor the formation of cassava seed banks, enabling the formation of new recombinants resulting from sexual reproduction (Martins & Oliveira, 2009).

Genetic diversity

Molecular analyses were carried out with 164 out of the 182 collected individuals, as gardens with less than three varieties were excluded from the analyses. A total of 42 alleles were found (mean of 6.5±0.59 alleles per locus) and 100% polymorphism. The average number of alleles per locus ranged from 4 (Qb) to 9 (Mt) among the four communities. High levels of genetic diversity were observed (H_O = 0.79, H_E = 0.69, on average). Higher levels of H_O than H_E were found, reflected in the fixation index, with all communities showing values below zero, which demonstrates the high heterozygosity, as observed by Tiago et al. (2019). The Vq community showed the highest observed heterozygosity (H_O = 0.84), while Mt had the highest gene diversity (H_E = 0.72) (Table 2).

The values found for the genetic diversity parameters were higher than those of other studies with traditional communities using SSR markers (Carrasco et al., 2016; Mühlen et al., 2019). However, they were similar to the values found by Tiago et al. (2019) (H_O = 0.701, H_E = 0.656, on average) for populations of five municipalities of the State of Mato Grosso, including the municipality of Jangada. The fixation index for all loci had values below zero, which shows the high heterozygosity, as observed by Tiago et al. (2019). The results indicate that the ethnobotanical diversity is directly proportional to the observed genetic diversity.

Table 2. Number of cassava varieties/community (*N*), average number of alleles per locus ($\bar{A}$), observed heterozygosity (H_O), expected heterozygosity (H_E), and fixation index (*f*) for each community in the municipality of Jangada, Mato Grosso State, Brazil.

Community*	*N*	$\bar{A}$	H_O	H_E	*f*
Mt	60	9	0.82	0.72	−0.14
Vq	40	6	0.84	0.70	−0.20
Ra	48	7	0.79	0.70	−0.15
Qb	16	4	0.74	0.65	−0.16
Mean	41	6.5	0.79	0.69	−0.16

*Mt: Mutum; Vq: Vaquejador; Ra: Ribeirão das Pedras Acima; Qb: Quilombo.

The AMOVA results show that most of the detected variability was within communities (88%) (Table 3). Similar results have been found in other studies with cassava, with a value of 92% within populations cultivated in northern Mato Grosso State (Pedri et al., 2019) and within communities in the south of the State of Mato Grosso (Carrasco et al., 2016). The high genetic diversity found within communities is due to several factors, including the maintenance of the sexual reproduction system, as it favors the emergence of variability via hybridization, originating new varieties that can be experimented and selected by farmers (Martins & Oliveira, 2009). Another factor would be the constant exchange of propagation material between farmers from different communities, promoting high gene flow, as verified in this research and other studies (Oler et al., 2019). A similarity between the managed collections was also found, mainly due to exchanges in the propagation circulation network (Oler et al., 2019; Santos et al., 2020).

Table 3. Molecular analysis of variance (AMOVA) for seven microsatellite loci evaluated in 164 cassava varieties from four communities located in the municipality of Jangada, Baixada Cuiabana, State of Mato Grosso State, Brazil.

Source of variation	Sum of squares	Variance component	Total variance (%)
Among communities	108.12	0.79	12
Within communities	889.73	5.56	88
Total	997.86	6.35	100

The Bayesian analysis classified local varieties into two groups (K = 2). Although genotypes of both groups occur in all evaluated communities, the predominance of one of the groups (red) was observed for the Mt and Vq communities, and genotypes of the other group (green) were observed in the Ra and Qb communities (Figure 5). Cluster analysis using Nei's distance (Nei, 1972) and the UPGMA method showed a similar pattern of clustering of communities, also classified into two groups, with one of the groups containing the Mt and Vq communities and the other the Ra and Qb communities (Figure 6). Two groups were also observed considering the cluster analysis carried out for swiddens using Nei's distance (Nei, 1972) and the UPGMA method (Figure 7). Mt farmers remained in the same group. Farmer Av, from the Vq community, showed higher genetic differentiation in his field. This farmer managed the second-largest collection of Vq, produced flour for the market, and sold fresh cassava at the free market. This farmer presented the most accurate knowledge about the identification and use of new varieties to incorporate them into the collection when asked about the management of "cassava seeds". This type of management may be influencing the genetic differentiation of the varieties cultivated by him.

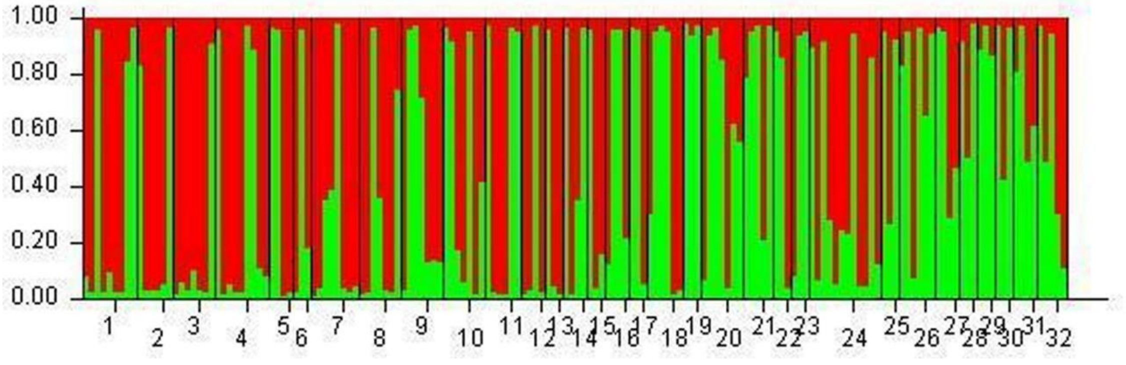

Figure 5. Clustering obtained by the Bayesian analysis using the Structure software for local cassava varieties from the communities Mt-Mutum (1-9), Vq-Vaquejador (10-19), Ra-Ribeirão das Pedras Acima (20-29), and Qb-Quilombo (30-32).

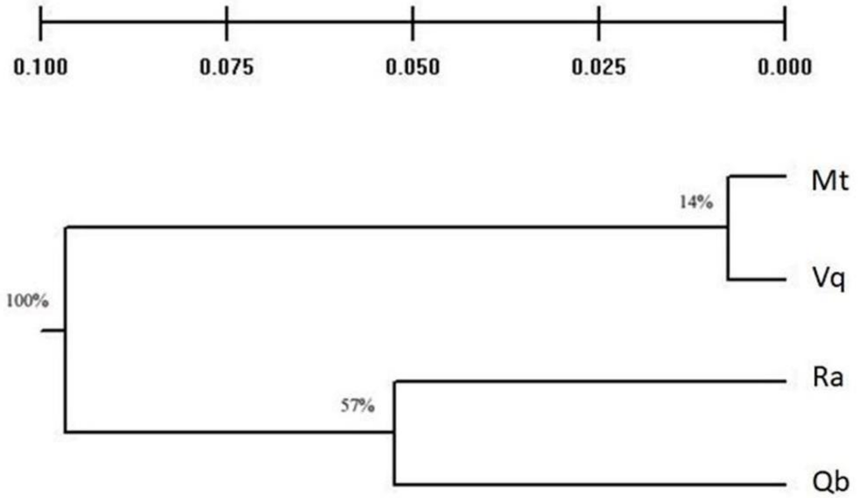

Figure 6. Cluster analysis generated by Nei's (1972) distance matrix and the UPGMA method for local cassava varieties collected in the Mutum (Mt), Vaquejador (Vq), Ribeirão das Pedras Acima (Ra), and Quilombo (Qb) communities.

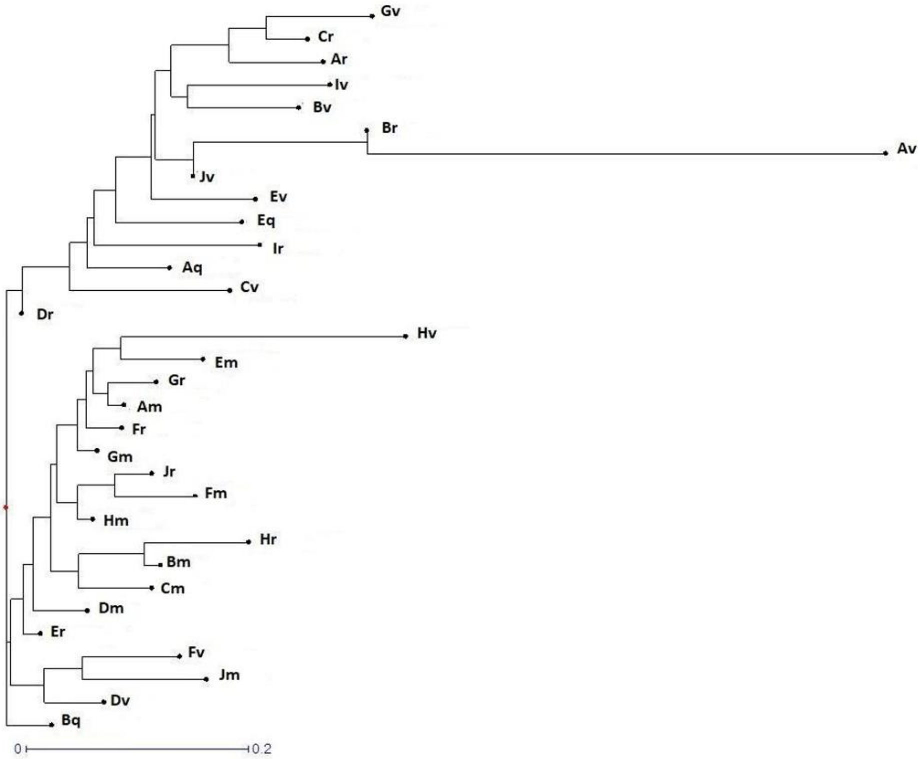

Figure 7. Cluster analysis of cassava fields evaluated using Nei's (1972) distance matrix and the UPGMA method. The lowercase letter indicates the initial of the community to which the farmer belongs (m: Mutum; v: Vaquejador; r: Ribeirão das Pedras Acima; q: Quilombo).

The flow drawn in the propagation network (Figure 4) coincides with the grouping based on the genetic similarity of the collection by the community in the two applied methods, with higher interaction between the Mt and Vq communities, as well as between Ra and Qb, which are geographically close, facilitating the exchange of material and probably contributing to this genetic similarity. Other factors such as kinship ties between residents can also influence. Farmer Er, manager of the largest managed collection among all studied farmers, maintained local varieties for possible future needs, testing, and aesthetic reasons. These practices are common among older farmers and should be spread among younger ones. Er was an active member of the propagule circulation network, mainly with the Vq and Mt communities, where he is related to some residents.

Consanguineous and sociocultural ties increase the functioning of the network, and the constant need to know and test new varieties is the essential characteristic for networks to exist (Thomas et al., 2011). Er presented potential as a central element in the management of the community's agricultural diversity. Called source-farmers by Elias et al. (2000), they play important roles in the maintenance of local diversity because they act actively in the social circulation network of propagating material. The circulation network of propagules was quite complex and important for the functioning of the dynamics of the four communities. However, the presence of other communities and even other municipalities in the network reveals the importance of a broader analysis involving municipalities adjacent to Jangada to understand the regional context of diversity conservation.

Conclusion

The results of this study allow us to conclude that cassava cultivation has an important social, economic, and cultural role in the studied communities. The selection of varieties used in the communities is directly linked to the final use of the product. The main use of cassava in the MT community is for self-consumption, while the crop stands out in the other communities as an important source of income for families, destined for flour production for commercialization. The frequency of the varieties was similar in the four communities, with few very common varieties and most varieties with only one occurrence. However, all communities showed high ethnobotanical and genetic diversity based on the diversity analyses, indicating that these farmers maintain diversity in their gardens. Although the interviewed farmers demonstrated relevant knowledge about the cultivated varieties, some worrying factors are emphasized in this study. The specialization of the collection for flour production, mainly in the Ra community, and the concentration of diversity only among older farmers, mainly in the Mt community, may represent risk factors for the reduction of diversity in the future. Some conservation strategies can be adopted in this context: a) proposals for participatory improvement should be implemented in regions that are more dependent on flour production and tend to choose collections guided by market requirements, with the choice of the most profitable varieties, without the abandonment of the others so that there is no simplification and homogenization of agroecosystems; b) government programs to encourage the settlement of younger farmers, even those who carry out part-time farming, in addition to raising awareness of the real value of agricultural diversity for the system resilience and autonomy, should be implemented in communities where diversity is mainly maintained by older farmers. The propagule circulation network proved to be quite complex, and the genetic proximity of local varieties cultivated by the closest communities, which had related farmers, seemed to be modulated by this network. The presence of other communities and even other municipalities in the network reveals the importance of a regional approach for future studies, aiming at more effective diversity conservation and genetic improvement programs.

Acknowledgements

To the residents of the Mutum, Vaquejador, Ribeirão das Pedras Acima, and Quilombo communities for their welcome and sharing. To the funding entities of this work, *Coordenação de Aperfeiçoamento de Pessoal de Nível Superior* (CAPES), *Empresa Brasileira de Pesquisa Agropecuária* (EMBRAPA), and *Fundação de Amparo à Pesquisa do Estado de Mato Grosso* (FAPEMAT). To *Empresa Mato-Grossense de Pesquisa, Assistência e Extensão Rural* (EMPAER) for the support in the field, *Conselho Nacional de Desenvolvimento Científico e Tecnológico* (CNPq) for the scholarship awarded to EAV, and the technicians and colleagues at ESALQ-USP for the support in the laboratory analyses. To Prof. Maria Christina de Mello Amorozo and Prof. Reinaldo Monteiro for their teachings and support in the discussions.

References

Albuquerque, U. P., Lucena, R. F. P., & Neto, E. M. F. L. (2010). Seleção dos participantes de pesquisa. In U. P. Albuquerque, R. F. P. Lucena, & L. V. F. C. Cunha (Orgs.), *Métodos e técnicas na Pesquisa Etnobiológica e Etnoecológica* (p. 83-106). Recife, PE: NUPPEA.

Amaral, C. N., Souza, G. C., Ritter, M. R., Loboruk, N., & Melo, R. S. P. (2017). Contribuição dos quintais na conservação do cerrado e da agrobiodiversidade: um estudo dos quintais tradicionais da Baixada Cuiabana. *Amazônica: Revista de Antropologia*, *9*(1), 294-314. DOI: https://doi.org/10.18542/amazonica.v9i1.5492

Amaral, C. N., Coelho-de-Souza, C. P., Schuch, I., & Souza, M. (2016). Contribuições da produção de autoconsumo em quintais para a segurança alimentar e nutricional e renda em Jangada, Baixada

Cuiabana, MT. *Guaju Revista Brasileira de Desenvolvimento Territorial Sustentável*, *2*(1), 102-119. DOI: https://doi.org/10.5380/guaju.v2i1.46425

Amorozo, M. C. M. (2010). Diversidade agrícola em um cenário de transformação: será que vai ficar alguém para cuidar da roça? In L. C. Ming, M. C. M. Amorozo, & C. W. Kffuri (Eds.), *Agrobiodiversidade no Brasil: experiências e caminhos da pesquisa* (p. 293-308). Recife, PE: NUPEEA.

Batagelj, V., & Mrvar, A. (2013). *Program for large network analysis pajek*. Retrieved on Jan. 10, 2023 from http://vlado.fmf.uni-lj.si/pub/networks/pajek/

Bellon, M. R., & Risoupolos, J. (2001). Small-scale farmers expand the benefits of improved maize germplasm: a case study from Chiapas, Mexico. *World Development*, *29*(5), 799-811.

Bittencourt, N. A. (2022). Direitos dos agricultores: o legado de Juliana Santilli na interface entre as relações jurídicas e a agrobiodiversidade brasileira. *Resenha*, *46*(2), 555-557. DOI: https://doi.org/10.1590/0103-11042022E237

Bittencourt, D. M. C. (2020). *Agricultura familiar: desafios e oportunidades rumo à inovação*. Brasília, DF: Embrapa.

Carrasco, N. F., Oler, J. R. L., Marchetti, F. F., Carniello, M. A., Amorozo, M. C. M., Valle, T. L., & Veasey, E. A. (2016). Growing manioc (*Manihot esculenta*) in Mato Grosso, Brazil: genetic diversity conservation in small−scale agriculture. *Economic Botany*, *70*(1), 15-28.

Chavarriaga-Aguirre, P. P., Maya, M. M., Bonierbale, M. W., Kresovich, S., Fregene, M. A., Tohme, J., & Kochert, G. (1998) Microsatellites in cassava (*Manihot esculenta* Crantz): discovery, inheritance and variability. *Theoretical and Applied Genetics*, *97*(3), 493-501. DOI: https://doi.org/10.1007/s001220050922

Doyle, J. J., & Doyle, J. L. (1990). Isolation of plant DNA from fresh tissue. *Focus*, *12*, 13-15.

Elias, M., Rival, L., & McKey, D. (2000). Perception and management of cassava (*Manihot esculenta* Crantz.) diversity among makushi Amerindians on Guyana (South America). *Journal of Ethnobiology*, *20*(2), 239-265.

Elias, M., Lenoir, H., & McKey, D. (2007). Propagule quantity and quality in traditional Makushi farming of cassava (*Manihot esculenta*): a case study for understanding domestication and evolution of vegetatively propagated crops. *Genetic Resources and Crop Evolution*, *54*, 54-59. DOI: https://doi.org/10.1007/s10722-005-2022-1

Evanno, C., Regnaut, S., & Goudet, J. (2005). Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology*, *14*(8), 2611-2620. DOI: https://doi.org/10.1111/j.1365-294X.2005.02553.x

Falush, D., Stephens, M., & Pritchard, J. K. (2007). Inference of population structure using multilocus genotype data: dominant markers and null allele. *Molecular Ecology Notes*, *7*(4), 574-578. DOI: https://doi.org/10.1111/j.1471-8286.2007.01758.x

Figueredo, P. E., Hoogerheide, E. S. S., Rondon, M. J. P., Barcelos, Q. L., & Zanetti, G. T. (2023). A agrobiodiversidade na agricultura periurbana de Sinop, Mato Grosso, Brasil, Amazônia legal. *Ciência Florestal*, *33*(1), 1-20. DOI: https://doi.org/10.5902/1980509867230

Hammer, O., Harper, D. A. T., & Ryan, P. D. (2001). PAST: paleontological statistics software package for education and data analysis. *Palaeontologia Electronica*, *4(*1), 1-9.

Huberman, A. M., & Miles, M. B. (1994). Data management and analysis methods. In N. K. Denzin, & Y. S. Lincoln (Eds.), *Handbook of Qualitative Research* (p. 428-444). Tousand Oaks, CA: Sage Publications.

Marchetti, F. F., Massaro Jr., L. R., Amorozo, M. C. M., & Butturi-Gomes, D. (2013). Maintenance of manioc diversity by traditional farmers in the state of Mato Grosso, Brazil: a 20-year comparison. *Economic Botany*, *67*(4), 313-323. DOI: https://doi.org/10.1007/s12231-013-9246-3

Martins, P. S., & Oliveira, G. C. X. (2009) Dinâmica evolutiva em roças de caboclos amazônicos. In I. C. G. Vieira, J. M. C. Silva, D. C. Oren, & M. Â. D'Incao (Orgs.), *Diversidade biológica e cultural da Amazônia* (p. 373-391). Belém, PA: Museu Paraense Emílio Goeldi.

Mba, R. E. C., Stephenson, P., Edwards, K., Melzer, S., Nkumbira, J., Gullberg, U., ... Fregene, M. A. (2001). Simple sequence repeat (SSR) markers survey of the cassava (*Manihot esculenta* Crantz) genome: towards an SSR based molecular genetic map of cassava. *Theoretical and Applied Genetics*, *102*(1), 21-31. DOI: https://doi.org/10.1007/s001220051614

Miller, M. (1997). *Tools for Population Genetic Analyses (TFPGA) 1.3: a Windows program for analysis of allozyme and molecular population genetic data*. Retrieved on May 20, 2018 from http://www.public.asu.edu

Mühlen, G. S., Alves-Pereira, A., Carvalho, C. R. L., Junqueira, A. B., Clement, C. R., & Valle, T. L. (2019). Genetic diversity and population structure show different patterns of diffusion for bitter and sweet manioc in Brazil. *Genetic Resources and Crop Evolution*, *66*(8), 1773-1790. DOI: https://doi.org/10.1007/s10722-019-00842-1

Nei, M. (1972). Genetic distance between populations. *American Naturalist*, *106*(949), 283-292. DOI: https://doi.org//10.1086/282771

Oler, J. R. L., Hoogerheide, E. S. S., Pinto, J. M. A., Tiago, A. V., Silva, J. F. V., & Veasey, E. A. (2019). Influence of the use of manioc on its genetic diversity conservation in a quilombo community in Mato Grosso, Brazil. *Genetics and Molecular Research*, *18*(3), 1-15. DOI: https://doi.org/10.4238/gmr18326

Oler, J. R. L., & Amorozo, M. C. M. (2017). Etnobotânica e conservação on farm de mandioca (*Manihot esculenta* Crantz) na agricultura de pequena escala no estado de Mato Grosso, Brasil. *Interações*, *18*(4), 137-153. DOI: https://doi.org/10.20435/inter.v18i4.1600

Peakall, R., & Smouse, P. E. (2006). GENALEX 6: genetic analysis in Excel - Population genetic software for teaching and research. *Molecular Ecology Notes*, *6*(1), 288-295. DOI: https://doi.org/10.1111/j.1471-8286.2005.01155.x

Pedri, E. C. M., Hoogerheide, E. S. S., Cardoso, E. S., Pinto, J. M. A., Santos, L.L., Yamashita, O. M., ... Rossi, A. A. B. (2019). Genetic diversity of cassava landraces cultivated in northern Mato Grosso State, Brazil, using microsatellite markers. *Genetics and Molecular Research*, *18*(3), 1-11. DOI: https://doi.org/10.4238/gmr18315

Peprah, B. B., Parkes, E. Y., Harrison, O. A., van Biljon, A., Steiner-Asiedu, M., & Labuschagne, M. T. (2020). Proximate composition, cyanide content, and carotenoid retention after boiling of provitamin a-rich manioc grown in Ghana. *Foods*, *9*(12), 1-12. DOI: https://doi.org/10.3390/foods9121800

R Development Core Team. (2016). *R: A language and environment for statistical computing*. Vienna, AT: R Foundation for Statistical Computing. Retrieved on Jan. 10, 2023 from http://www.R-project.org

Ribeiro, D. D., & Ribeiro, W. M. (2017). "Nossa forma de produzir": estudo de variedades crioulas em sítios camponeses de Orizona e Vianópolis, GO. *Geoambiente On-line*, *28*, 110-126. DOI: https://doi.org/10.5216/revgeoamb.v0i28.45009

Santos, M. N., Zárate-Salazar, J. R., Carvalho, R., & Albuquerque, U. P. (2020). Intraspecific variation, knowledge and local management of manioc (*Manihot esculenta* Crantz) in the semiarid region of Pernambuco, Northeast Brazil. *Environment, Development and Sustainability*, *22,* 2881-2903. DOI: https://doi.org/10.1007/s10668-019-00323-6

Schuelke, M. (2000). An economic method for the fluorescent labelling of PCR fragments. *Nature Biotechnology*, *18*(2), 233-234. DOI: https://doi.org/10.1038/72708

Silva, M. C. M., Cordeiro, A. G. M., Tiago, A. V., Pedri, E. C. M., & Rossi, A. A. B. (2022). Levantamento e caracterização fenotípica de etnovariedades de mandioca cultivadas em assentamentos rurais no estado de Mato Grosso, Brasil. *Research, Society and Development*, *11*(7), 1-15. DOI: https://doi.org/10.33448/rsd-v11i7.29731

Siqueira, M. V. B. M., Pinheiro, T. T., Borges, A., Valle, T. L., Zatarim, M., & Veasey, E. A. (2010). Microsatellite polymorphisms in manioc landraces from the cerrado biome, Mato Grosso do Sul, Brazil. *Biochemical Genetics*, *48*(9-10), 879-895. DOI: https://doi.org/10.1007/s10528-010-9369-5

Souza, G. F., Hoogerheide, E. S. S., Reis, J. C., Duarte, G. S. D., & Silva, J. F. V. (2016). Conservação on farm da mandioca: etnobotânica e aspectos socioeconômicos na comunidade Rios dos Couros, Cuiabá, MT. *Cadernos de Agroecologia*, *11*(2), 1-15.

Sunwar, S., Thornstro, C. G., Subedi, A., & Bystrom, M. (2006). Home gardens in western Nepal: opportunities and challenges for on-farm management of agrobiodiversity. *Biodiversity and Conservation*, *15*, 4211-4238. DOI: https://doi.org/10.1007/s10531-005-3576-0

Thomas, M., Dawson, J. C., Goldringer, I., & Bonneuil, C. (2011). Seed exchanges, a key to analyze crop diversity dynamics in farmer-led on-farm conservation. *Genetic Resources and Crop Evolution*, *58*, 321-338. DOI: https://doi.org/10.1007/s10722-011-9662-0

Tiago, A. V., Hoogerheide, E. S. S., Pedri, E. C. M., Rossi, F. S., Cardoso, E. S., Pinto, J. M. A., ... Rossi, A. A. B. (2019). Genetic diversity and population structure of cassava ethno-varieties grown in six municipalities in the state of Mato Grosso, Brazil. *Genetics and Molecular Research*, *18*(4), 1-17. DOI: https://doi.org/10.4238/gmr18357