

Evaluation of cassava (*Manihot esculenta* Crantz) genetic diversity in traditional varieties and sexual plants using microsatellites (SSRs)

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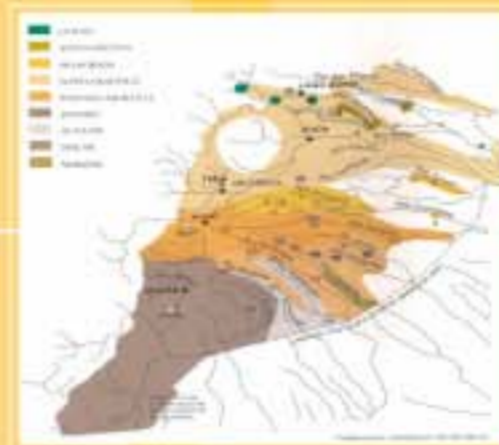
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Introduction

In traditional agrosystems cassava is the main subsistence crop. In the amazonian region, Napo Province shows the largest agricultural area where subsistence crops cover 35% of the cultivated surface (Fig 1 and 2). The "chacra" is the agroforestral production system in this region; the particular feature of this system presents a high diversity found in cassava crops; it's common to find various varieties growing in the same "chacra" (around 40 varieties) (Second & Iglesias, 2001; Elias et al., 2000). Genetic characterization of amazonian landraces carried out by Lozada (2000) showed an important genetic diversity in Napo sweet varieties. In French Guiana, Elias et al. (2001) found a high polymorphism at inter and intravarietal levels in Makushi landraces. These results allow us to propose the existence of particular mechanisms at the origin and maintenance of cassava diversity taking into account that cassava is a vegetatively reproduced crop. Traditional farmers carry out a dynamic management of the crop at different levels; among the main diversity generating activities are: a permanent interest in acquiring new varieties (Fig 3), supporting an active exchange of cutting stems and conserving and maintaining cuttings of plants from volunteer seedlings after selection (Elias & McKey, 2001). The Quichua traditional community at Santo Domingo de Archidona recognize around 31 varieties and they perform exchange of cuttings between them. The evaluation, documentation and comprehension of the mechanisms generating this diversity, with special emphasis in volunteer seedlings management, allow us to value, recognize and rescue cassava crop traditional management by quichua farmers.



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Objectives

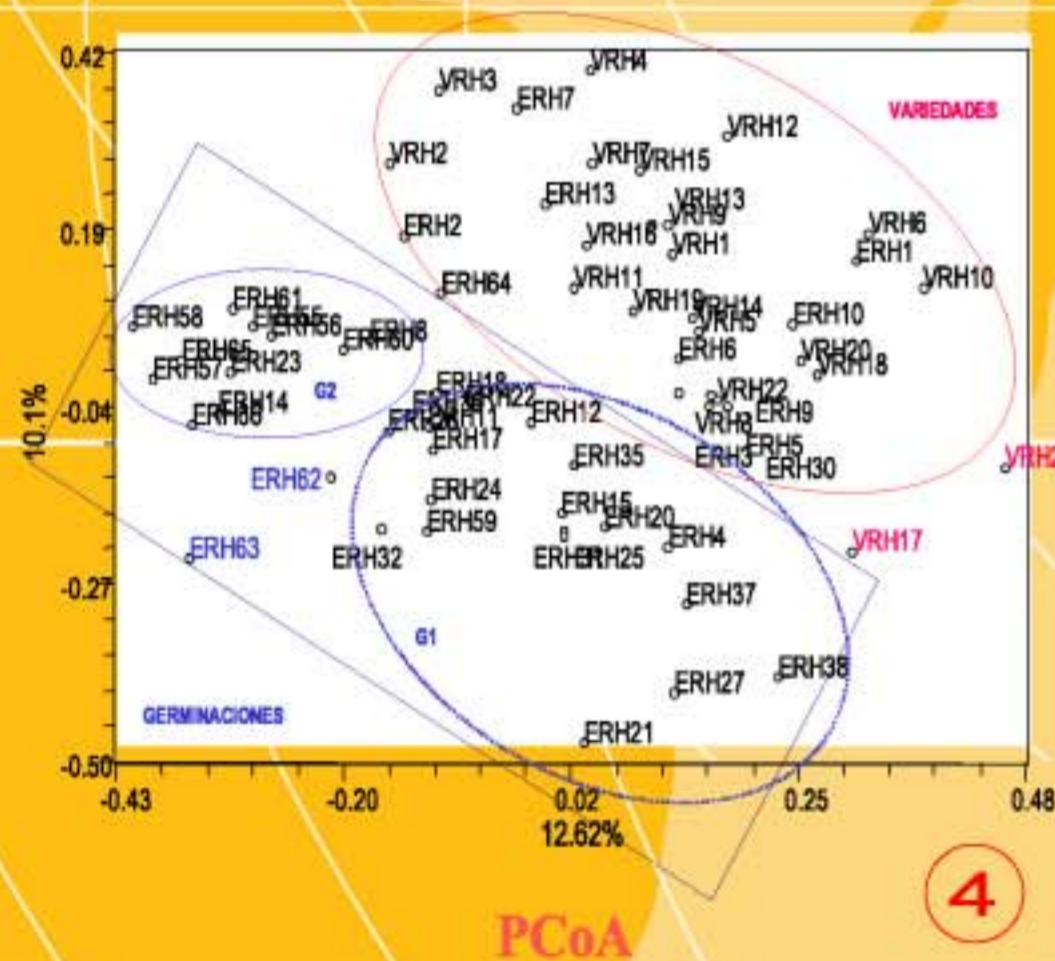
- Evaluate cassava genetic diversity in traditional varieties and in volunteer seedling populations using SSRs
- Establish the traditional management incidence in cassava crop diversity at a local level

Materials and Methods

- Sample collection was carried out in a single quichua family "chacra" at Santo Domingo de Archidona, Napo province.
 - A total of 66 foliar samples were collected
 - 22 landraces representing the 73% of total landraces reported by local farmers
 - 44 volunteer seedlings, 32 from the same chacra where the landraces were sampled and 12 from a "chacra" 100 m away
- Samples were analyzed using 15 microsatellite loci, eight designed by Mba et al. (2001) and seven designed by Chavarriaga et al. (1998).
- Data was analyzed with PopGene 1.31, multivariate analysis (PCoA) and clustering analysis (UPGMA) in NTSYS program.

Results and discussion

14/15 loci (93,3%) were polymorphic. 44 alleles were found in cassava varieties and 45 alleles in volunteer seedlings population. We report new alleles in sweet varieties reported before only in bitter cassava varieties. Five rare alleles were found in the whole sample set. In spite of cassava clonal multiplication, clones (identical genotypes) were not observed. An important intravarietal and intervariatal diversity was detected; the 22 landraces were different. Diversity inside varieties could generate confusions in the local classification: varieties morphologically similar were classified under the same name while being genetically different. Notwithstanding, the differentiation coefficient (F_{st}) remains low (0,04), the whole maintains his heterogeneity ($N_m=5,3$). One of the subpopulation of volunteer seedlings is close to the traditional varieties group; low differentiation between varieties and some volunteer seedlings could be explained by the cross pollination between varieties that gave way to the seeds (these varieties were similar or probably the same landraces analyzed in this study) (Fig 4). The other volunteer seedling subpopulation appears more distant from the varieties group, representing a genetic contribution for crop diversity. The incorporation of volunteer seedlings in this study allows that they could be evaluated with the rest of traditional varieties with the chance of being selected by quichua farmers if the root presents interesting agronomic characteristics (Fig 5) and with the advantage that they will increase crop genetic variability in account that they are from cross pollination.



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Aknowledgments

Institut de Recherche pour le Développement & ????????????

Conclusions

The important genetic variability found in a single farm shows a dynamic management of the crop by quichua farmers as is found in other traditional groups. Origin and maintenance of the crop genetic diversity at the local level could be explained essentially by two mechanisms: the incorporation of cuttings from volunteer seedlings (that will generate intra and intervariatal diversity) and an active exchange of cuttings between farmers inside the community (Fig 6).



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