Genetic diversity of Guatemalan avocado using SSR molecular marker

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Introduction

Avocado (*Persea americana* Mill), one of the most widely consumed fruits world wide, originated in the Sierra Nevada region in California eight to five million years ago (1). In Guatemala, a high genetic diversity has been reported by morphological characterizations, but due to cross-pollination and interracial hybridizations, these characterizations present complications and cannot detail the total genetic richness (2). The main objective of this study was to analyze the genetic diversity of tentative Guatemalan avocado collected through the main areas of its natural distribution in order to understand the genetic structure of the populations and identify potential resources of germplasm for conservation and plant breeding programs.

Methodology

189 individuals were sampled from seven populations located in eight departments of the country (Figure 1a). DNA was extracted from young leaves and fingerprinted with 11 SSR loci (3) and the fragments were measured by capillary electrophoresis. Data analysis – genetic diversity indexes (GenAlEx (4)), clustering analysis (Structure (5))

Figure 1. a) Collection sites and location of populations. **b)** Assignement of probabilities for the seven populations of native avocado in each group inferred by STRUCTURE.

Table1. Measures of genetic diversity of seven populations of native Guatemalan avocado.

Pop.	N	Na	Ar	Ho	He	F
Sac-Chimal	75	14.18	6.94	0.61	0.79	0.24
Chimal	16	9.91	6.21	0.68	0.80	0.15
Toto-Qui	36	14.91	8.16	0.54	0.84	0.37
Hue-Qui	23	10.91	8.26	0.53	0.81	0.35
Sol	9	6.73	7.49	0.38	0.74	0.48
BV	10	8.10	6.37	0.48	0.78	0.39
AV	20	10.18	8.11	0.55	0.80	0.32
Total	189	10.70	7.36	0.54	0.79	0.33

N = population size, Na = number of alleles, Ar = allelic richness Ho = observed heterozygosity, He = expected heterozygosity, F = fixation index
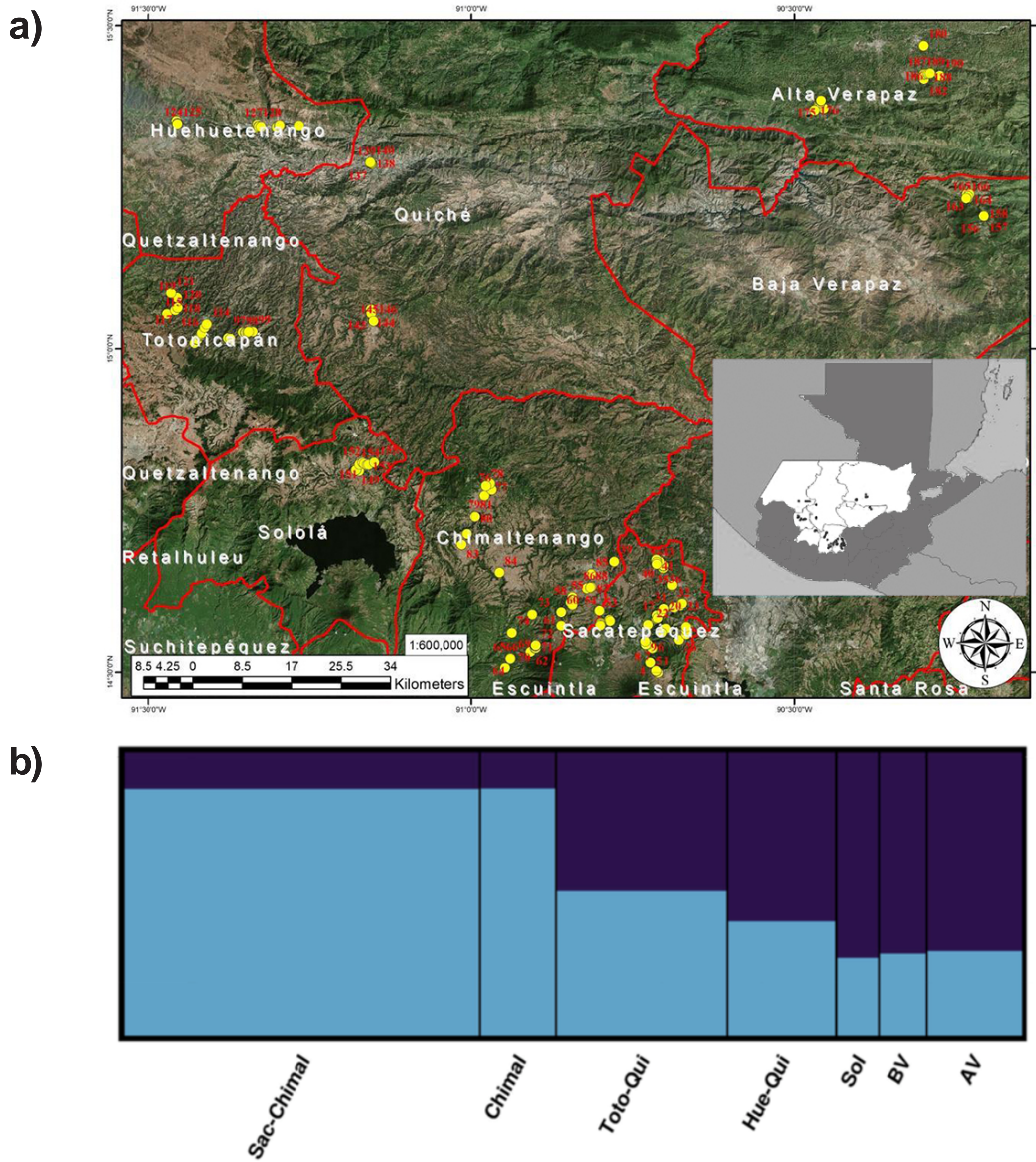

Figure 2. Percentage of molecular variance

Results

The results showed that population structure is composed from two genetic clusters (Figure 1b). The population Toto-Qui,Hue-Qui and AV showed high diversity and allelic richness, whereas population BV and Chimal presented lower levels of genetic diversity (Table 1). The analysis of molecular variance (AMOVA) showed that only 2 % genetic variation existed among population, while 65 % existed within individuals and 33 % existed among individuals (Figure 2)

Conclusions

The lack of population structure is attributed to the process of selection, the system of cross-pollination, the exchange of seeds and the process of domestication to which the avocado is still subject. Protection of the phytogenetic resource is suggested, as well as a complementary agromorphological characterization to establish an adequate strategy of exploitation through plant breeding programs.
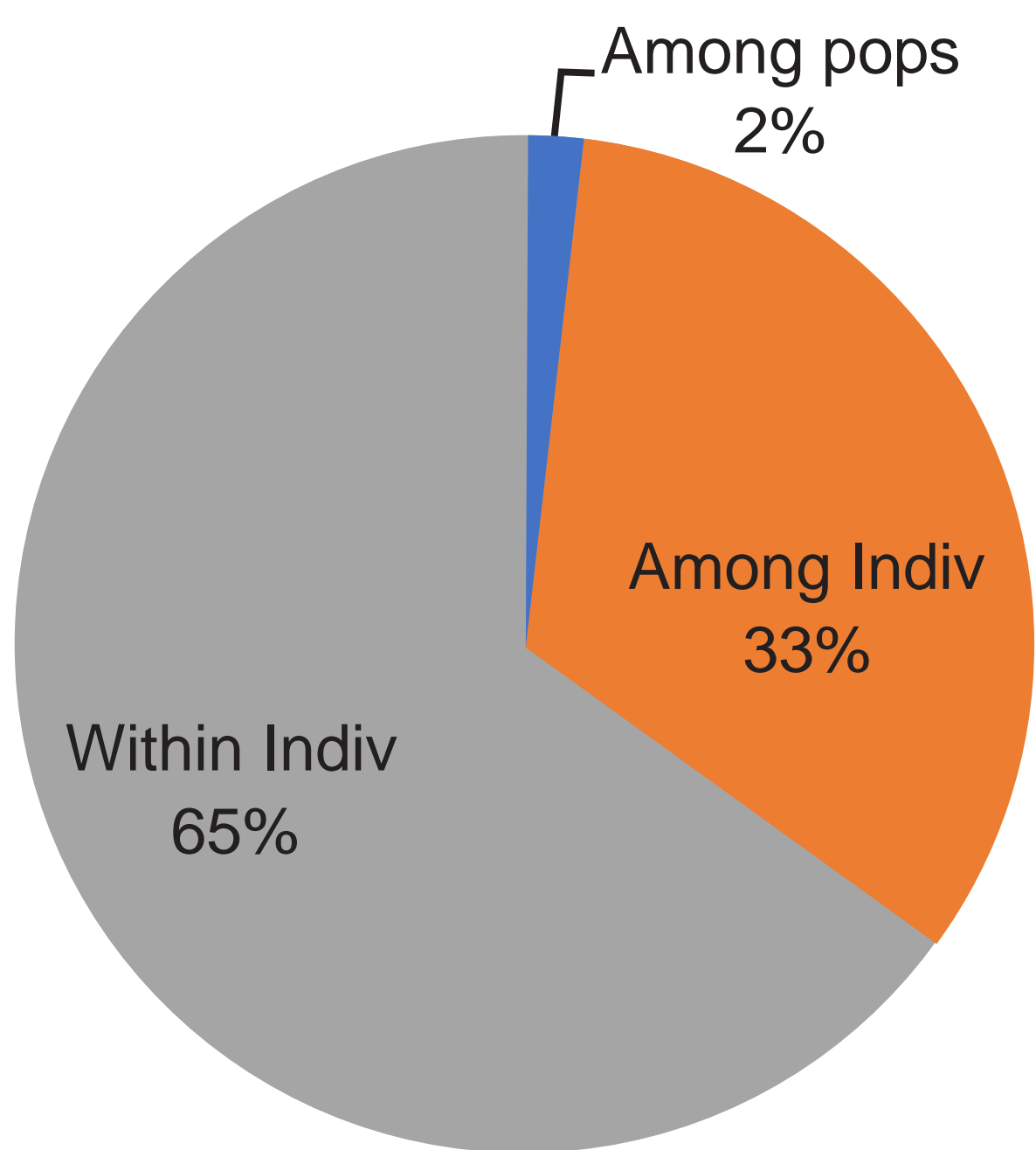
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