The purpose of this study was to compare wild and cultivated Inga edulis Mart. populations’ genetic structure spanning the Peruvian Amazon and to identify the level of differentiation among studied populations. Does the domesticated form of the species have local origin? Materials and methods We evaluated a total of 259 trees, 197 cultivated and 62 wild, sampled in 27 geographically different populations (Table 1). The sexually mature trees were selected randomly and the minimum average distance between two sampled individuals was 200 m. Young leaves were collected and preserved in silica gel. The total genomic DNA was extracted for each sample and genotyped with four microsatellite primers: (P15, Inga03, Inga08 and Inga33). Diversity parameters were calculated and cultivated populations were compared with the wild populations. Hierarchical analysis of molecular variance (AMOVA) was done. To assess the population structure, we estimated the number of genetic clusters (K). Due to the weak population structure, we used a "lociprior" model, which incorporated a priori sampling information. Two groups (cultivated/wild) of populations were used as priors. The number of clusters (K) was set at each value from one through twenty-eight, and the simulation was run ten times at each K value to confirm the repeatability of the results.

Results

We identified 71 alleles, with an average of 17.8 alleles per locus. For the 27 populations with at least 5 samples, the average number of alleles was 5.7, the average allelic richness 4.4, the observed heterozygosity 0.59, and the expected heterozygosity 0.69. The heterozygote deficit was non-significant, and the inbreeding coefficient was 0.153. Twelve populations were not in Hardy-Weinberg equilibrium. These populations were distributed randomly across the I. edulis sampled range and across cultivated and wild populations (Tab. 2). We compared the wild vs. the cultivated populations, and significant deviation from the null expectation emerged. The allelic richness and the observed heterozygosity were lower in the group of cultivated populations. The level of differentiation among populations was significantly higher in the cultivated compared to the wild populations (Tab. 3). A hierarchical analysis of molecular variance revealed that a majority of the genetic diversity was partitioned within populations (78.8%), 14.3% was partitioned among populations within groups (wild and cultivated) and 6.9% was partitioned between cultivated and wild groups (Tab. 4). Results of Bayesian clustering were interpreted only for K = 2 (Fig. 1) and K = 3 (Fig. 2). Analysis of similarity coefficients as well as ΔK indicated that two and three clusters best explained the genetic structure of I. edulis populations. (Fig. 3 and 4).

Table 1. Type of populations sampled (Cultivated or Wild), study site (Site), population code (Pop.), sample size (N), geographic location - GPS coordinates in WG84 (Latitude (S) and Longitude (W)) and altitude in meters above sea level.

Table 2. Diversity parameters per population. sample size (N), average number of alleles per locus (A), allelic richness (R), observed heterozygosity (H), expected heterozygosity (H), inbreeding coefficient (Fis), Populations deviating from Hardy-Weinberg equilibrium at P<0.05 are marked with an asterisk (*).

Table 4. AMOVA between cultivated and wild populations, among populations within cultivated and wild populations and between I. edulis populations, degrees of freedom (df), sum of squared deviation (SS), % variance explained (P), significance test (P).

Conclusions

According to the Bayesian structure results we inferred that the cultivated material in Peruvian Amazon has different origins.

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Figure 1. Results of Bayesian clustering for K = 2, plotted in the map of Peru. Populations assigned to two clusters (green and red) corresponding to the I. edulis wild (bigger black-lined pie charts) and cultivated populations (smaller no-lined pie charts) in the Peruvian Amazon.

Figure 2. Results of Bayesian clustering for K = 3, plotted in the map of Peru. Populations assigned to three clusters (violetial blue and red) corresponding to the I. edulis wild (bigger black-lined pie charts) and cultivated populations (smaller no-lined pie charts) in the Peruvian Amazon.

Figure 3. Number of clusters (K).

Figure 4. DeltaK = mean(ΔK(K)/ std(ΔK(K)).