



Tropentag, September 9-11, 2020, virtual conference

“Food and nutrition security and its resilience
to global crises”

Genetic Diversity of Aguaje (*Mauritia flexuosa*) in Peruvian and Ecuadorian Amazon

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Abstract

Mauritia flexuosa (aguaje) is a dioecious indigenous species from the family Arecaceae important for local people and also for Amazon forest as a whole. The specific environments along the banks of large rivers or inside the lowland jungle forest, where water is retained and where nutrients are slowly decomposed, are called aguajales. Particularly these swampy areas, where *M. flexuosa* occurs in abundance, provide a refuge for different kinds of fauna and flora. People from the local communities living in the Amazon depend on its nutritive fruits. The fact that it is a dioecious species presents a number of difficulties in cultivation. Therefore, a large part of the production is still obtained from wild populations, usually by cutting the female trees. Unfortunately, this bad management of the fruit collection leads to degradation of aguajales and to biodiversity loss.

The main objective of this research was to assess the intra-population and inter-population genetic diversity of *M. flexuosa* in Peruvian and Ecuadorian Amazon by SSR markers. Totally, 145 trees from 15 populations were sampled and successfully analysed using seven polymorphic microsatellite loci. The populations were characterised by high values of genetic diversity and very low levels of inbreeding. The high molecular variance was determined especially among individuals. According to STRUCTURE analysis, no different genetic composition was indicated in the populations. The UPGMA diagram divided populations into two main groups corresponding to the region's isolation; (1) Ecuador and (2) Peru. A very low correlation between geographic and genetic distances was determined using a Mantel test.

The results can be explained by the high level of gene flow along the Amazonian rain forest, where the rivers are used as bio corridors. Also, the human activity through the history of the Amazonian probably has had a significant impact on the *M. flexuosa* distribution. Based on the high genetic diversity, the selection of superior individuals for further breeding can be explored.

Keywords: Arecaceae, biodiversity, genetic variability, microsatellites, population genetics

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