



Genetic variability of *Myrciaria dubia* in Peruvian Amazon

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INTRODUCITON

Camu-camu (*Myrciaria dubia*, McVaugh) is a **fruit bearing tree that grows naturally in the whole Amazonian basin** [1].The fruits are valued for **their high content of vitamin** C. The ascorbic acid content is in range between **845 and 7,355 mg/100g of pulp**, which is about 30 times higher content of vitamin C then an orange. That is why the commercial interest in this species has been growing on national and also on international level [2, 3, 4]. Nevertheless, the information about genetic diversity of this species is still low, as most of the research was focused on the ascorbic acid content.

RESULTS

The average expected heterozygosity was 0.58 ,which is higher value than observed heterozygosity with average 0.49. The inbreeding coefficient was 0.16 and the average number of alleles per locus was 12.17 and the allelic richness ranged from 2.20 to 3.90.

The populations were divided into three different clusters. In cultivated populations, their approximate origin was quite difficult to determine according to lack of information about other populations in studied area. All the results indicated a high genetic variability, probably due to the distance between isolated populations. However, we can observe similarity of populations located on or near the same stream flow. Migration of this species through the forest is less probable. The inbreeding coefficient was quite low compared to other studies [5, 6, 7].



OBJECTIVES

- To assess the intra- and interpopulation genetic diversity of wild and cultivated populations of camu-camu in the area of Iquitos and Pucallpa by using SSR primers.
- To determine the approximate origin of cultivated populations.



Figure 1. Plantation of camucamu in Loreto department

Figure 2. Verious stages of ripeness. Middle fruit os whith highest content of vitamin C

MATERIALS AND METHODS

In total, **31 populations** have been sampled; 252 samples of **21 wild populations** from Peruvian departments Loreto gathered on field of IIAP and 133 samples from **10 cultivated populations** (30 from Iquitos and 103 from Pucallpa) (Figure 4, 5, 6). DNA was extracted from the leaves by modified **CTAB method**. Sven SSR primers were used for final analysis. Several genetic software were used to detect major indexes of variability.

Table 1. Main measures of genetic diversity for all six loci

Locus	k	Но	Не	HW	Ht	Fis	Allelic richness
MDI006	4	0.4632	0.4123	0	0.5013	-0.1233	2.20
MDI015	10	0.4199	0.5781	0	0.7270	0.2737	3.40
MDI004	11	0.3138	0.4644	0	0.5613	0.3243	2.57
MDI010	15	0.9554	0.7407	0	0.7761	-0.2898	3.32
MDI009	24	0.4347	0.6654	0	0.8340	0.3467	3.90
MDI003	9	0.3295	0.6062	0	0.7862	0.4564	3.37
Average		0.49	0.58		0.70	0.16	12.17

k: number of detected alleles at the locus, Ho: observed heterozygosity,

He: expected heterozygosity, HW: significance of deviation from Hardy-Weinberg equilibrium, Ht: the expected heterozygosity in total population over loci, Fis: inbreeding coefficient Figure 6. Graphical representation of cultivated population nearby city Pucallpa divided into three clusters (3-SFA, 9-SJM, 10-SRS, 11-FRA, 13-SJP, 29-Y1, 30-Y2, 31-Y3)



Figure 7. Graphical representation of cultivated population nearby city Iquitos and with division into three clusters (6- IG, 7-IM)

CONCLUSION





Figure 4. Division of all the populations into three clusters (W- wild population, C-cultivated population)



The levels of genetic diversity in our study were quite high, that can be caused by natural origin of populations and still quite low selection and domestication.

Although this study is a result of the combination of both our data and the data of Šmíd et al. (2017), it still represents a fraction of the knowledge that can be gained about this species. It would be beneficial if this research was going to continue, especially if optimized primers tested by two studies were available.

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Figure 3. Map of Peru with the study sites marked in pink

Figure 5. Graphical representation of wild populations with division into three clusters (1JSB, 2-MT, 4-SUNI, 5-YL, 8-Y5, 12-MY,14-TAAF, 15-TAHU, 16-TAO, 17-TC MIX, 18THT, 19-PM, 20-Pc, 21-PC, 22-CU, 23-CC, 24-Ct, 25-NN, 26-NY, 27-IP, 28-TH)

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