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“Solidarity in a competing world —
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Morphological and Genetic Diversity of Camu-Camu (*Myrciaria dubia* McVaugh) in Peruvian Amazon

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Abstract

Camu-camu (*Myrciaria dubia* McVaugh) is currently one of the most important fruit species that is grown in the Peruvian Amazon, as well as in Brazil, Colombia or Bolivia. Larger plantations were established only in the last two decades and a substantial part of the production is still obtained by collecting fruits from the wild. Domestication of the species is still at its very beginning; most of the farmers cultivate the plants without any breeding or just after simple selection. The aim of this study was to characterise the morphological and genetic variability of cultivated and natural populations of camu-camu in the Peruvian Amazon and also to compare the variability among and within these populations. In total we have sampled 13 populations; 10 wild populations in Iquitos region, three cultivated populations in Pucallpa in Peruvian Amazon. For genetic analysis, the leaf tissue samples were collected from ten individuals from each population ($n=126$), and for morphological data were collected from five trees of each population ($n=65$). To assess the genetic diversity, we used seven microsatellite primers that were developed from available DNA sequences. Using various genetic softwares, major indexes of variability were detected and dendrograms of relatedness of populations and individuals were created. The statistical analysis did not reveal statistically significant differences for most of the morphological descriptors, except for the fruit parameters. Surprisingly, the trees from wild populations had higher fruit and pulp weight and their fruits contained less seeds compared to cultivated populations. The observed heterozygosity was 0.347 and 0.404; expected 0.516 and 0.506; inbreeding coefficient was 0.328 and 0.200 for wild and cultivated populations, respectively. Wild populations could be divided according to the dendrogram into two completely different groups. In cultivated populations, their approximate origin was determined. All the results indicated a high genetic variability but also a high degree of inbreeding. This can be explained by isolation of the populations from each other or low number of individuals in the population. This high level of diversity can be explored for selection of superior individuals and further possibilities of breeding.

Keywords: Genetic diversity, microsatellites, morphological diversity, PCR, population genetics