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Evolutionary history of three *Baracoffea* species from western Madagascar

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Introduction

The wild species of the Coffea genus present a very wide morphological, genetic and biochemical diversity. These species are often more resistant to diseases, pests and environmental variations than the two species currently cultivated worldwide: *C. arabica* (Arabica) and *C. canephora* (Robusta). Wild species are now considered to be a crucial resource for climate change adaptation of cultivated coffee trees. Within the *Coffea* genus, 79 species are native to the Indian Ocean islands of Comoros, Mayotte, Mauritius, Réunion and Madagascar, out of a total of 141 taxa worldwide. Among them, a group of 9 species called "Baracoffea", are particularly atypical in their morphology and adaptation to the sandy soils of the dry deciduous forests of western Madagascar. Here, we have attempted to shed light on the evolutionary history of three Baracoffea species*: C. ambongensis, C. boinensis* and *C. bissetiae* by analyzing their chloroplast and nuclear genomes and by analyzing the climate data of their area of origin.

Materials/Methods

Coffea ambongensis J.-F.Leroy ex A.P.Davis & Rakotonas*., C. boinensis* A.P.Davis & Rakotonas. *and C. bissetiae* A.P.Davis & Rakotona, was collected at the Antsanitia village, Ankarafantsika National Park and the Ankarafantsika region, respectively. This study includes GPS data from the following articles: (Razafinarivo et al. 2012) and (Rimlinger et al. 2020). Some positions were extracted from the *Global Biodiversity Information Facility* (GBIF) website (www.gbif.org).

The Illumina sequencing was performed by HiSEQ 2500, 2X150 bp and available at NCBI: BioProject PRJNA898910.

The Plastid genome reconstruction and nuclear SNP was done similarly to Charr et al., 2020. The newly assembled plastid sequences obtained in this study are deposited at NCBI (ON101707, ON101708 and ON117418). The maternal and nuclear phylogeny was reconstructed similarly to Charr et al., 2020.

DNA content was measured by flow cytometry at the Imagif Cell Biology platform (Gif-sur-Yvette, France) according to Razafinarivo et al. 2012. Genome size data for 35 Malagasy species were extracted from Razafinarivo et al. 2012.

Environmental parameters: Climatic data were extracted from GPS coordinates of each species and from WorldClim information (http:// www.worldclim.org).

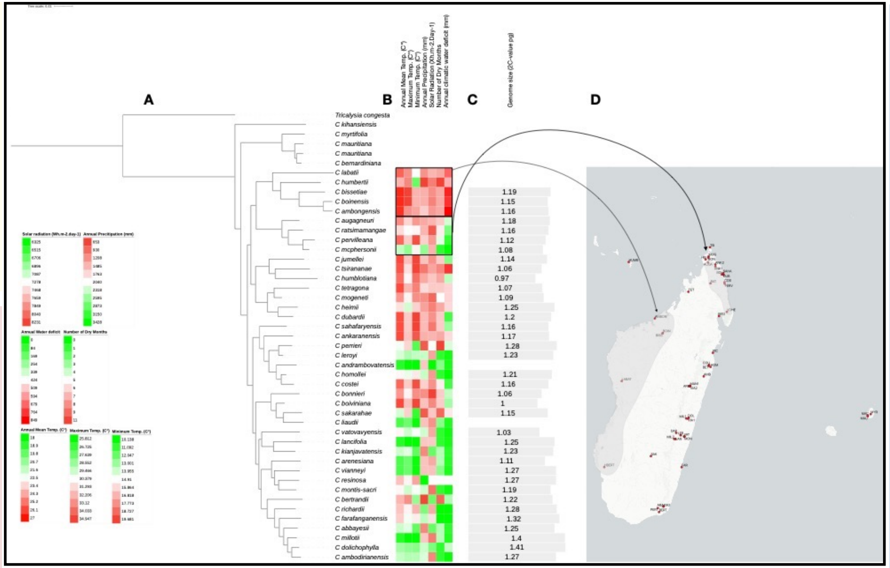

Figure 1: Nuclear phylogeny, geographic distribution, genome size and bioclimatic data for *Coffea* species in Madagascar. A. Maximum likelihood nuclear tree (see Figure 2). B. Climatic data (annual temperature, hottest and coldest month, annual rainfall, solar radiation, annual water deficit and number of dry months in the year) for the geographical positions of species in Madagascar. C. Size of 2C genomes in pg. D. Map of geographical positions of species. The distribution zones of Baracoffea and the Subterminal clade are shown in grey.

Results/Discussion

We assembled the complete chloroplast genomes and extracted 28,800 SNP (Single Nucleotide Polymorphism) markers from the nuclear genomes. These data were used for phylogenetic analysis of Baracoffea with *Coffea* species from Madagascar and Africa (Fig1A). Our data support the monophyletic origin of Baracoffea within the *Coffea* of Madagascar, and reveal a recent divergence with a sister clade of four species: *C. augagneuri, C. ratsimamangae, C. pervilleana* and *C. McPhersonii*, belonging to the Subterminal botanical series. Using Worldclim data, we show Baracoffea evolve in the bioclimatic zone of dry deciduous forests, where temperatures are high, rainfall is low and the number of dry months is high, whereas its sister clade evolves in a dry north-western region, but contains remnants of humid forests and monsoon rainforests (Fig1B/D). This information suggests that the Baracoffea clade has diversified and adapted uniformly to the dry climate of western Madagascar, whereas its sister clade has undergone contrasting adaptations. Interestingly, we observed a correlation between genome size and climate aridity (Fig1C, and data not shown), suggesting that climate adaptation of Coffea species has a strong impact at the genetic level.

Conclusion/Perspectives

In conclusion, in this work we show that the baracoffea group, made up of 9 species, has evolved to adapt to the dry climates of western Madagascar, while its sister clade composed of four SubTerminales Coffea species has adapted to the climates of the heterogeneous environments of north of the island (generally a dry region, but containing remnants of humid forests and monsoon rainforests and bordered by zones with very distinct climates (sub-humid, humid and mountain)). The acquisition of genomic data for these species will ultimately enable us to understand the molecular mechanisms of adaptation at both genetic and genomic levels. Particularly, our objectives in the near will be to elucidate the relation between aridity and the genome size variation, is,h Baracoffea as model.

References:

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