

Evolutionary history of three *Baracoffea* species from western Madagascar

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Rationale:

The genus *Coffea* comprises a total of 130 species, of which 79 are native to the Indian Ocean islands such as Comoros, Mauritius, Reunion and Madagascar. This considerable number of species in IOI, suggest an intense diversification in this territory in a relative short time (Hamon et al., 2017). Among these *Coffea* species there is an atypical group composed of 9 species: The Baracoffea 'alliance' found exclusively in the tropical dry forests of western Madagascar and restricted to sandy soils. However, to date, very few information exist about their evolutionary history and few molecular data are available in public repositories.

Methods:

Plant Material: *Coffea ambogensis* J.-F. Leroy ex A.P. Davis & Rakotonas., *C. boinensis* A.P. Davis & Rakotonas. and *C. bisetiae* A.P. Davis & Rakotona, collected at the Antsanitia village, Ankarafantsika National Park and the Ankarafantsika region, respectively.

Illumina sequencing: HiSeq 2500, 2X150 bp.

Plastid genome reconstruction and nuclear SNP calling: Plastid genome reconstruction was done similar to Charr et al., 2021.

Phylogenetic analyses: The maternal and nuclear phylogeny was reconstructed similarly to Charret al., 2021.

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

Results:

In this study, we produced genomic sequences for three Baracoffea species: *C. ambogensis* (14.7 Gbp), *C. bisetiae* (13.8 Gbp) and *C. boinensis* (17.5 Gbp). Complete chloroplast genomes were assembled, and 28,800 nuclear Single Nucleotide Polymorphism markers were recovered to construct maternal and nuclear phylogenies of *Coffea* including Baracoffea species. The phylogenetic trees obtained indicate the monophyly of Baracoffea species supporting the taxonomy proposed by Davis et al., 2008. The nuclear phylogeny of *Coffea* species from Madagascar indicates the divergence of Baracoffea with a group of species originating from the north of Madagascar and belonging to the Subterminales serie (*C. augagneuri*, *C. ratsimamangae*, *C. pervilleana* and *C. vahemarensis*). Climatic data when associated to the nuclear phylogenetic tree indicate an adaptation of Baracoffea to dry environment ~7 Mya.

Conclusions & Perspectives:

Baracoffea species have diverged from species of the subterminate series species 7 Mya, adapting to high temperatures and solar radiation as well as low annual rainfall. Further genomic and comparative analyses with the *C. canephora* genome (Denoeud et al., 2014) will be carried out in the future to identify the repertoire of Baracoffea-specific genes and investigate their putative adaptation-related function.

References:

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