



Complete chloroplast genome of *Lafoensia*

From 2019-2020 | Total budget € 30,000

For phylogenetic and biogeographic reconstruction of *Lafoensia* Vand (Lythraceae)

Lafoensia is a comprehensive component of the forests and savannas of South America. The lack of knowledge of the genus presents difficulties for the exploration of its species that have been recognized for containing active principles to the pharmacological industry. *Lafoensia* is widely distributed across different biomes and biodiversity hotspots in the Neotropics. Distribution areas of some of the species are non-overlapping, resulting in a patchy pattern with species confined to distinctive habitats, such as the cerrado, campos rupestres, and the submontane forests of the eastern Andes. Using a genome-skimming approach, the extranuclear genetic data of chloroplast genomes will be used in phylogenetic analysis of *Lafoensia*, and the use of molecular clock models will help explain the evolutionary and biogeographic patterns observed. This project is a collaboration between the Brazilian botanist from Embrapa and Dr. Freek Bakker from WUR. The permanence of the Brazilian researcher in The Netherlands was supported by a grant from National Council for Scientific and Technological Development (CNPq - Ministry of Science and Technology) and the sequencing services by the National Institutes of Science and Technology (INCT-Biosyn/CNPq) and Embrapa. WUR ensured access to the most advanced knowledge and tools on chloroplast genome analysis. The approach is innovative and represents a breakthrough for botanical research in Brazil.

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