

## Proposition de sujet de Master 2, 2024/2025

Titre du stage : Genetic delimitation of tree species in French Guiana: development and evaluation of transcriptomic SSR-Seq markers in the genus *Eschweilera* (Lecythidaceae)

Thème du projet d'unité : T1 Histoire évolutive et réponse au CC ; T4 Socio-écosystèmes, conservation/restauration de la biodiversité

Encadrant.e.s :

Niklas Tysklind (UMR Ecofog), Myriam Heuertz, Olivier Lepais (UMR Biogeco)  
[niklas.tysklind@ecofog.gf](mailto:niklas.tysklind@ecofog.gf), [myriam.heuertz@inrae.fr](mailto:myriam.heuertz@inrae.fr), [olivier.lepais@inrae.fr](mailto:olivier.lepais@inrae.fr)

Lieu du stage : 69 route d'Arcachon, 33610 Cestas

Contexte scientifique :

The botanical identification of closely related tropical tree species in the forest can be subject to errors due to similar morphology among species, especially when only vegetative characters are available and multiple related species occur in sympatry. Genetic markers can be used to delimit such species (Heuertz et al. 2020), but these markers must be sufficiently conserved across species to amplify across all species while sufficiently divergent among species to reliably delimit species. Furthermore, they must be variable within species, to allow assessing within-species population genetic parameters.

### Matériel & Méthodes

In this M2 internship project, we propose to develop and to evaluate transcriptome-based microsatellite (SSR, simple sequence repeat) markers to efficiently and cost-effectively delimit tree species of the genus *Eschweilera*, an ecologically important genus with potential for timber harvesting in French Guiana. We have recently produced a reference genome for *Eschweilera coriacea* and transcriptomes for five *Eschweilera* species (3 samples per species). Based on these resources, we propose to identify conserved regions among *Eschweilera* species that can be genotyped using a high-throughput pipeline available at the Bordeaux Genome-Transcriptome Facility, PGTB (Lepais et al. 2020). The proposed steps are the following 1) Identification of single copy transcribed regions of the genome conserved across different *Eschweilera* species; 2) Identification of SSRs on these regions and development of Simple Sequence Repeat sequencing (SSRseq) to genetically delimit the different species; 3) Genotyping by sequencing of a test collection of *Eschweilera* samples from French Guiana to ascertain species membership and compute population genetic diversity metrics on each of the species delimited.

We have a collection of *Eschweilera* samples available at the regional level in French Guiana (600 available DNA samples), and at the local level (400 tissue samples), to assess diversity and differentiation of closely related species in sympatry and in allopatry. Funds for data production are available through the G-MANAGE project within RRI-Tackling at the University of Bordeaux.

## Collaborations :

Niklas Tysklind, UMR Ecofog, Guyane ; Olivier Bruneau, ONF Guyane

## Profile du candidat :

We seek a biologist or bioinformatician with interest in the development of bioinformatic workflows and the analysis of sequencing data. If the candidate is interested in laboratory work, we can offer some training in DNA extraction and genetic/genomic applications.

## Références citées :

Heuertz, M., Caron, H., Scotti-Saintagne, C., Pétronelli, P., Engel, J., Tysklind, N., Miloudi, S., Gaiotto, F.A., Chave, J., Molino, J.F., Sabatier, D., Budde, K.B., 2020. The hyperdominant tropical tree *Eschweilera coriacea* (Parvifolia clade, Lecythidaceae) shows higher genetic heterogeneity than sympatric *Eschweilera* species in French Guiana. *Plant Ecol. Evol.* 153, 67–81.

Lepais, O., Chancerel, E., Boury, C., Salin, F., Manicki, A., Taillebois, L., Dutech, C., Aissi, A., Bacles, C.F.E., Daverat, F., Launey, S., Guichoux, E., 2020. Fast sequence-based microsatellite genotyping development workflow. *PeerJ* 8, e9085.