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The Dicorynia guianensis population genomic structure mirrors the distribution of environmental variables in French Guiana

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bonnier.ju@gmail.com



Background V



Effective forest management can protect forests and enhance adaptation to climate change. In French Guiana, timber exploitation and climate change are threatening *Dicorynia guianensis*, a drought-sensitive tree that plays a crucial role in timber harvests $\frac{1}{2}$. Understanding its genetic adaptation to environmental variations through landscape genomic studies is essential to designing better management programs.

Objective: identify significant outlier loci associated with environmental variation in *Dicorynia guianensis* in French Guiana

Material: whole genome resequencing of 87 individuals distributed over 11 sites with varying environmental conditions

Methods: outlier analysis methods, based on genetic structure and genotype-environment association methods³

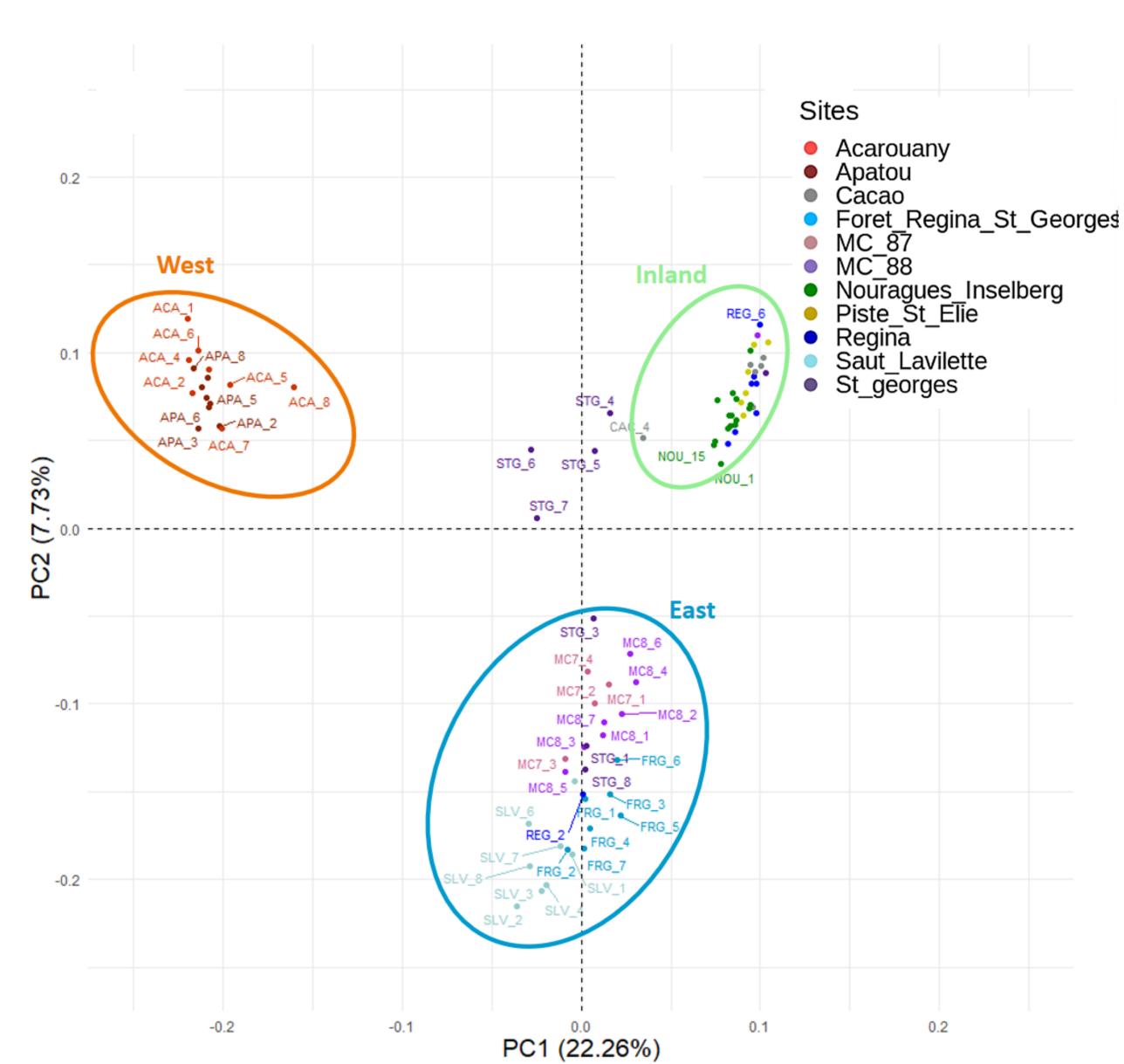


Figure. Principal component analysis (PCA) based on 599,959 SNP markers and conducted on the sampling sites using the first two components (PC1 and PC2).

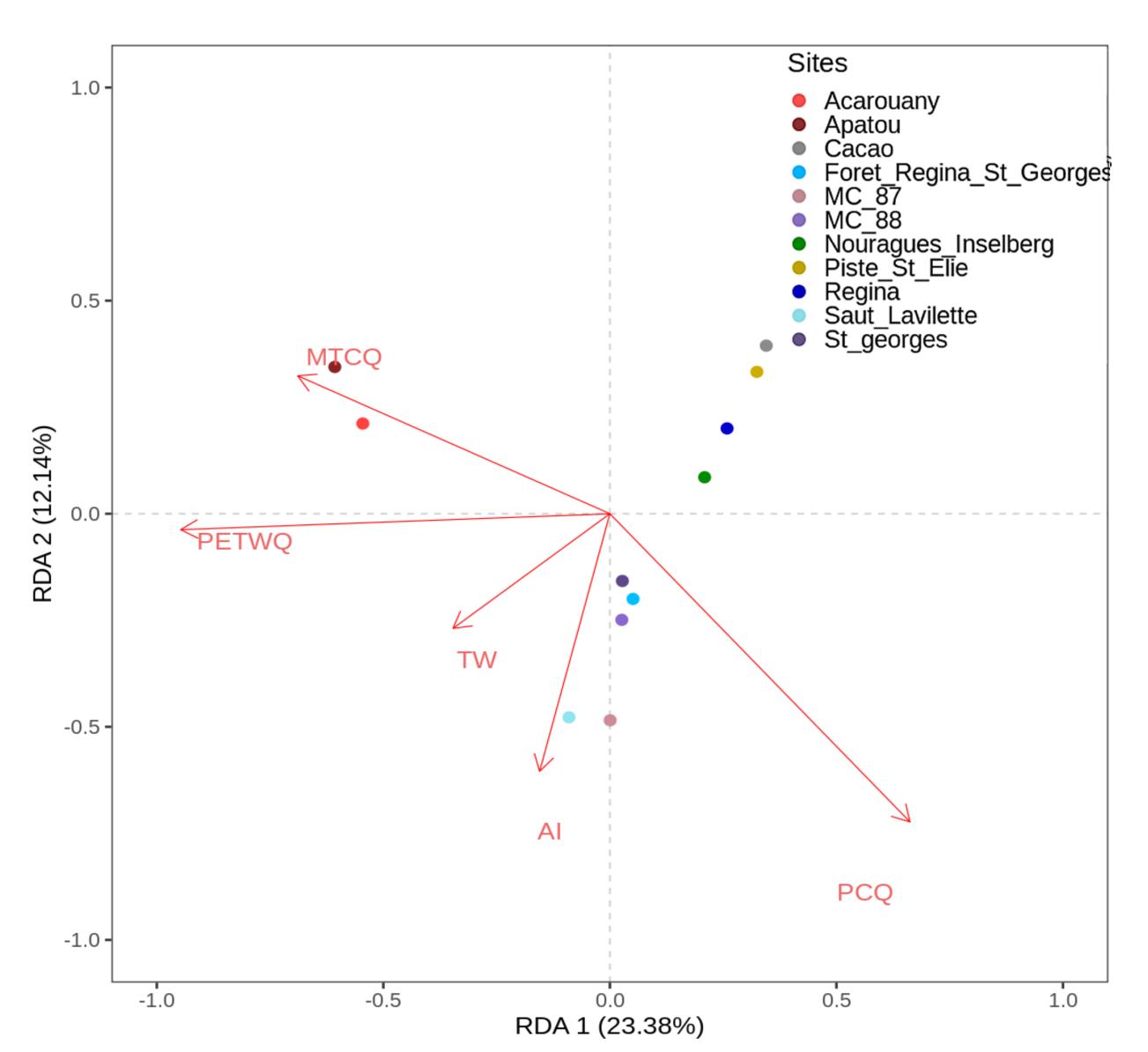
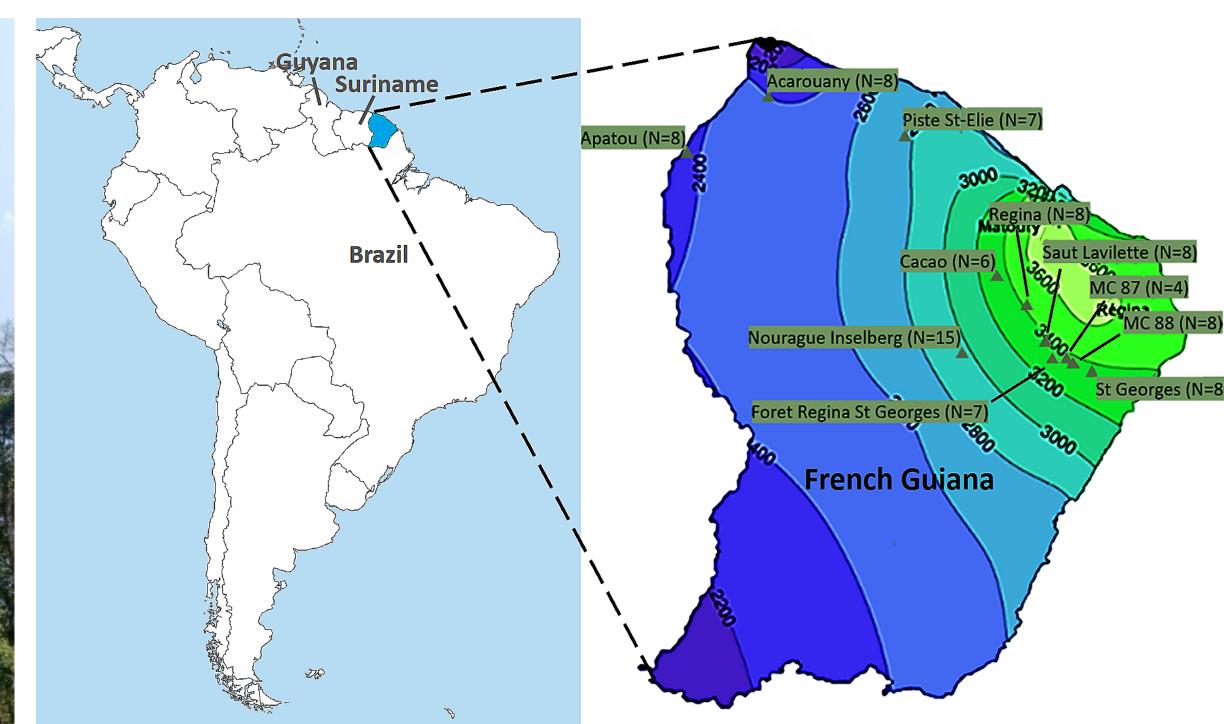


Figure: Biplot of redundancy analysis (RDA) illustrating the impact of environmental variables on genetic variation at 11 study sites for Dicorynia guianensis in French Guiana.

- Mean temperature of the coldest quarter (MTWQ)
- Aridity index (AI)
- Potential evapotranspiration of the wettest quarter (PETWQ)
- Topographic wettest index (TW)
- Precipitation of the coldest quarter (PCQ)



Figures. On top, geographic distribution of sampling sites of Dicorynia guianensis in French Guiana along the rainfall gradient with the number of individuals (N) in each site. On the left, picture of Dicorynia guianensis in sampling area.

Genetic structure and environmental variation



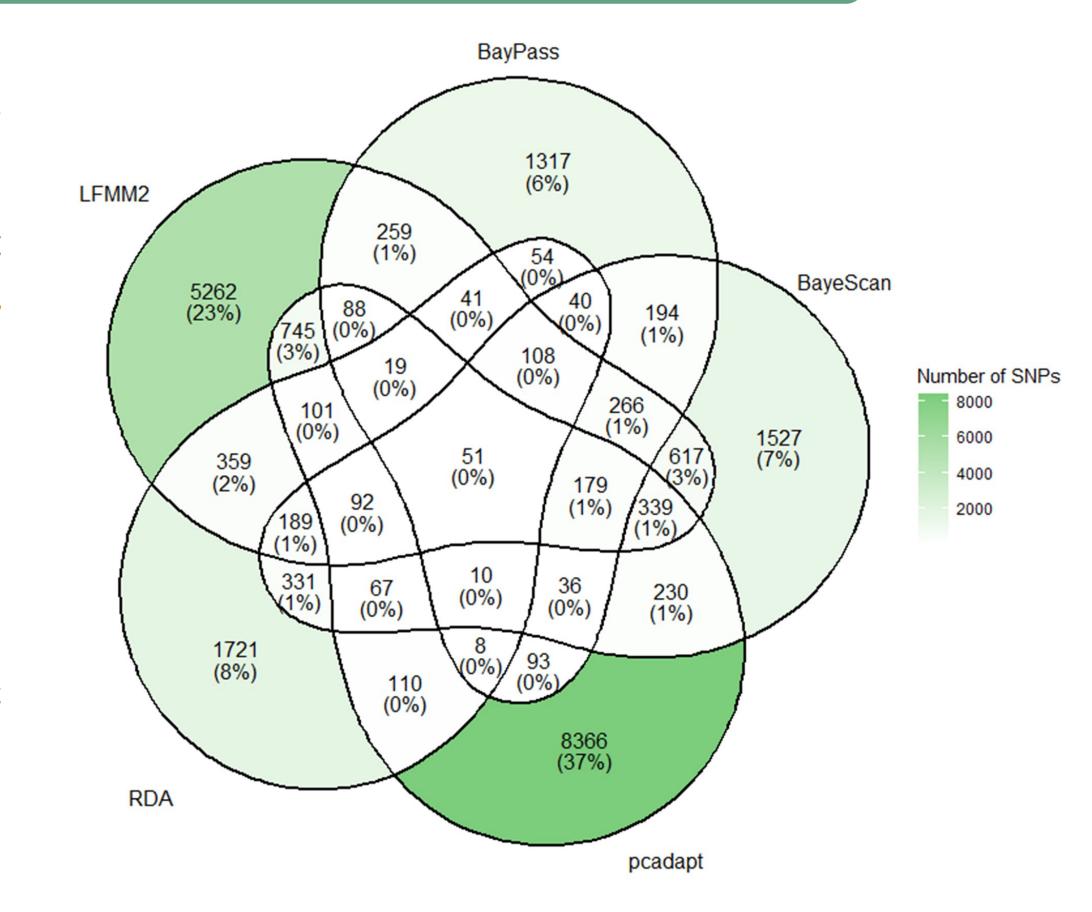
- 3 clusters: west, inland, and east, improving the previously described population structure 4,5
- Regions characterized by varying environmental conditions, mainly influenced by rainfall during the rainy season

First signs of local adaptation



- 5 different methods to detect evidence of selection.
- . 459 SNPs were retained by at least four methods, highlighting robust signals of selection.

Precipitation and evapotranspiration during rainy season are the most significant variables modulating local adaptation and in shaping the genetic



Forest management perspective



- Our results showcase the critical role of specific environmental factors, specially heavy rainfall during the rainy season, as strong drivers of local adaptation.
- . Using genomic offset calculations, we observed spatial patterns of maladaptation risk in D. guianensis in French Guiana.

Our results advocate for the integration of patterns of genetic structure and local adaptation into management plans by (1) protecting genetically diverse populations; (2) developping region-specific strategies to cope with environmental change

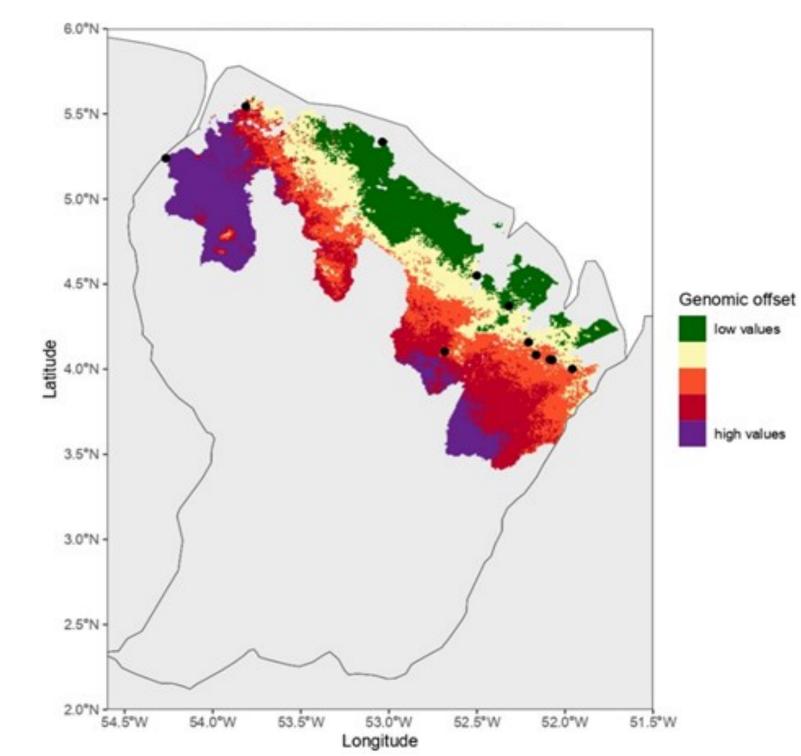


Figure. Spatial projection of adaptive genetic turnover in the permanent forest domain (DFP) in French Guiana.

References

- 1._Flora, C. Origine et prédiction de la variabilité de la durabilité naturelle chez Dicorynia guianensis Amsh. (Université de Guyane, 2018). doi:10/
- 2. Guariguata, M. R., Cornelius, J. P., Locatelli, B., Forner, C. & Sánchez-Azofeifa, G. A. Mitigation needs adaptation: Tropical forestry and climate change. Mitig Adapt Strateg Glob Change 13, 793-808 (2008).
- 3. Rellstab, C., Gugerli, F., Eckert, A. J., Hancock, A. M. & Holderegger, R. A practical guide to environmental association analysis in landscape genomics. Molecular Ecology 24, 4348-4370 (2015).
- 4. Bonnier, J. et al. Population genetic structure and demographic history of the timber tree Dicorynia guianensis in French Guiana. Tree Genetics &
- Genomes 20, 2 (2024). 5._Caron, H. et al. Spatial and temporal distribution of chloroplast DNA polymorphism in a tropical tree species. Molecular Ecology 9, 1089–1098 (2000).















