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PAST DEMOGRAPHIC HISTORY OF *Astrocaryum sciophilum*: CHLOROPLAST GENETIC STRUCTURE AND RESTRICTED SEED DISPERSAL

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1. INTRODUCTION

Existence of Quaternary refuges in the Neotropics has long been debated since Haffer (1969) and remains controversial for the Guiana shield despite recent paleoecological (Tardy, 1998) and phylogeographic data (Caron, 2000; Dutech 2003). Several theories have been developped:

▪ **Quaternary refuge theory** (Haffer, 1969): the climate changes induced fragmentation of the forest cover, which in some places was replaced by savannas. Remaining fragments of forest acted as isolated refuges for fauna and flora, leading to high species diversification by allopatric speciation.

▪ The **Disturbance-Vicariance theory** does not imply a reduction of forest cover. Instead, it suggests that the 5 to 6°C cooling in temperature allowed colonization of forests by Andean species (Colinvaux *et al.*, 2004). Several colonisation-regression events occured, leading to changes in communities' composition.

▪ An **intermediate theory** has been developped for the Guianan Shield. During drier periods, wet forests were preserved in some refuges along the coast (macro-refuge) and at the basis of rocky formations called inselbergs (micro-refuges), located in the centre and the south of the Guianan Shield (figure 1). Outside the refuges, migration of taxa originating from Venezuelan drier forest induced a change in forests'composition.

Using genetic data, we aim at reconstructing the past demographic history of an understorey palm to test these different theories and to identify potential routes of recolonization in French Guiana.

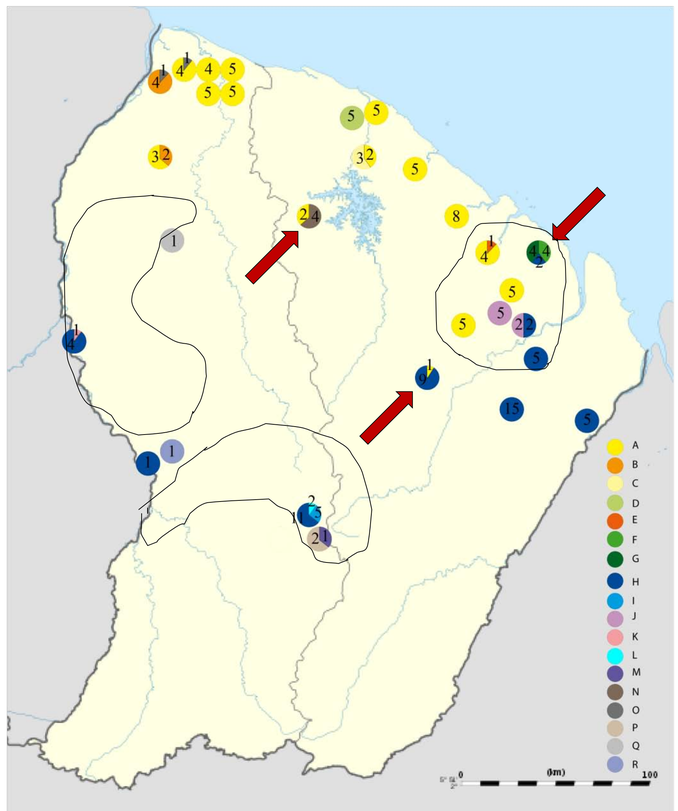

Figure 1: Distribution of the cpDNA haplotypes in French Guiana. Numbers indicate the number of individuals. Red arrows indicate admixture zones. Refuges inferred by Tardy (1998) are circled in black.

2. THE MODEL

Astrocaryum sciophilum (Miq.) Pulle

- endemic to the Guiana Shield
- sciaphilous species, only growing in understorey
- mean first age at reproduction of 170 years
- pollinated by bees
- slow colonisation speed: average dispersal distance of 11 meters
- dispersed by agoutis, acouchis and squirrels (figure 3)

➔ Suitable model for genetic analysis to infer demographic changes in response to climate variations from the Quaternary

Figure 2: *Astrocaryum sciophilum*

Figure 3: Agouti (*Dasyprocta leporina*), main disperser of *Astrocaryum sciophilum*

3. MATERIALS AND METHODS

- 166 individuals (38 populations,1-5 individuals/population)
- 9 outgroups (8 *Astrocaryum*, 1 *Bactris*)
- 5 cpDNA regions (intron rps16, rps16-trnQ, intron trnG, psbM-trnD and atpI-atpH). Primers and PCR conditions are described in Shaw et al. (2007).
- Sequences edited and aligned manually using Bioedit v7.0. Insertion/deletion and microsatellite length polymorphims coded as single-base polymorphisms.
- Data analysis conducted using DNAsp v.5, Network 4.5.
- Genetic structure and isolation by distance assessed using SPAGeDI.

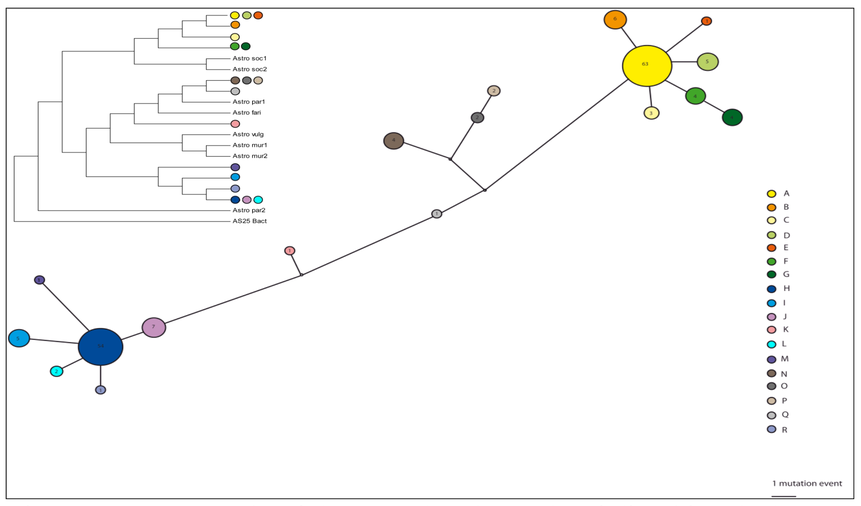

Figure 4: cpDNA haplotype network and relationships between haplotypes and outgroups . Size of the circles are proportional to the sample size, indicated by the numbers.

4. RESULTS

- 18 different haplotypes, 2 of them frequent (A: 38%, H: 33,7%)
- 10 haplotypes with 3 or less individuals
- Only a few populations with more than 1 haplotype
- 3 different distant groups, closer to other Astrocaryum species than to each other
- Phylogeographic signal within populations (Nst = 0.84, Gst = 0.73, p =0.008)
- Phylogeographic signal among populations (p<0.0001) → Isolation by Distance pattern

5. DISCUSSION AND PERSPECTIVES

We detected a strong genetic structure at the scale of the French Guiana, which was further correlated with geographic distance. This isolation-by-distance pattern was explained by limited seed and pollen dispersal (mean seed dispersal distance = 11 m). Three different groups of haplotypes were identified : 'blue', 'yellow' and 'gray'. The haplotype network showed star-liked shapes with many different haplotypes diverging slightly from the two most common ones (A & H, see Figure 1). This pattern is often characteristic of expansion events.

Moreover, we detected three geographic zones where highly divergent haplotypes co-existed (Kaw, Nouragues, Trinité Mounts, Figure 1). These areas may correspond to contact zones of different recolonization routes. Overall, our results do no support the intermediate theory. Furthermore, we did not ind higher frequencies of rarea haploypes in the areas identified by Tardy (1998), so our results do not support the refuge theory either.

In addition to chloroplastic sequences, we will use nuclear microsatellite markers 1) to get a better understanding of the demographic history of A. sciophilum, 2) to estimate more precisely pollen and seed dispersal distances with parentage analysis.

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