



MOLECULAR PHYLOGENY OF THE GENUS *PALISOTA* RCHB. EX ENDL. (COMMELINACEAE)

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CONTEXT - The genus *Palisota*:

- ✓ Poorly known **monocot genus**.
- ✓ Largest genus **endemic to Africa** in the Commelinaceae (33 spp.) (Faden, 1998 ; Bidault & Van der Burg, 2019).
- ✓ Includes **terrestrial herbaceous plants**, ranging from small rosettes to robust shrub-like herbs. (Bidault & Van der Burg, 2019).
- ✓ **Important component of the understory of tropical rainforests** (Faden, 2007).
- ✓ **Complex taxonomic history** and overall difficulty to identify informative morphological characters (Bidault & Van der Burg, 2019).
- ✓ **No formal classification and no phylogeny published** for the genus.
- ✓ But recent **taxonomic works** with revamped **species delimitations and new species descriptions** (Bidault & Van der Burg, 2019 ; Van der Burg & Bidault, 2020).

OBJECTIVES OF THE STUDY

1. Test the **monophyly of the genus**.
2. Provide a first insight in the **phylogeny of *Palisota***.
3. Check if it is possible to identify clear **morphological patterns**.

MATERIAL & METHODS

TAXONOMIC SAMPLING:

Using both herbarium and silica-gel preserved material, we were able to constitute a sampling **that accounts for 24 out of the 33 species** described to date and that is **representative of the morphological and ecogeographic diversity of the genus**. Also, 8 samples pertaining to 5 Commelinaceae genera were included to serve as outgroups.

PHYLOGENETIC ANALYSIS:

We have conducted **Bayesian and maximum likelihood analyses** on a dataset of **43 accessions** (representing 24 *Palisota* species) and **five DNA regions (4710 bp)**: **four chloroplast regions** (gene *matK* and three intergenic spacers, *rpl32-trnL*, *rps16-trnK* and *trnL-trnF*) and **one nuclear spacer** (the nuclear ribosomal region ITS).

CONSTITUTION OF A MORPHOLOGICAL MATRIX:

In order to check for morphological patterns in the phylogeny, we selected and compiled **20 key morphological traits for the 24 *Palisota* species sampled**.

RESULTS & DISCUSSION

A. A FIRST PHYLOGENETIC FRAMEWORK FOR *PALISOTA*

- ✓ In accordance with all recent taxonomic treatments, *Palisota* is **strongly supported as monophyletic** (see figure 1).
- ✓ The genus is divided into **four main clades**, three of which are strongly supported as monophyletic (clades A, B and C); clade D is only supported in Bayesian analyses (PP=0.94).
- ✓ The deep nodes of the phylogeny suggest that clades B, C and D are forming a monophyletic grouping (PP = 1) **but basal relationships in *Palisota* are not supported in bootstrap analyses**.

RESULTS & DISCUSSION (continued)

B. AN EVOLUTION TOWARDS TWO TYPES OF ECOLOGICAL STRATEGIES?

- ✓ Of the 20 characters coded for the study, **12 were highly homoplastic** and **8 seem to show strong phylogenetic signal** (showed in figure 2). These latter morphological traits are related with (1) the **habit of the plants**, (2) the **shape, position and pubescence of the inflorescences**, (3) the **number of flowers per cyme** (cincinnus), and (4) the **shape of the fruit pedicels** as well as the **color and shape of the fruits**.
- ✓ We observed a **morphological homogeneity** between two main groups (grade ABC versus clade D), which lead us to suggest two types of ecological strategies for *Palisota* species:
 1. Species of **grade ABC**, that are **erect herbs or shrubs** with **terminal and rather elliptical inflorescences** and **subspherical fruits**.
 2. Species of **clade D**, that are **rosette and creeping species**, closer to the ground and less visible, with **mostly axillary and globular inflorescences**, and **pepper like fruits**.

Figure 2 : Morphological diversity of *Palisota* species in a phylogenetic context

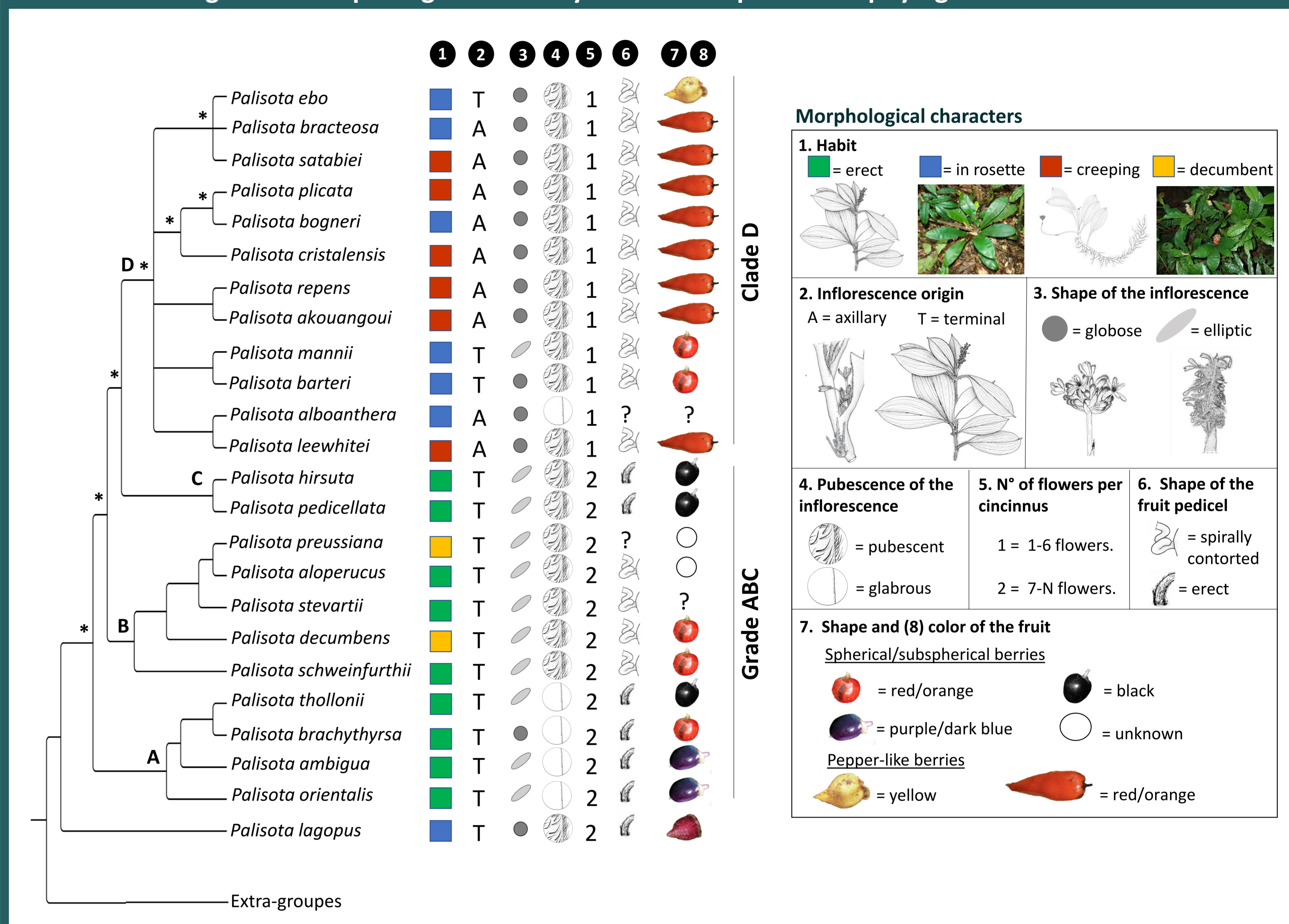


Figure 2. Morphological matrix of eight coded characters related to *Palisota* phylogeny. The tree used is derived from Bayesian analysis of the matrix obtained by concatenating the chloroplast and ITS sequences. We present the simplified majority consensus (cladogram): the extra-groups have been lumped into one branch, one specimen per *Palisota* species has been maintained, and the values at the nodes have been removed in order to simplify visualization. Legend: * = nodes with bootstrap support < 50%. Drawings of D. Geffard-Kuriyama, H. de Vries, L. Longou and photos of E. Bidault, N. Texier, G. Prenner and G. Take.

Figure 1 : Molecular phylogeny of the genus *Palisota*

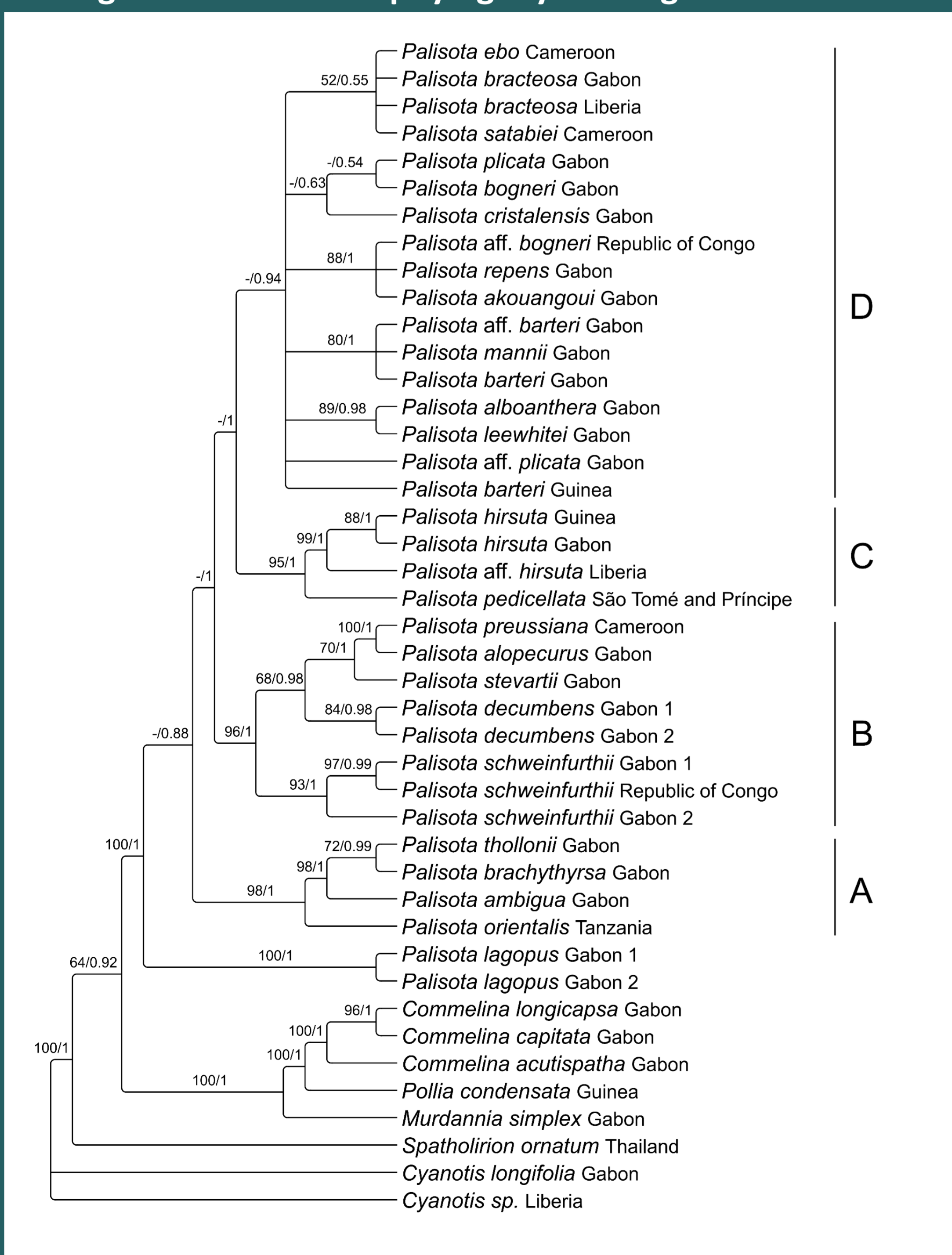


Figure 1. Majority rule consensus tree (cladogram) from a Bayesian analysis of the matrix obtained by concatenating the chloroplast and ITS sequences (43 specimens; 4710 base pairs). The values at the nodes correspond to the bootstrap supports (BS) obtained in the maximum likelihood analysis followed by the posterior probability (PP) values obtained with the Bayesian analysis. The values are shown only if they are greater than 50%.

Figure 3 : Phylogenetic context of the geographical distribution of the species

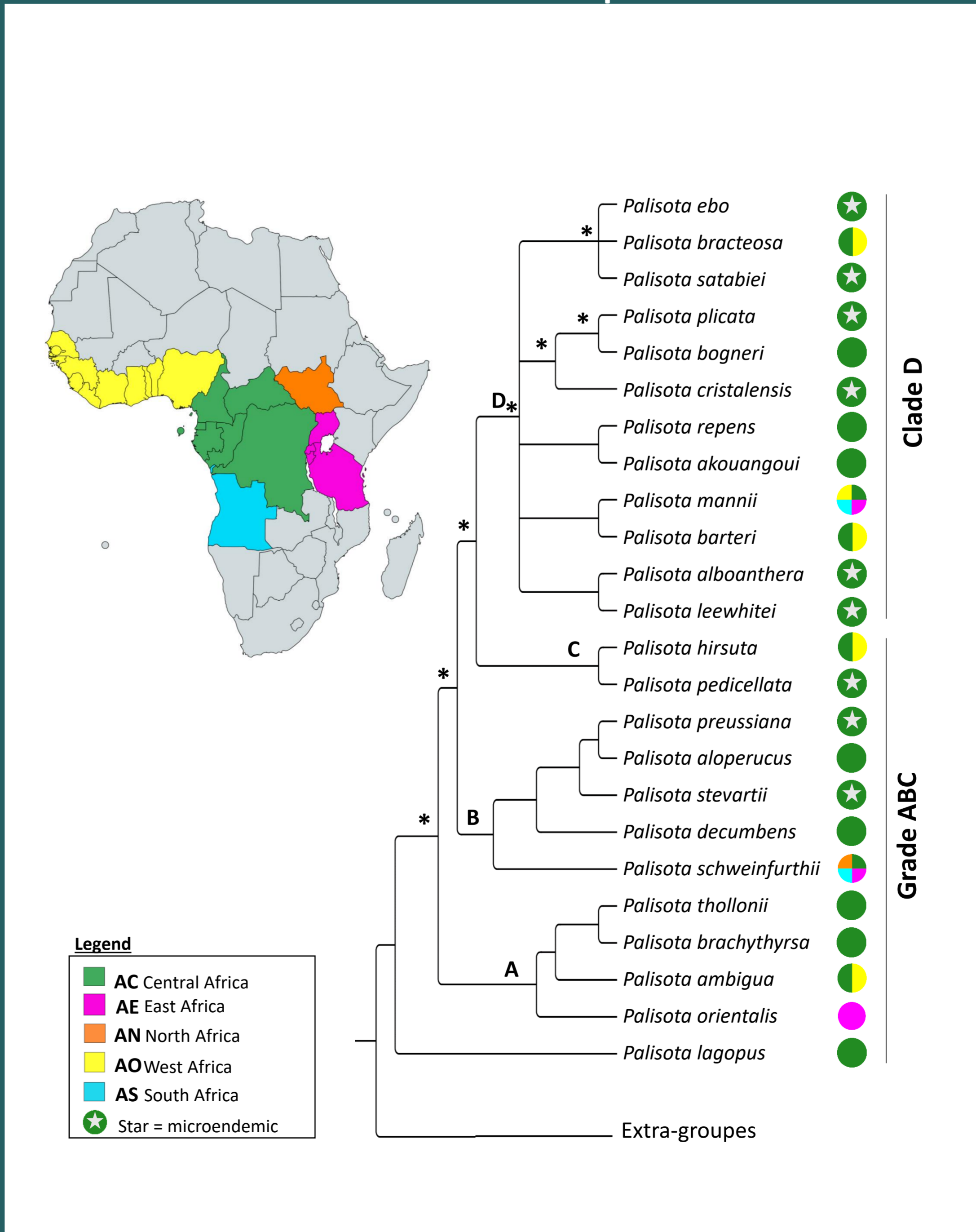


Figure 3. Geographical distribution of *Palisota* species in relation with the phylogeny of the group. We present the simplified majority consensus (cladogram). Legend: * = nodes with bootstrap support < 50%. Map generated with mapchart.net®.

C. NO STRONG GEOGRAPHICAL STRUCTURING

- ✓ A priori **little geographical structuring** in the clades.
- ✓ **Micro-endemism** in **grade ABC** (3/9 spp.) related to strong **geographical constraints**?
- ✓ Significant **micro-endemism** in **clade D** (6/9 spp.) related to former **refuge areas**?

CONCLUSIONS:

We confirmed the **monophyly of *Palisota*** and gave a first insight in the phylogenetic systematics of the genus. Whereas **basal relationships are still poorly supported**, we were able to use the phylogenetic framework to distinguish **two contrasting morphological groupings (grade ABC and clade D)**. No phylogenetic pattern was detected concerning species geographic ranges.

PERSPECTIVES:

- ✓ Add informative molecular regions to the analysis in order to **increase resolution** and support (e.g. nuclear markers).
- ✓ **Perform ancestral state reconstruction** for a series of key morphological characters, in particular for the eight phylogenetically significant traits identified here.
- ✓ **Identify regions of endemism** and infer dates of divergence for the group. This will ultimately allow for robust **biogeographic analyses**.



References:

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Acknowledgments :

We thank the curators of AAU, BR, BRLU, HBG, MO and P for permission to sample DNA from specimens held in their collections; this work was funded in part by the Research starting grant of the Ecology, Systematics and Evolution lab of University Paris-Saclay.