

# Evolution of diets in Phyllostomidae

## A contribution based on molecular phylogeny data

By Yann Gager, Fidel Botero & Emmanuel Douzery

Phylogénie moléculaire - Institut des Sciences de l'Évolution (UMR 5554 CNRS)  
Université Montpellier 2 - Montpellier, France



### General context

- **Taxonomy:** Phyllostomidae belongs to Chiroptera: Yangochiroptera: Noctilionoidea.
  - **Biogeography:** Central & South America.
  - **Life history traits:** High diversity of **species** (~160), with a high diversity of **diets** : arthropods, frogs, bats, lizards, blood, nectar, pollen, fruits, flowers & leaves.
  - **Phylogeny:** Difficulties to resolve the internal relationships of the family.  
Only 55 Phyllostomidae (+ 7 outgroups) were sampled in the molecular phylogeny study of Baker et al (2003).
  - **Evolution:** **Insectivorous** ancestral character state proposed for the last common ancestor of the family based on morphological traits (Wetterer 2000).
- Need for an updated molecular phylogeny to test this hypothesis !

### Material and methods

**Dataset :** Compilation from NCBI Genbank & concatenation of 4 mitochondrial genes (12S rRNA, 16S rRNA, CYB and CO1) + one nuclear gene (RAG-2) = a **supermatrix of 6,883 aligned sites**.

**Phylogenetic analysis :** Maximum likelihood (ML) inference (PAUP\* with a GTR + Gamma + INV model).

#### Trophic level data :

87 species + 2 outgroups

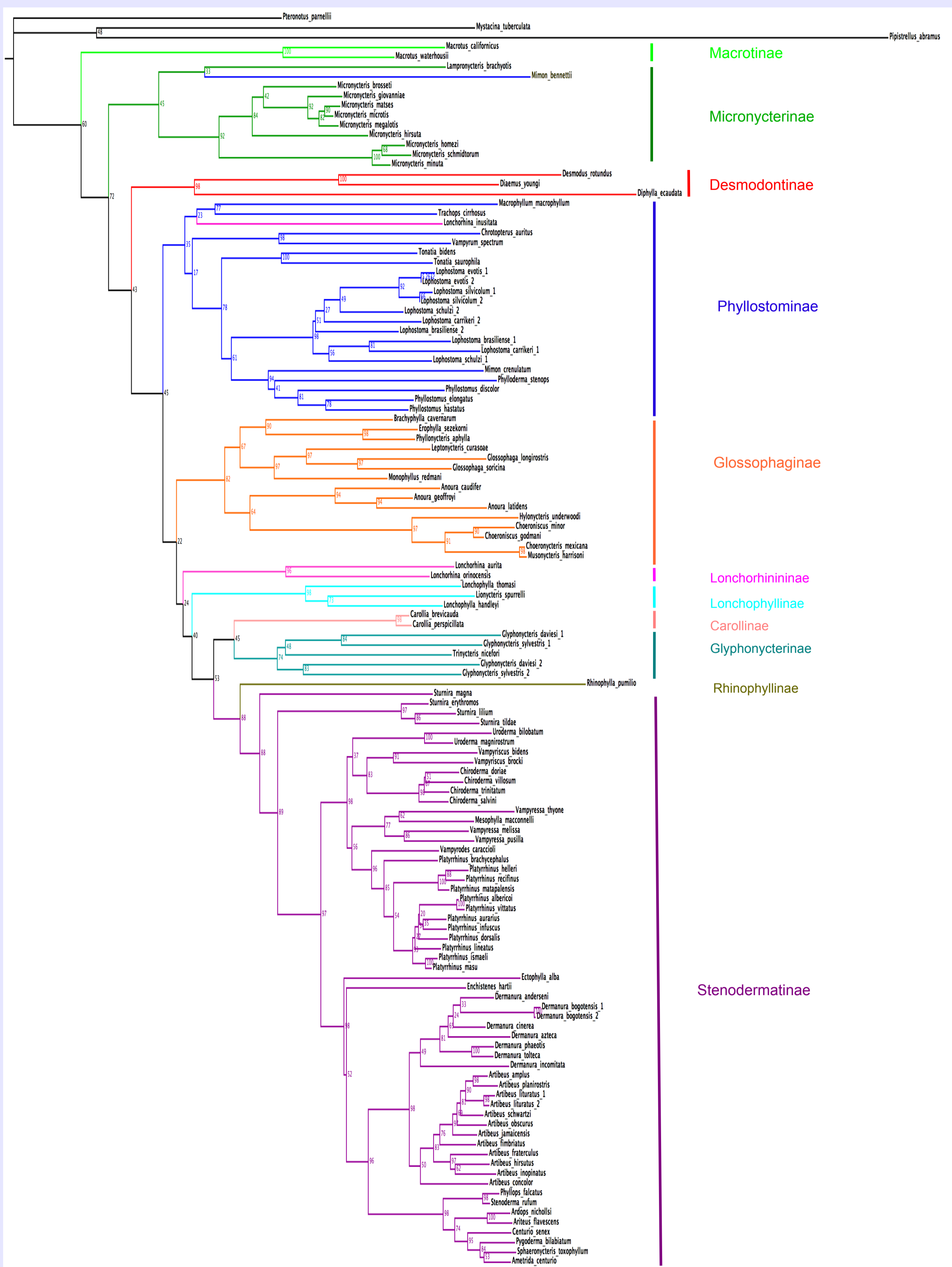
3 trophic levels used (Jones et al 2009) :

- > **Animalivory** : ■ Arthropods + Vertebrates (including blood) ;
- > **Phytophagy** : ■ Fruits, nectar-pollen-flowers, leaves ;
- > **Omnivory** : ■ At least one category of animalivory & phytophagy.

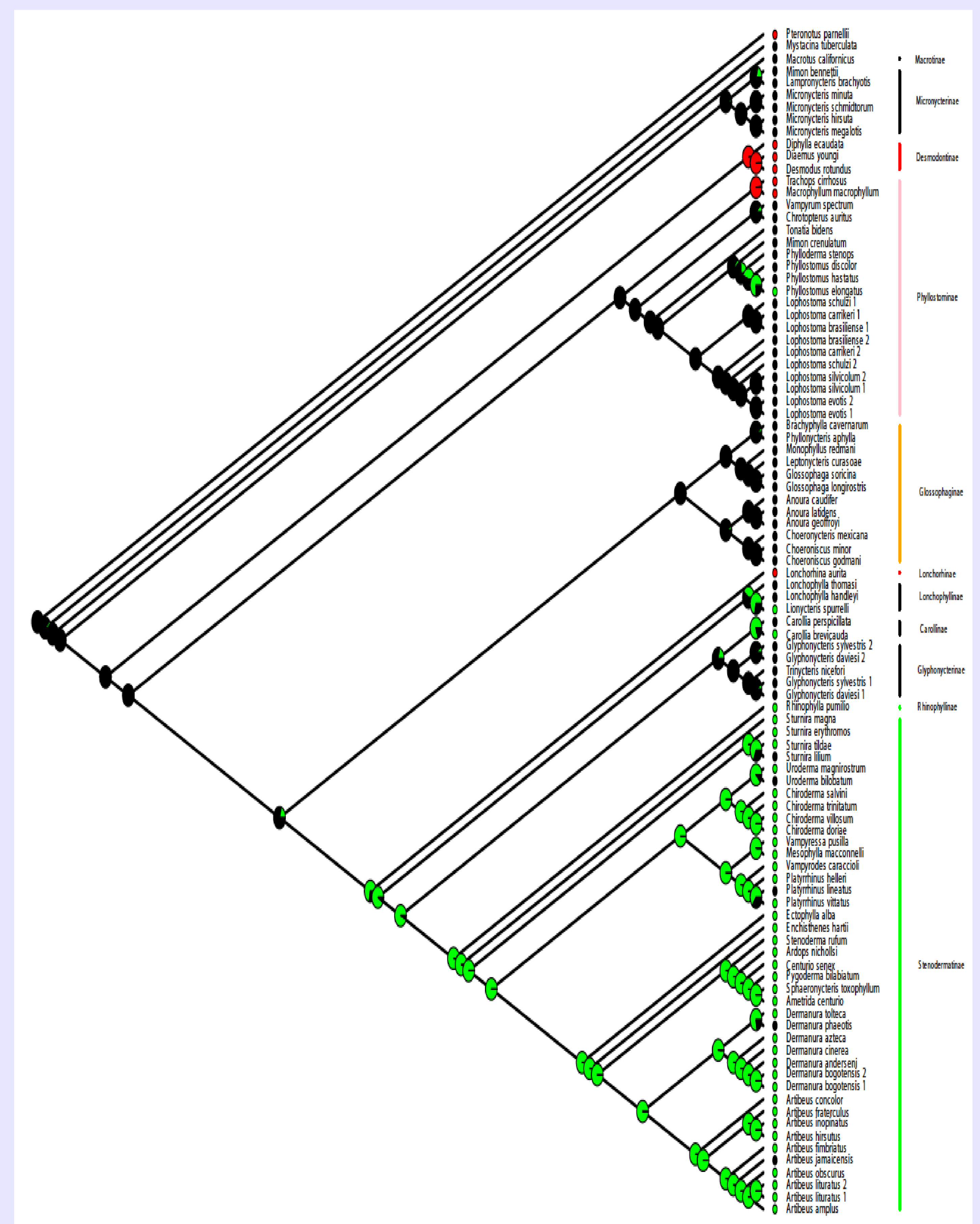
#### Ancestral Character Estimation :

Use of the function ACE (Paradis et al 2006): package Analyses for Phylogeny & Evolution (APE) within the software R.

**Fig. 1 :** Molecular phylogeny of Phyllostomidae from a ML analysis using the mitochondrial + nuclear supermatrix for 120 species. Bootstrap node support is provided.



**Fig. 2 :** Cladogram showing the diet ancestral character estimations based on available trophic level information (Jones et al 2009).



### Results & Discussion

✗ Molecular phylogeny of Phyllostomidae including more than 100 species (Fig. 1).

✗ Congruence with the classification proposed by Baker et al (2003).

✗ **First use of a probabilistic approach in the ancestral character state estimations** (of diets) to resolve a bat evolutionary ecology question.

✗ **Omnivorous diet for the last common ancestor of the Phyllostomidae**, maybe preferentially insectivorous (cf. Baker et al 2003, Datzmann et al 2010).

✗ One likely apparition of **haematophagy** and one independent apparition of strict **animalivory** (red disks on Fig. 2).

✗ Evidence for a **phytophagous** terminal crown (green disks on Fig.2).

✗ **Diphyly** of **nectarivorous** bats (Glossophaginae & Lonchophyllinae) as suggested by Datzmann et al (2010).

### References

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### Contact

yann.gager@orange.fr  
fidel.botero@gmail.com  
emmanuel.douzery@univ-montp2.fr