

Genetic diversity and population structure of two endemic and sympatric flying fox species from the Comoros archipelago (*Pteropus livingstonii* and *P. seychellensis comorensis*)



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1 Introduction

The Livingstone's flying fox (*Pteropus livingstonii*) and the Comorian flying fox (*P. seychellensis comorensis*) are two endemic fruit bat species of the Comoros islands known for their importance in the ecosystem functioning as pollinators and seed dispersers. These two species coexist in some of their roosting and feeding sites but seem to differ in their ecology, diet and reproductive behavior. Both species are highly threatened by habitat loss in the Comoros archipelago, and suffer from the highest deforestation rate in the world, estimated to 9.3% every year. This habitat loss, the low genetic diversity but also the lack of gene flow between population from each island may make them highly vulnerable to extinction. Assessing the effect of habitat loss on genetic diversity and population structure for the two flying fox species is a challenge in order to implement conservation plans.

How genetic approaches can help to assess relevant habitat management and conservation strategy for both flying fox species in the Comoros islands.

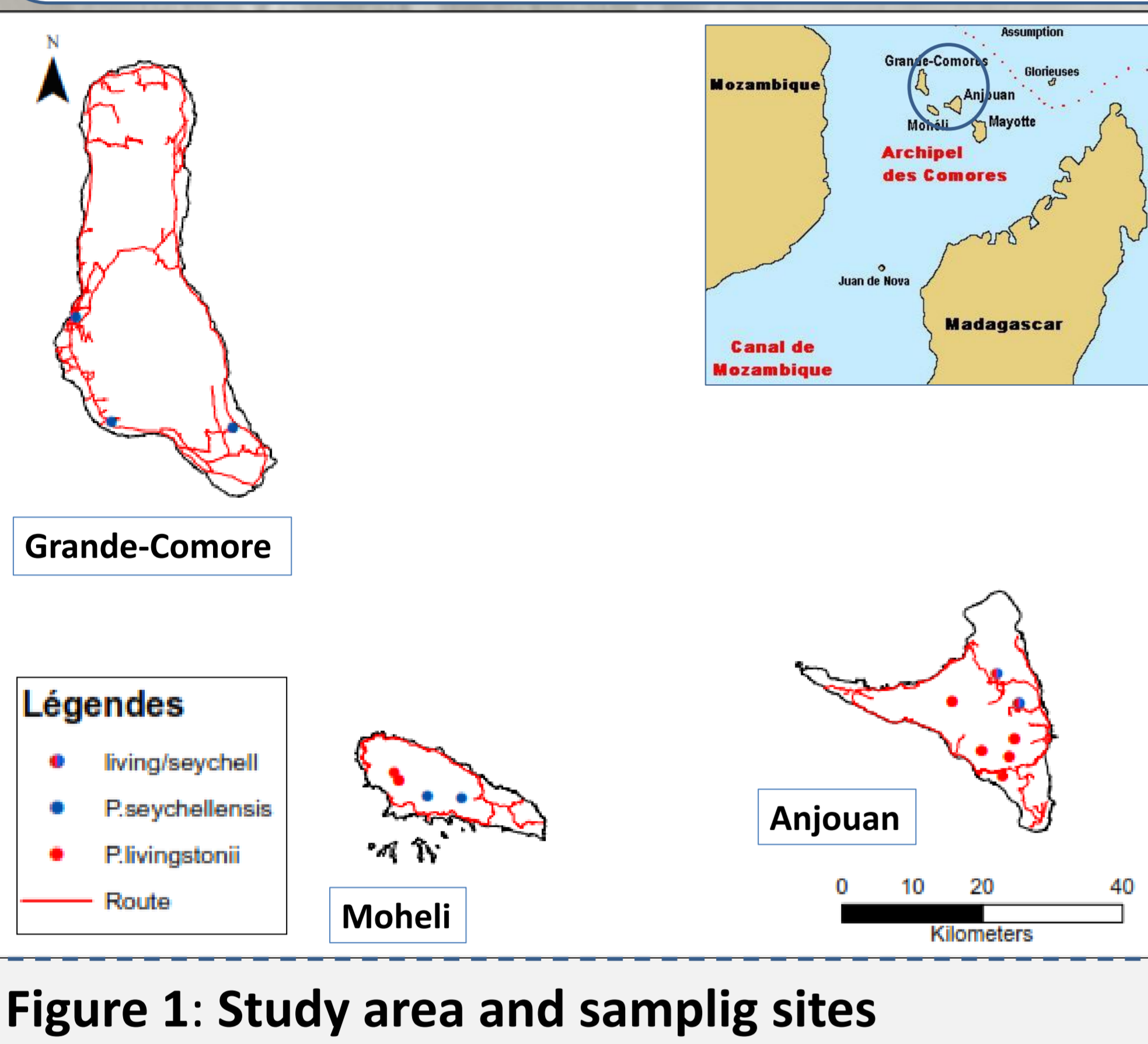


Figure 1: Study area and samplig sites

2 Materials and Methods

Sample collections:

- Faecal samples were collected below each rooting tree and tissue samples were collected using physical captures of individuals by mist nets.

Laboratory process:

- DNAs were extracted at the Degraded DNA platform (LABEX CeMEB)
- DNA amplifications were carried out using mtDNA (460 bp cytochrome b marker) at the Genetic Markers in Ecology Service (SMGE), CEFE, Montpellier.

Data analyses:

- Phylogenetic approaches (phylogenetic tree and network) for the genetic structure characterization between population
- Analyze of the mitochondrial polymorphism

3 Results

Sampling, amplification and species identification:

- 258 samples collected (227 faecal samples and 31 tissues)
- 112 samples are successfully amplified with the Cytb: 59 for *P. livingstonii* and 53 for *P.s. comorensis* with a PCR amplification rate of 43,41%
- Bias of species identification: 5 samples (5,8 %)

Genetic Diversity:

- Low rate of genetic diversity: *P.s. comorensis* (haplotypes number: $h=3$; heliotypic diversity: $Hd=0,50$); *P.livingstonii* ($h=8$; $Hd=0,79$) (Figure 2)

Genetic Structure:

- Lack of population structure between islands for *P.s. comorensis*
- *P. livingstonii* shows specific haplotype for each island highlighting that population from each island are structured for this species (Figure 2)

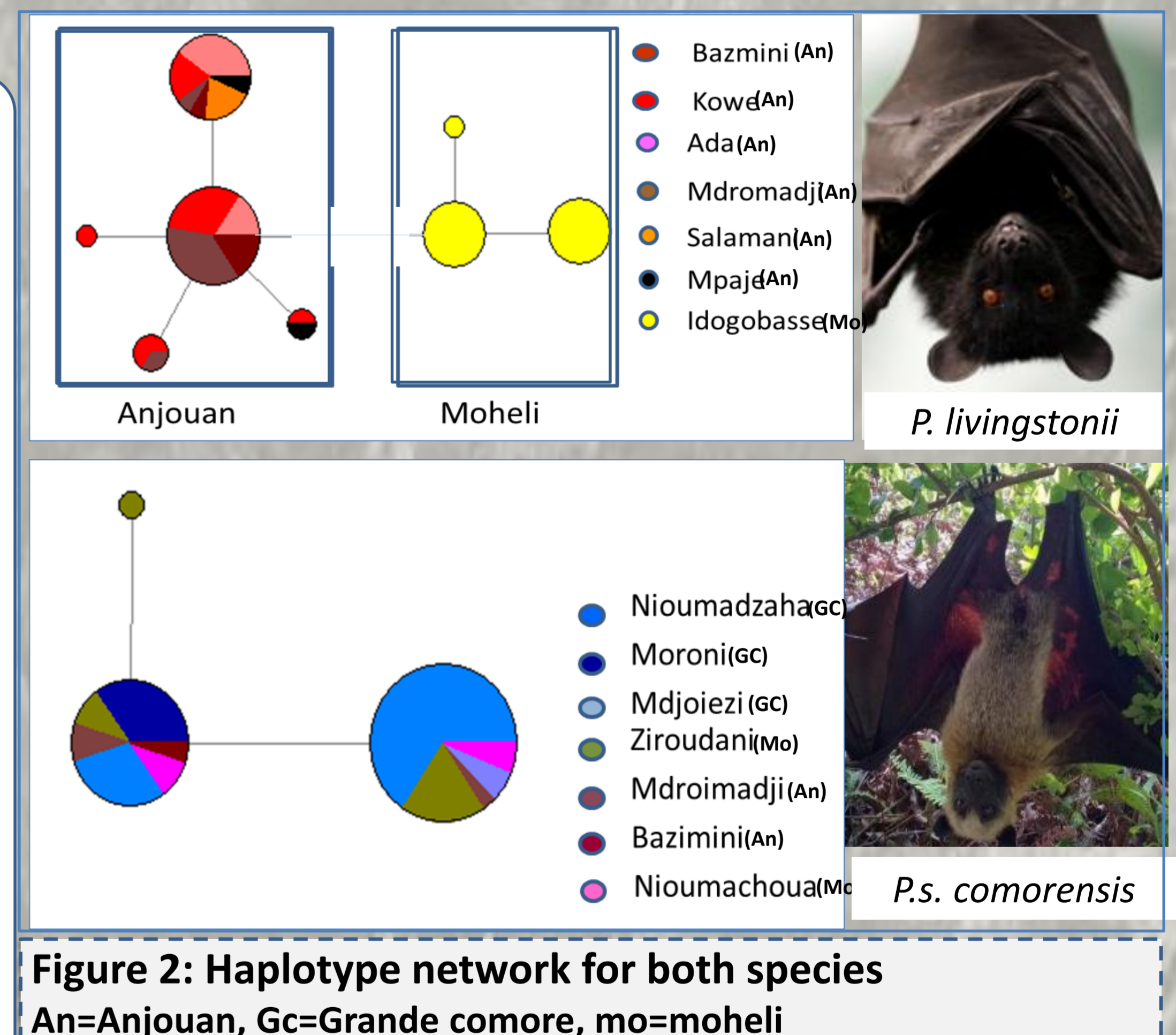


Figure 2: Haplotype network for both species
An=Anjouan, Gc=Grande comore, mo=mohéli

4 Conclusion & perspectives

- The lack of genetic structuration for *P.s. comorensis* indicates the presence of gen flow between the three island of Comoros separated by about 40-80 km in the contrary to *P. livingstonii* which presents specific haplotype for each island.
- Difference in the migratory and dispersal capacity for both species probably due to their wing morphology traits.
- *P. livingstonii* shows high diversity compared to its congener probably due to its demographic history and colonization events in the Comoros islands more former that *P.s.comorensis*.
- In the continuity of this study, our faecal and tissues samples are amplified using 9 microsatellite loci (O'Brien, 2007) for both species in order to understand the genetic interaction at fine scale between population. Genotyping study will be generalized in the ensemble of individuals.

References: O'Brien J., McCracken G.F., Say L. and Hayden T.J. (2007). Rodrigues Fruit Bats (*Pteropus Rodricensis*, Megachiroptera: Pteropodidae) Retain Genetic Diversity despite Population Declines and Founder Events. *Conservation Genetics*, 8, 1073–1082.

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