



THE MISSING LINK: WHAT ABOUT CENTRAL EASTERN ATLANTIC KOGIA SPP?

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Introduction

- The Kogiidae family was almost completely unknown until the early 2000s due to their cryptic and elusive behaviour and similar appearance, nowadays we are able to reconstruct their population genetics thanks to the use of new molecular techniques

Objectives

- Fill in a knowledge “gap” present in Kogiidae’s population structure in the Central Eastern Atlantic area
- Compare the obtained sequences with the ones already present in online molecular banks (Chivers et al., 2005; Viricel et al., 2012; Nishida et al., 2023; Plön et al., 2023)

Materials and Methods

- DNA-Extractions were performed for 42 samples (see Table 1)
- Primers used for amplification from Chivers (2005) analysing two regions of the mitochondrial DNA: a portion of the Control Region and a portion of the Cytochrome B
- All samples were Sanger sequenced

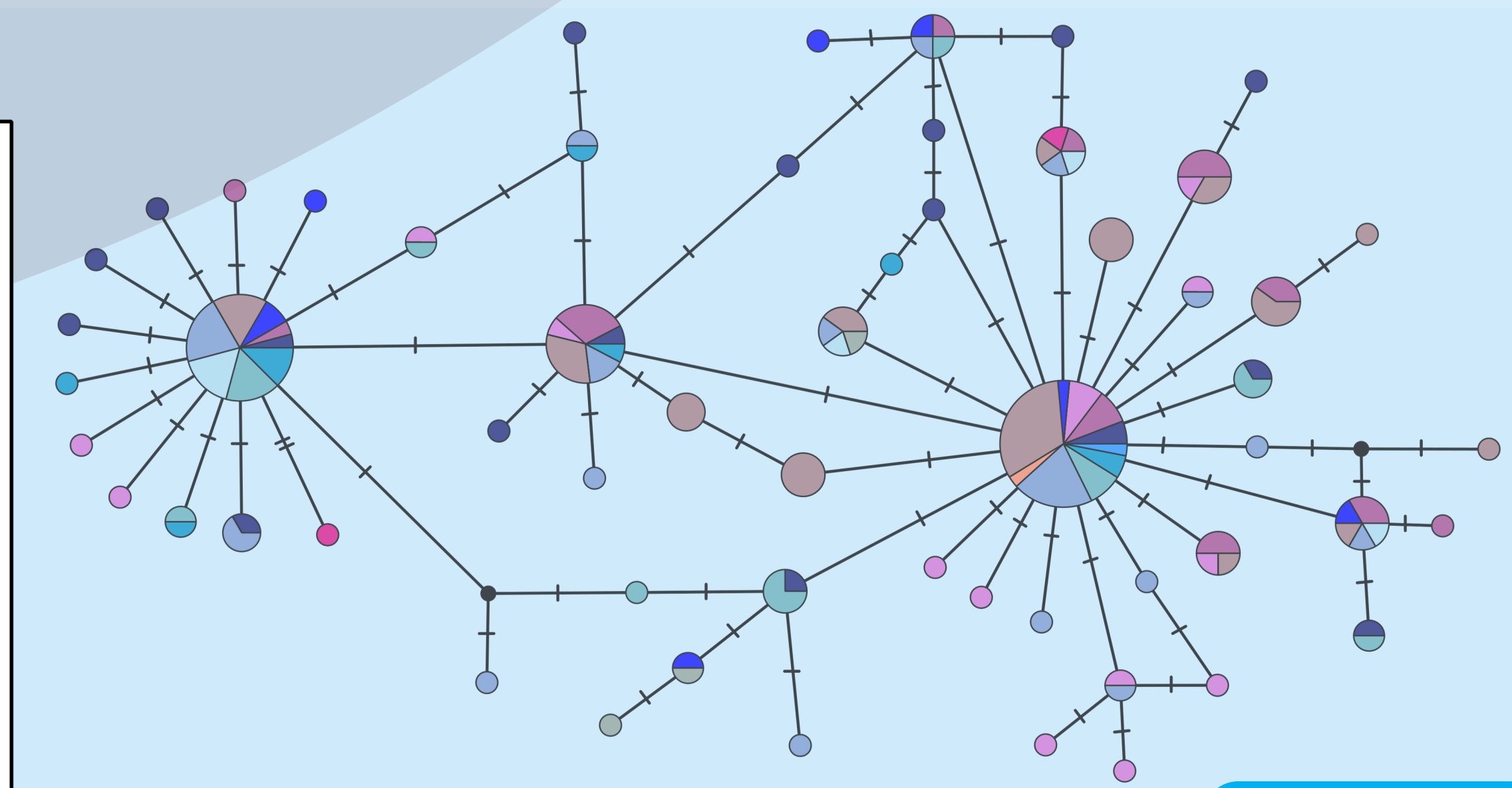
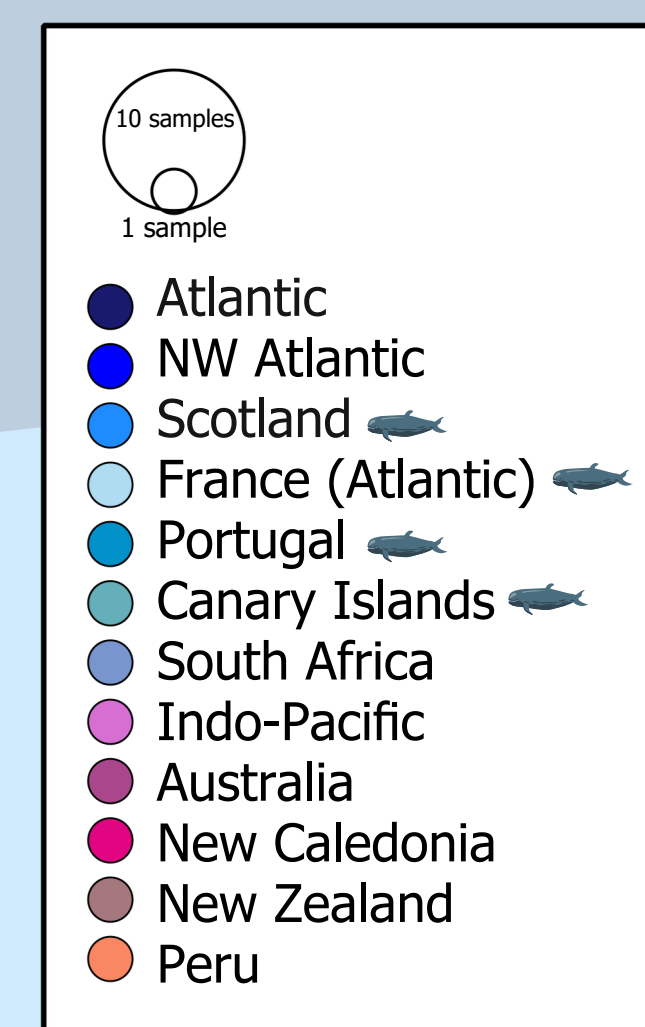
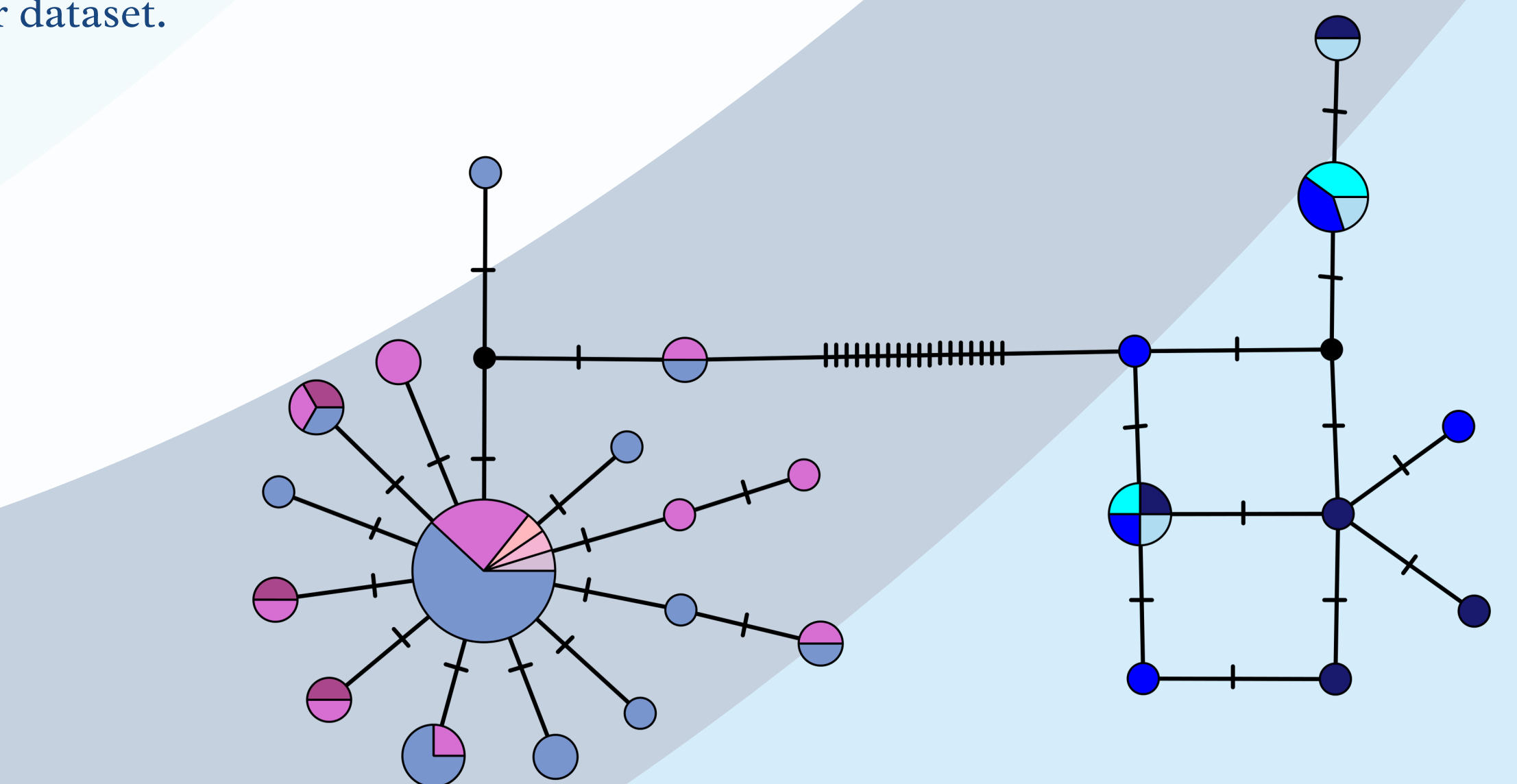
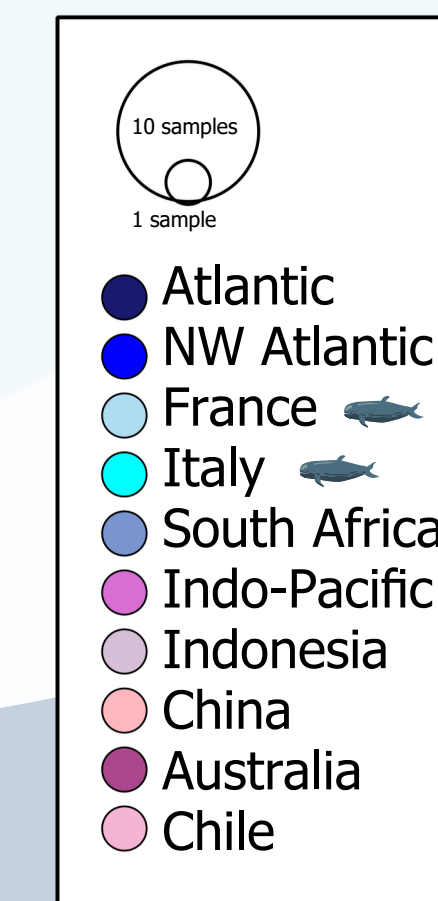
	CANARY ISL.	ITALY	PORTUGAL	FRANCE (ATL.)	UK
Kb	17	0	10	8	4
Ks	0	1	0	2	0

Table 1: Total sample set

Phylogenetic analysis

- Merge of a global database with all the available sequences on GenBank for both Control Region and Cytochrome B
- All the sequences were visually checked, cleaned and trimmed before being aligned using *Physeter macrocephalus* as the outgroup
- Creation of Median-Joining haplotype networks for both species and markers

Figure 1,2: Ks (above) and Kb (below) Median-Joining haplotype networks for Cytochrome B marker.
🐳 = samples from our dataset.



Results

- Kogia breviceps*’ total phylogenetic trees for both Control Region and Cytochrome B markers suggest a close evolutionary relationship among populations, while *Kogia sima* presents a strong mtDNA divergence between Indo-Pacific and Atlantic specimens
- The difference observed in mtDNA diversity and population structure between *Kogia breviceps* and *Kogia sima* suggests a dissimilarity in their evolutionary history and in the gene flow between oceans
- In one case, a sample identified as *Kogia breviceps* during carcass retrieval, clustered among *Kogia sima*’s haplotypes in the phylogenetic reconstruction

Conclusions

- Genetic analysis constitutes a valuable tool for their understanding and conservation status
- The results obtained confirm the patterns found worldwide: *Kogia breviceps* presents signs of persistent genetic flow between populations, while *Kogia sima*’s population structure shows distinct clades between the oceanic basins
- Some genetic characteristics found in these animals could suggest hints about their – still unknown – behaviour
- More samples are needed to get a clearer picture about their populations structure and the genetic flow between oceans and in between group inhabiting the same areas

References

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