

Genetic insights into the Mediterranean expansion of *Pinna rudis* following the decline of *Pinna nobilis*

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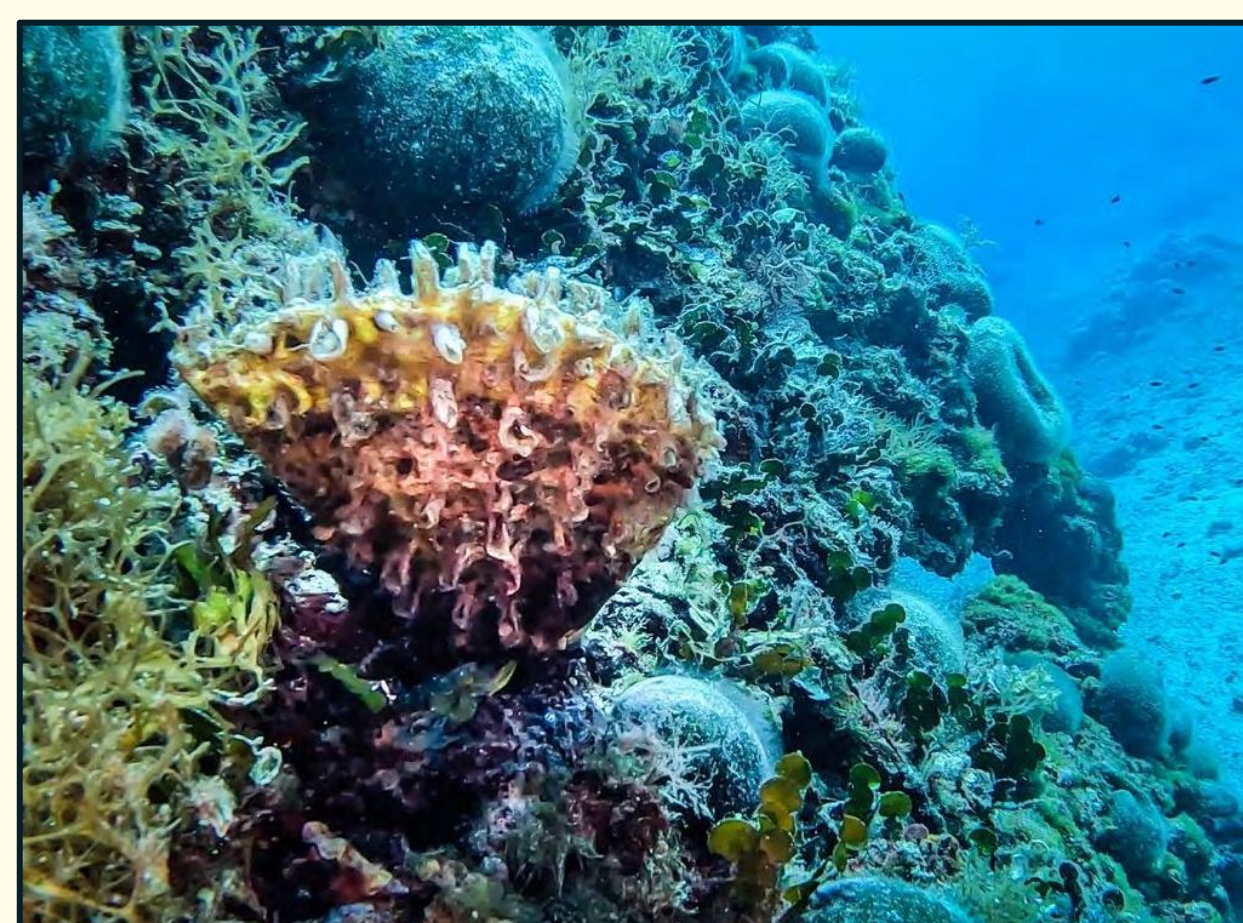
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Introduction



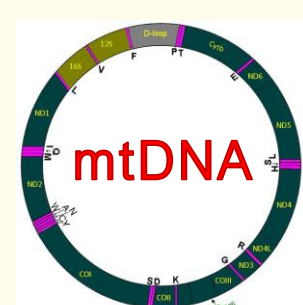
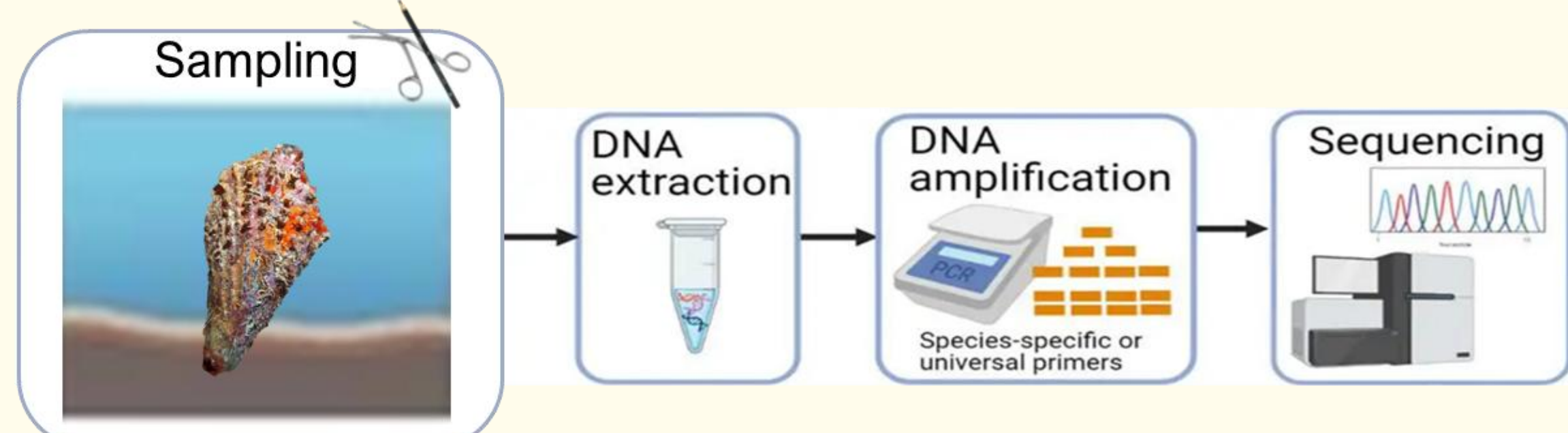
Pinna rudis



- Commonly known as the **rough pen shell**, is a close relative of the endangered Mediterranean *P. nobilis*;
- Despite its **Atlanto-Mediterranean distribution**, it remains quite less common in the Mediterranean;
- Following the **mass mortality of *P. nobilis***, it appears to be expanding into its **vacant ecological niches**.

This study investigates the **genetic variability** and **evolutionary relationships** of *P. rudis* populations in the Mediterranean through **phylogeographic** and **phylogenetic analyses**.

Materials and Methods

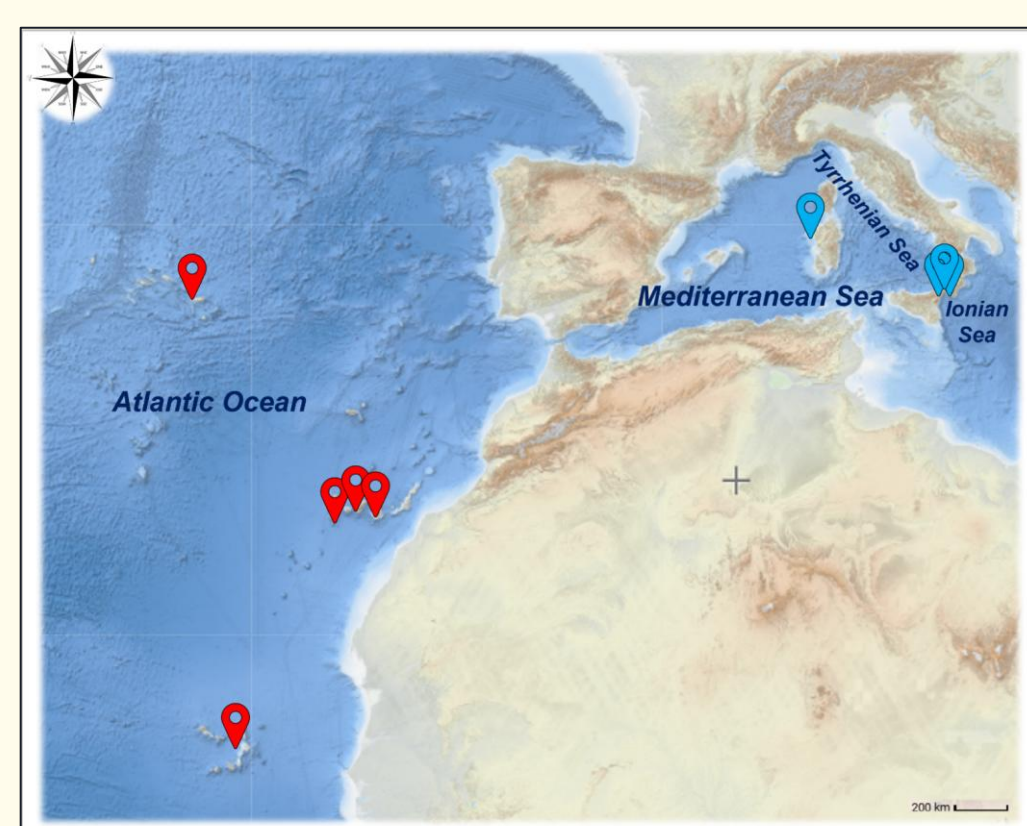


MOLECULAR MARKER:
Cytochrome c Oxydase Subunit I (COI)

115 analysed sequences (615 bp):

82 newly generated

33 taken from GenBank



These sequences represent *P. rudis* populations from various **Mediterranean and Atlantic locations**.

Figure 1. Geographic areas of origin of the sequences analysed in this study. Blue pins represent sequences newly generated, red pins represent sequences from the GenBank database.

Results

The preliminary results indicate a **lack of genetic structure on a geographic basis** between Mediterranean and Atlantic *P. rudis* populations.

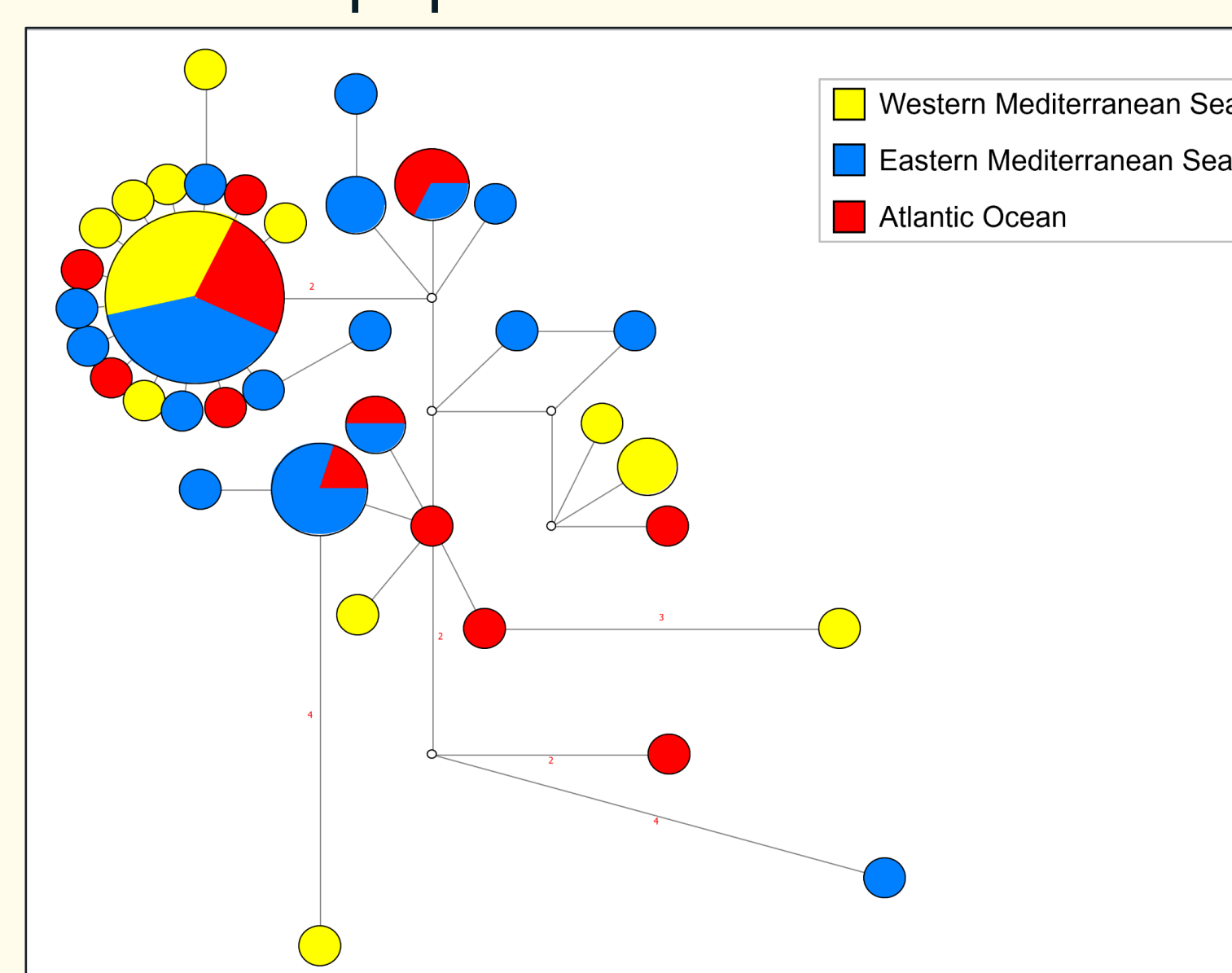


Figure 2. Network analysis (Median-Joining).

Network analysis (Fig. 2): homogeneous distribution of the most common haplotype, consistent with a typical founder effect; high dispersal capacity of the most adapted haplotypes in the Mediterranean Sea and Atlantic Ocean.

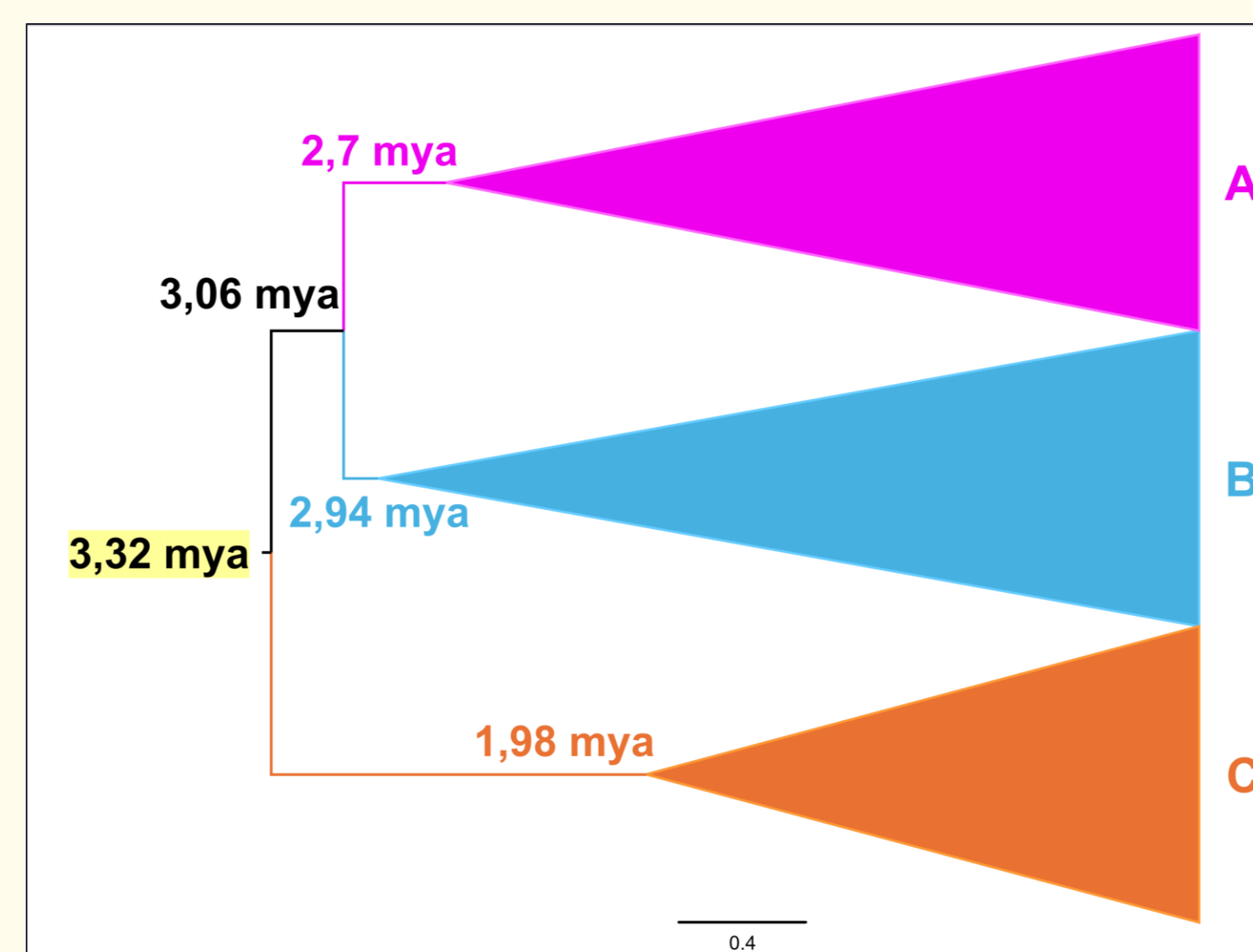


Figure 3. Graphical representation of the ultrametric Beast tree.

Ultrametric tree (Fig. 3): common ancestor dating to approximately 3.3 Mya, from which three main genetic clusters (A, B, and C) originated.

- Clusters **A** and **B**, **contemporary** and **closer** to the **earliest *P. rudis* ancestors**, date back to around **3 Mya**;
- Cluster **C** is **more recent**, with a **divergence time** of approximately **1.9 Mya**.

Our genetic data further suggest that *P. rudis* and *P. nobilis* are nearly **contemporaneous species**, with the latter originating around **2.5 Mya** (Sanna et al., 2024), and they likely share a **common Atlantic ancestor**.

Conclusion

This is the **first extensive genetic study** on *P. rudis* populations in the **Mediterranean**, providing crucial insights into **species conservation and management**.