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AIMS OF THE STUDY

Loggerhead turtles (*Caretta caretta*) are widely distributed and threatened marine turtles, and have been grouped into nine discrete population segments (DPS; NMFS, 2009). Several factors contribute to the separation of these DPS, including the described existence of barriers to gene flow between them. This is the first study on the genetic diversity of loggerhead populations nesting in southern Mozambique.

METHODS

The following procedures were conducted:

- Collection of 63 samples from muscle tissue between 2010 and 2013
- Extraction of DNA with Quiamp
- Sequencing 817 bp fragment from mtDNA Dloop
- Genotyping 21 nuclear loci (microsatellites).

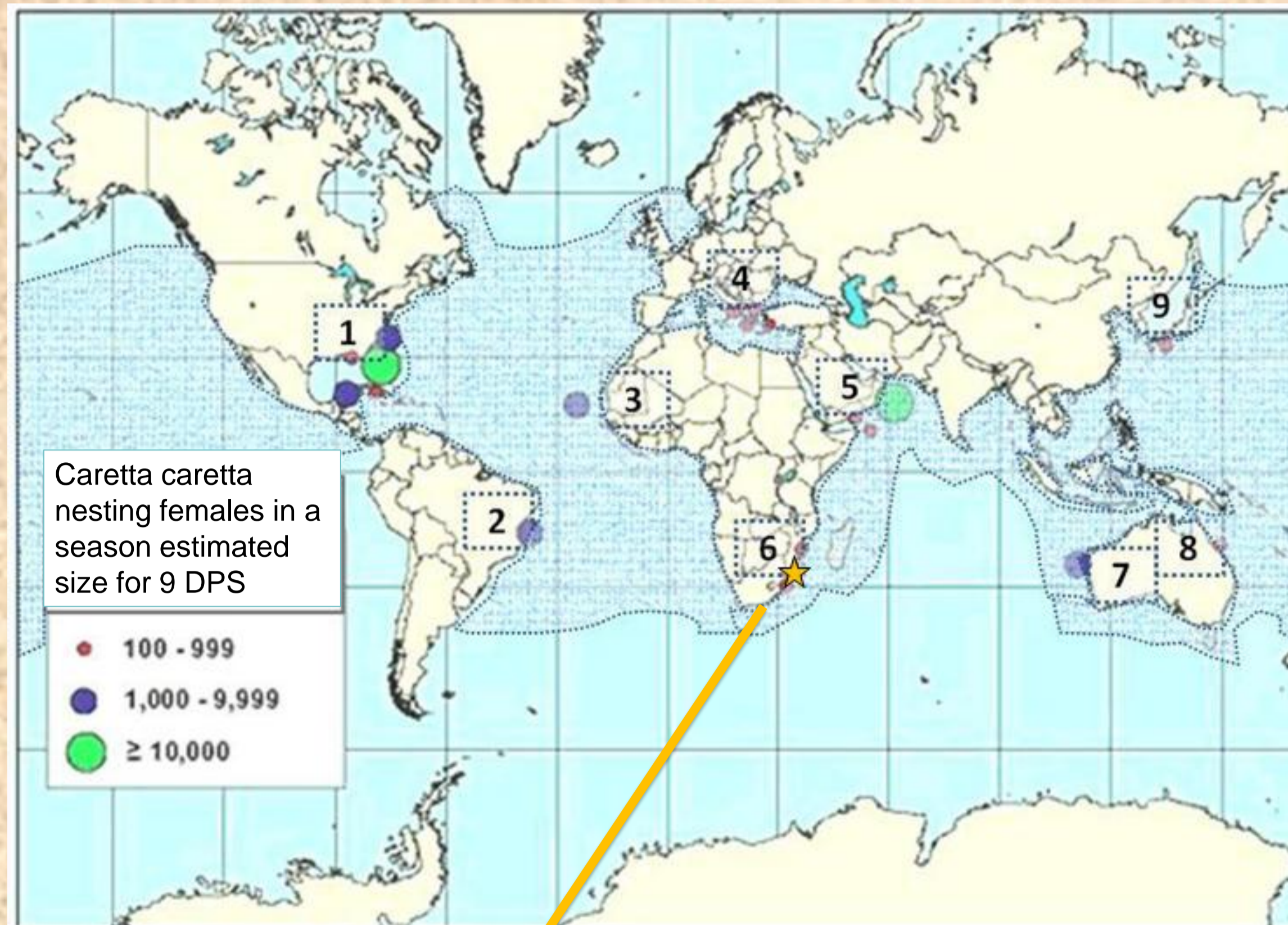


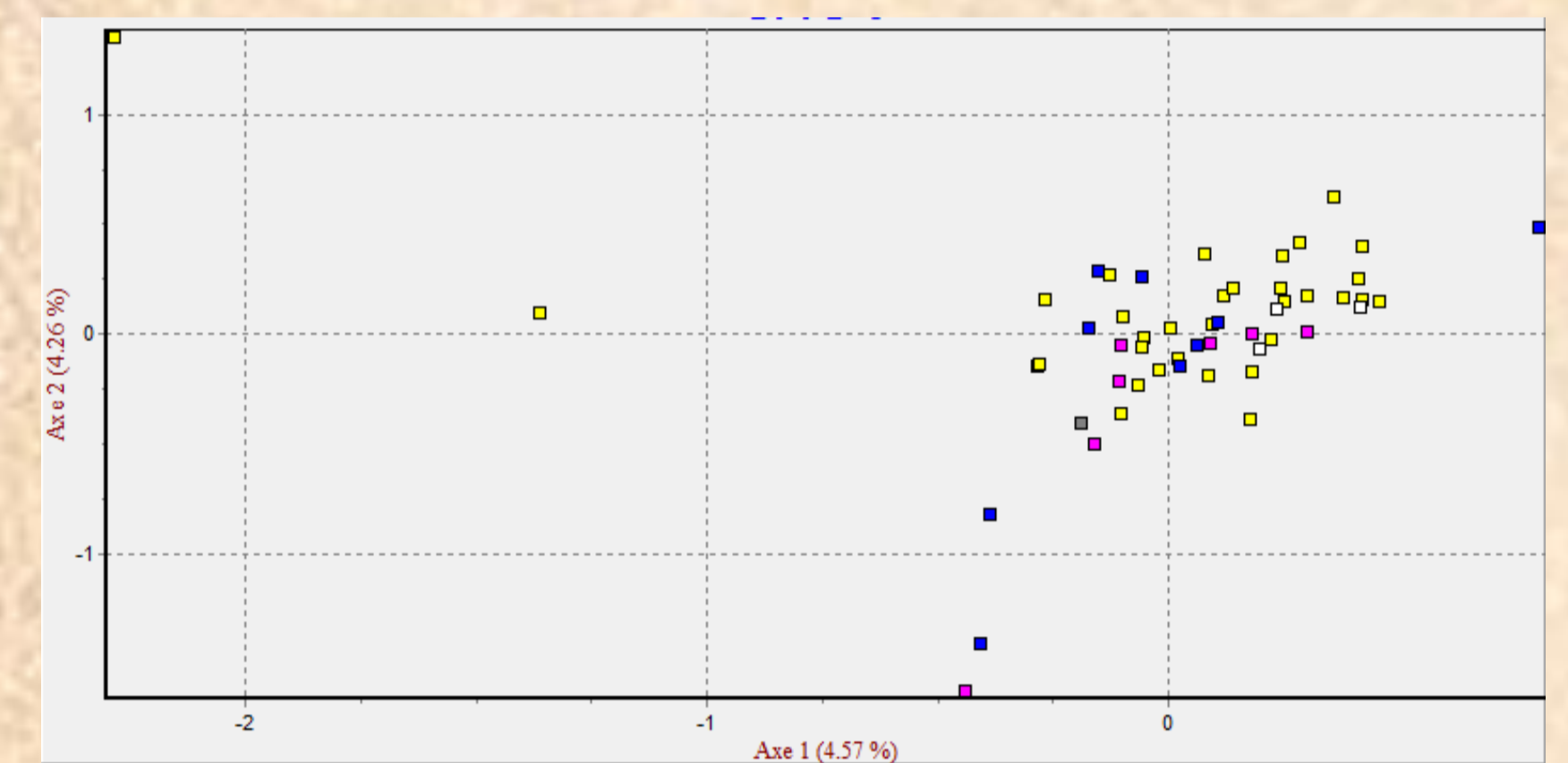
Photo: Raquel Fernandes



Photo: Eduardo Videira



Microsatellite analysis did not show any clear genetic differentiation whether the artificial geographic partitions were considered *a priori* or not. (genetic distance -FST, Bayesian inference and Factorial Correspondence Analysis -AFC, respectively done in Genepop, Structure and Genetix software).



RESULTS & DISCUSSION

The ADN_m analysis showed that there are two haplotypes in this population, CC-A2.1 and CC-I1.

Nucleotide diversity (π) was 0.00005 and haplotypic diversity (h) was 0.033. This is the first study to describe the CC-I1 haplotype, which seems to be a private haplotype of the POPMR nesting population.

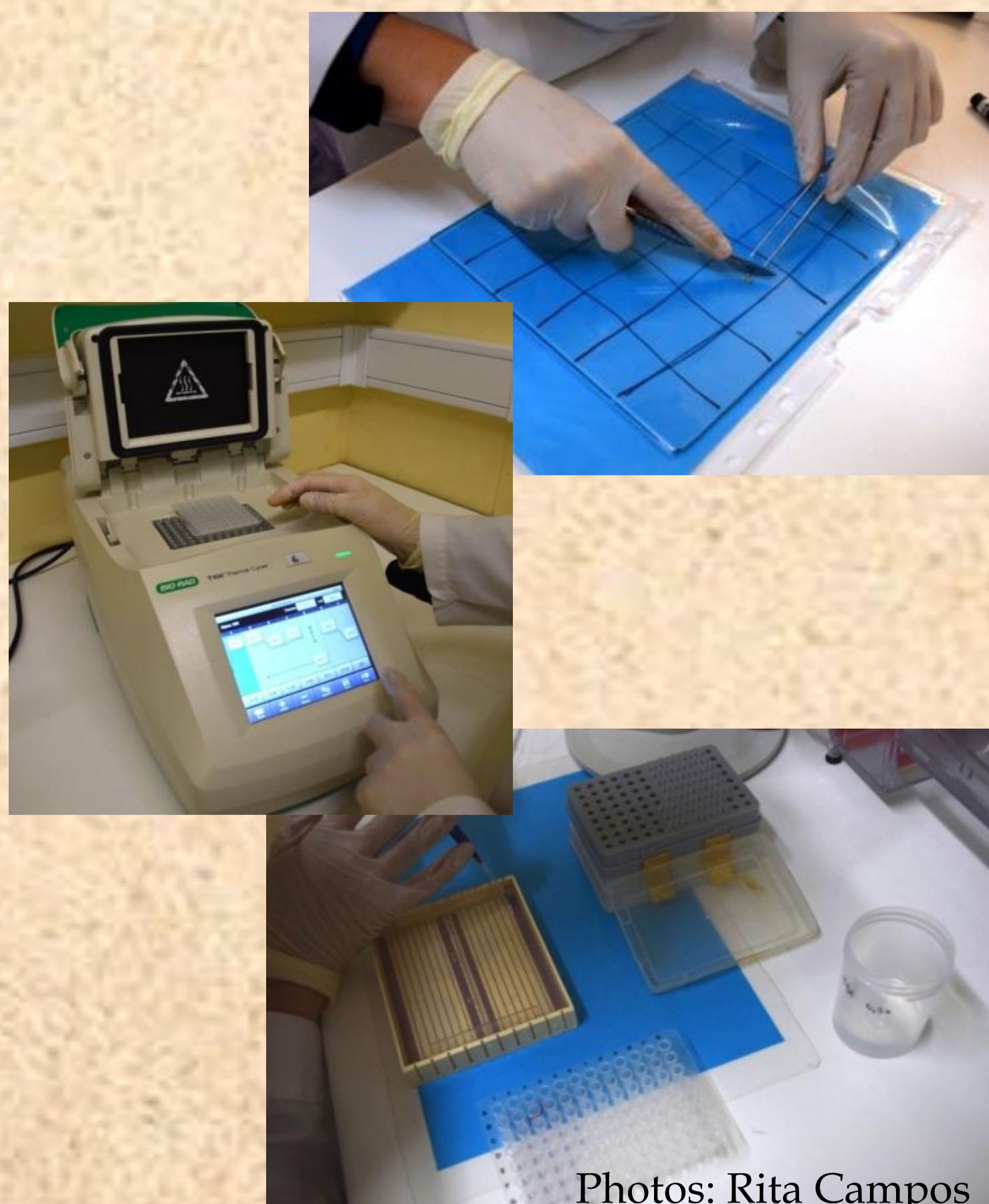
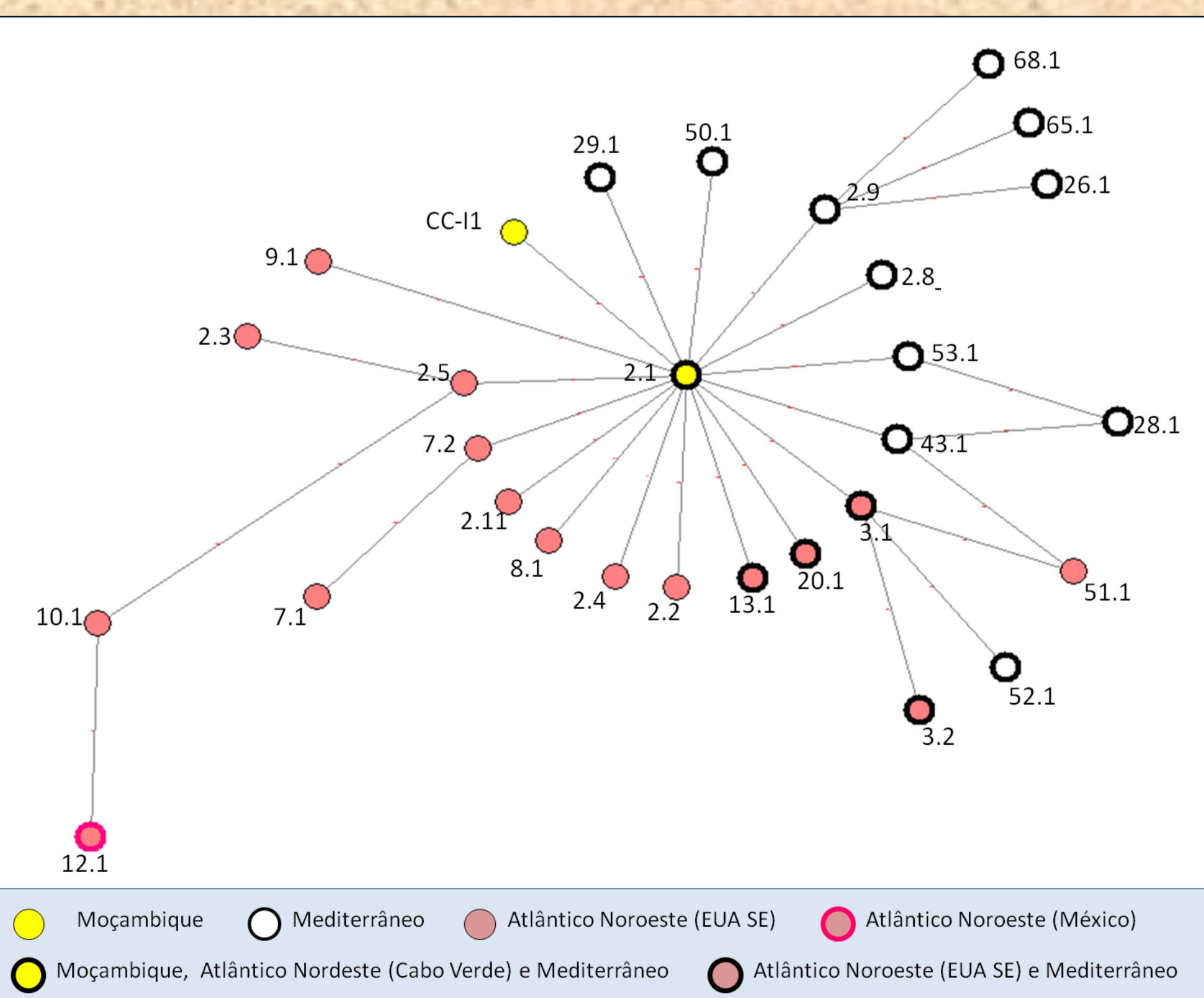
The CC-A2.1 haplotype is present in several populations that nest in the Mediterranean beaches, and less commonly, in the Northwest Atlantic (e.g. Florida) and Northeast Atlantic (e.g. Cape Verde) beaches (Shamblin *et al.*, 2014).

The expected heterozygosity (H_e) average for the POPMR population was 0.675 ± 0.271 .

The effective population (N_e) estimate for loggerhead turtles given by the LDNE software was 276 to 428 (depending on the lowest allelic frequency used), whereas with the ONeSAMP software was 193. Several models were used to detect the occurrence of a bottleneck (using the software Bottleneck) but only one case of a possible recent demographic bottleneck was found, which shows the low likelihood of a recent demographic bottleneck.

CONCLUSION

- This study reinforced the hypothesis of recent (during the Pleistocene) colonization of the Indian Ocean beaches from the Atlantic Ocean, enabled by the weakening of the cold Benguela current and strengthening of the warm Agulhas current, which temporarily removed the Cape of Good Hope thermal barrier for temperate turtle species.
- The H_e for the POPMR population was lower than what was estimated for southeast United States populations ($H_e = 0.862 \pm 0.092$), for the same set of loci. The smaller genetic diversity could be explained by non-representative sampling or because the population is effectively smaller.
- The absence of structuring did not allow the setting of geographic population limits, indicating the possibility of gene sharing between loggerhead turtles from the southern Mozambique, South Africa, and probably, although to a lesser degree, Madagascar and Oman.
- Even though the data obtained in this study do not indicate a recent demographic bottleneck, the low genetic variability and the reduced effective population size suggest that the nesting loggerhead turtle population in the POPMR may be susceptible to environmental changes or anthropogenic threats. The results of this study also suggest that the conservation efforts for this species in the southern Mozambique should take into consideration the fact that we are dealing with a single population, without a clear structuring between the different beaches.



Photos: Rita Campos

ACKNOWLEDGEMENTS

Thanks to CIBIO, CTV, POPMR, Peace Parks Foundation, Toyota Mozambique, Petromoc, the AGIR Programme, We Effect, British Chelonia Group, Critical Ecosystem Partnership Foundation, Universidade Eduardo Mondlane (UEM). The data is part of a MSc thesis submitted to the UEM. To access the full thesis, please visit Centro Terra Viva's publications page at: www.ctv.org.mz

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