

# Genetic population structure and connectivity of the mud creeper *Terebralia palustris* (Linnaeus, 1767) in Kenya and Madagascar.

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## INTRODUCTIONS

- Genetic diversity covers the genetic variation among individuals within a population and among populations. Species diversity is regulated by combined biological and physical process. Divergence is caused by evolutionary process.
- Great dispersal potential is associated with high gene flow.
- the "South Equatorial Current" (SEC) in the Indian Ocean could facilitate dispersal by drifting propagules and planktonic larvae in the Eastern African region.
- Terebralia palustris* (Linnaeus), the largest prosobranch dominating the surface of the muddy substrates of mangrove forests, have a planktonic larvae but the duration is still unknown. Not much information is available about *T. palustris*.

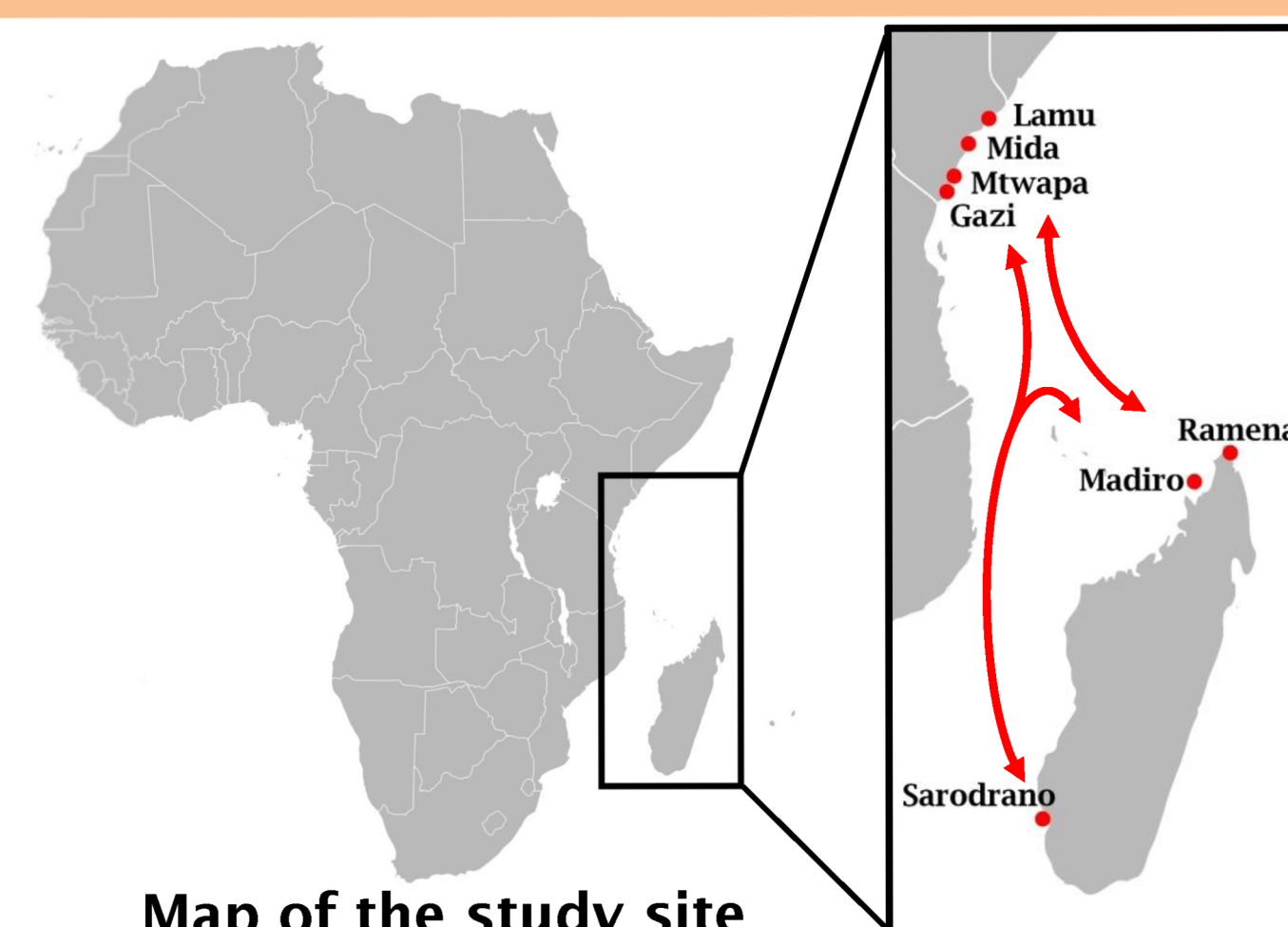


Figure of a *Terebralia palustris*

## OBJECTIVES

To investigate:

- the genetic diversity of the four sampled sites in Kenya (Lamu, Mida, Mtwapa and Gazi) and Madagascar (Sarodrano, Madiro and Ramena (see map). There is a probability to include Tanzania in the study.
- the connectivity among *T. palustris* populations in short scale (within each country) and bigger scale (between country).
- Implication for conservation



Map of the study site

## METHODOLOGY

### • Sample collection:

Tissue were collected and stored (in Ethanol 96°) waiting for DNA extraction.



### • DNA extraction, amplification and sequencing:

DNA extraction using QIAGEN® kit. CO1 amplification through PCR using Folmer (1994)'s primer.



### • Genetic diversity:

estimation of the haplotype and nucleotide diversity using the Programme Arlequin.

### • Phylogenetic analysis

### • Historical demography and genetic population structure:

Test the hypothesis of neutral evolution using Tajima's D test and Fu's Fs test.

## RESULTS

- Analysis will be based on approximately 680bp partial sequence of mitochondrial CO1 from 134 individuals.
- "h" value and "π" percentage value will be calculated to estimate level of genetic diversity.
- Analyses of molecular variance (AMOVA) will reveal the spatial population differentiation among sample sites.
- Hierarchical AMOVA will show the homogeneity of population.
- Genetic population structure will be investigated and will indicate level of gene flow.
- The population structure in the Eastern African region will be estimated.

***Terebralia palustris* is still out of the list of endangered species at present, but the widespread destruction of the mangrove forests upon which it is dependent may lead to that direction.**