

Genetic diversity and connectivity of *Seriatopora hystrix* along the East Coast of Africa

Buitrago Carol, Rosa Maria van der Ven and Marc Kochzius
Marine Biology, Vrije Universiteit Brussel (VUB), Pleinlaan 2, 1050 Brussels, Belgium

Introduction

- ❖ Coral reefs are the most diverse marine ecosystems in the world; nearly three-quarters of them are either gone or threatened [3].
- ❖ Reefs provide livelihood to approximately 16 million people in the coastal regions of Kenya, Tanzania, and Mozambique (mainly from fishing and tourism) [2].
- ❖ These reefs have been severely impacted by climate change (bleaching) as well as anthropogenic activities (unsustainable fishing, pollution and sedimentation from construction and coastal development) [2].
- ❖ Recovery of affected coral populations depends on both the availability of parental stock for new recruitment and the connectivity patterns among subpopulations.
- ❖ This research aims to elucidate the connectivity patterns of the scleractinian coral *Seriatopora hystrix* along the East Coast of Africa by assessing genetic diversity and connectivity among subpopulations. This provides scientific support for conservation and implementation of Marine Protected Areas (MPAs).

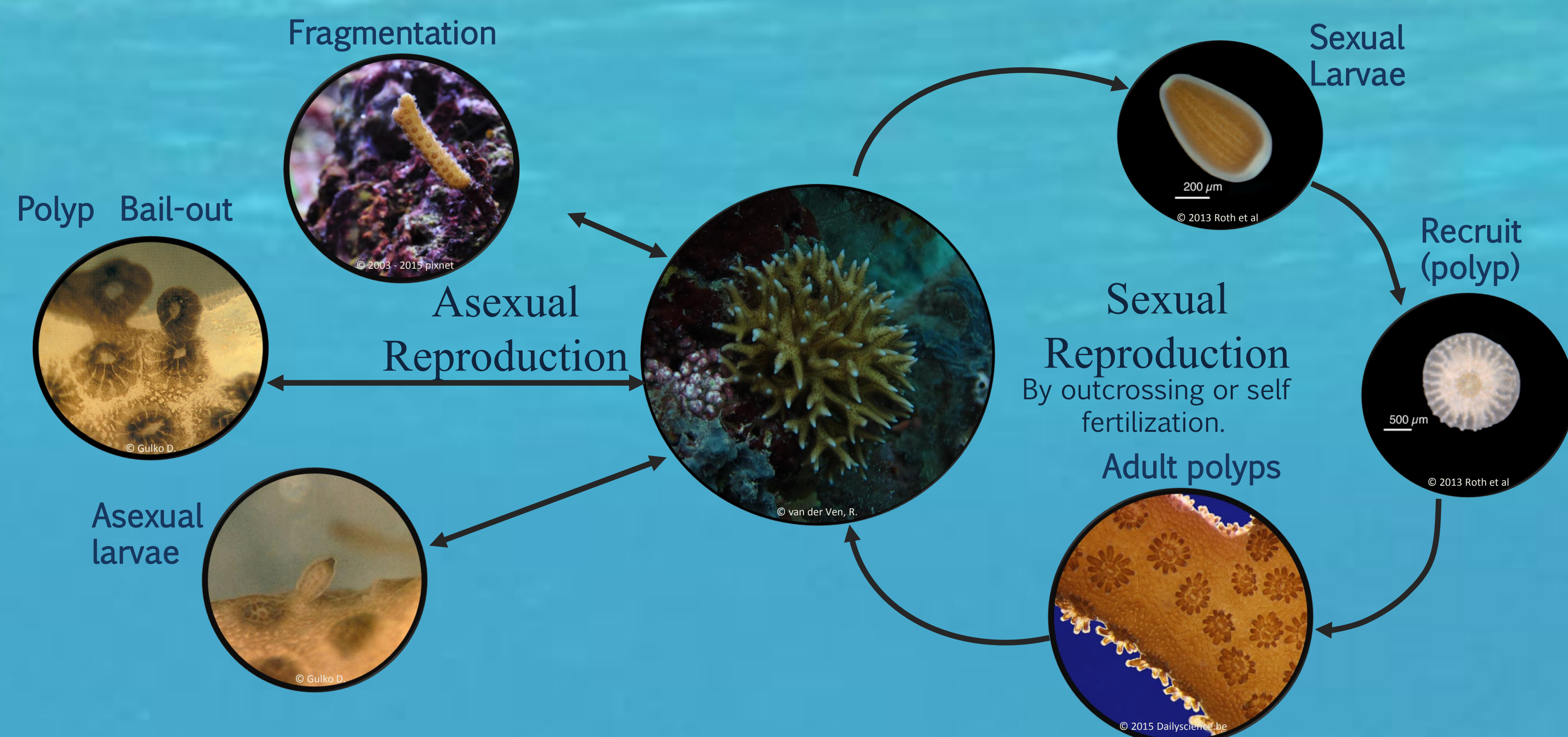


Fig. 1 Reproduction strategies of *Seriatopora hystrix*. Asexual reproduction by fragmentation, polyp bail-out and asexual larvae, and sexual reproduction by either outcrossing or self fertilization.

Seriatopora hystrix

- ❖ Hermaphroditic scleractinian coral species found in the Indo-Pacific.
- ❖ Rapid growth and high reproductive output either sexual or asexual (**Fig.1**); likely to recolonize reefs that have been disturbed [4].
- ❖ Larvae can settle within ten to hundred meters of their parental colony [6], although long dispersal of sexual and asexual propagules can occur [8].

Research Hypotheses

1. Along the East Coast of Africa, we expect to find high level of genetic structuring within and between subpopulations of *S. hystrix*.
2. Higher connectivity between sample sites in Tanzania and Kenya (distance correlated) as compared to those from Mozambique. This due to a genetic break caused by the split of the South Equatorial Current (SEC) (**Fig. 2**)

Materials & Methods

Sampling

- Tissue samples (1-2 cm branch fragments) of 238 *S. hystrix* colonies from 10 sites (**Fig. 2**)
- 2 m distance among colonies to avoid neighboring clones.

Lab Processing

1. DNA extraction.
2. DNA quantification.
3. Microsatellites selection and primer testing [1, 7].
4. Multiplex PCR design.
5. Fragment Analysis.

Analysis of data

6. Scoring Microsatellite.
7. Analysis of Molecular Variance (AMOVA), Principal Components (PCoA), Heterozygosity (F-statistics) and Clonality.
8. Estimation of genetic distances within and between subpopulations (F_{ST}).
9. Determination of genetic structure and clustering analysis of populations.

Study Area

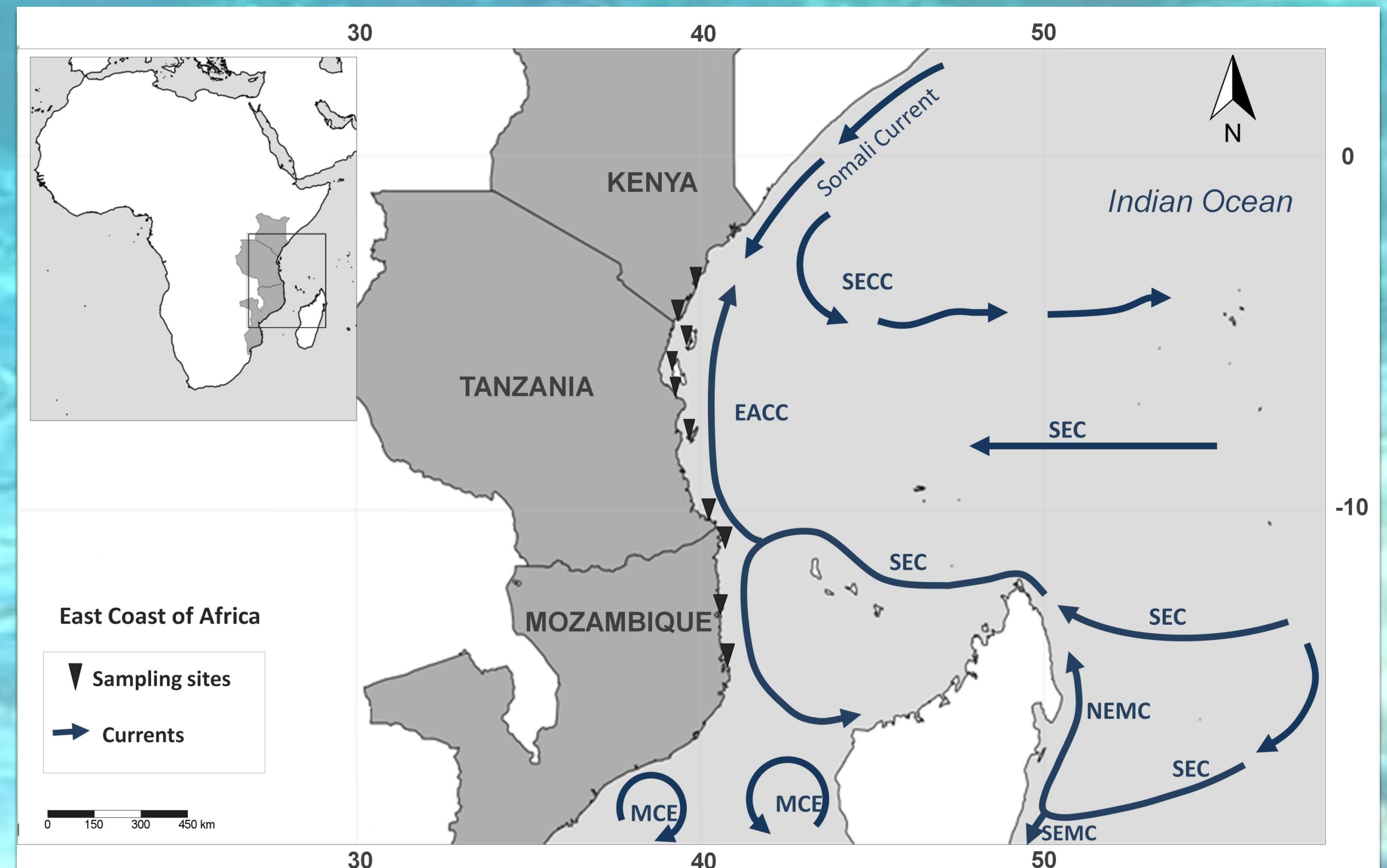


Fig. 2. Sampling sites in Kenya, Tanzania and Mozambique. Sampling sites are represented by black triangles. The ocean currents are shown by blue arrows: the South Equatorial Current (SEC), South East Madagascar Current (SEMC), North East Madagascar Current (NEMC), East African Coastal Current (EACC), and the Mozambique Channel eddies (MCE) during the Southeast Monsoon [0, 5].

Preliminary results

- 13 polymorphic microsatellite markers were selected and used in two multiplex PCRs (**Fig. 3**).

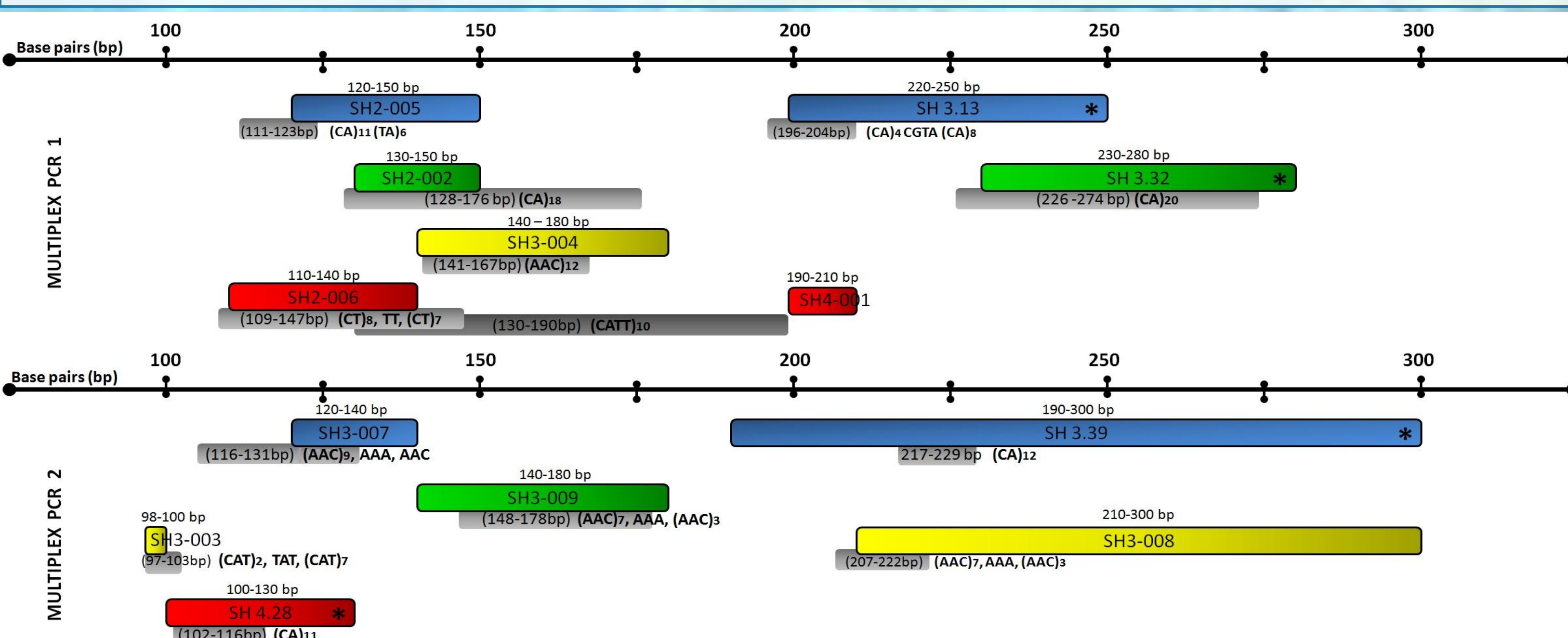
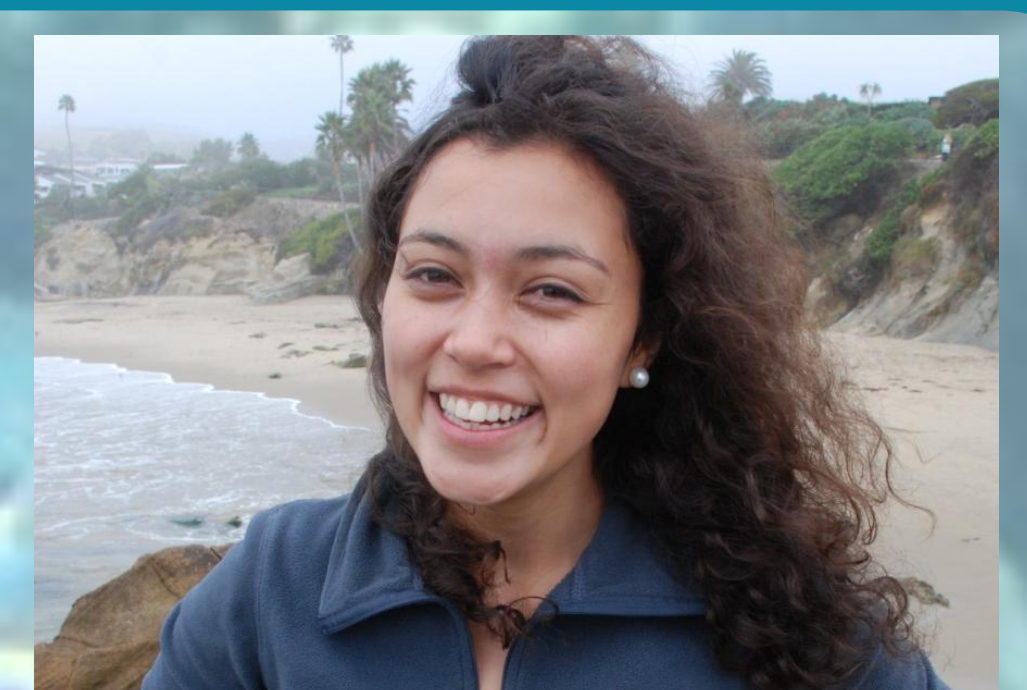


Fig. 3. Arrangement of two Multiplex PCRs. *S. hystrix* microsatellites (SH) are indicated in each colored box. Colors represent the fluorescent label used: 6FAM (blue), HEX (green), Cy5 (yellow) and Atto 565 (red). Seven microsatellites were used in the first reaction and six in the second. Experimental lengths are indicated on top of each colored box, while theoretical lengths are both represented and indicated in the grey boxes. The repeat motifs are indicated in bold letters. Primers for these microsatellites were developed for the species in Australia [7] and in the Red Sea (*) [1].

Contact Information:

Carol Buitrago López
MSc Biology – Specialisation Human Ecology
Marine Biology Research Group
Pleinlaan 2 - 1050 Brussels, Belgium
cnathaly@vub.ac.be



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