Genetic population structure of the stony coral *Seriatopora hystrix* in the Indo-Malay Archipelago

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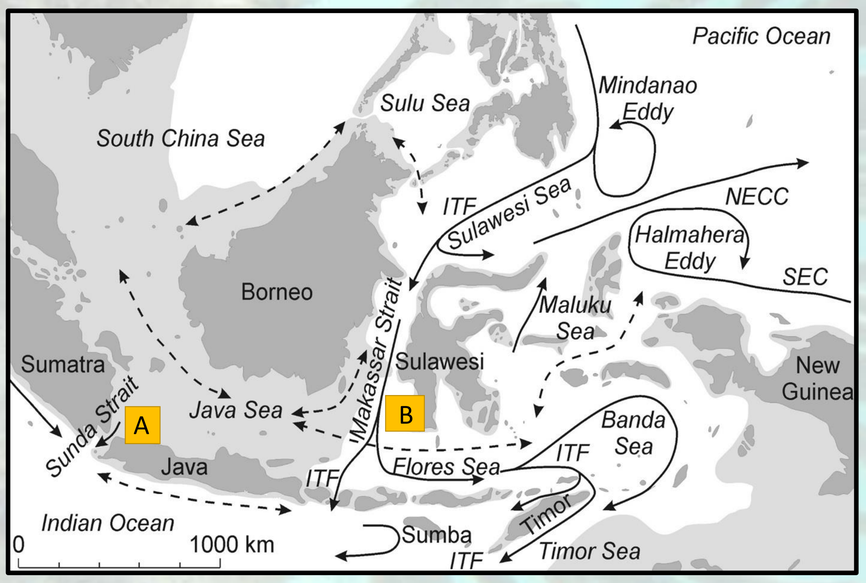
Background

- Coral reefs are renowned to be some of the most diverse marine ecosystems on earth.
- Coral ecosystems contribute to local economies through tourism (diving & sedimentation) and fishing (the provision of food). More important they protect adjacent shorelines from wave action, storms and erosion [1].
- Approximately 75% of coral reefs worldwide are threatened by both local and global stressors with the highest threat in Southeast Asia where ±95% of the coral reefs are threatened [1-2].
- Marine protected areas (MPAs) can be a powerful management tool to increase connectivity and maximize coral resilience.

Species of Study

- ***Seriatopora hystrix*** is a hermaphroditic scleractinian brooding coral living in symbiosis with zooxanthellae.
- The species is native to East Africa, the Red Sea and western Indo-Pacific [3].
- Characterised by rapid growth, a variety of reproduction strategies and the capability for short- and long-distance dispersal [4].



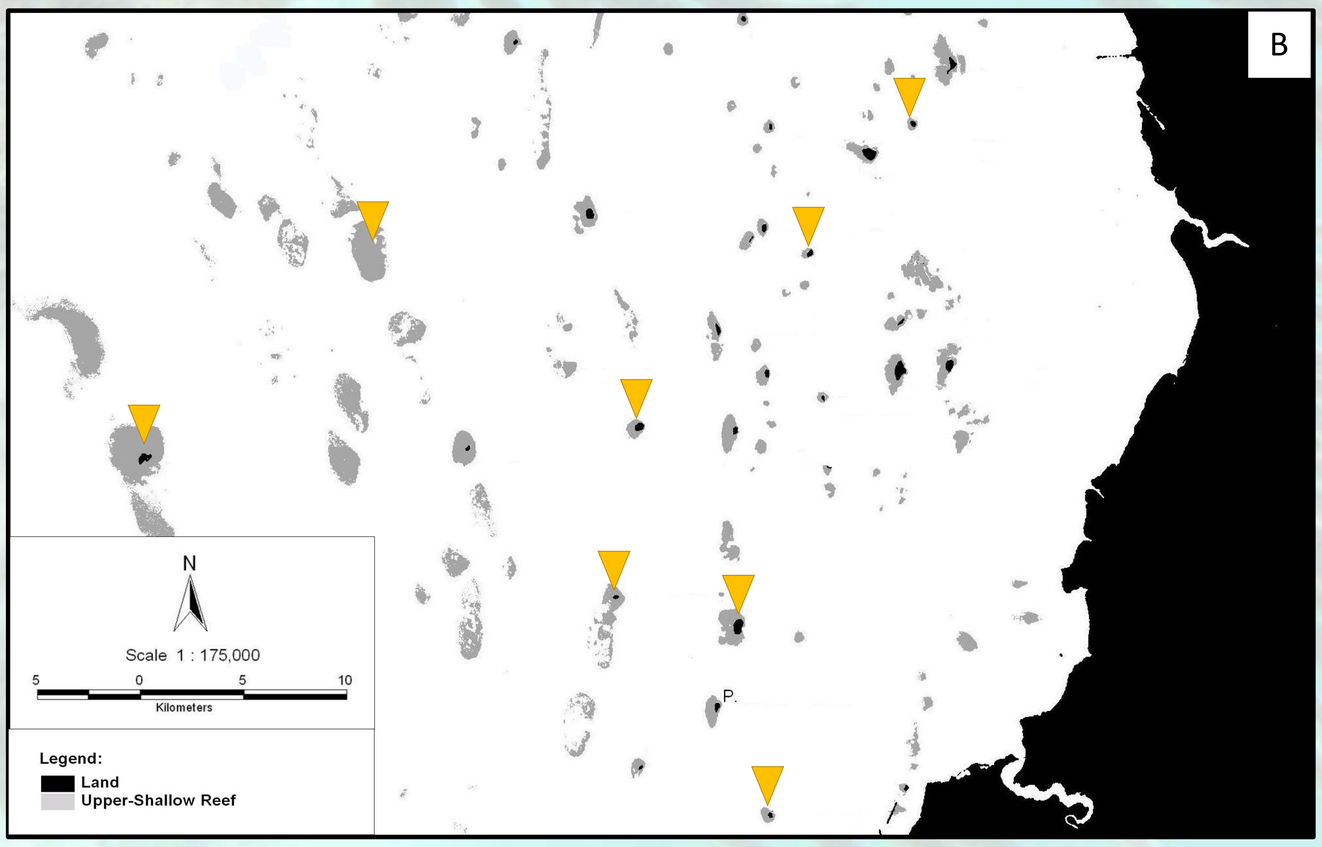


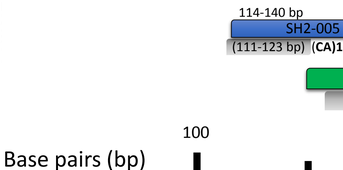
Fig. 1: Map of the Indo Malay Archipelago. [A] Pulau Seribu: 5 sampling site off Jakarta in Java. [B] Spermonde Archipelago: 8 sampling sites off the southwest coast of Sulawesi. ITF: Indonesian Throughflow, NECC: North Equatorial Counter Current and SEC: South Equatorial Current. Source (B): Landsat ETM + Satellite Image, Acquisition Year 2002.

Research Objectives

- Acquiring knowledge on genetic population structure and hence connectivity patterns among subpopulations by measuring genetic diversity (allelic richness and heterozygosity).
- *Hypothesis: Allelic compositions will be different between the two studied sites and within Spermonde Archipelago, due to isolation by distance.*
- This study will provide necessary scientific information to support MPA implementations and effective management.

Material & Methods

1. *Seriatopora hystrix* tissue samples: 303 samples from 13 locations (Fig. 1)



2. DNA extraction and quantification
3. Microsatellites selection and primer validation.
4. Multiplex PCR design
5. Fragment length analysis with a DNA capillary sequencer
6. Microsatellite scoring
7. Statistical analysis: Principal Components (PCoA), heterozygosity (F-statistics) , GeneAlEx (AMOVA + Mantel test), STRUCTURE (Bayesian cluster analysis)
8. Calculating genetic divergence within and among subpopulations

Preliminary Results

10 Polymorphic microsatellites were selected
Two primermix setups were designed for multiplex PCR

Fig. 2: Two microsatellite primermix designs. The different microsatellites are color coded according to their fluorescent labels: 6FAM (blue), HEX (green), Cyanine 3 (yellow) and Atto 565 (red). Experimental lengths are indicated on top of the boxes, while theoretical lengths and repeat motifs (bold) are indicated in the grey boxes. The microsatellite primers were designed for species in the Red Sea(*)[6] and Australia [5]. SH: *Seriatopora hystrix*.

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