

Connectivity of the coral *Acropora tenuis* in Spermonde Archipelago

INTRODUCTION

- **Coral reefs** have the highest species biodiversity of all marine ecosystems. However, since they are declining globally due to anthropogenic impacts, conservation is essential.
 - **Marine Protected Areas (MPA)** are an important conservation tool. MPA's should be arranged in networks, because coral reefs are scattered/patchy habitats. This ensures connectivity and increases resilience.
- Hermatypic corals are ecosystem engineers that build the three-dimensional structure of the reef.
Insights of population dynamics help to develop management strategies for conservation.

Exploring the Indonesian region in Sulawesi,
study of a hermatypic, mass-spawning coral:
Acropora tenuis in Spermonde Archipelago.

Research objectives

A. population structure on a local scale:

What is the composition of genetic diversity?
(allelic richness + heterozygosity)

Hypothesis: Genetic diversity is shaped by local sea surface currents.

B. gene flow and connectivity on a global scale:

Is there migration and/or dispersal across the Indian Ocean?
(F-statistics + Mantel test + AMOVA + Bayesian cluster analysis)

Hypothesis: There are two distinct genotype clusters: an African and an Indonesian cluster.



Fig 1: Adult colonies of *Acropora tenuis*.
(Picture: Puspita Sutrisno, 2013)

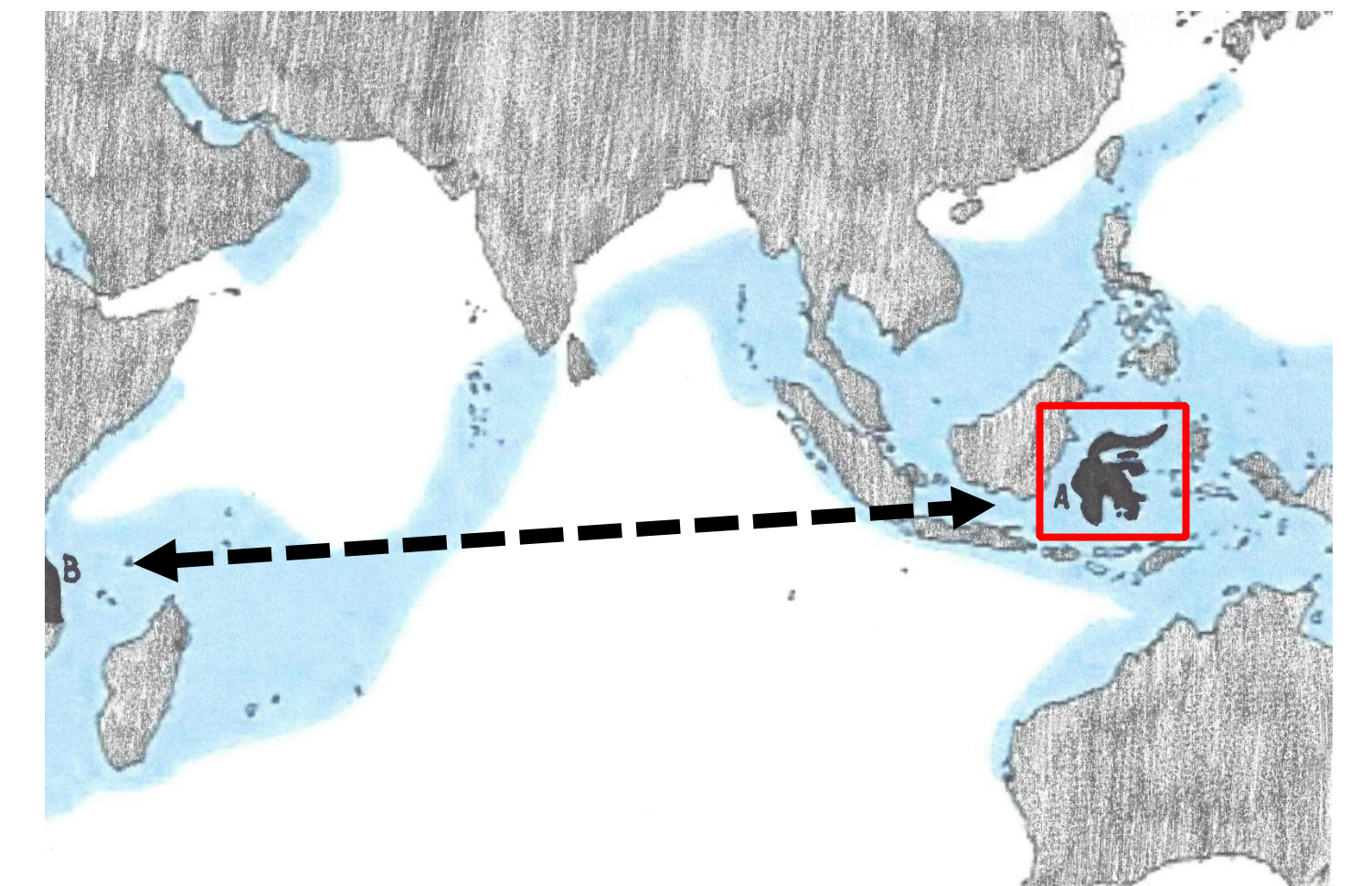


Fig 2: Distribution map of *Acropora tenuis*.
(A) the Spermonde archipelago, Sulawesi, ID
(B) the coast of Tanzania. (Veron, 2000)

SAMPLING



Code	Sites in Spermonde	#
BL	Barang Lompo	4
BT	Bone Tambung	3
SL	Sarapo Lompo	5
LA	Lanyukang	8
BA	Badi	24
KL	Kodingareng Lompo	15
KK	Kodingareng Keke	17
KA	Kapoposang	4
Sample Total		80

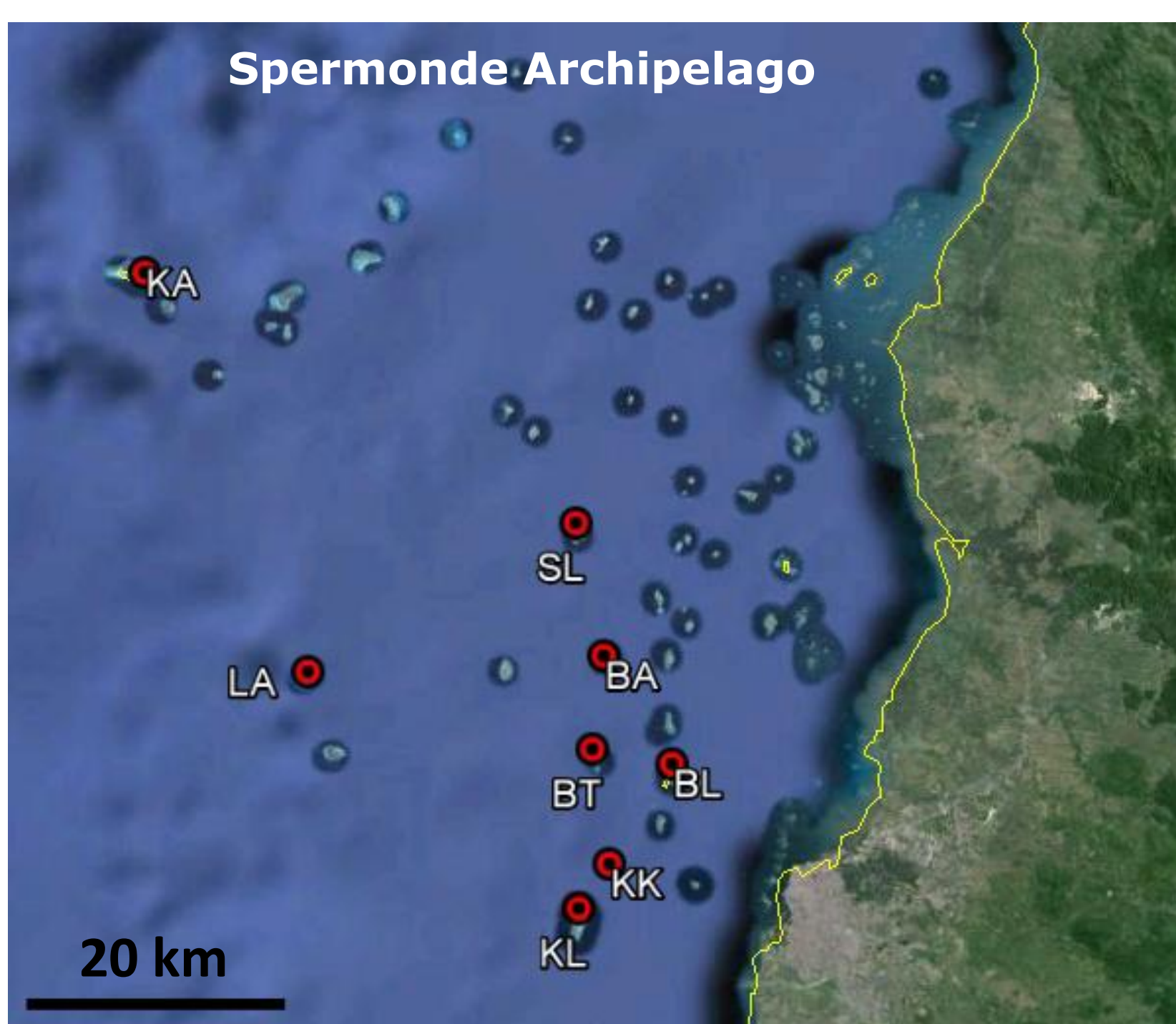


Fig 3: Samples collected in Spermonde, SE-Sulawesi.
TOP RIGHT– Table of sampling sites: site code, site name and number of samples collected there.
DOWN– Spatial distribution of the collection sites.

MATERIAL & METHODS

Acropora tenuis coral branch: 80 samples from 8 locations.

- Genomic DNA extraction and purification
- Microsatellite analysis (SSR length polymorphism)
 1. 7 markers from (Underwood *et al.*, 2009) + 9 markers from literature search (NEW)
 2. Primer validation + Multiplex PCR with fluorescent labeled primers
- DNA capillary sequencer
 1. Fragment Length Analysis of PCR products
 2. Scoring of fragment lengths

Genotypes = length polymorphisms of microsatellites

- Statistical analysis of the length polymorphism
Fstat (F-statistics), GenAlEx (AMOVA + Mantel test),
STRUCTURE (Bayesian cluster analysis):
- Data comparison with samples from the Tanzanian coast
Dataset from a previous study (Rosa van der Ven, 2012)
Measure of gene flow and connectivity

RESULTS

- Successful primer validation + Multiplex PCR for the 7 markers (Underwood *et al.*, 2009)
Successful fragment length analysis → scoring process ongoing.
- Primer validation for the 9 NEW markers ongoing.