Connectivity of the Skunk Clownfish (*Amphiprion akallopisos*) in the Indian Ocean.

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INTRODUCTION

- Coral reefs are threatened worldwide
- Marine Protected Areas (MPAs) are implemented to:
  - Preserve species and genetic diversity
  - Provide spill-over (larval export) to adjoining (non-protected) coral reefs
- To function correctly, MPAs should be connected
- Model species *A. akallopisos* abundant & easy to sample
- Economical value: aquarium trade

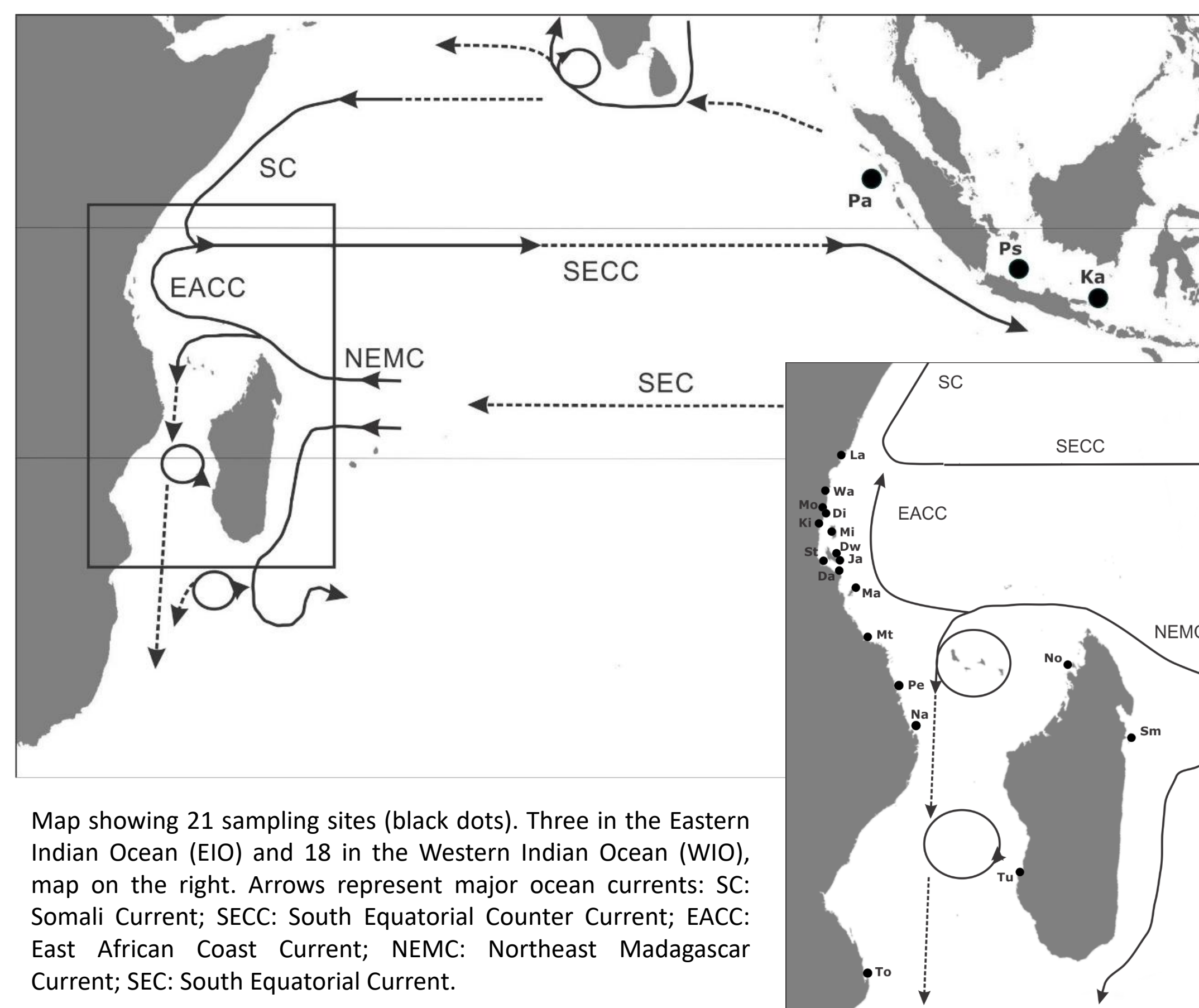*Amphiprion akallopisos* (photo: M. Kochzius)

Research questions:

1. What are the patterns of connectivity and gene flow among populations in the Indian Ocean?
2. Are results based on mitochondrial DNA and nuclear DNA congruent?

MATERIAL AND METHODS

SAMPLING

- A total of 387 fin tissue samples were collected while SCUBA diving at 21 sites.
- Tissues were preserved in 96 % ethanol.

Map showing 21 sampling sites (black dots). Three in the Eastern Indian Ocean (EIO) and 18 in the Western Indian Ocean (WIO), map on the right. Arrows represent major ocean currents: SC: Somali Current; SECC: South Equatorial Counter Current; EACC: East African Coast Current; NEMC: Northeast Madagascar Current; SEC: South Equatorial Current.

GENETIC ANALYSIS

- **Mitochondrial DNA (mtDNA)**
  - Control Region universal primers CR-A & CR-E.
  - Alignment: 337 bp
- **Microsatellite markers: 13 loci**
- **Haplotype network (TCS)**
- **Pairwise Fst - AMOVA (Arlequin)**
- **Bayesian inference (Structure)**
- **Principal Component Analysis (PCA) (AdGenet)**
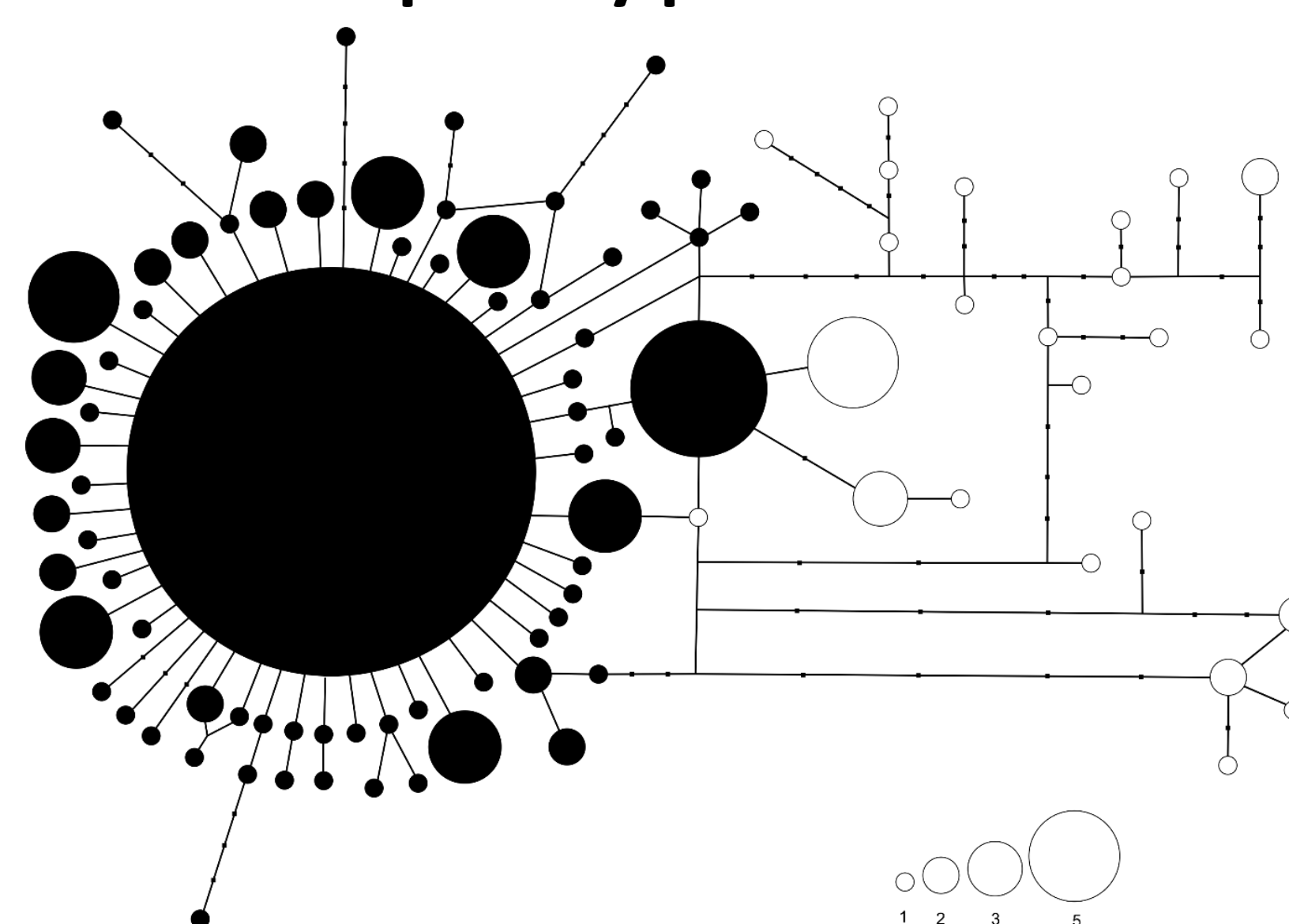
RESULTS

AMOVA (p<0.001)

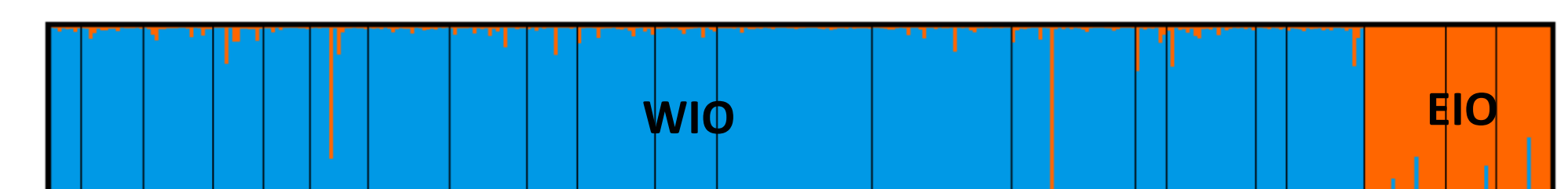| mtDNA	Microsat
EIO-WIO	EIO-WIO
Φ_{ct} = 0.63	F_{ct} = 0.11
St-Marie – Eafr	Mad – Eafr
Φ_{ct} = 0.34	F_{ct} = 0.014
	Watamu – WIO
	F_{ct} = 0.013

Haplotype network

Haplotype network: circles represent haplotypes from in the WIO and white circles haplotypes from the EIO; size of the circles corresponds to the number of individuals as indicated in lower black left corner, with the largest circle representing 217 individuals; lines represent one, small dots additional mutational steps.
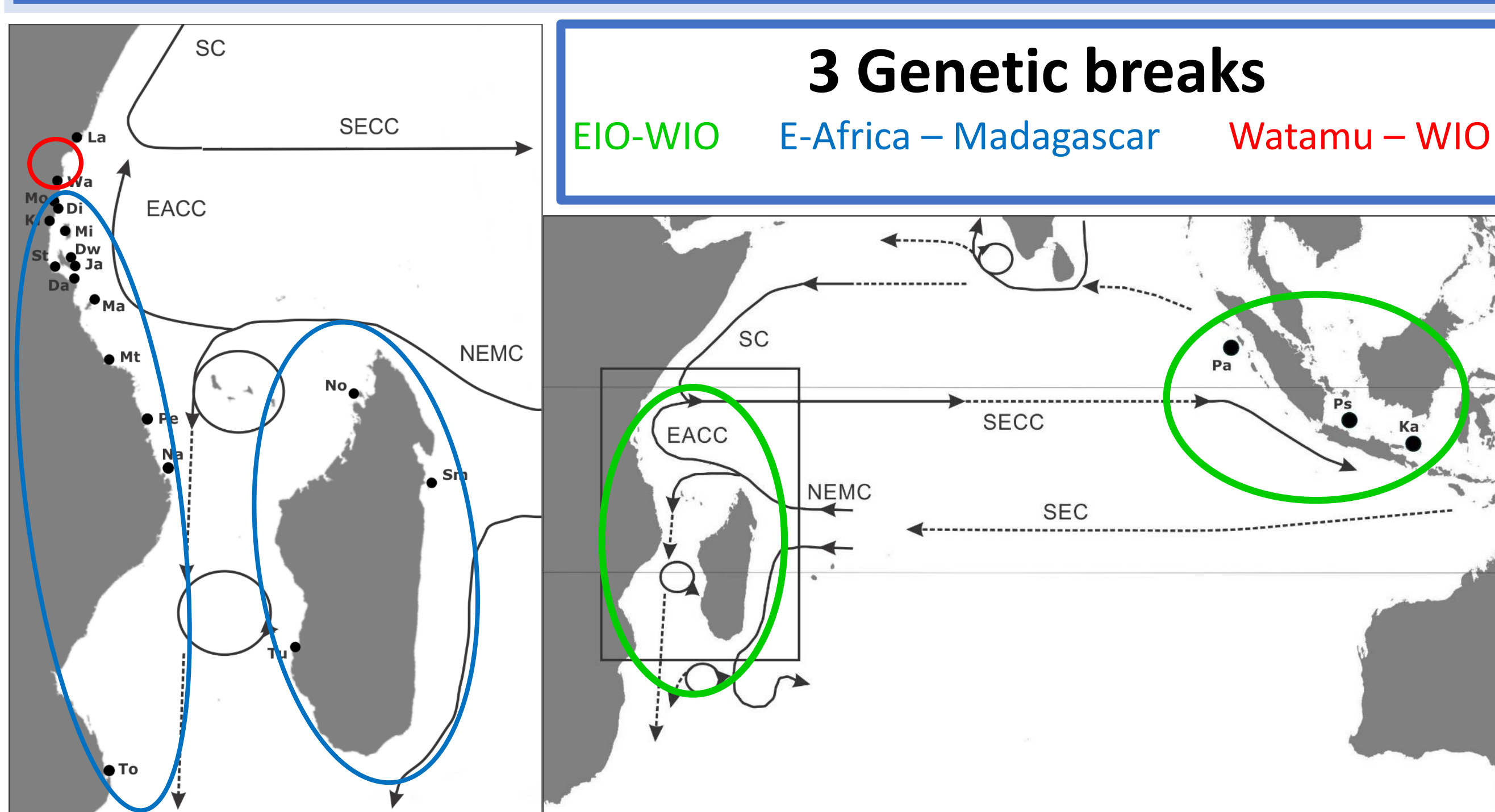
PCA

Scatterplot of PCA: Individual genotypes appear as dots linked to the mean value of the population surrounded by 95% inertia ellipses. Eigenvalues show the amount of information contained in each successive principal component with the x-axis constituting the first and the y-axis constituting the second principal component.

Structure

CONCLUSION

3 Genetic breaks

EIO-WIO | E-Africa – Madagascar | Watamu – WIO

1. **Highly restricted gene flow between EIO and WIO populations**
2. **Shallow population Structure within the WIO**
   - Sea surface currents may restrict larval dispersal among WIO populations
   - Alternatively: Watamu reef differentiated as a result of chaotic genetic patchiness
3. **Microsats and mtDNA are congruent in detecting population structure between WIO and EIO but identify genetic breaks at different locations within the WIO**