

## **Theme: Biodiversity and diversification processes**

### **Using genetic approach to estimate reef fish connectivity in the South-West Indian Ocean and help in the design of Marine Protected Areas network**

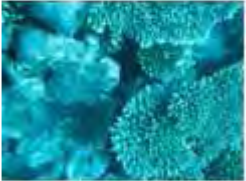
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Marine Protected Areas (MPAs) are designed to increase ongoing efforts done to preserve marine diversity. Existing marine reserves in the South West Indian Ocean appeared largely ineffective and remain insufficient as a whole for the protection of marine reef diversity (Mora *et al.* 2006). In fact, for a real efficiency to preserve biodiversity, MPA may be integrated in a dense network. By using genetic information, our project aims to characterize the natural spatial structure of fish stocks before trying to maintain it, and then, to contribute to the ongoing design of MPAs network in the South West Indian Ocean. This project focuses on three key reef fish species (*Lutjanus kasmira*, *Epinephelus merra* and *Myripristis berndti*) with the main question: do each genetic structure provide similar pattern of connectivity or not? At a first step, genetic diversities and differences were surveyed at the mitochondrial control region of 125 *E. merra*, 144 *L. Kasmira* and 157 *M. berndti* collected in four localities of the South West Indian Ocean (La Reunion, Mayotte, Glorieuses and Seychelles). Patterns observed on the three species show interesting similarities, with, for example, no differences encountered between fishes sampled in the distant sites of Mayotte and La Reunion, whereas some differences could be observed between the closer sites of Mayotte and Glorieuses. It seems that some sites keep a signal of a different colonisation history that could hide present connectivity. These results are now being complemented by the use of microsatellite and the addition of samples from eight other sites, to better delineate strictly isolated populations from strongly connected ones, and thus help managers to identify priority areas for the development of new MPAs within the regional network.



# Connectivity of Marine Protected Areas in South-Western Indian Ocean:

Using population genetics of reef fish to  
contribute to the design of MPAs network

- Delphine MUTHS & Jérôme BOURJEA -





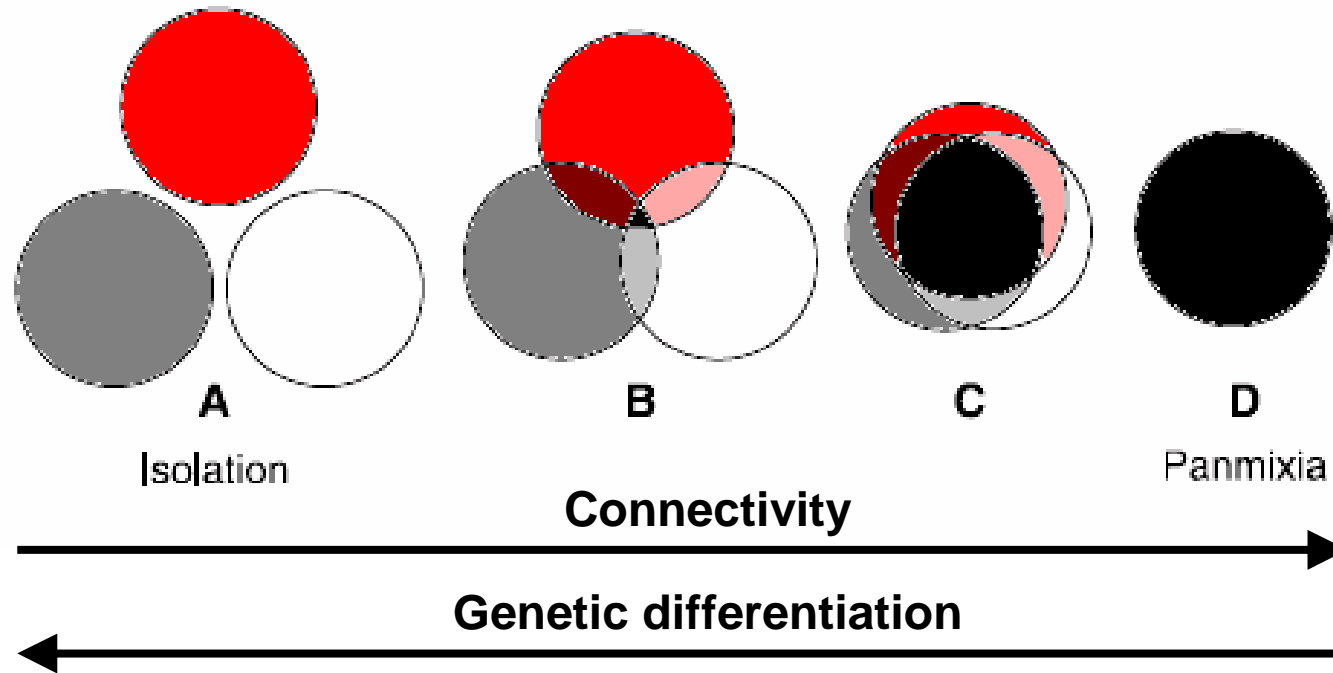
- A MPA is an area delimited in sea, which aims to protect biodiversity in a sustainable perspective
- BUT, for a real efficiency, MPAs need to be integrated in a dense network of representative, individually well-managed and connected MPAs (Mora *et al.*, 2006 - Science )



26 actual MPAs in the SWIO

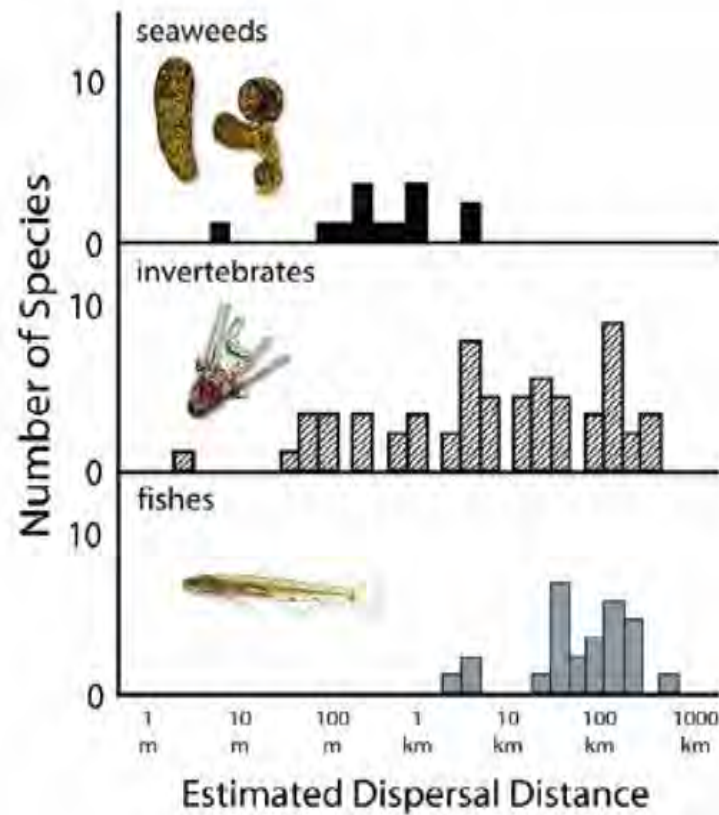
- How could we estimate the scale of connectivity in marine environment?

- Using **population genetics** to estimate efficient connectivity:





- Marine habitats are often thought as a well-mixed environment with no boundaries. In fact genetic data help to show that dispersal is often very limited:

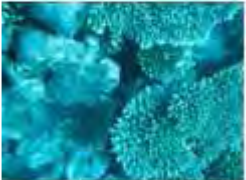


Kinlan & Gaines, 2007 – Ecology: Literature compilation based on genetic data

- Which is the scale of connectivity for reef fish in the SWIO?

## Strategy of our project CAMP:

- 1/ Elaborate a **regional strategy of sampling** and use **population genetics methodology**
- 2/ Better understand actual **exchanges** between populations and help to localize the most isolated areas
- 3/ Precise **colonisation history** of the SWIO
- 4/ Contribute to the design of **the most efficient MPAs network** in the SWIO



## Strategy of our project:

- 3 species of fishing interest

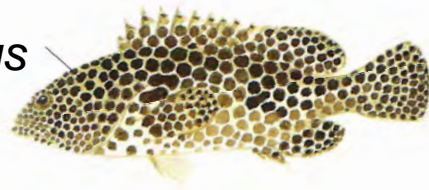
- *Lutjanus kasmira*



- *Myripristis berndti*

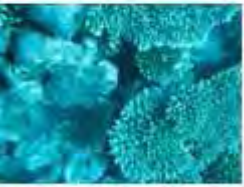
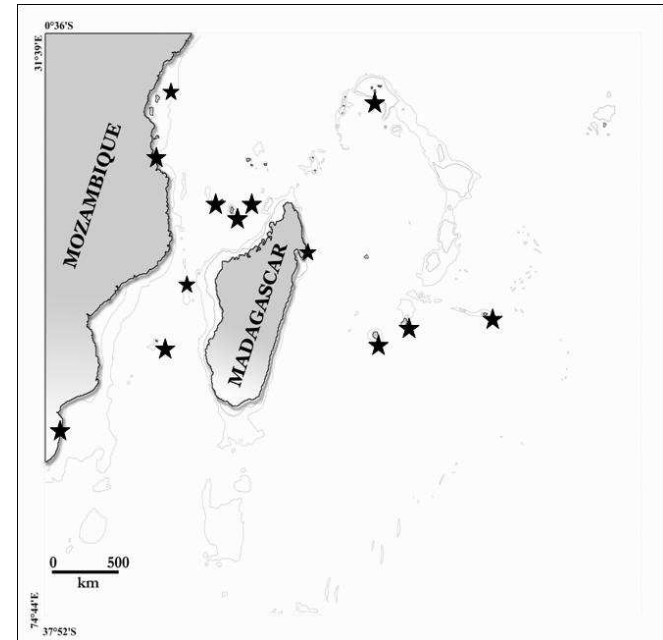


- *Epinephelus merra*



- 2 genetic markers: mitochondrial DNA sequencing & microsatellite genotyping

- 13 expected sampling sites



## Preliminary results:

- 3 species of fishing interest

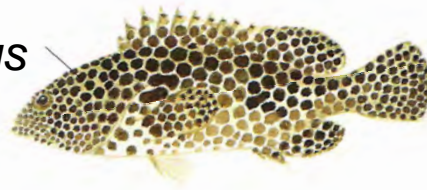
- *Lutjanus kasmira*



- *Myripristis berndti*

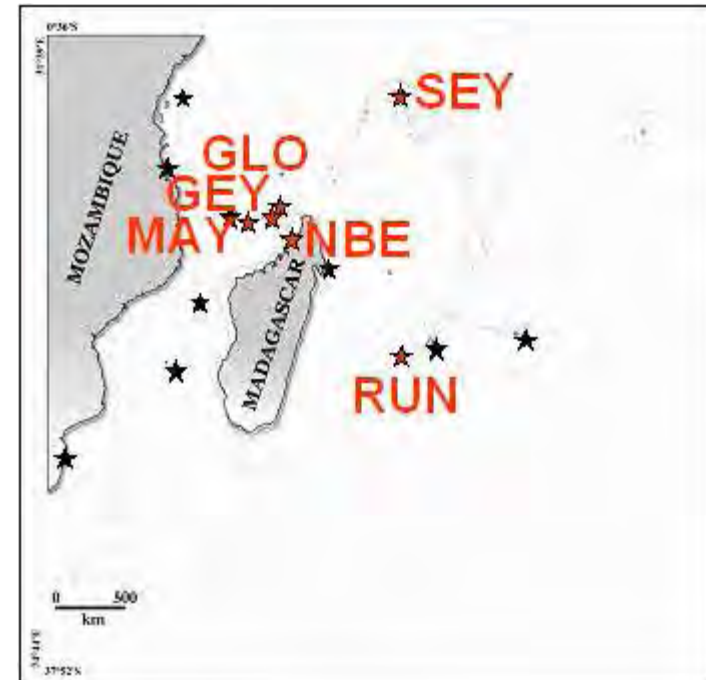


- *Epinephelus merra*



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mitochondrial DNA sequencing  
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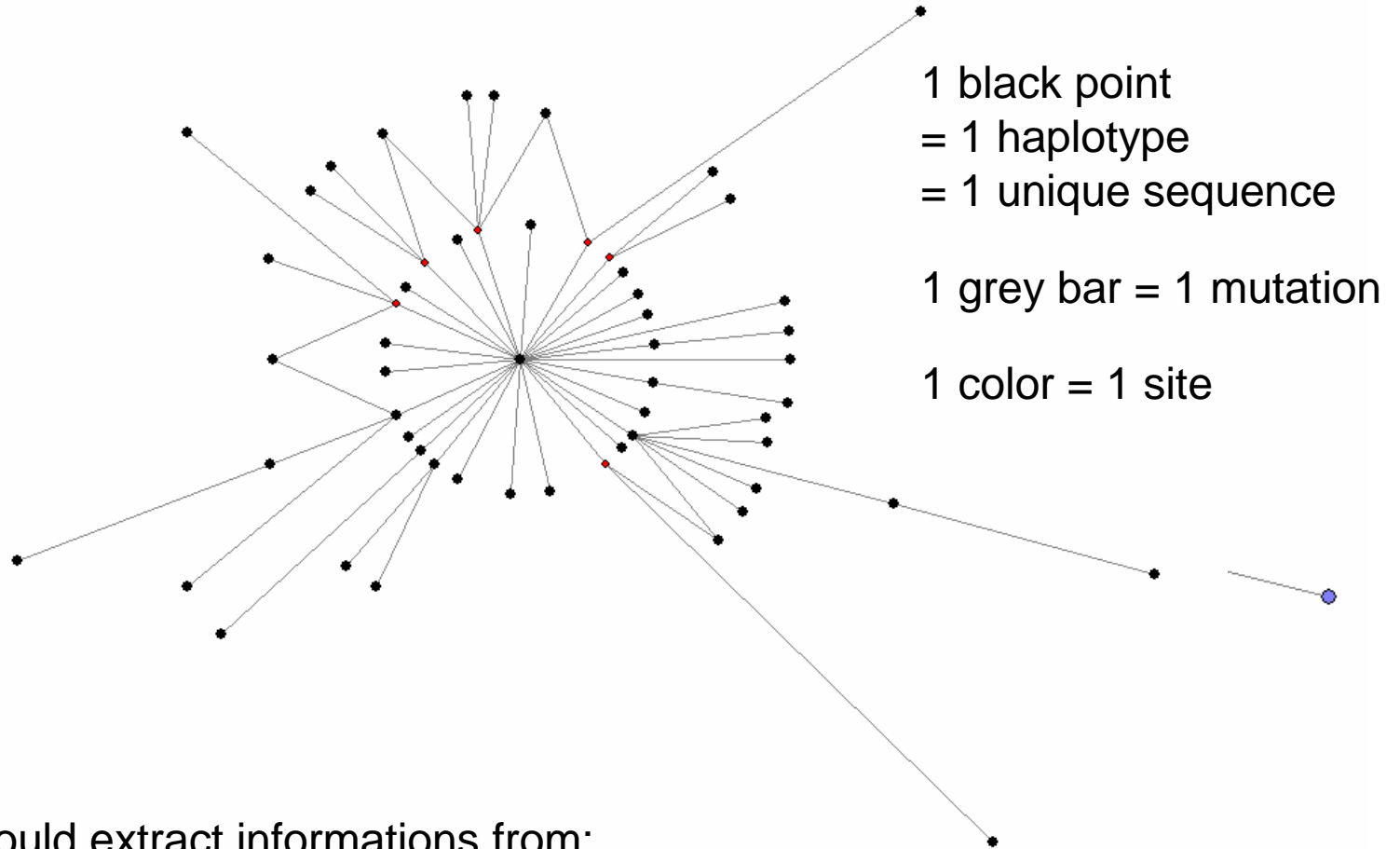
- 6 of the 13 expected sampling sites



Is there similar connectivity pattern and/or isolated areas between these 3 species?



### Example of haplotype network :



We could extract informations from:

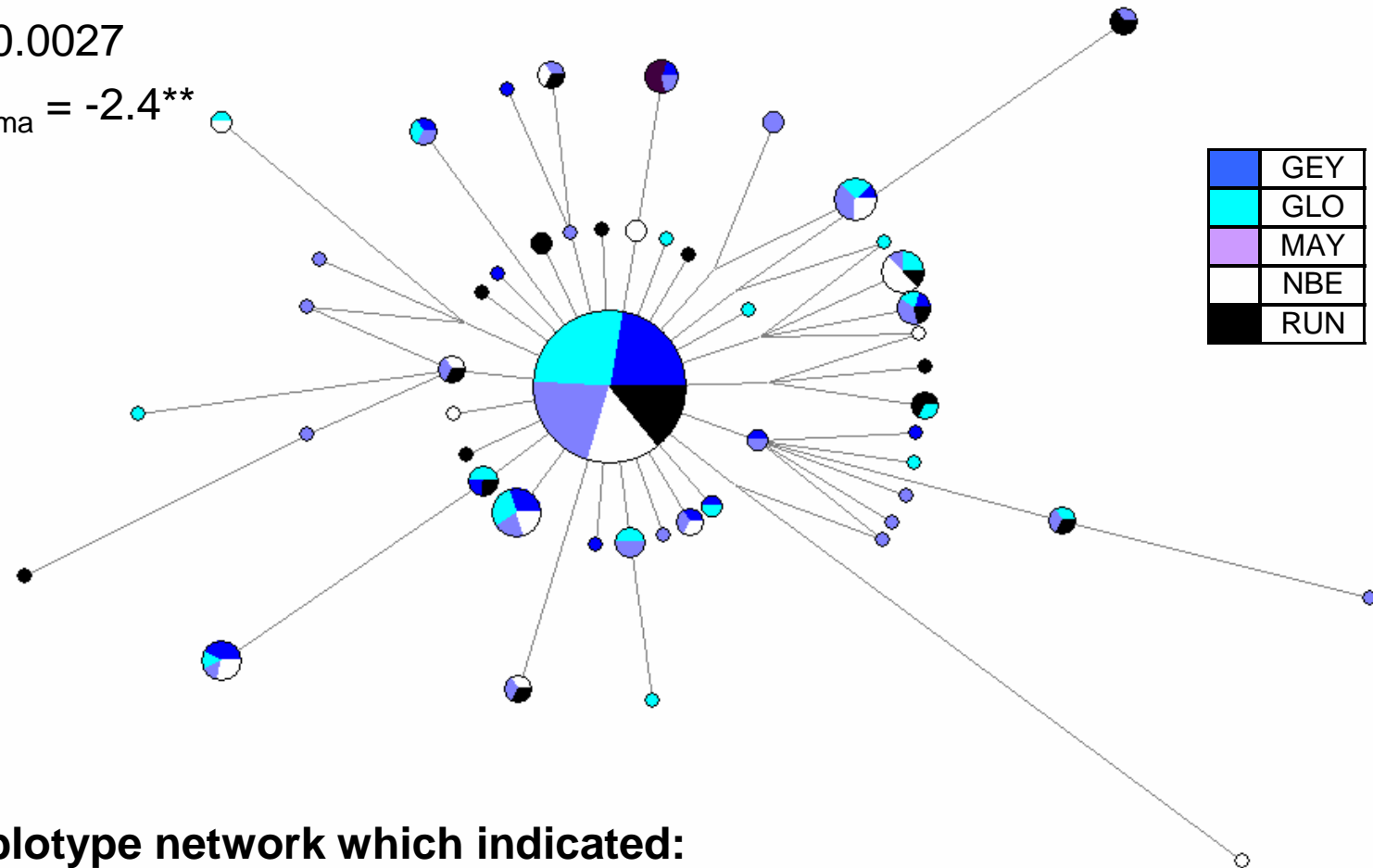
- the morphology of the network
- the frequency of the different haplotypes
- the geographical representation of each haplotype

## Results for *Lutjanus kasmira*:

$H_d = 0.781$

$\pi = 0.0027$

$D_{Tajima} = -2.4^{**}$



### Haplotype network which indicated:

- A star-like pattern, typical of a population in extension (in agreement with a significant  $D_{Tajima}$ )
- A main central haplotype = a unique colonisation event
- Haplotypes homogeneously represented between sites



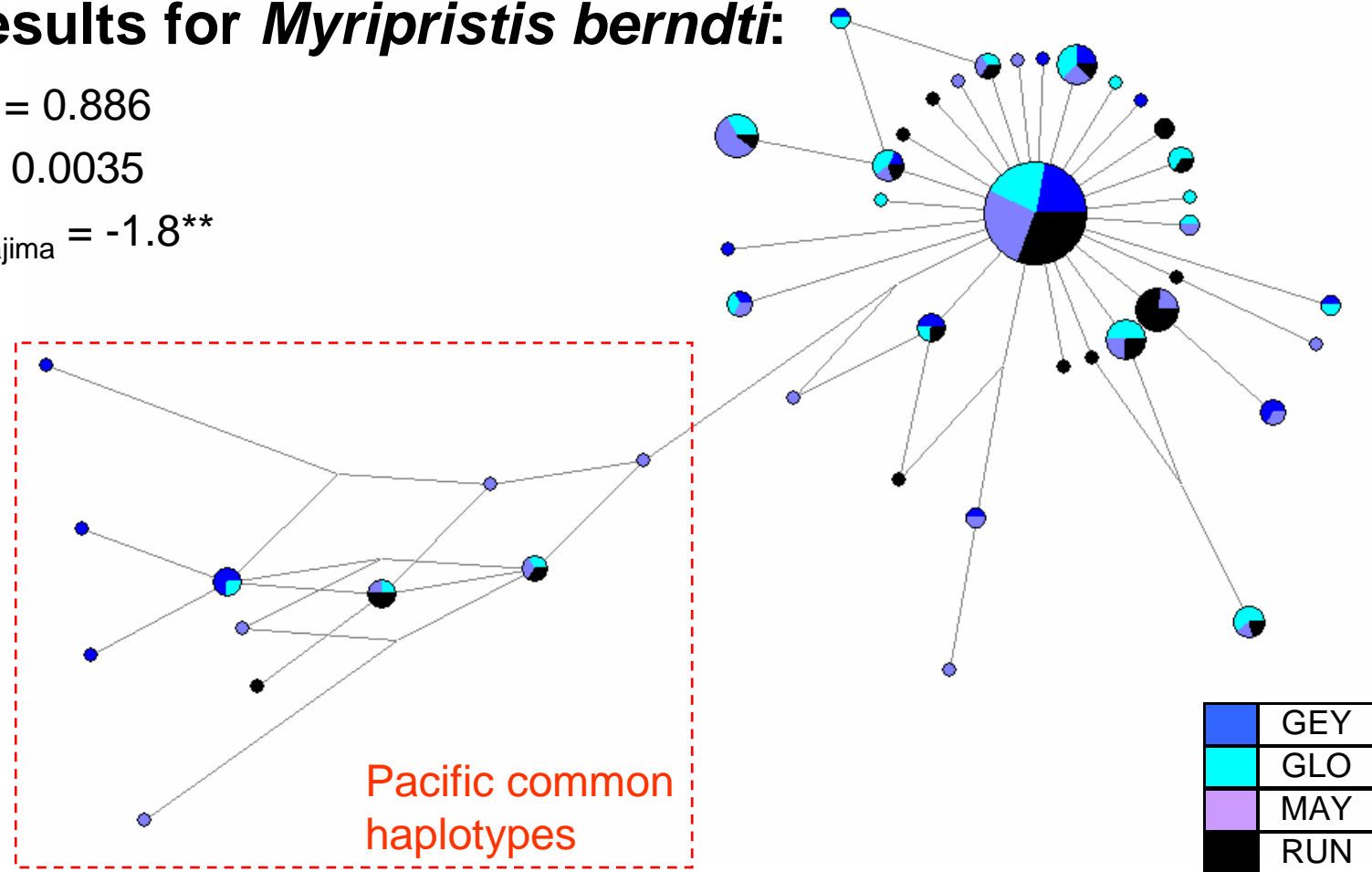


## Results for *Myripristis berndti*:

$H_d = 0.886$

$\pi = 0.0035$

$D_{Tajima} = -1.8^{**}$



### A more complex haplotype network with:

- A divergent branch indicating connection with Pacific fish, that is long-distance connectivity
- Haplotypes homogeneously represented between sites

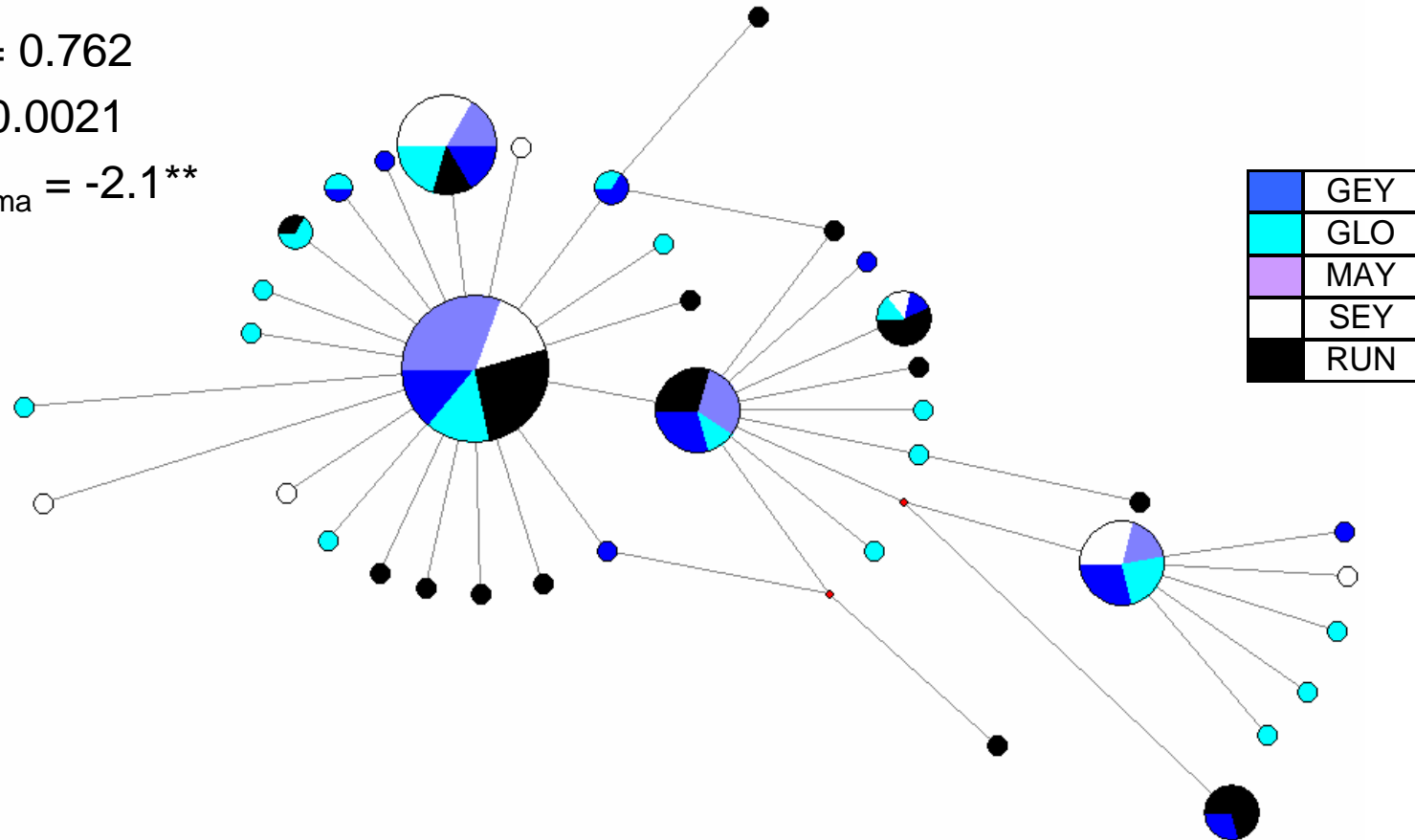


## Results for *Epinephelus merra*:

$H_d = 0.762$

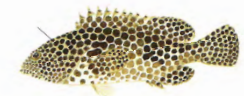
$\pi = 0.0021$

$D_{Tajima} = -2.1^{**}$

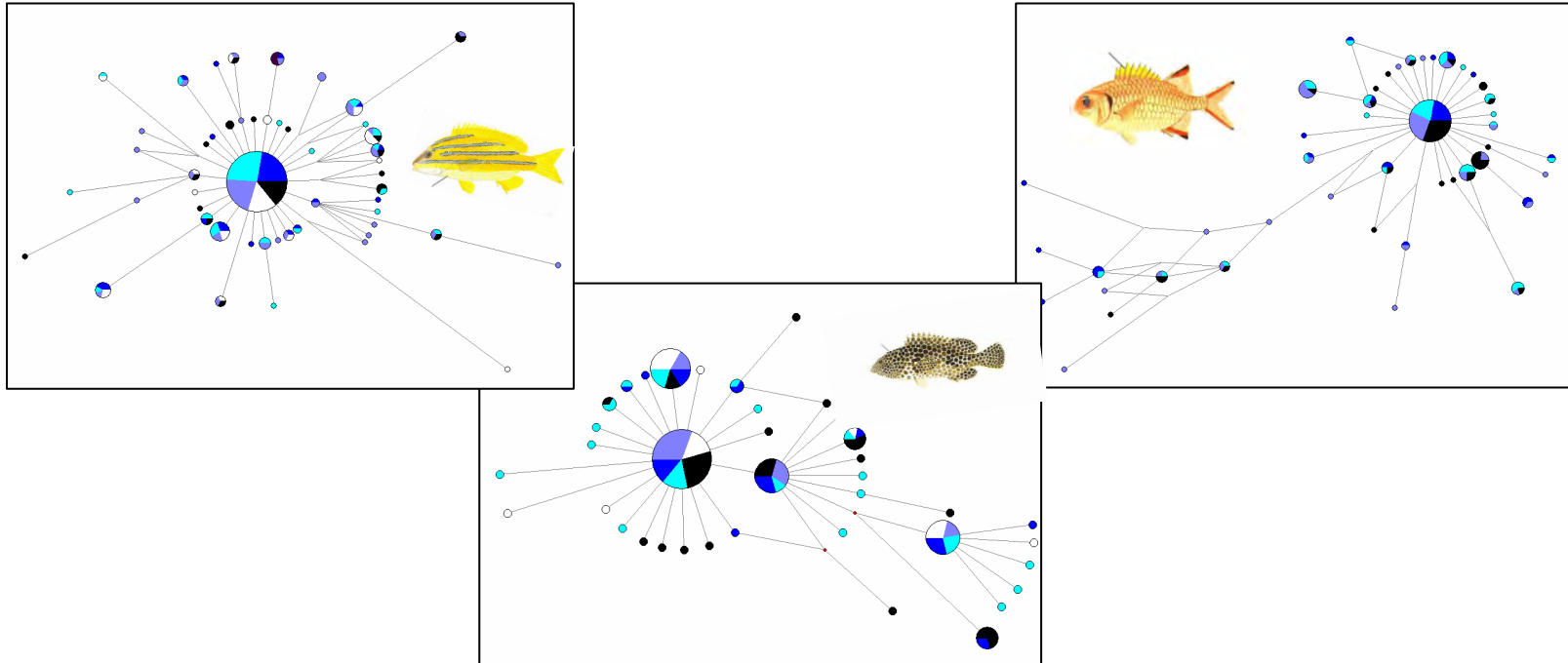


**Even more complicated network which indicated:**

- A few well-represented haplotypes = ancestral polymorphism retention, giving evidence of multiple colonisation events
- A significant  $D_{Tajima}$  = population still in extension
- Haplotypes homogeneously reparted between sites



## Comparison of the results for the 3 species



### For the 3 species:

- Different stories : more recent expansion for *L. kasmira*, more complex for *E. merra*
- A diversity globally shared between the different sites

→ An other genetic indicator is the calculation of **Fst**, that is fixation index between pair of sites

## Fst Results for *the 3 species*:

**Fst** = Fixation index between populations

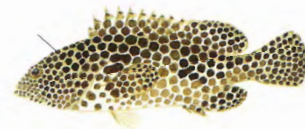
More Fst → 1, more populations are differentiated



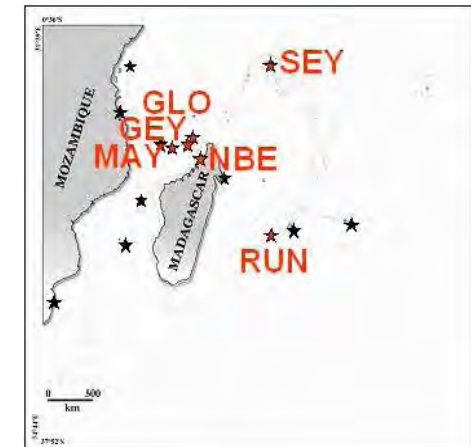
	GEY	GLO	MAY	NBE
GLO	-0.010			
MAY	0.007	-0.001		
NBE	0.006	-0.003	-0.006	
RUN	0.017	0.008	-0.004	0.002



	GEY	GLO	MAY
GLO	0.004		
MAY	0.002	-0.009	
RUN	0.010	0.008	-0.001

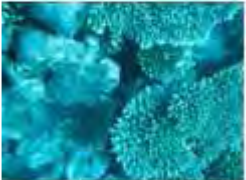
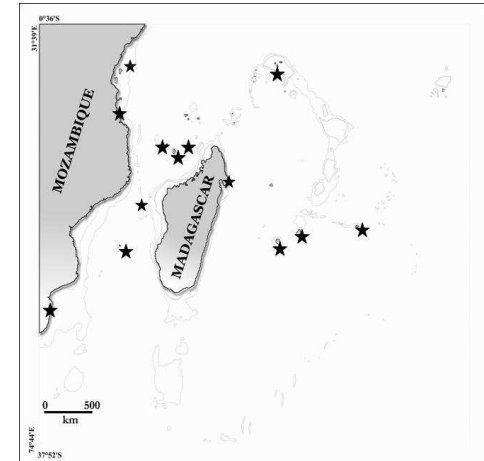


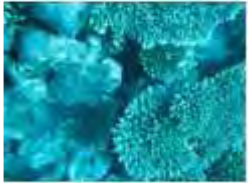
	GEY	GLO	MAY	SEY
GLO	-0.016			
MAY	0.016	0.016		
SEY	-0.013	-0.014	0.024	
RUN	<b>0.053*</b>	<b>0.057*</b>	-0.042	<b>0.072*</b>



## Preliminary results give interesting perspectives:

- Continue the sampling for the CAMP project in the other SWIO sites
- Develop the 2<sup>nd</sup> genetic marker, *i.e.* microsatellite, for the 3 species: *obtain the best mapping of exchanges between populations*
- Integrate all the genetic results in a global ecological background (*oceanic currents, biogeographical boundaries, ...*)
- Communicate synthetic results (cartography) to assessment & authorities: *Help to understand the MPAs connections and isolated areas*





## Many thanks to:

- people who help us for fish sampling,

- to our main partners:

- Réserve Naturelle Marine de La Réunion – France
- Marine Park of Mohéli – Comoros
- Seychelles Fishing Authority – Seychelles
- SA Institute of Aquatic Biology – South Africa
- Mauritius Oceanographic Institute – Mauritius (in progress)



- to our financial supports:

- WIOMSA (MASMA Grant)
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- TCO



- Thanks for your attention -