

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

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

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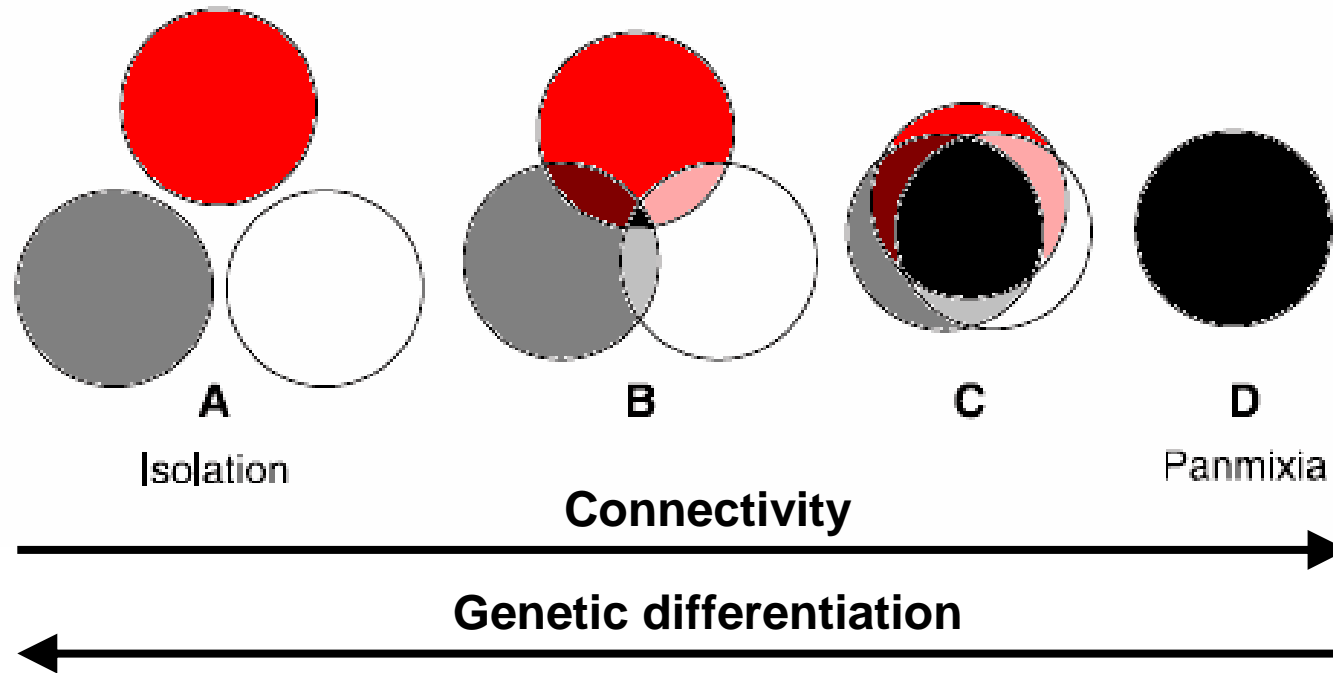
- A MPA is an area delimited in sea, which aims to protect biodiversity in a sustainable perspective
- BUT, for a real efficiency, MPAs need to be integrated in a dense network of representative, individually well-managed and connected MPAs (Mora *et al.*, 2006 - Science)



26 actual MPAs in the SWIO

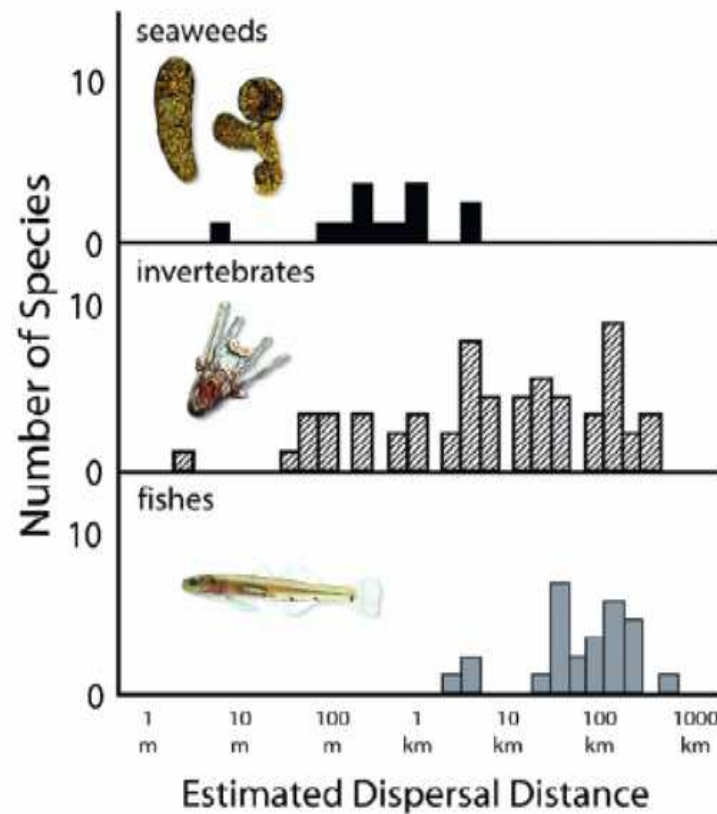
- How could we estimate the scale of connectivity in marine environment?

- 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:

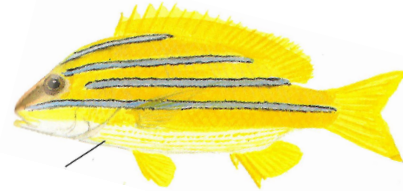
- 1/ Elaborate a **regional strategy of sampling** and use **population genetics methodology**
- 2/ Better understand actual **exchanges** between populations and help to localize the most isolated areas
- 3/ Precise **colonisation history** of the SWIO
- 4/ Contribute to the design of **the most efficient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



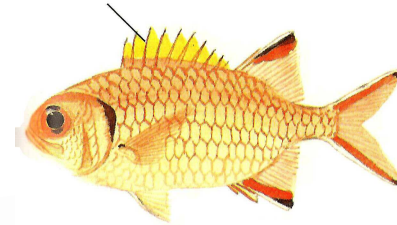
Strategy of our project:

- 3 species of fishing interest

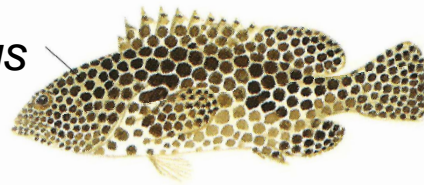
- *Lutjanus kasmira*



- *Myripristis berndti*

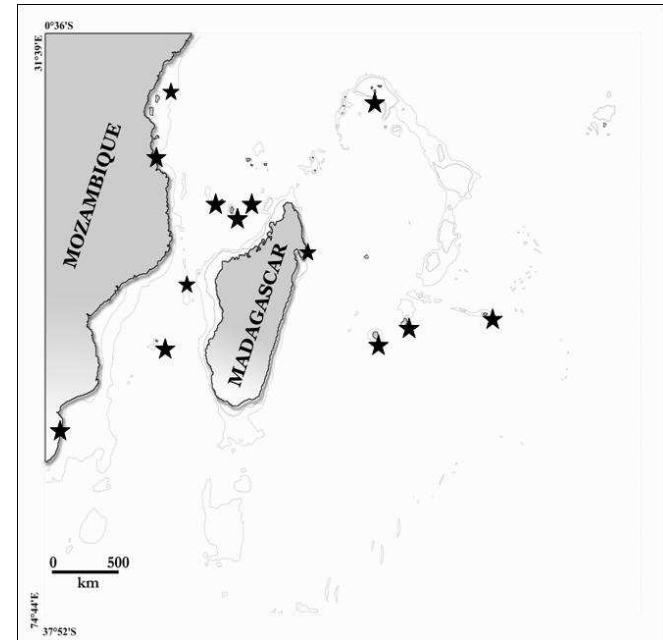


- *Epinephelus merra*



- 2 genetic markers:
mitochondrial DNA sequencing
& microsatellite genotyping

- 13 expected sampling sites

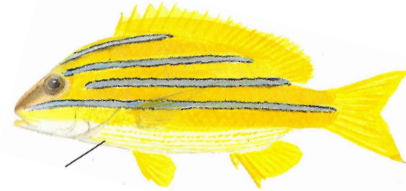




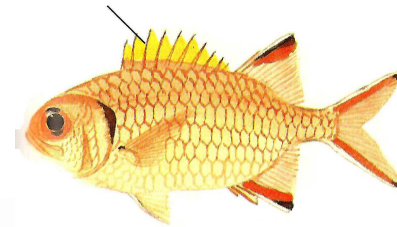
Preliminary results:

- 3 species of fishing interest

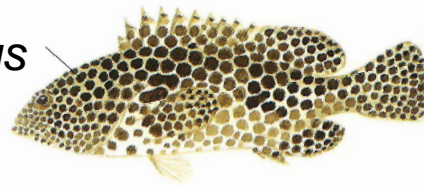
- *Lutjanus kasmira*



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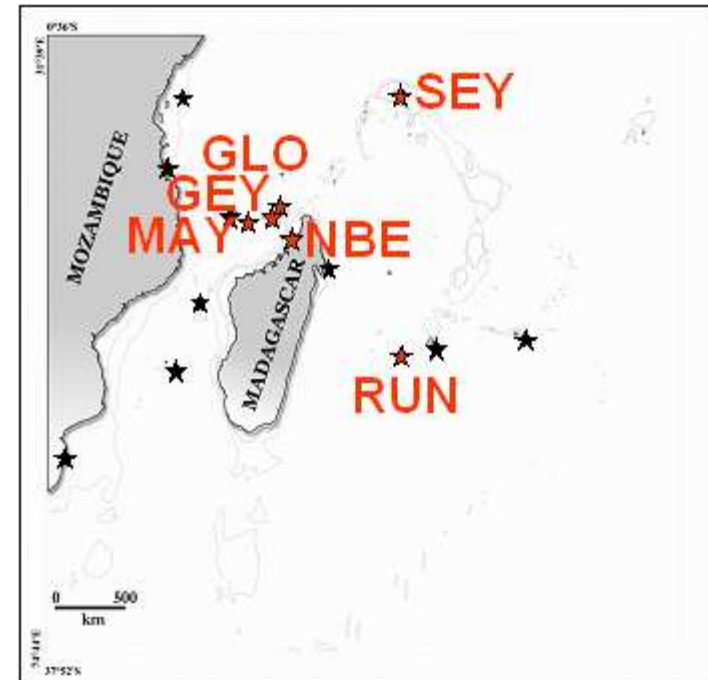


- *Epinephelus merra*



- 2 genetic markers: mitochondrial DNA sequencing & microsatellite genotyping

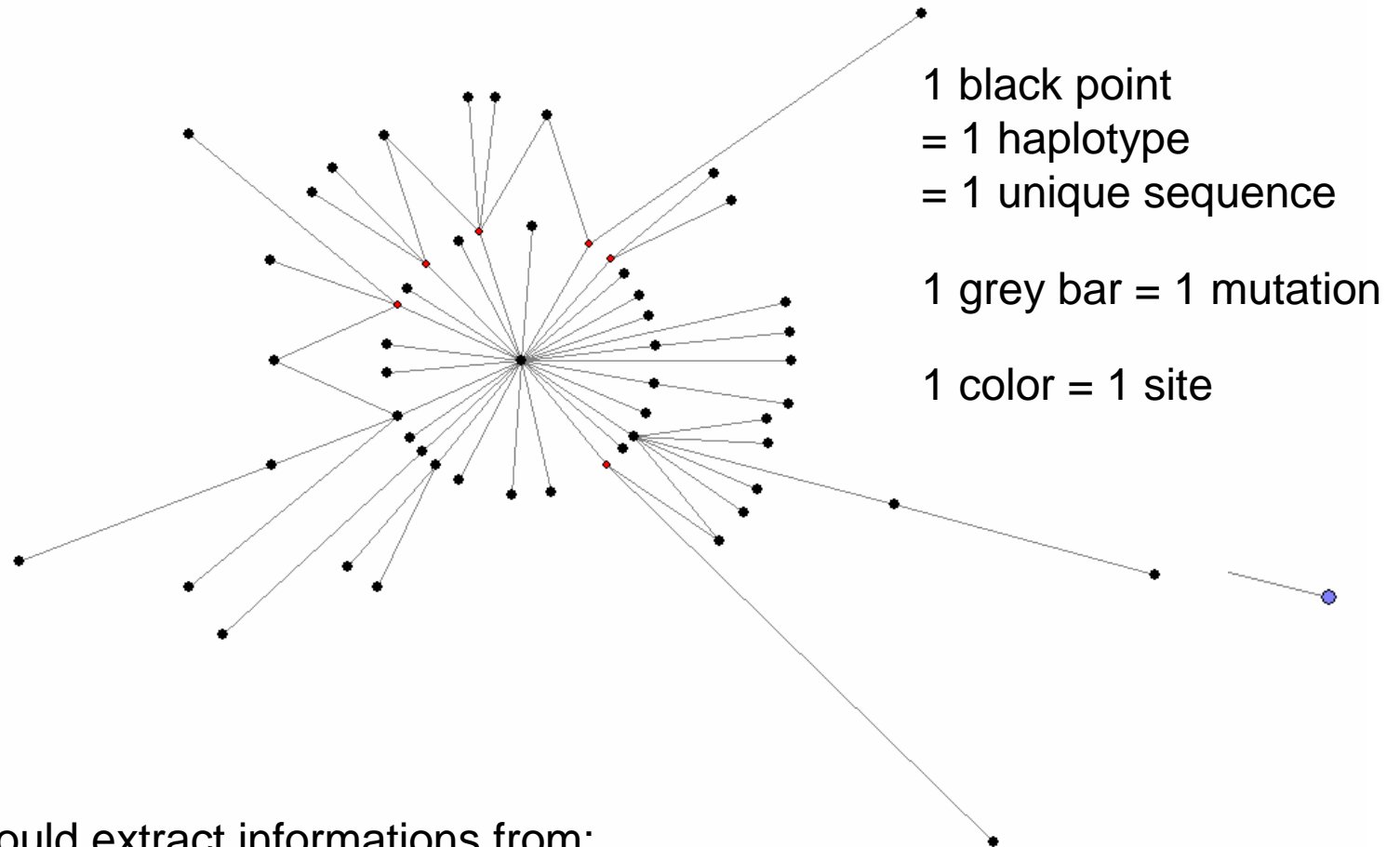
- 6 of the 13 expected sampling sites



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



Example of haplotype network :



We could extract informations from:

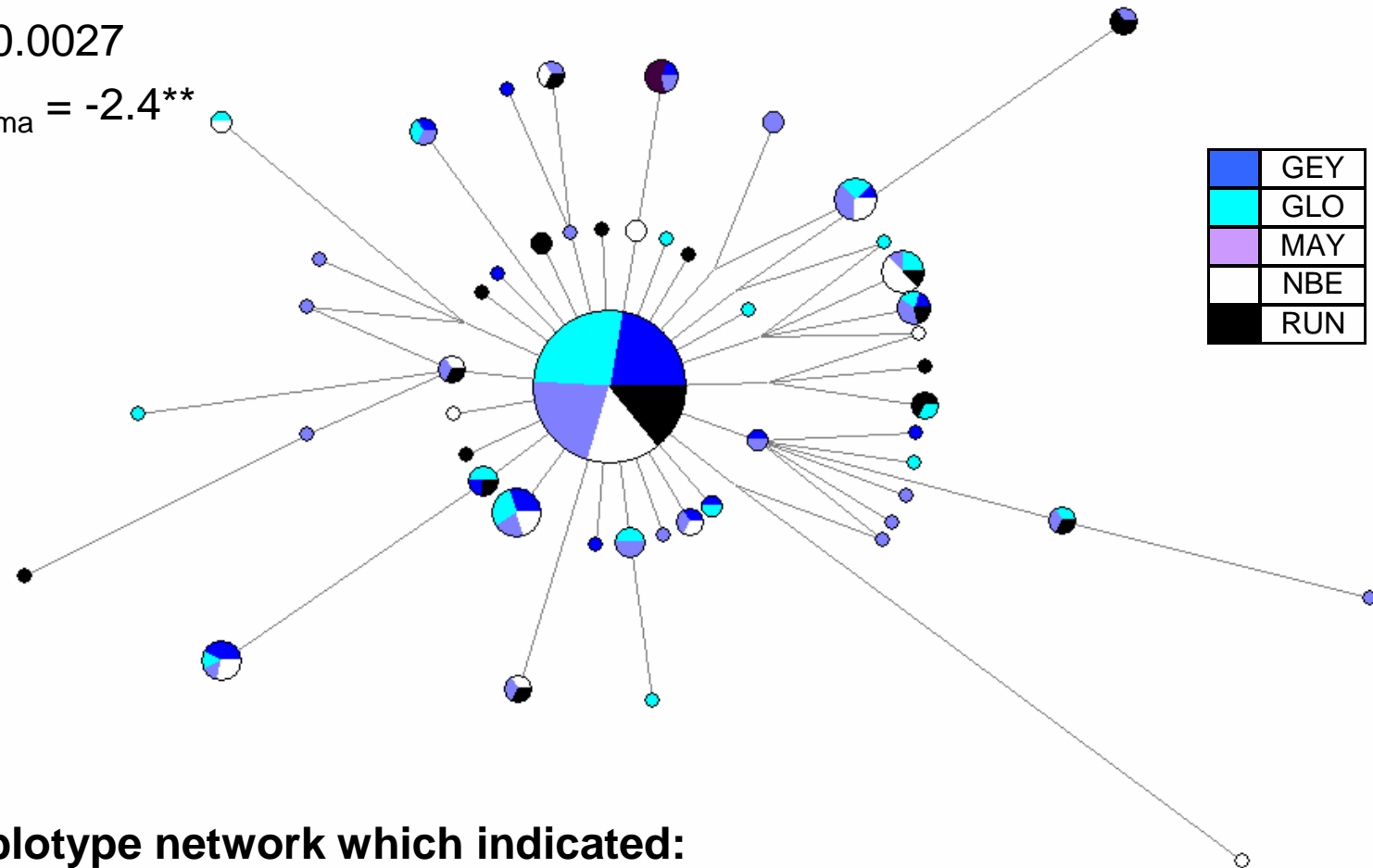
- the morphology of the network
- the frequency of the different haplotypes
- the geographical representation of each haplotype

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



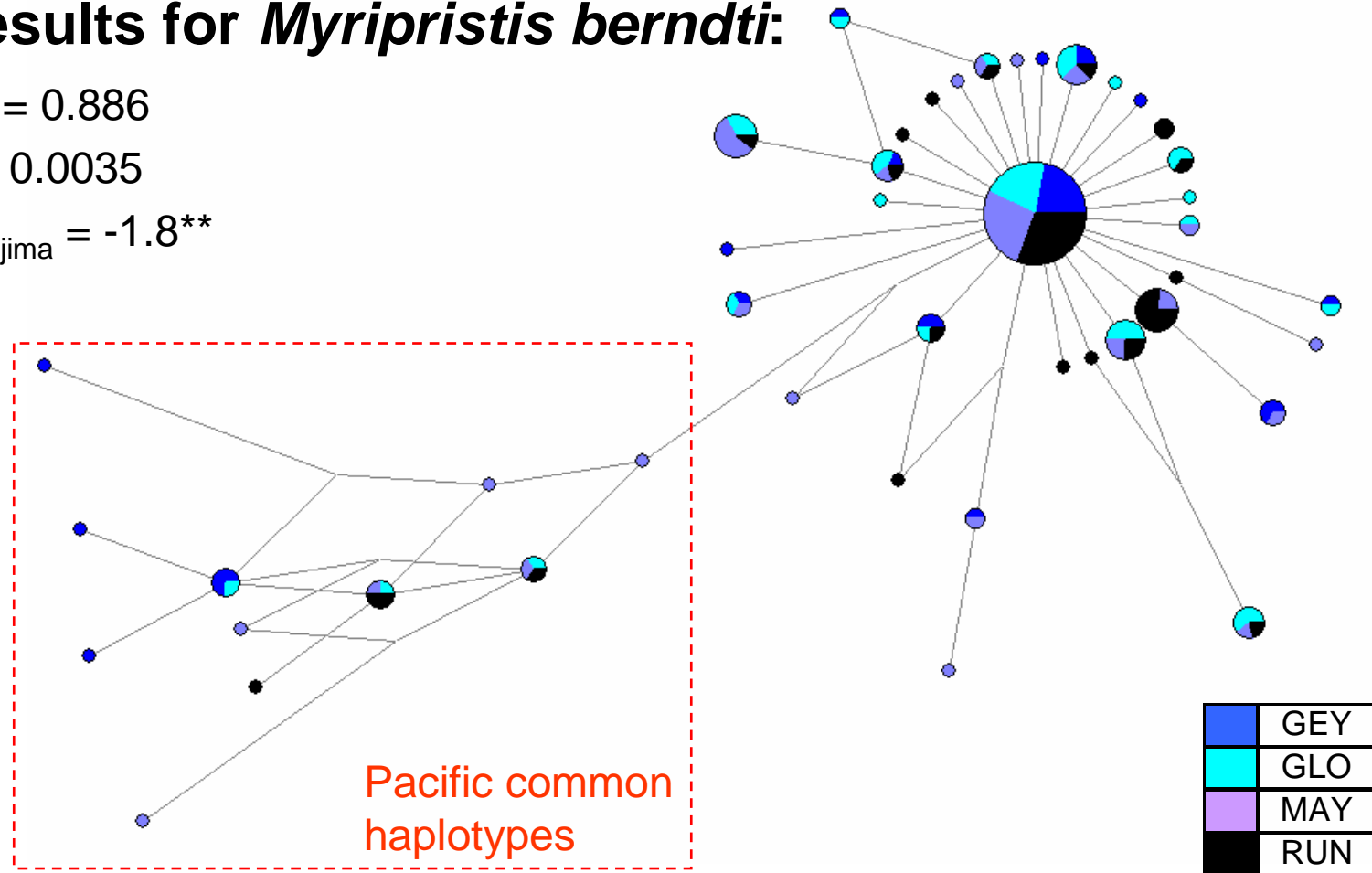


Results for *Myripristis berndti*:

$H_d = 0.886$

$\pi = 0.0035$

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



A more complex haplotype network with:

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

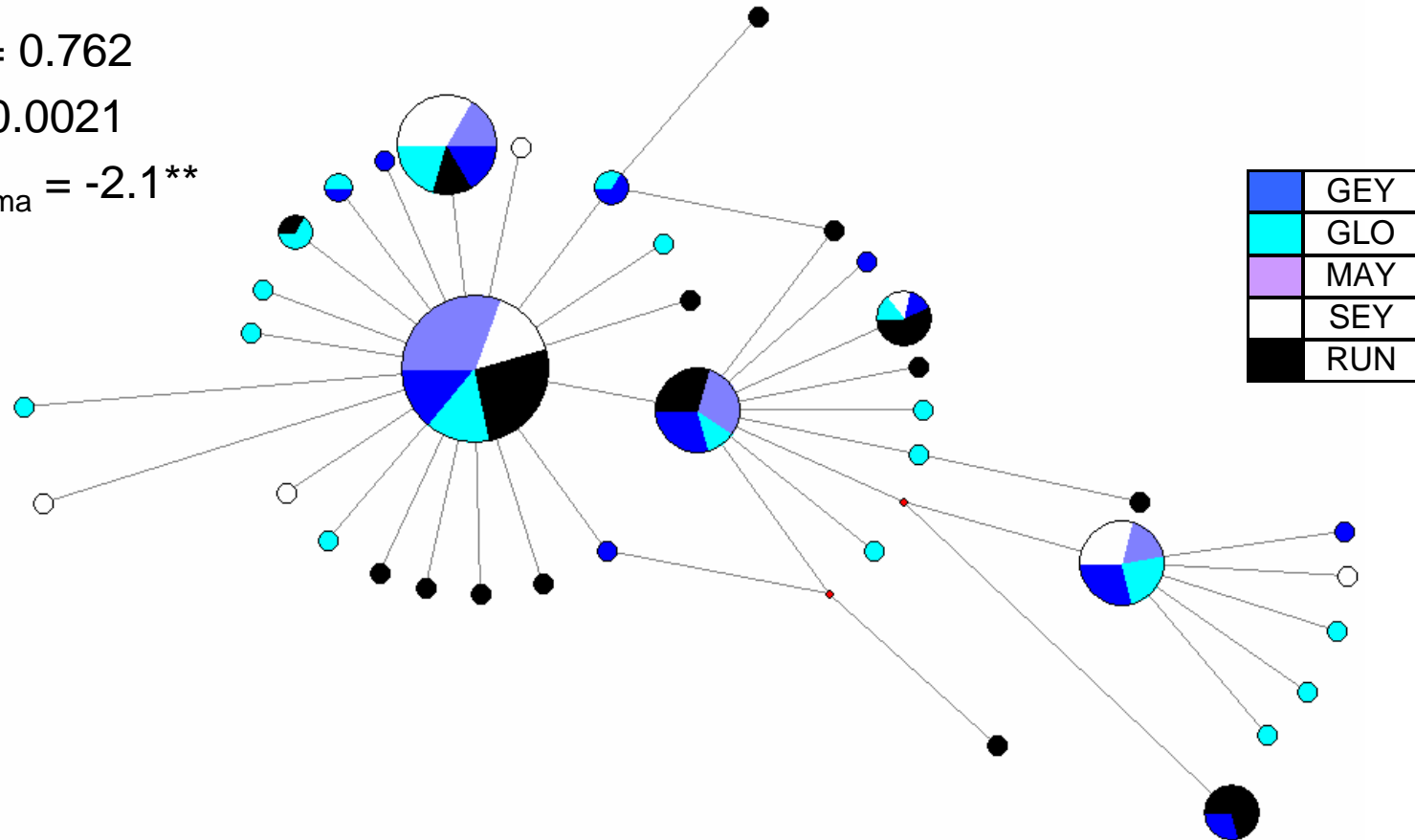


Results for *Epinephelus merra*:

$H_d = 0.762$

$\pi = 0.0021$

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

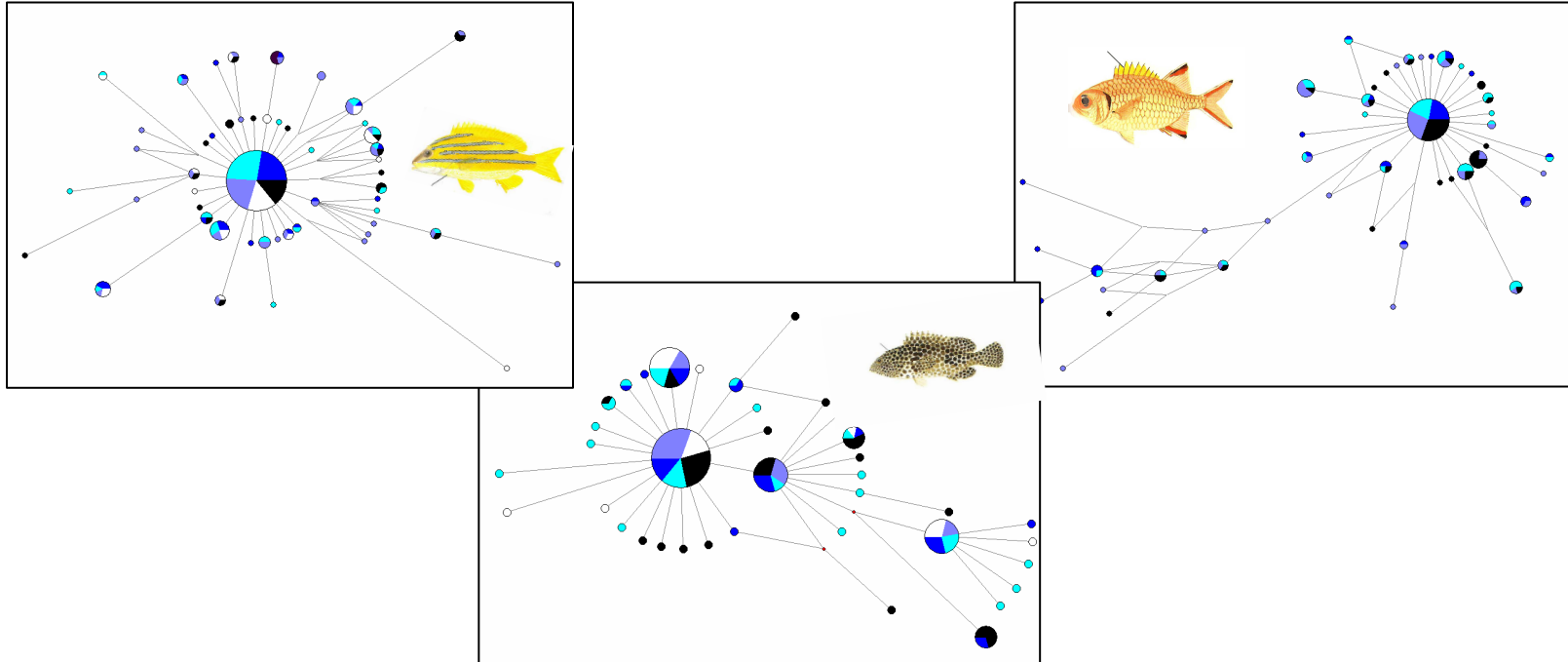


Even more complicated network which indicated:

- 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

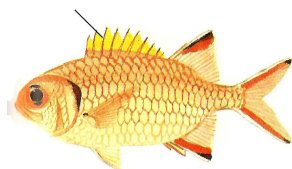


For the 3 species:

- 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*:



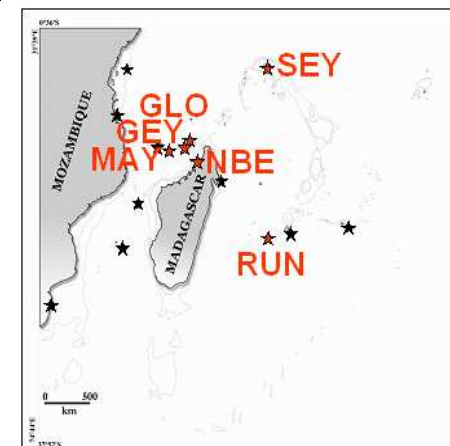
	GEY	GLO	MAY	NBE
GLO	-0.010			
MAY	0.007	-0.001		
NBE	0.006	-0.003	-0.006	
RUN	0.017	0.008	-0.004	0.002

	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	0.053*	0.057*	-0.042	0.072*

Fst = Fixation index between populations

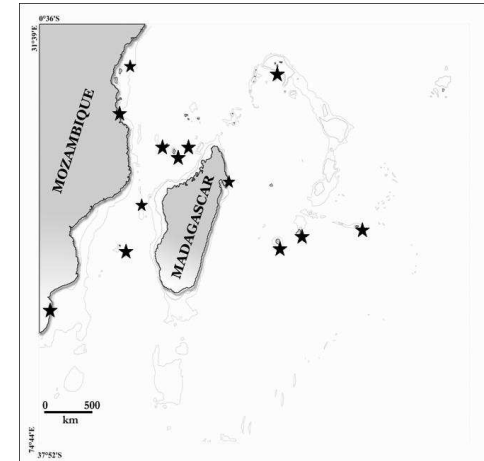
More Fst → 1, more populations are differentiated

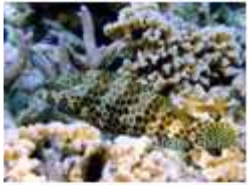


Preliminary results give interesting perspectives:



- Continue the sampling for the CAMP project in the other SWIO sites
- Develop the 2nd 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)
- POCT-OI (Europe, France, La Réunion)
- TCO



CAMP 3001

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- Thanks for your attention -