

Molecular ecology and phylogenetics of deep-sea species in the North Atlantic

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Institute of Zoology

LIVING CONSERVATION

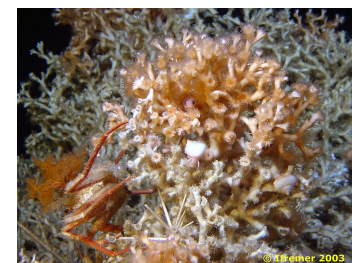
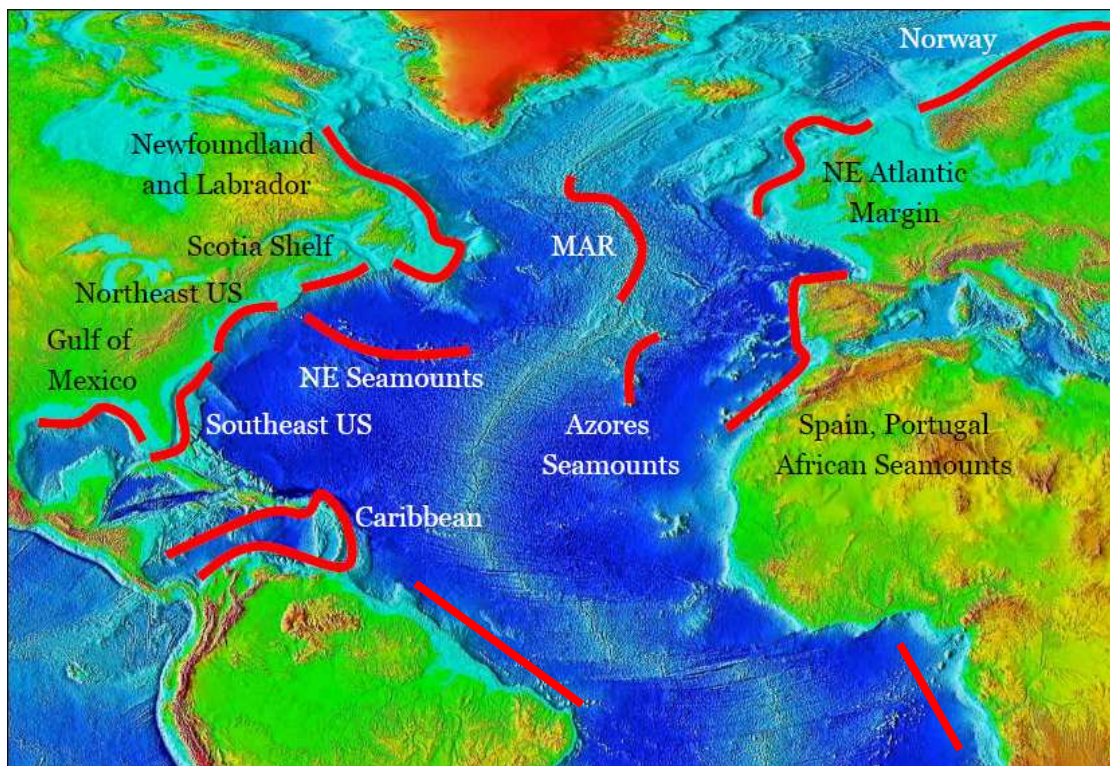
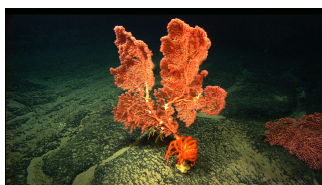
The talk



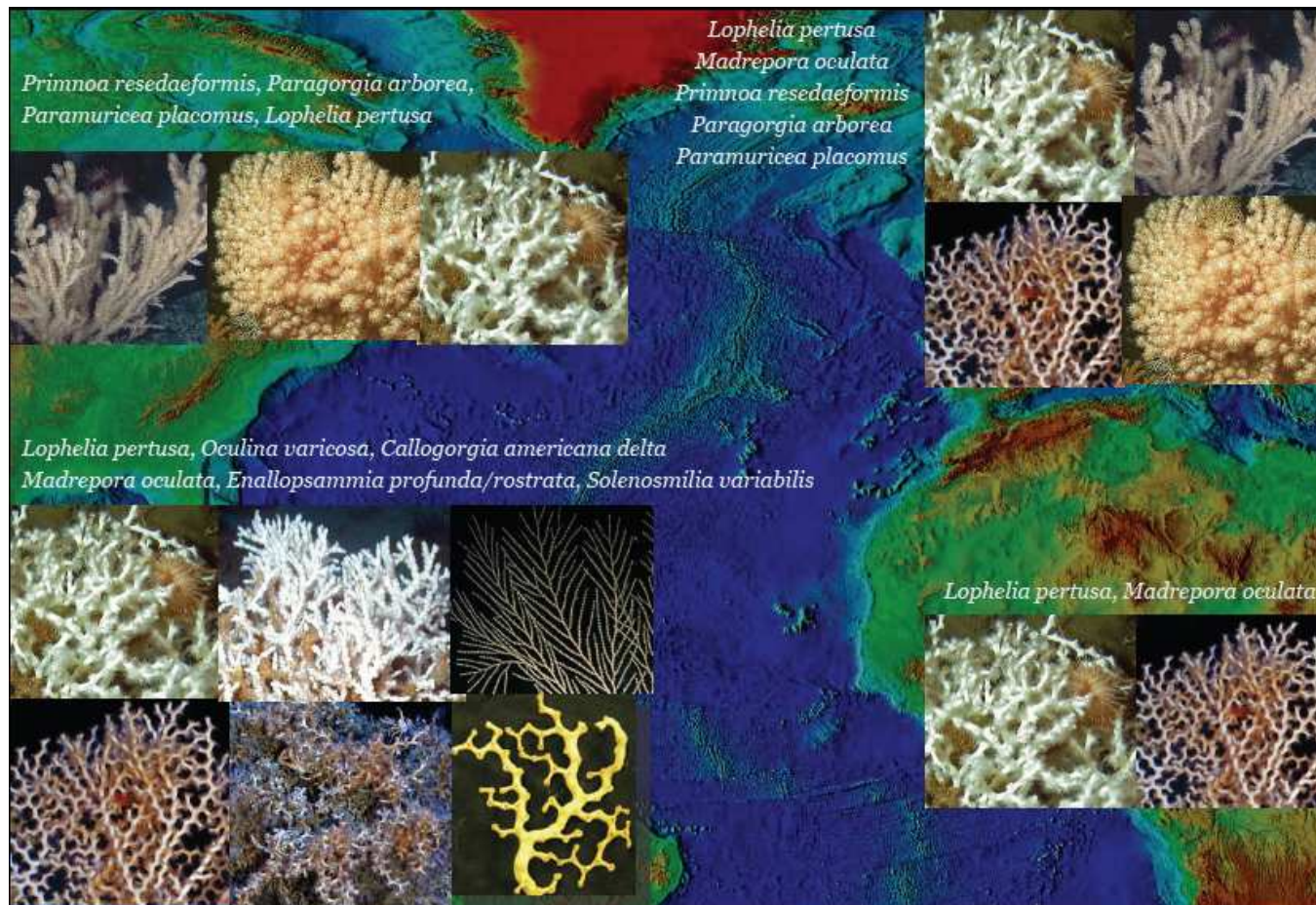
- **North Atlantic**
- **Studies**
 - Deep-sea fish
 - *Lophelia pertusa*
 - Other corals
- **Hypotheses**

Coral regions – North Atlantic

ZSL



Differences in species composition of coral communities



Erik Cordes

Modelling species distributions: Environmental Niche Factor Analysis (ENFA)

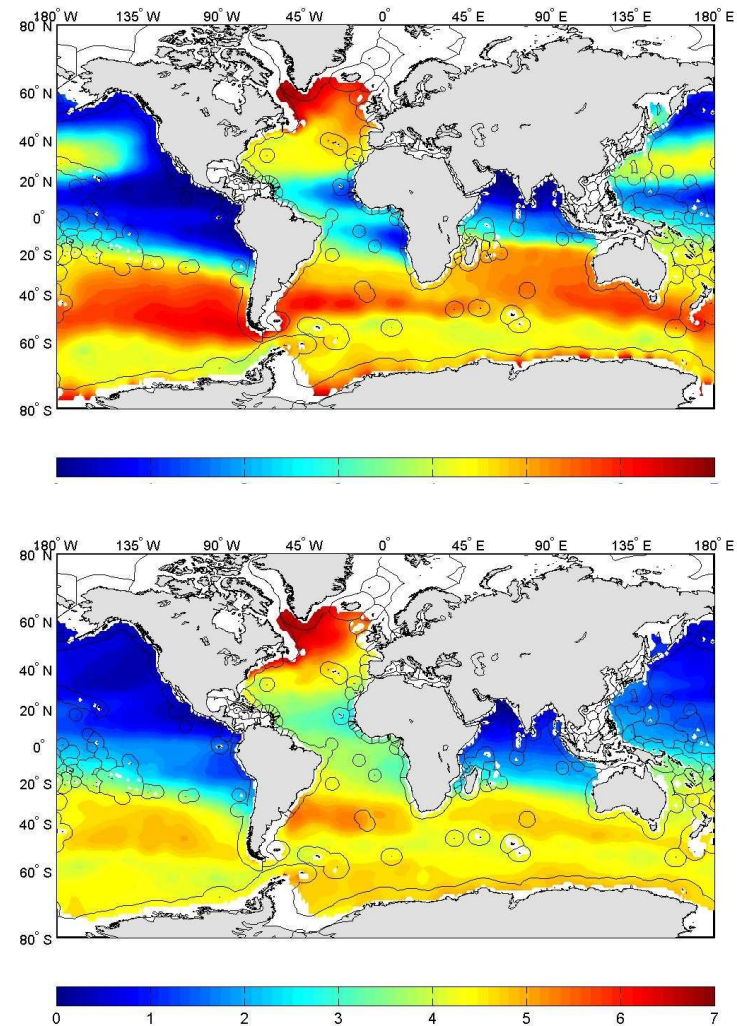


ENFA compares the observed distribution of a species, or group of species, to the background distribution of environmental factors.

It assesses how different the environmental niche a taxonomic group occupies is relative to the mean background environment (its 'marginality'), and how narrow this niche is (its 'specialization').

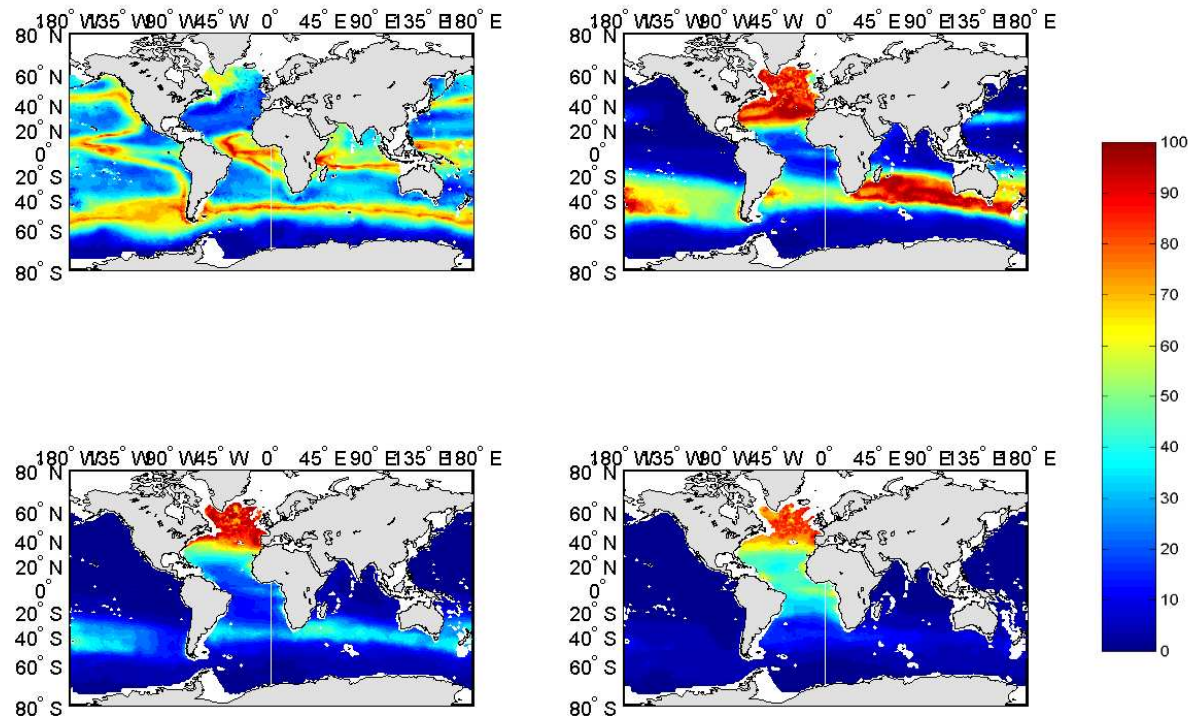
Why ENFA?

Because the coral database is a "presence only" dataset.



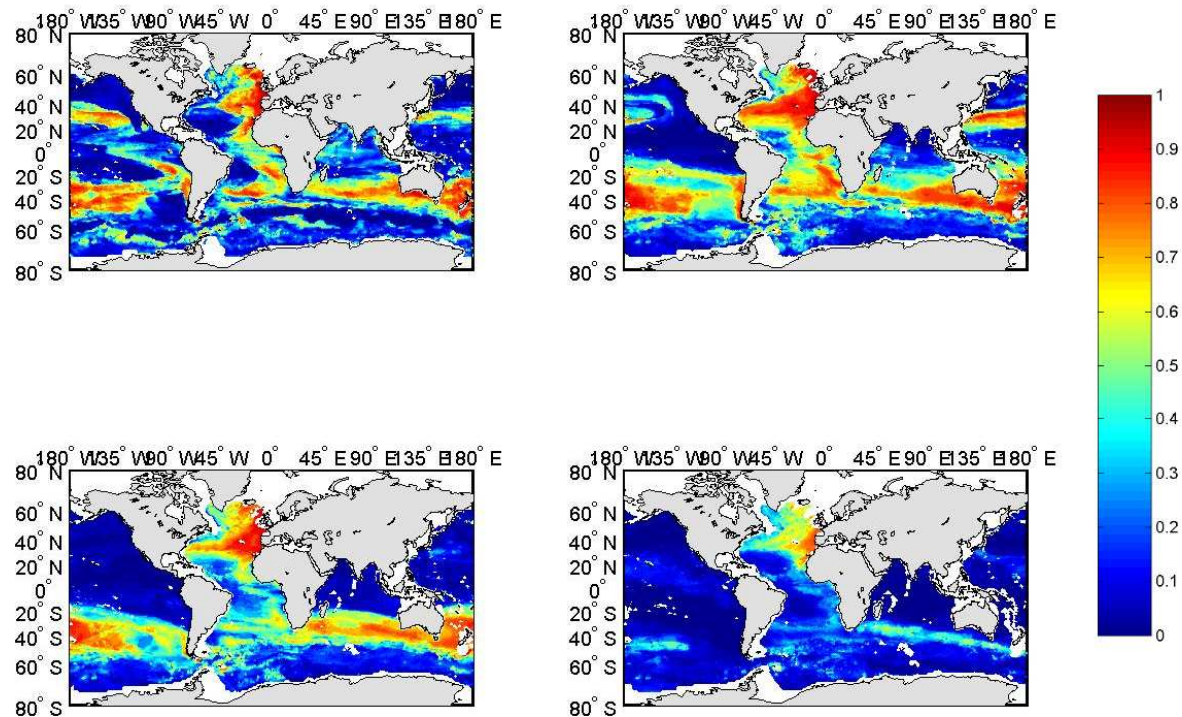
Aragonite $\mu\text{mol kg}^{-1}$ at 500m & 1000m depth

Scleractinian habitat suitability



Tittensor et al., In press J. Biogeogr.

Scleractinian habitat suitability – Maximum Entropy



Tittensor et al., In press J. Biogeogr.

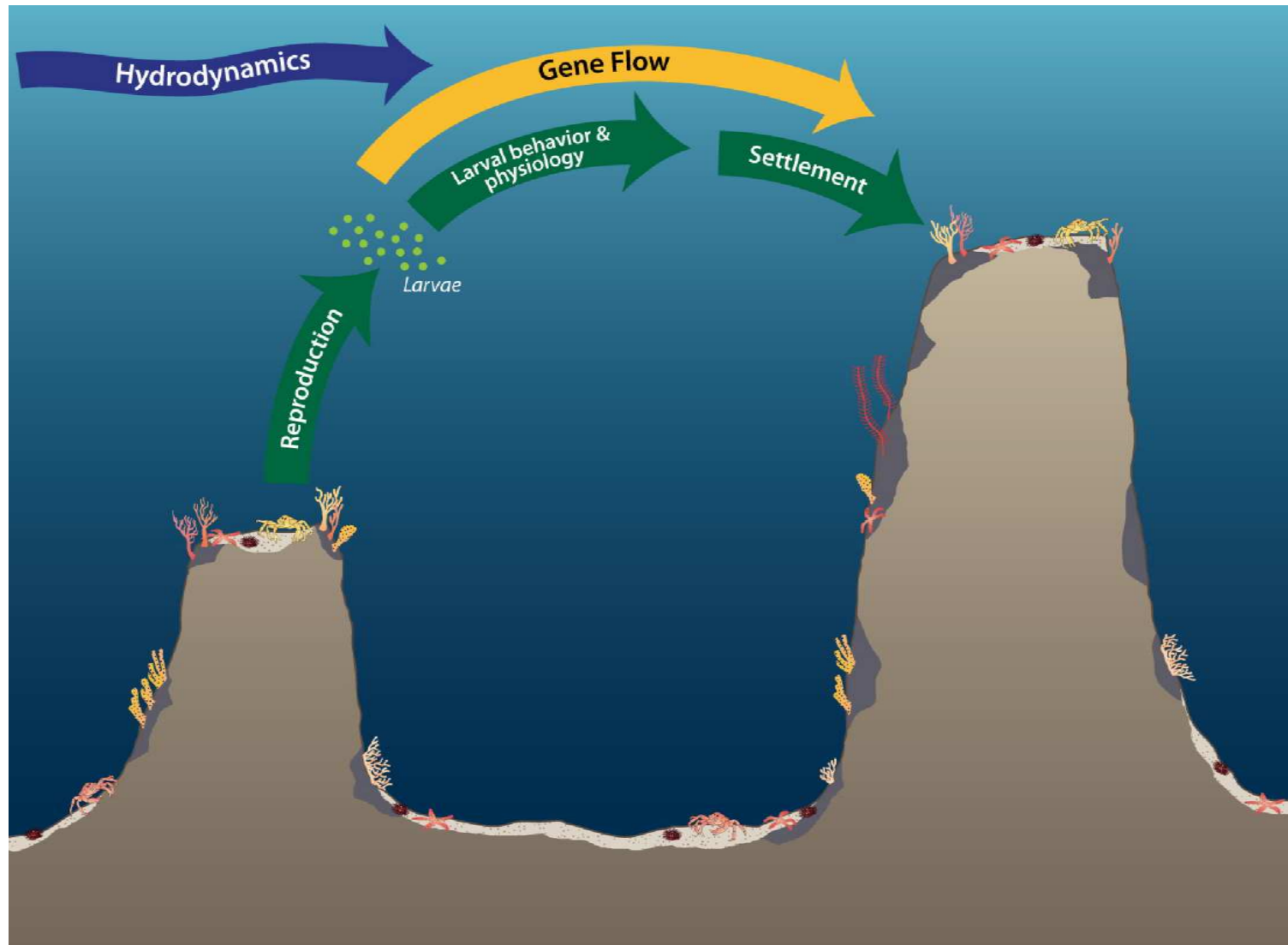
Explained specialization by physical factors



1 = marginality; rest = specialisation

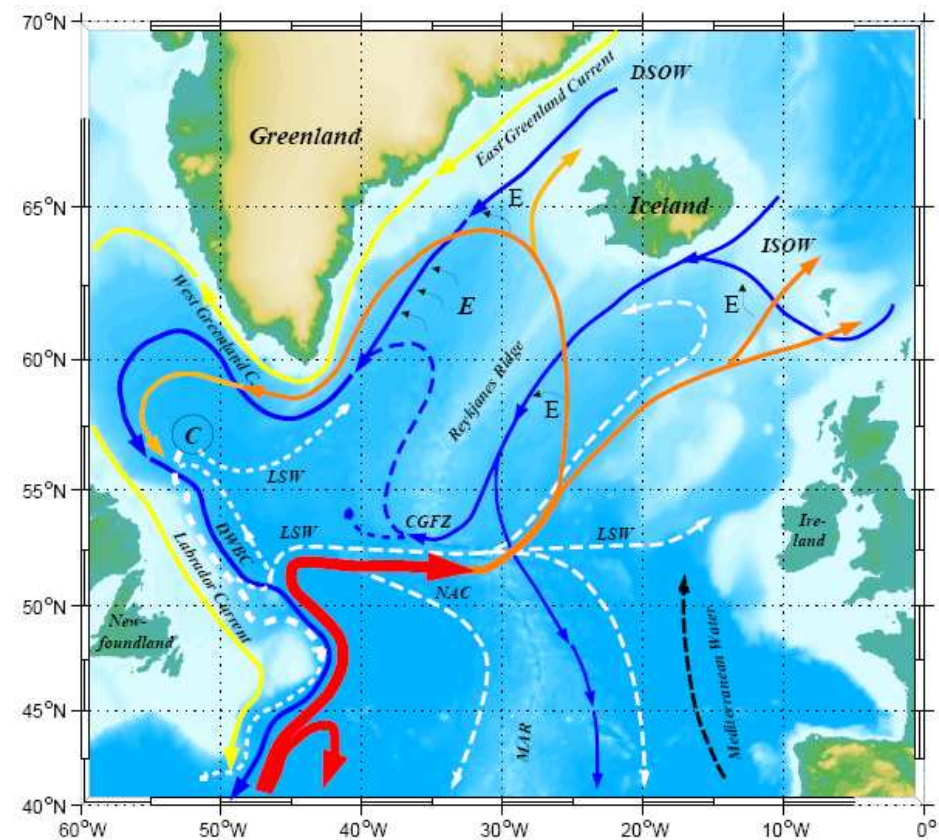
Factor	1	2	3	4	5	6	7	8	9
Alkalinity (total)	-0.242	0.057	0.104	0.147	0.002	0.545	0.131	0.334	0.486
Delta CO3 (aragonite saturation state)	0.317	0.245	0.174	0.682	0.293	0.144	0.190	0.034	0.330
Depth	-0.233	0.085	0.020	0.181	0.035	0.399	0.012	0.020	0.217
Dissolved oxygen	0.204	0.037	0.565	0.147	0.535	0.057	0.351	0.359	0.408
Export productivity	0.149	0.003	0.000	0.009	0.007	0.005	0.010	0.026	0.034
Nitrate	-0.325	0.550	0.139	0.053	0.039	0.002	0.687	0.048	0.304
Percent oxygen saturation	0.271	0.023	0.731	0.104	0.592	0.316	0.028	0.097	0.352
Phosphate	-0.328	0.786	0.149	0.265	0.021	0.132	0.066	0.023	0.054
Primary productivity	0.306	0.014	0.003	0.047	0.014	0.076	0.117	0.035	0.149
Salinity	0.179	0.052	0.027	0.088	0.090	0.267	0.114	0.138	0.201
Silicate	-0.361	0.017	0.105	0.072	0.161	0.173	0.225	0.600	0.359
Total CO2 (DIC)	-0.315	0.064	0.156	0.587	0.481	0.543	0.476	0.278	0.041
Temperature	0.283	0.020	0.165	0.123	0.094	0.008	0.207	0.537	0.152
Water velocity	-0.042	0.005	0.000	0.009	0.004	0.028	0.007	0.008	0.068
<i>Explained specialisation</i>	<i>0.095</i>	<i>0.218</i>	<i>0.171</i>	<i>0.107</i>	<i>0.092</i>	<i>0.072</i>	<i>0.064</i>	<i>0.050</i>	<i>0.037</i>

Connectivity of populations



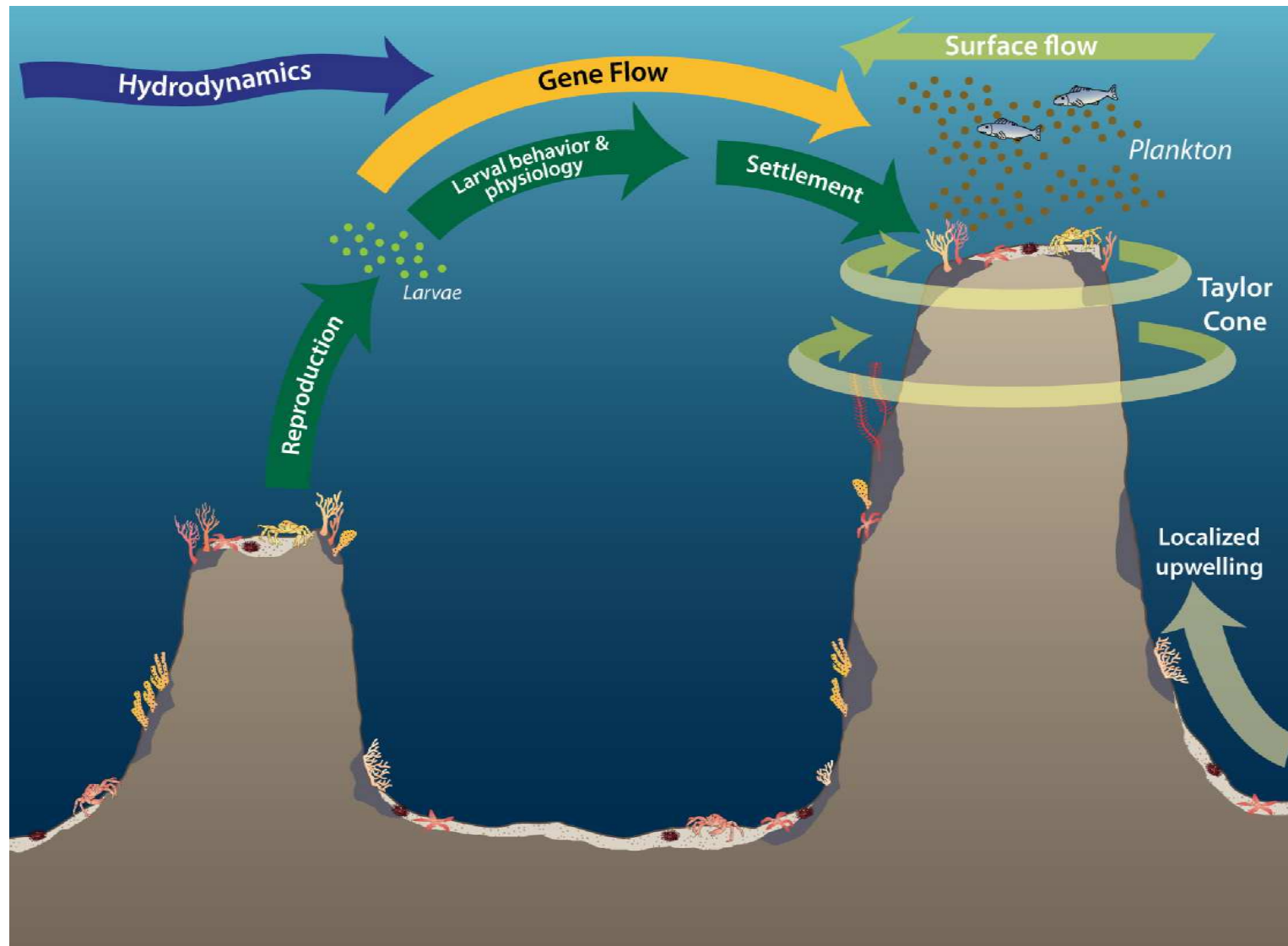
Tim Shank

North Atlantic currents



E: Entrainment C: Convection CGFZ: Charlie Gibbs Fracture Zone MAR: Middle Atlantic Ridge
DWBC: Deep Western Boundary Current NAC: North Atlantic Current
LSW: Labrador Sea Water ISOW: Iceland Scotland Overflow Water DSOW: Denmark Strait Overflow Water

Barriers to dispersal



Tim Shank

Methods for inferring migration.



- 1) Indirect (inferring effective migration). Genetic methods to estimate gene flow from genetic differences among populations (Slatkin et al., 2003; Benzie 1999); different gene regions evolve at different rates so must pick markers yield appropriate scale. Genetic markers for assignment of individuals to populations (Mantel et al., 2005; Jones et al., 2005).
- 2) Direct (assigning sources populations, natal origins, or parents). Larval and adult tags (Jones et al., 1999; Alamayet al., 2007). Fish otolith chemistry (Thorrold et al., 2001).

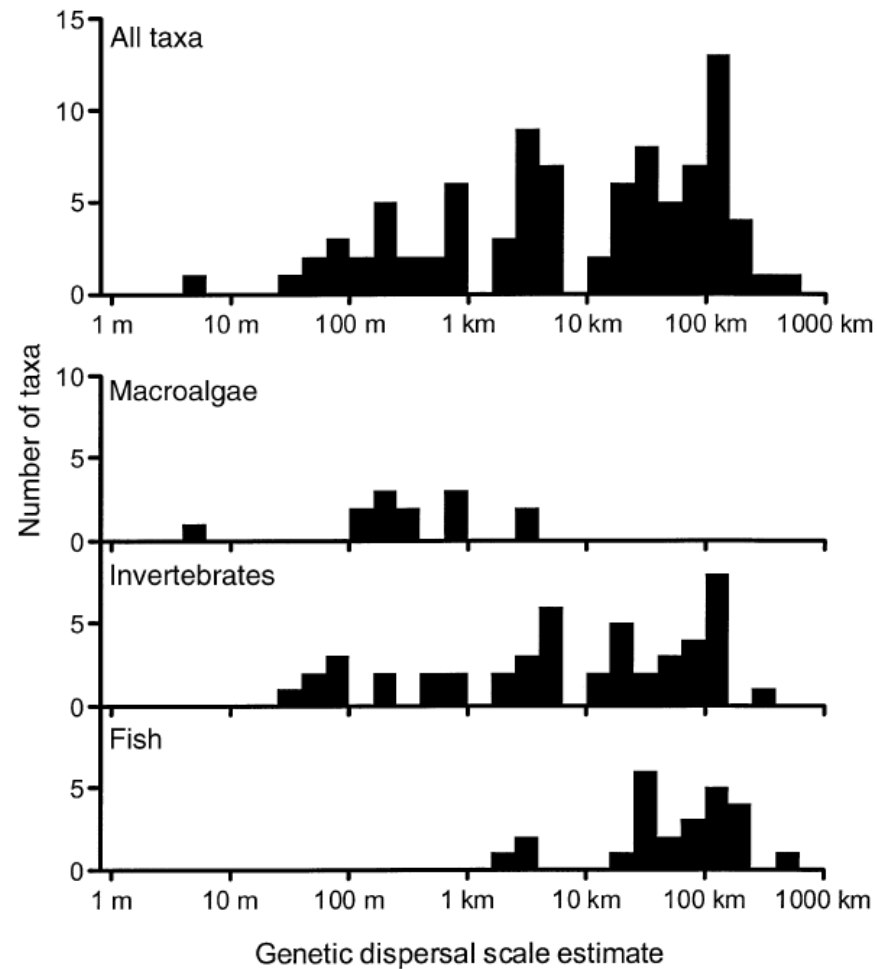
Dispersal scales of marine taxa



Dispersal distances based on genetic isolation by distance slopes.

Note the extreme heterogeneity in dispersal distances

Kinlan & Gaines, 2003
Ecology 84: 2007-2020



Deep-sea fish in the NE Atlantic



Pagellus bogaraveo



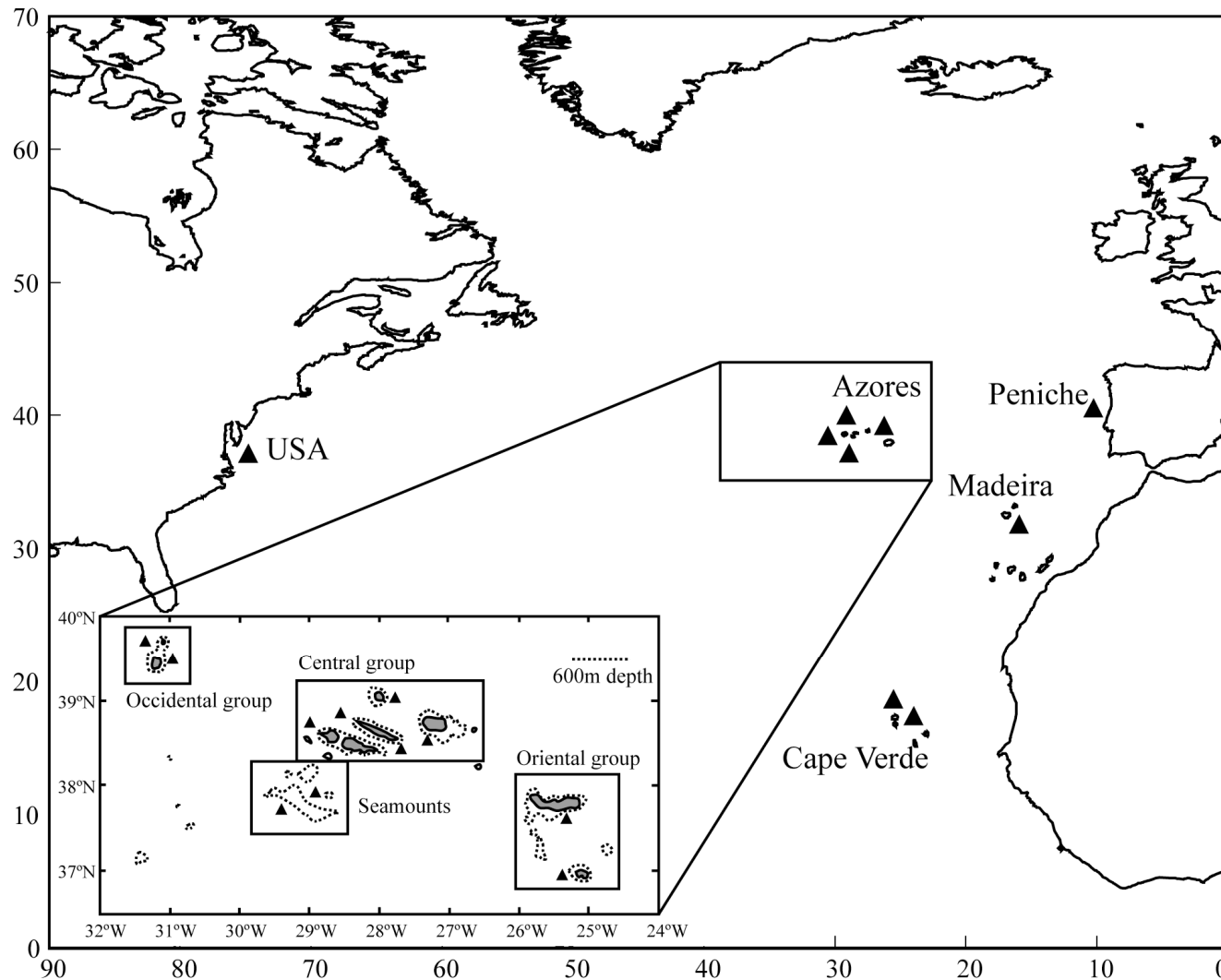
PMN Cambraia Duarte



*Helicolenus
dactylopterus*

T Østergaard

Sample localities: *Pagellus* / *Helicolenus*



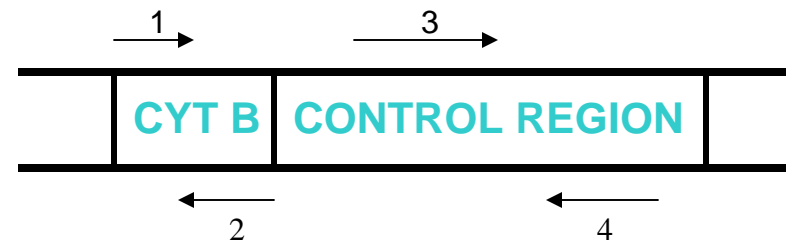
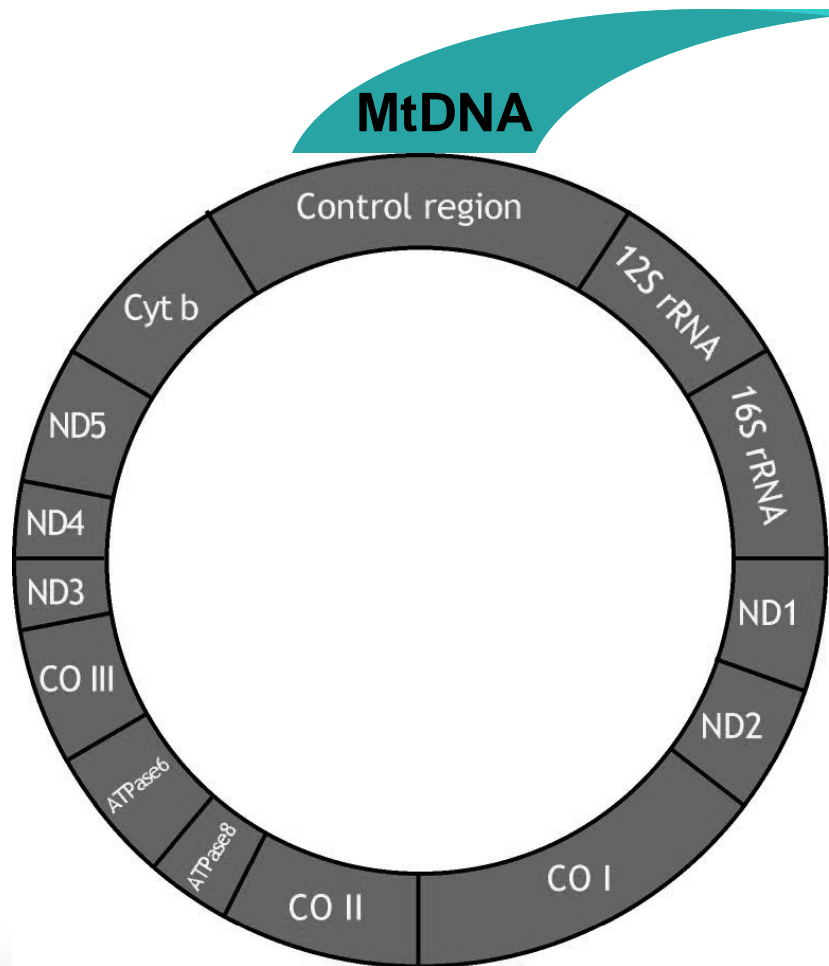
Aboim et al., 2005

Mitochondrial DNA Sequence analyses



METHODOLOGY

MOLECULAR MARKERS



Universal primers:

1- Cyb-glu-I-cp- TGACTTGAAGAACCACCGTTG

2-CB2-H-CCCTCAGAATGATATTTGTCCTCA

3- L-Pro-1-ACTCTCACCCCTAGCTCCCAAAG

4-H-DI-C-1-CCTGAAGTAGGAACCAGATGCCAG

Pagellus bogaraveo

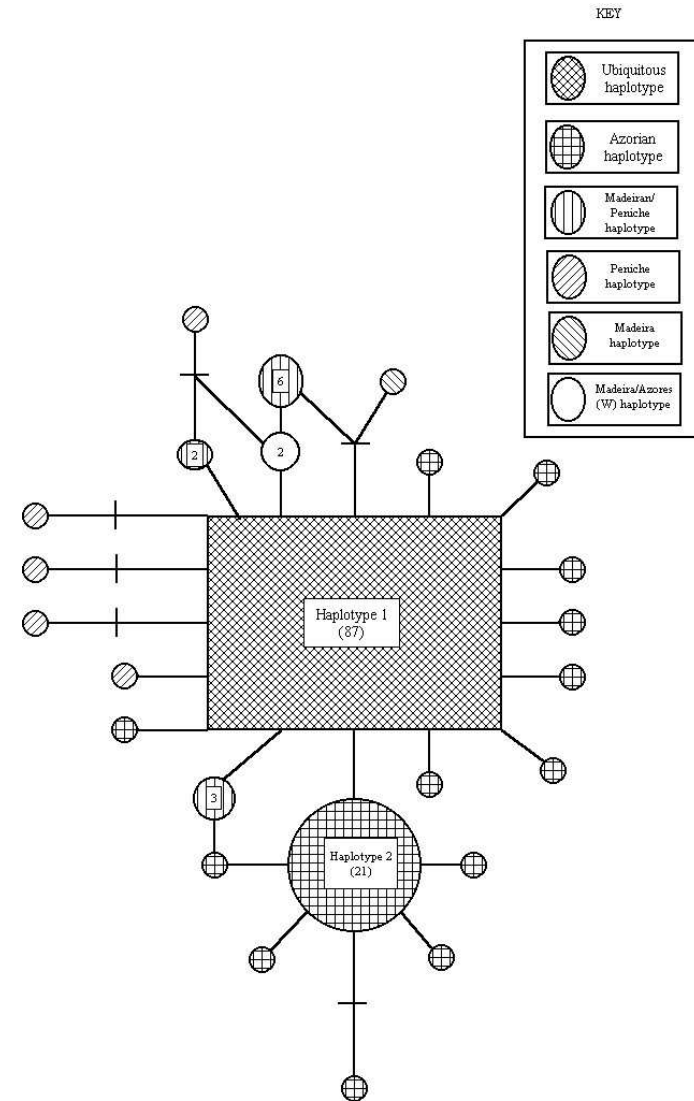


Minimum-spanning
network analysis D-Loop

Size of box = nos. of
individuals with
haplotype

Mutation events shown
by lines

Azores-only haplotypes



Stockley et al *Marine Biology* **146** (4): 793-804

F-statistics



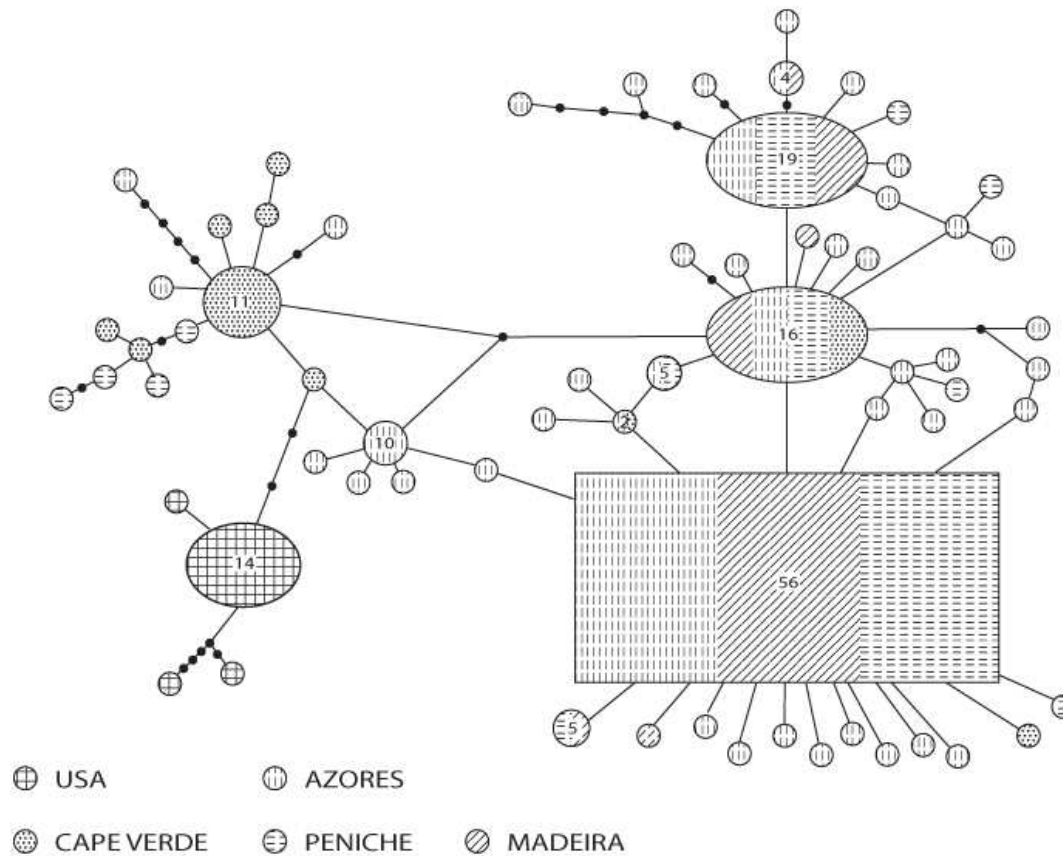
- F_{ST} is a measure of genetic differentiation between populations.
- Value 1 = complete differentiation
- Value of 0 = identical populations
- Even quite low values of F_{ST} can be significantly different.
- Sample size and number of genetic loci examined can be important.

Pairwise F_{ST} s (above = microsats below = D-loop)



	Azores West	Azores East	Azores Central	Princess Alice Bank	Portuguese Slope	Madeira
Azores West	X	0.00227	0.0030	0.00169	0.01833***	X
Azores East	0.06322	X	-0.0068	0.0084	0.02051***	X
Azores Central	0.04136	-0.03118	X	0.00125	0.01888***	X
Princess Alice Bank	0.10182*	-0.02573	-0.01040	X	0.01793***	X
Portuguese slope	0.22960***	0.07615*	0.09960*	0.03889*	X	X
Madeira	0.18804**	0.04858	0.07268**	0.03108*	-0.02075	X

D-loop *Helicolenus* - minimum spanning network



Aboim et al 2005 *Molecular Ecology* 14: 1343-1354

F_{ST} values for pairwise population comparisons: *Helicolenus dactylopterus*.



F_{ST} values	Azores (oriental)	Azores (ocidental)	Azores (central)	Azores Seamounts	Peniche	Madeira archipelago	NW Atlantic	Cape Verde archipelago
Oriental	—	−0.0115	−0.0117	−0.0116	0.0048	−0.0075	0.7583***	0.3036***
Ocidental	0.0002	—	0.0167	−0.0085	0.0034	−0.0101	0.7326***	0.2711***
Central	−0.0123	0.0052	—	0.0083	0.7173	0.0191	0.7665***	0.3317***
Seamounts	0.0082	−0.0043	−0.0004	—	−0.0077	−0.0189	0.6904***	0.2346***
Peniche	0.0270	0.0279	0.0188	0.0096	—	−0.0162	0.7173***	0.2434***
Madeira	−0.0027	−0.0068	0.0053	0.0013	0.0069	—	0.7272***	0.2349***
NWA	0.7910***	0.7408***	0.7714***	0.7315***	0.7159***	0.7531***	—	0.6587***
Cape Verde	0.4154***	0.3668***	0.3778***	0.3119***	0.2509***	0.3440***	0.6845***	—

Beryx splendens and *B. decadactylus*



Ken Sulak, USGS
Life on the Edge 2004.

F_{ST}	<i>Beryx splendens</i>		<i>Beryx decadactylus</i>
	control region	cyt <i>b</i>	control region
Azores x Madeira	-0.020	0.023	-0.0155
Azores x Cape Verde	-0.006	0.042	0.2359***
Madeira x Cape verde	-0.018	0.018	0.1622***

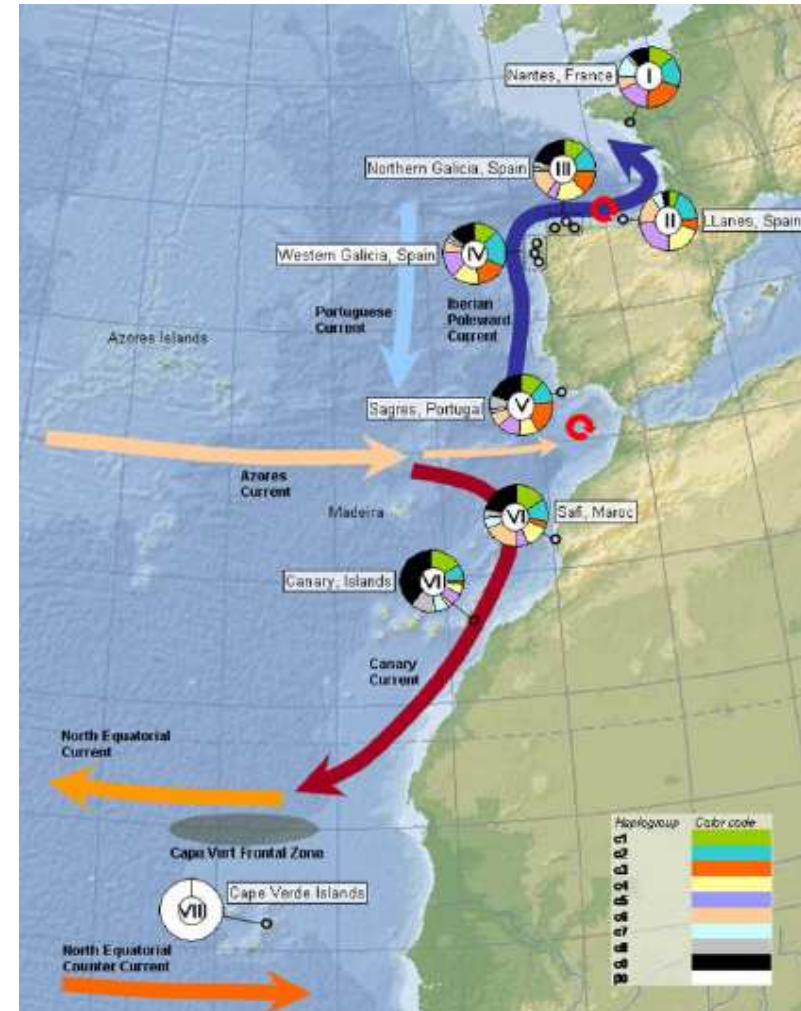
B. splendens and *B. decadactylus*: pairwise comparisons for F_{ST} . *** = significant at $P < 0.001$ (after sequential Bonferroni correction).

Haplotype frequencies: *Pollicipes pollicipes*



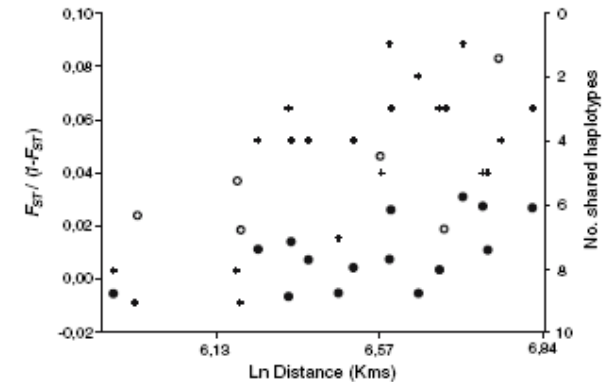
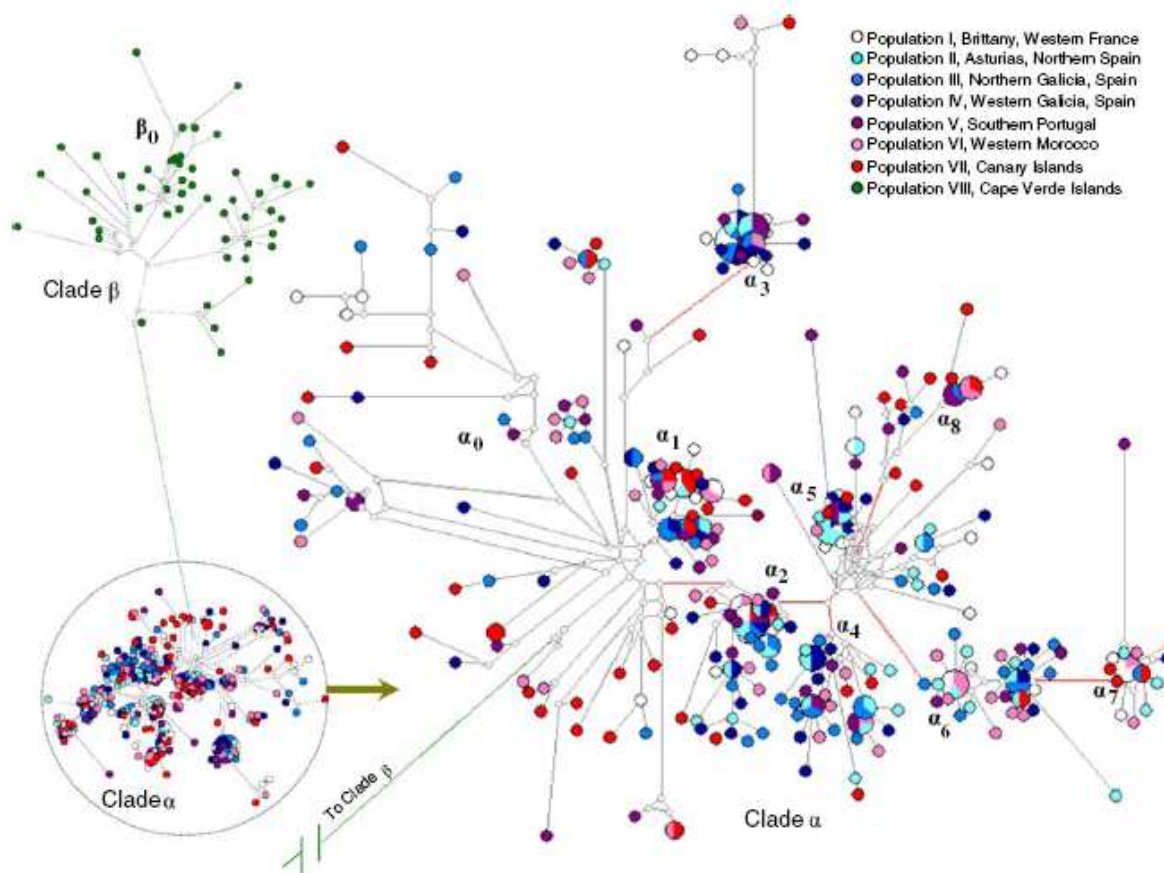
MCCIP

Sequencing of mt 12SrRNA and
tRNA^{MET}



Quintero *et al* (2007) Mar Biol 153: 47-60

Haplotype network *Pollicipes pollicipes*



Isolation by distance
(except Cape Verde)

Haplotype network
Quintero *et al* (2007) Mar Biol 153: 47-60

Cape Verde Frontal System



- The Azores and Canary Islands are potentially connected by the Azores Current and its extension, the Canary Current (Machíz et al., 2006). These currents may act as a pathway to allow the dispersal of larvae between these areas and, similarly, larval transport is also possible between the Azores and Madeira (Machíz et al., 2006).
- From the Azores, the Canary current approaches the eastern North Atlantic where it is deflected south by wind and the meridional blocking of the African continent. The Canary current then flows south to Cape Blanc where it then moves offshore along the Cape Verde Frontal System.
- This is a strong thermohaline front that acts as a barrier between the well-ventilated sub-tropical gyre (North Atlantic Central Water) and quasi-stagnant waters to the south (Klein & Siedler, 1995). It is almost certainly a major barrier to dispersal & gene flow.

Polyprion americanus

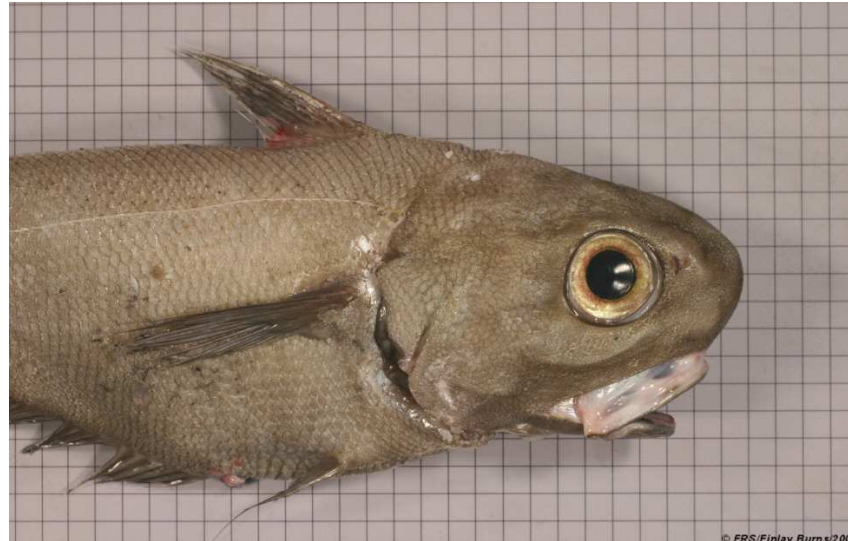


Two populations, one in North Atlantic, one in South Atlantic (ND1 gene).



IUCN

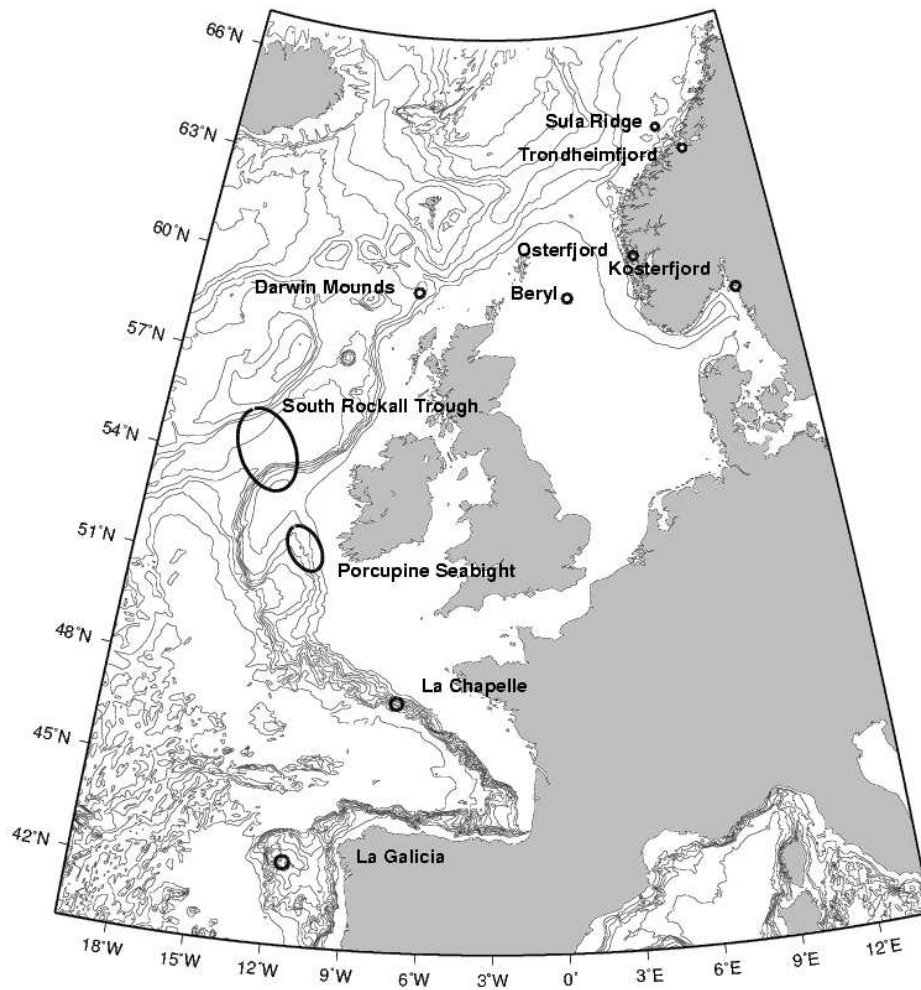
Coryphaenoides rupestris



Finlay Burns, FRS

Some evidence based on allozymes of population differentiation between NE and NW Atlantic and northern and southern Mid-Atlantic Ridge (Duschenko 1988) .

Genetic population structure in *Lophelia pertusa*



David Billett, National Oceanography Centre

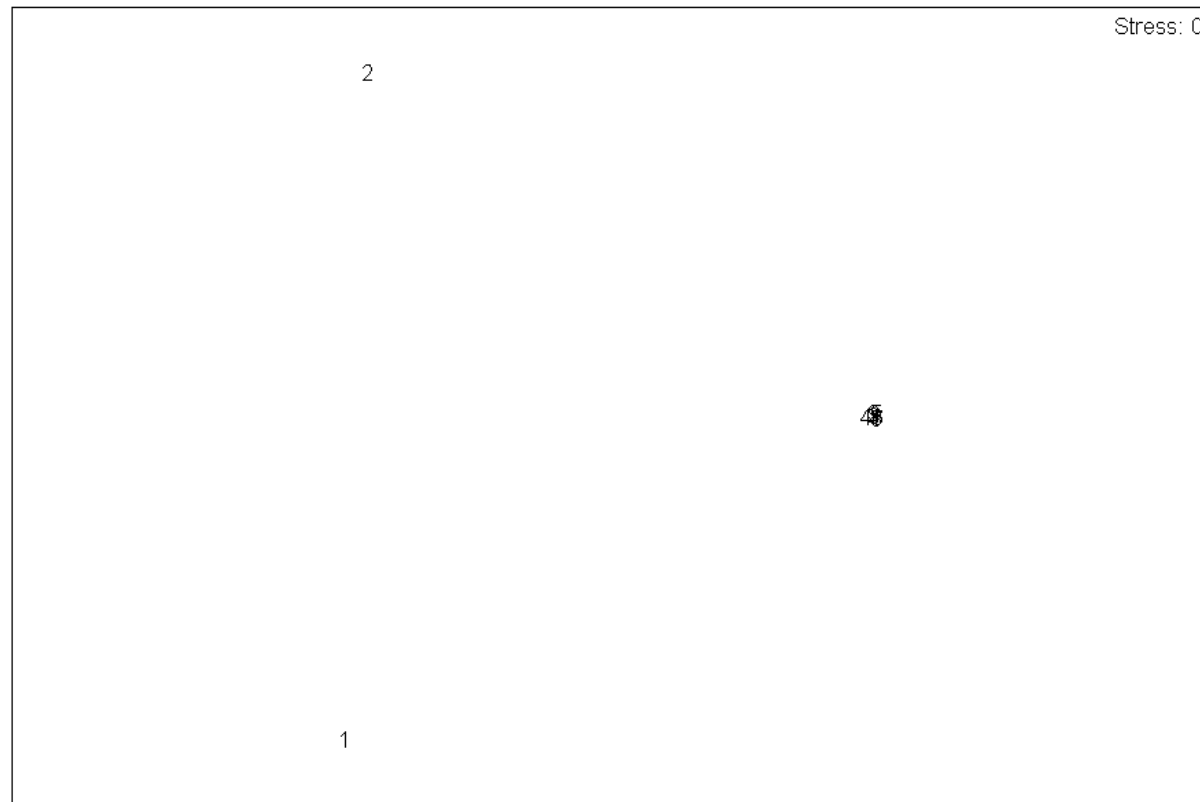
Le Goff-Vitry, et al. (2004) *Molecular Ecology*. **13**: 537-549

Genotypic diversity



Sampling area	Genotypic diversity (G/N)
Kosterfjord	1.000
Osterfjord	0.667
Trondheimfjord	1.000
Sula Ridge	1.000
North Sea (Beryl Alpha platform)	1.000
North Rockall Trough (Darwin Mounds)	0.415
South Rockall Trough	1.000
Porcupine Seabight	0.796
La Chapelle	0.875
La Galicia	0.854

Gene - flow



Multidimensional scaling of pairwise genetic distances (Shriver et al.'s stepwise weighted genetic distance (1995))(Osterfjord: 1; Trondheimfjord: 2; Sula Ridge: 3; North Sea (Beryl Alpha platform): 4; North Rockall Trough (Darwin Mounds): 5; South Rockall Trough: 6; Porcupine Seabight: 7; La Chapelle: 8; La Galicia: 9)

Gene flow between populations

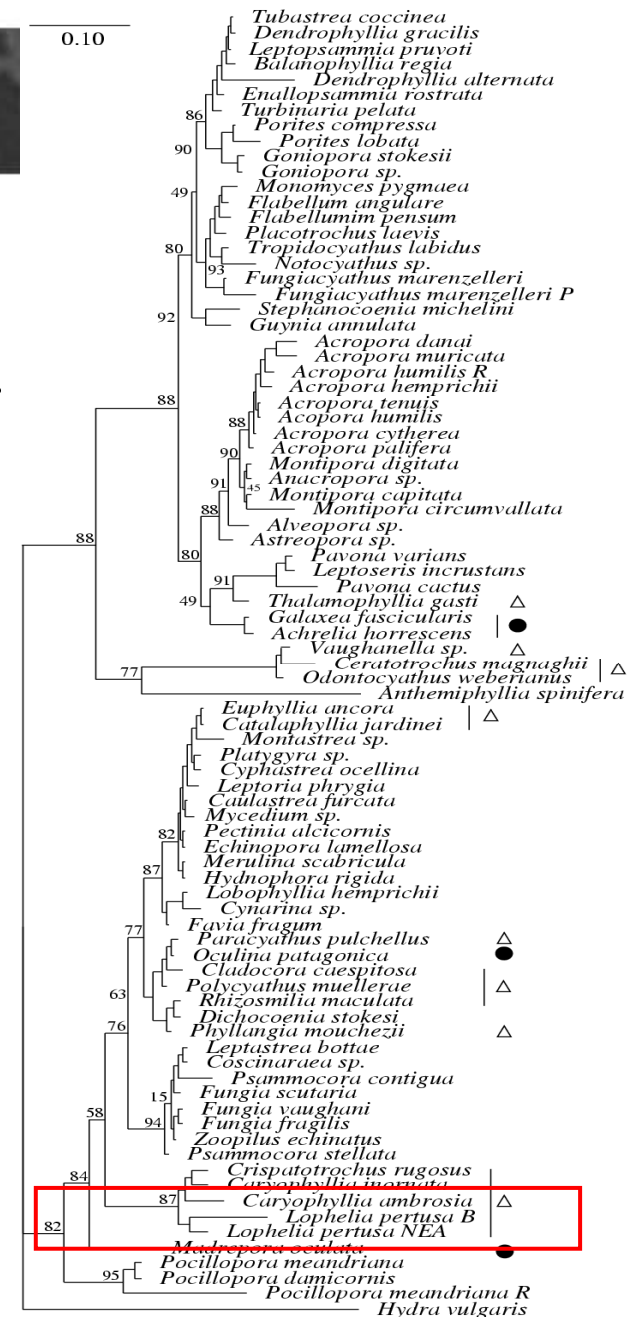


	OF	TF	SR	NS	NRT	SRT	PS	LC	LG
OF		<i>0.30</i>	<i>0.33</i>	<i>0.43</i>	<i>0.49</i>	<i>0.52</i>	<i>0.70</i>	<i>0.37</i>	<i>0.80</i>
TF	<i>0.26</i>		<i>0.69</i>	<i>1.06</i>	<i>1.11</i>	<i>1.25</i>	<i>1.42</i>	<i>0.78</i>	<i>1.79</i>
SR	<i>0.25</i>	<i>1.08</i>		<i>1.28</i>	<i>0.89</i>	<i>1.91</i>	<i>3.69</i>	<i>1.39</i>	<i>2.21</i>
NS	<i>0.24</i>	<i>0.70</i>	<i>2.24</i>		<i>1.54</i>	<i>2.06</i>	<i>2.91</i>	<i>1.41</i>	<i>3.58</i>
NRT	<i>0.24</i>	<i>1.23</i>	<i>5.03</i>	<i>1.31</i>		<i>1.59</i>	<i>1.91</i>	<i>1.19</i>	<i>3.27</i>
SRT	<i>0.16</i>	<i>0.70</i>	<i>-39.84</i>	<i>0.89</i>	<i>2.14</i>		<i>4.06</i>	<i>4.81</i>	<i>5.26</i>
PS	<i>0.16</i>	<i>1.46</i>	<i>9.83</i>	<i>1.52</i>	<i>2.02</i>	<i>1.64</i>		<i>3.23</i>	<i>5.41</i>
LC	<i>0.24</i>	<i>1.48</i>	<i>36.78</i>	<i>3.07</i>	<i>-98.80</i>	<i>4.80</i>	<i>7.06</i>		<i>4.10</i>
LG	<i>0.23</i>	<i>1.14</i>	<i>5.35</i>	<i>2.51</i>	<i>3.23</i>	<i>2.45</i>	<i>4.52</i>	<i>9.64</i>	

Pairwise estimates of number of migrants per generation for θ (Weir and Cockerham, 1984) (above the diagonal) (Weir and Cockerham, 1984) and Rho (Goodman, 1997) (below the diagonal)

Phylogenetic analysis mitochondrial 16S rDNA

Phylogram resulting from the Bayesian analysis. Probabilities of the partitions, expressed in percentages, are shown at node labels. The scale unit is the mean of the posterior probability density. A capital letter by the species indicates the origin of the sample (R - Réunion Island; B - off Brazil; N E A - North East Atlantic; P - Porcupine Seabight). Symbols show representatives of the families *spot*= *Caryophylliidae*, *triangle*= *Oculinidae*



Systematics of *Lophelia pertusa*



In NE Atlantic region = single species

High genetic distance between NE Atlantic
and Brazilian *Lophelia pertusa* (6.96)

(estimated using F84 model with gamma distribution and a coefficient of variation of 1.2657)

Brazilian and NE Atlantic *Lophelia*
reproductively isolated for a long time

Conclusions



- Clear evidence of genetic structure amongst populations of deep-sea fish and shallow- / deep-water invertebrates in NE Atlantic.
- *Lophelia pertusa* shows a pattern of low to moderate genetic differentiation along continental slopes but marked differentiation between fjord / slope populations, also between the GoM and NW Atlantic and between NE and NW Atlantic
- Levels of genetic differentiation between populations of octocorals and antipatharians depend on the species and probably relate to life history, regional historical patterns of dispersal / colonisation and patterns of currents and the distribution of habitats.

Questions



- What is the range of mean / maximum dispersal distance for cold-water corals?
- What parameters / factors promote dispersal or act as barriers to dispersal / gene flow?
- How does life history interact with these factors?
- How do corals reproduce (sexuality, mating systems, larval development)?
- How is this likely to influence management of deep-sea coral communities?
- Where are deep-sea corals and associated communities found and what influences their distribution and diversity?

Current projects



- Coralfish

Multinational coral study focusing on the Azores, Iceland, Mediterranean and other areas of European continental shelf.

- Azores coral studies

Detailed studies of coral occurrence off the Azores islands (submersible survey, by-catch studies)

- HERMES

- South Atlantic octocoral communities

Detailed study of octocoral by-catch from toothfish long lining.

- SW Indian Ocean

ROV cruise to the SW Indian Ocean Ridge – benthic biodiversity.