

# Antarctic life on the precipice

(marine biology)

## *Workshop 5*



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Table IV. Antarctic and Southern Ocean Science Horizon Scan questions in cluster 'Antarctic life on the precipice'.

## Antarctic life on the precipice

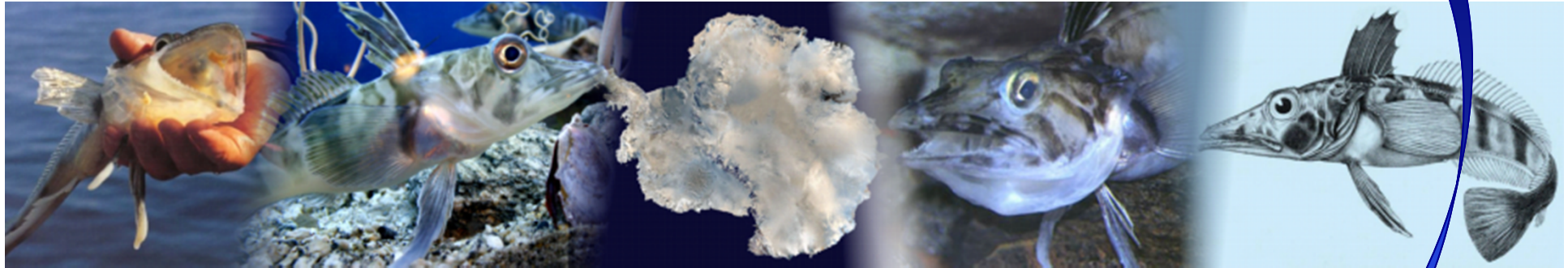
Antarctic life on the precipice	
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44. How fast are mutation rates and how extensive is gene flow in the Antarctic and the Southern Ocean?	How will the risk of spreading emerging species in the Antarctic and Southern Ocean be affected? ( <i>Cross-cuts 'Human'</i> )
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47. How do events in the Earth's history? ( <i>Cross-cuts 'Dynamic Earth'</i> )	59. How will linkages between marine and terrestrial systems change in the future?
48. How do life on Earth respond to warmer climate conditions in the past?	60. How will linkages between marine and terrestrial systems change in the future?
49. How will threshold transitions vary over different spatial and temporal scales, and how will they impact ecosystem functioning under future environmental conditions?	61. How will increased marine resource harvesting impact Southern Ocean biogeochemical cycles? ( <i>Cross-cuts 'Human'</i> )
50. What are the synergistic effects of multiple stressors and environmental change drivers on Antarctic and Southern Ocean biota?	62. How will deep sea ecosystems respond to modifications of deep water formation, and how will deep sea species interact with shallow water ecosystems as the environment changes?
51. How will organism and ecosystems respond to a changing soundscape in the Southern Ocean? ( <i>Cross-cuts 'Human'</i> )	63. How can changes in the form and frequency of extreme events be used to improve biological understanding and forecasting? ( <i>Cross-cuts 'Antarctic atmosphere'</i> )
52. How will next-generation contaminants affect Antarctic and Southern Ocean biota and ecosystems?	64. How can temporal and spatial 'omic-level' analyses of Antarctic and Southern Ocean biodiversity inform ecological forecasting?
53. What is the exposure and response of Antarctic organisms and ecosystems to atmospheric contaminants (e.g. black carbon, mercury, sulfur, etc.), and are the sources and distributions of these contaminants changing? ( <i>Cross-cuts 'Antarctic atmosphere' and 'Human'</i> )	65. What will key marine species tell us about trophic interactions and their oceanographic drivers such as future shifts in frontal dynamics and stratification?
54. How will the sources and mechanisms of dispersal of propagules into and around the Antarctic and Southern Ocean change in the future?	66. How successful will Southern Ocean Marine Protected Areas be in meeting their protection objectives, and how will they affect ecosystem processes and resource extraction? ( <i>Cross-cuts 'Human'</i> )
	67. What <i>ex situ</i> conservation measures, such as genetic repositories, are required for the Antarctic and Southern Ocean? ( <i>Cross-cuts 'Human'</i> )
	68. How effective are Antarctic and Southern Ocean conservation measures for preserving evolutionary potential? ( <i>Cross-cuts 'Human'</i> )

# Genomic basis of icefish adaptation to cold

- ✓ no hemoglobin
- ✓ no myoglobin expression in skeletal muscle

- ✓ remodeling of the cardiovascular system
- ✓ high mitochondrial density

O<sub>2</sub>



Increased  
request for structural and functional  
components of mitochondria ?

- **Kock KH** (2005a) Antarctic icefishes (Channichthyidae): a unique family of fishes: A review, Part I. *Pol Biol*, 28: 862-895.
- **O'Brien KM**, Mueller IA (2010) The unique mitochondrial form and function of Antarctic channichthyid icefishes. *Integr Comp Biol*, 50: 993-1008.
- **Ruud JT** (1954) Vertebrates without erythrocytes and blood pigment. *Nature*, 173: 848-850.
- **Sidell BD et al.** (1997) Variable expression of myoglobin among the hemoglobinless Antarctic icefishes. *PNAS*, 94: 3420-3424.

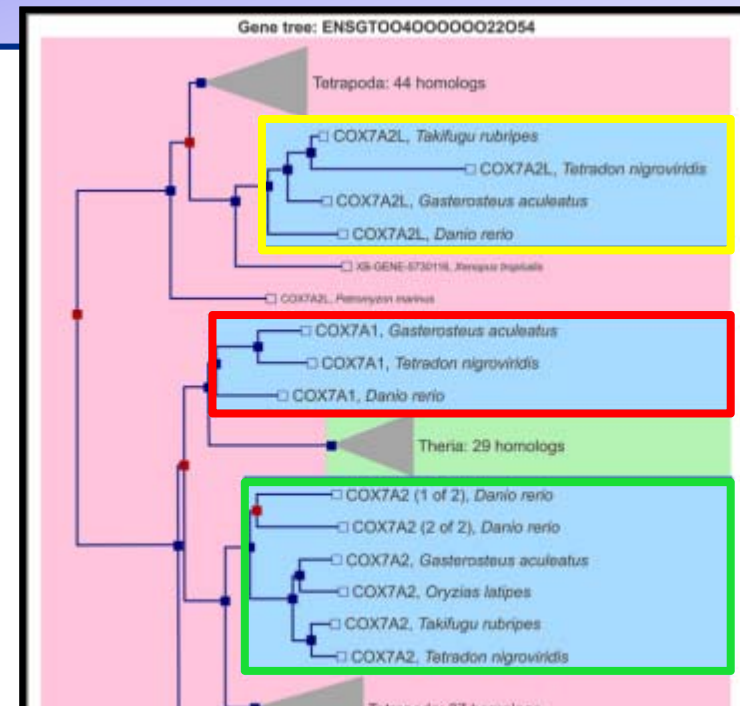
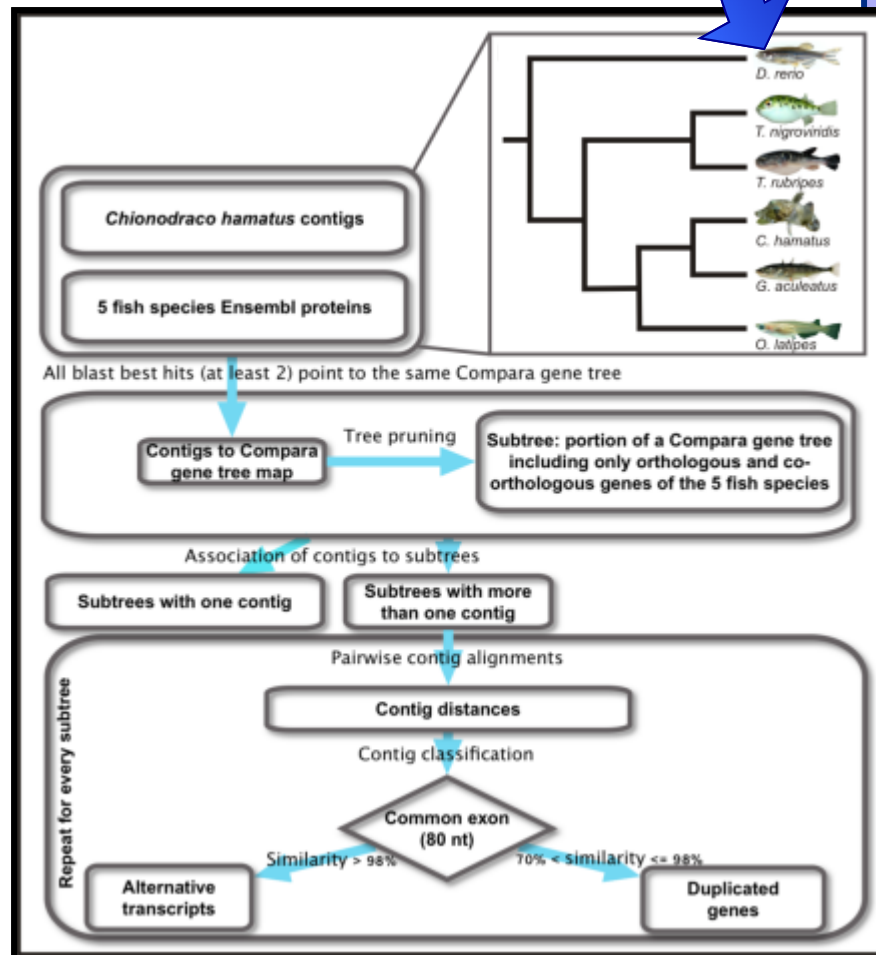
# Genomic basis of icefish adaptation to cold

## TRANSCRIPTOME

- ✓ Normalized, skeletal muscle
- ✓ ~340,000 good-quality 454-reads
- ✓ ~24,000 contigs (48% annotated)

## BIOINFORMATIC PIPELINE

Transcripts were univocally assigned to groups of orthologous genes of **5 model fish** with sequenced genome

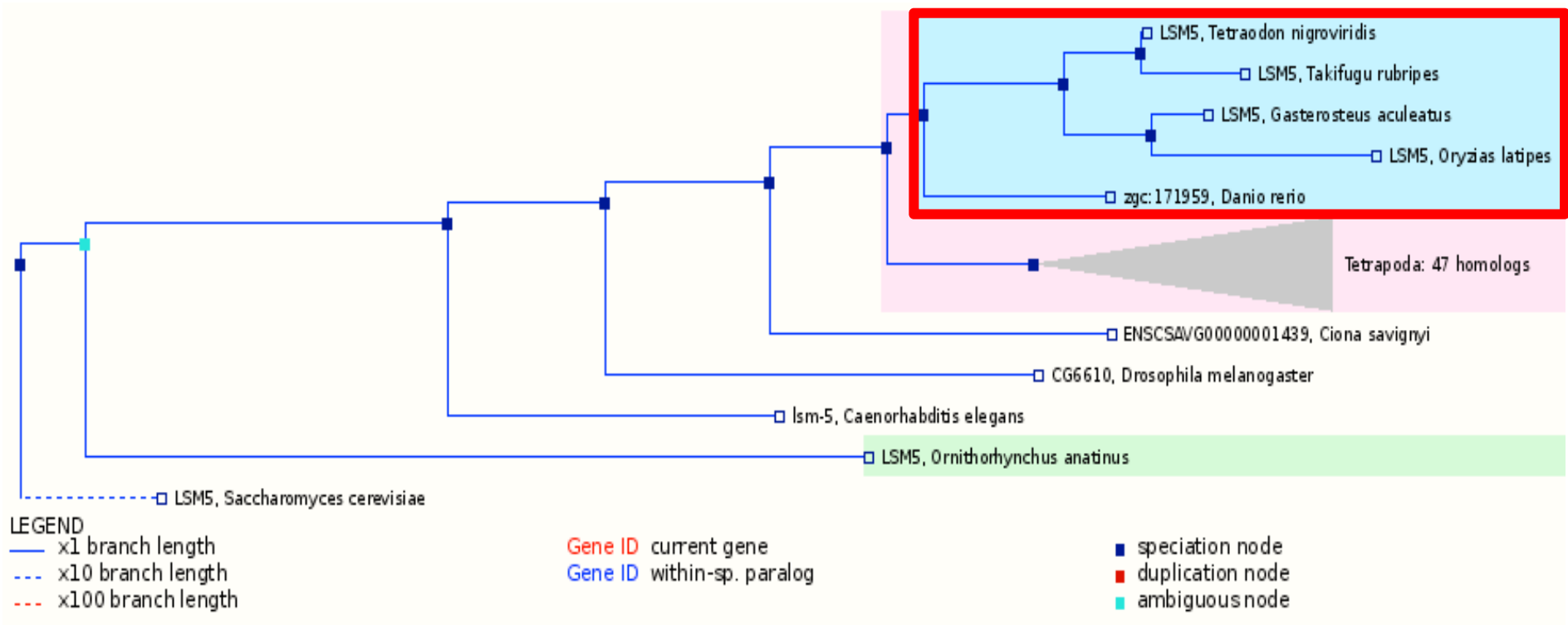


- ✓ the number of *C. hamatus* genes pointing to each orthologous group was recorded

# Genomic basis of icefish adaptation to cold

## Ch - 4 transcripts

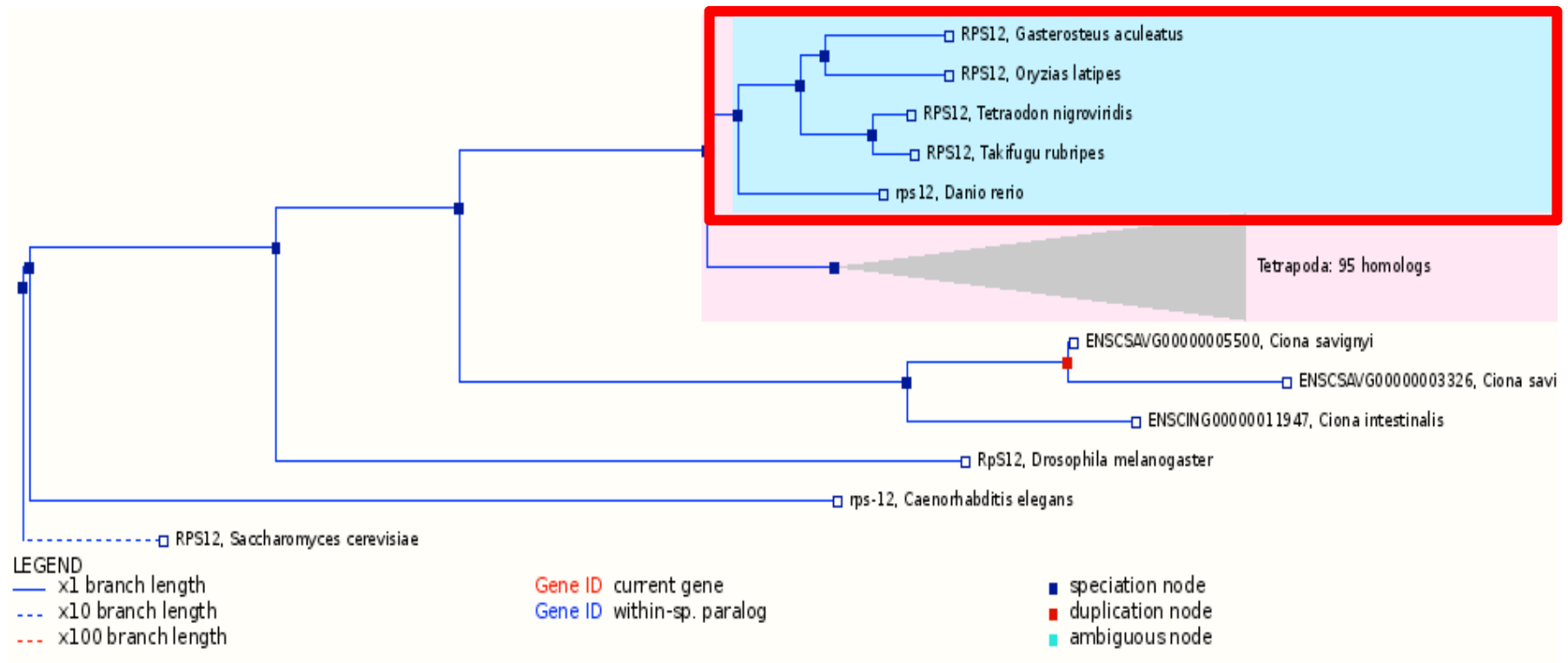
Tree	Ch	Dr	Ga	OI	Tr	Tn
ENSGT00390000001455	4	1	1	1	1	1
LSM5 homolog, U6 small nuclear RNA associated						



# Genomic basis of icefish adaptation to cold

## Ch - 5 transcripts

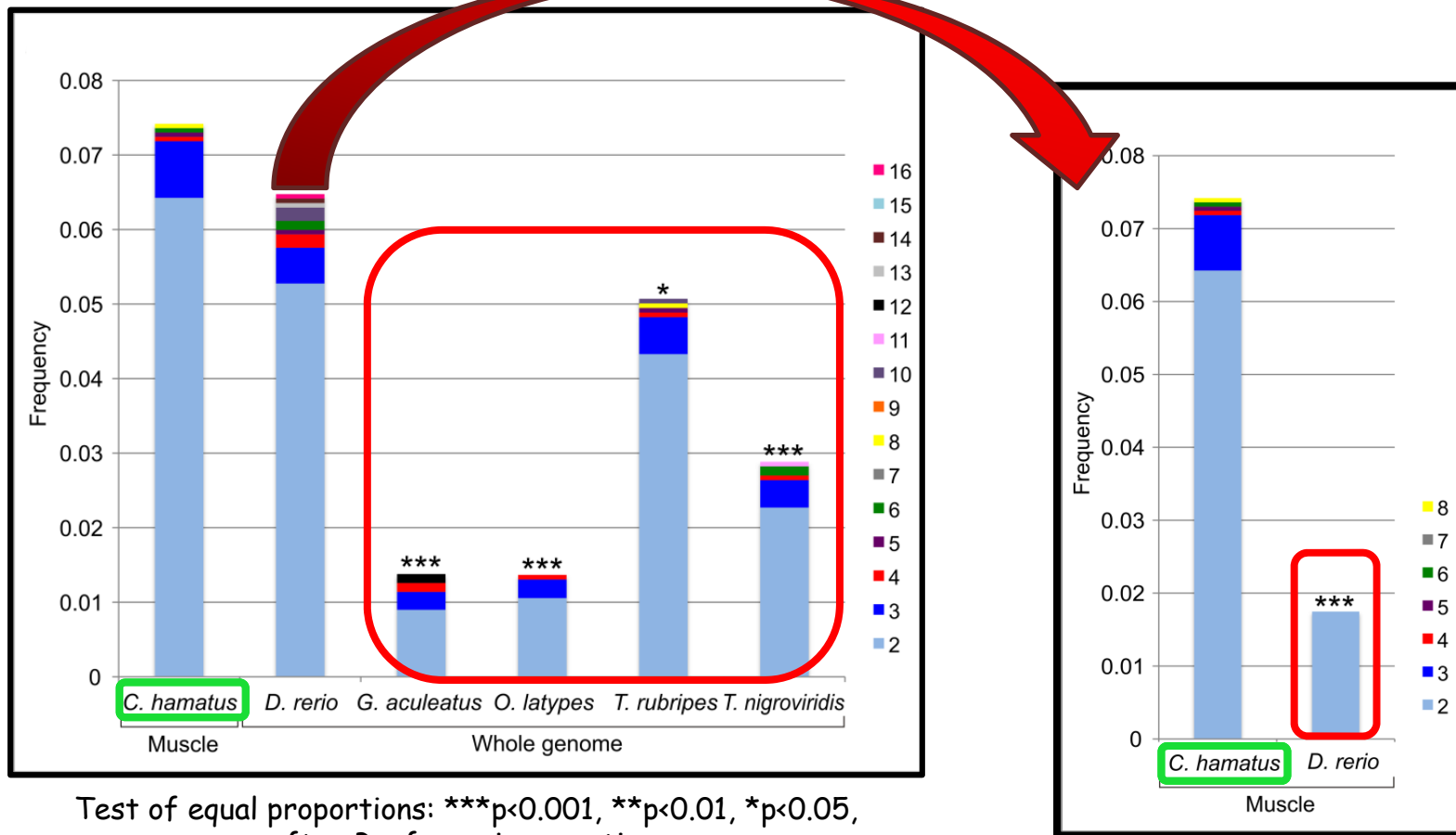
Tree	Ch	Dr	Ga	OI	Tr	Tn
ENSGT0039						
0000018318	5	1	1	1	1	1



# Genomic basis of icefish adaptation to cold

- ✓ 124 orthology groups with *C. hamatus* lineage-specific duplications
- ✓ 2 to 8 gene copies in each group (mean 2.3)


Statistical comparison of the proportion of lineage-specific duplicates found in *C. hamatus* and in each of the 5 model species



# Genomic basis of icefish adaptation to cold

## Functional enrichment of duplicated genes

- ✓ Enriched functional terms are related to:
  - protein translation
  - oxidative phosphorylation
  - organelle organization and biogenesis
- ✓ at least 34 out of 124 duplicated genes encode proteins with mitochondrial localization



Significant enrichment  
for mitochondrial  
proteins ( $p=0.0235$ )

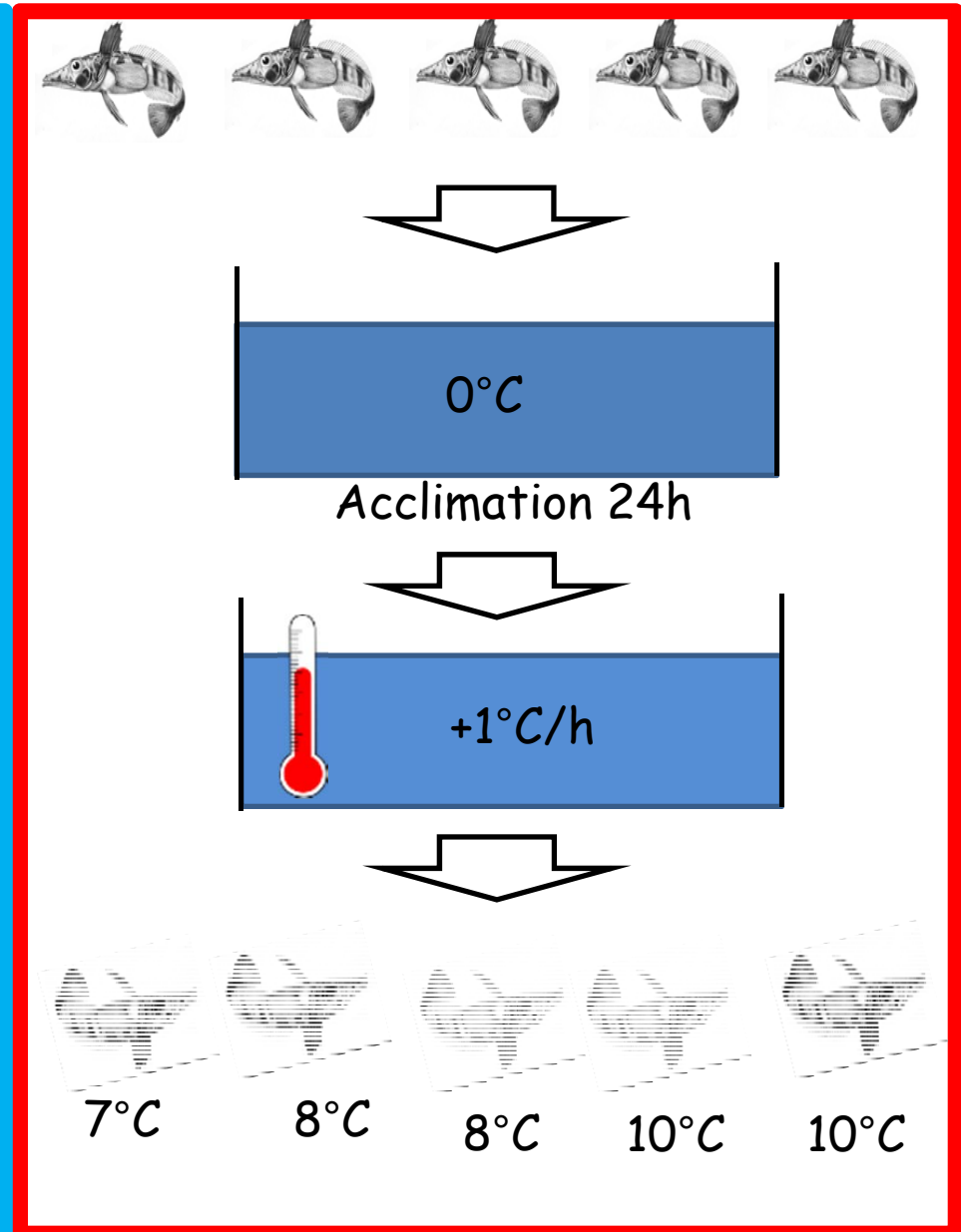
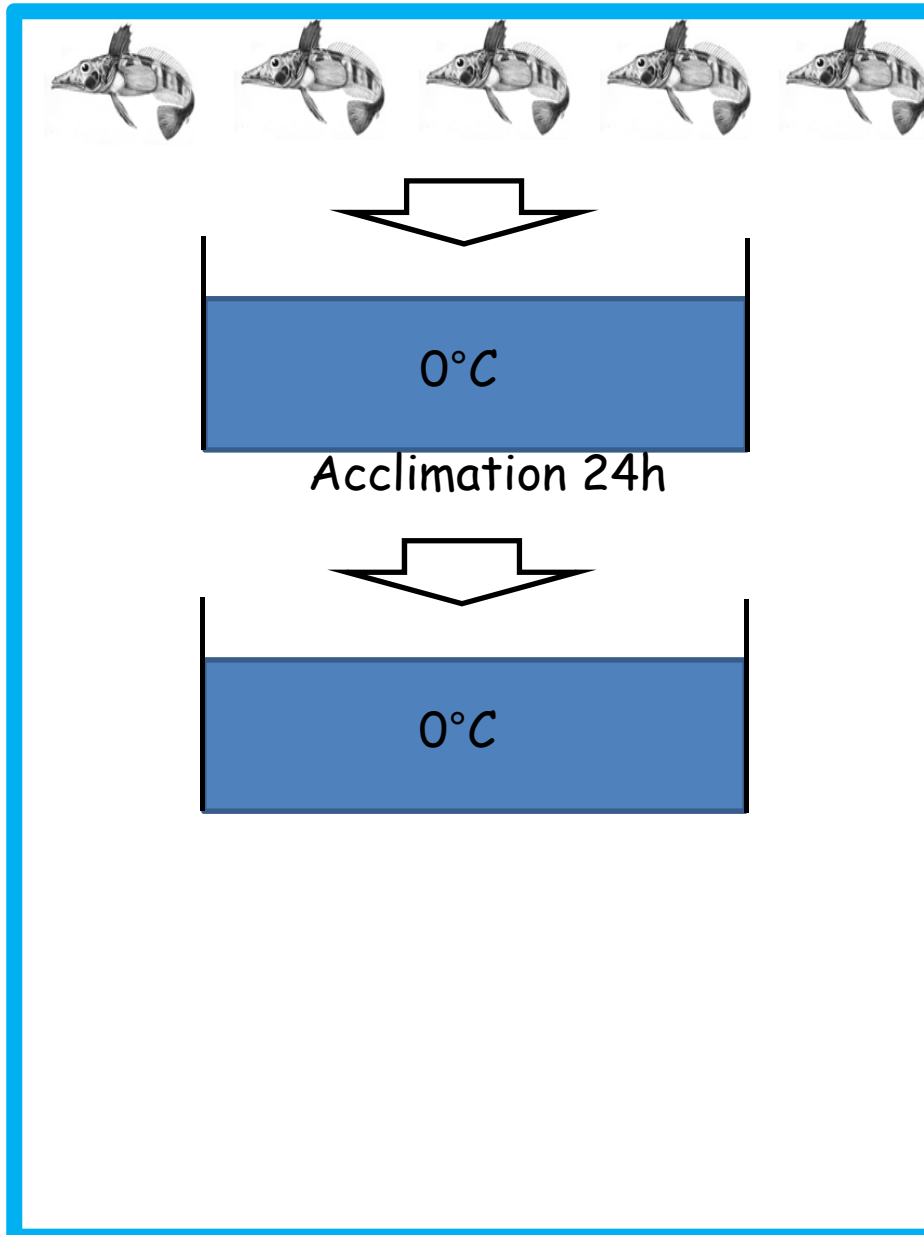
- ✓ Confirm the **trend of genomic expansion** accompanying the evolutionary history of Antarctic notothenioids
- ✓ Suggest that the maintenance of duplicates in the icefish genome may be associated, at least in part, to a **selective pressure for increased mitochondrial density/function**



# icefish transcriptomics and heat shock response

CTRL

EXPOSED TO HIGHER TEMPERATURE



# icefish transcriptomics and heat shock response

## Gene expression analyses

control vs. exposed



102 transcripts **down-regulates** (in the exposed group)

107 transcripts **up-regulates** (in the exposed group)

### Down-regulation

of several transcripts involved in **inflammatory and immune response**  
(e.g. interleukin-6 receptor subunit alpha, c-type lectin domain family 4,  
chemokine 4, chemokine 13)

### Up-regulation

of several transcripts involved in **Glycolysis / Gluconeogenesis**.

Potential impact of **mitochondrial and thermal stress on the  
bioenergetics and reserve respiratory capacity**.

in progress...

Whole genome sequencing of *Chionodraco hamatus*  
(illumina + PacBio technology)

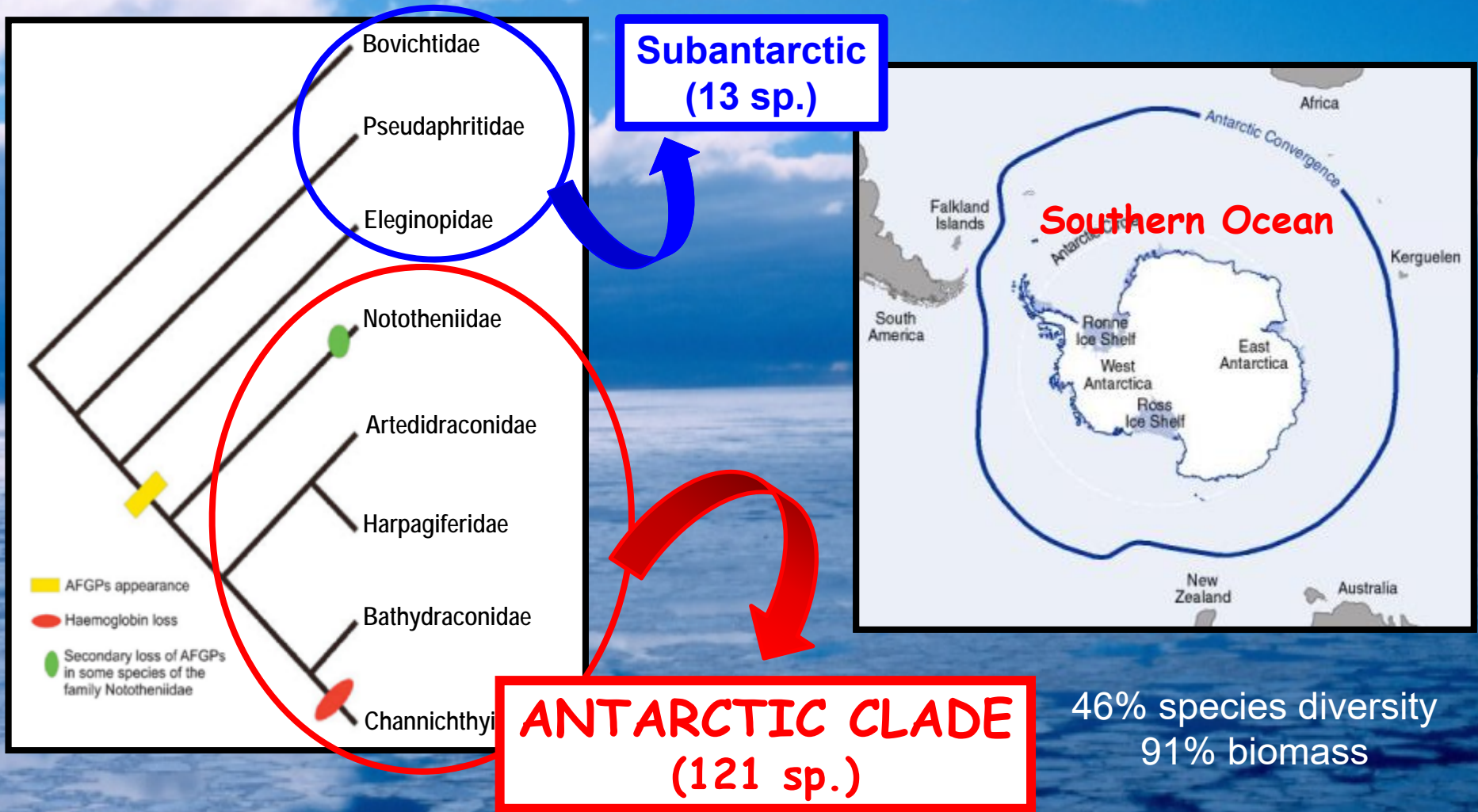


Table IV. Antarctic and Southern Ocean Science Horizon Scan questions in cluster 'Antarctic life on the precipice'.

## Antarctic life on the precipice

43. What is the genomic basis of adaptation in Antarctic and Southern Ocean organisms and communities?	55. How will invasive species and range shifts of indigenous species change Antarctic and Southern Ocean ecosystems? ( <i>Cross-cuts 'Human'</i> )
44. How fast are mutation rates and how extensive is gene flow in the Antarctic and the Southern Ocean?	56. How will climate change affect the risk of spreading emerging infectious diseases in Antarctica? ( <i>Cross-cuts 'Human'</i> )
44. How fast are mutation rates and how extensive is gene flow in the Antarctic and the Southern Ocean?	57. How will climate change affect the Antarctic intertidal zone impact of biological invasions? Existing and future Southern Ocean biota? ( <i>Cross-cuts 'Human'</i> )
46. How will threshold transitions vary over different spatial and temporal scales, and how will they impact ecosystem functioning under future environmental conditions?	59. How will linkages between marine and terrestrial systems change in the future?
47. How do subglacial systems inform models for the development of life on Earth and elsewhere? ( <i>Cross-cuts 'Eyes on the sky'</i> )	60. What are the impacts of changing seasonality and transitional events on Antarctic and Southern Ocean marine ecology, biogeochemistry and energy flow?
48. Which ecosystems and food webs are most vulnerable in the Antarctic and Southern Ocean, and which organisms are most likely to go extinct?	61. How will increased marine resource harvesting impact Southern Ocean biogeochemical cycles? ( <i>Cross-cuts 'Human'</i> )
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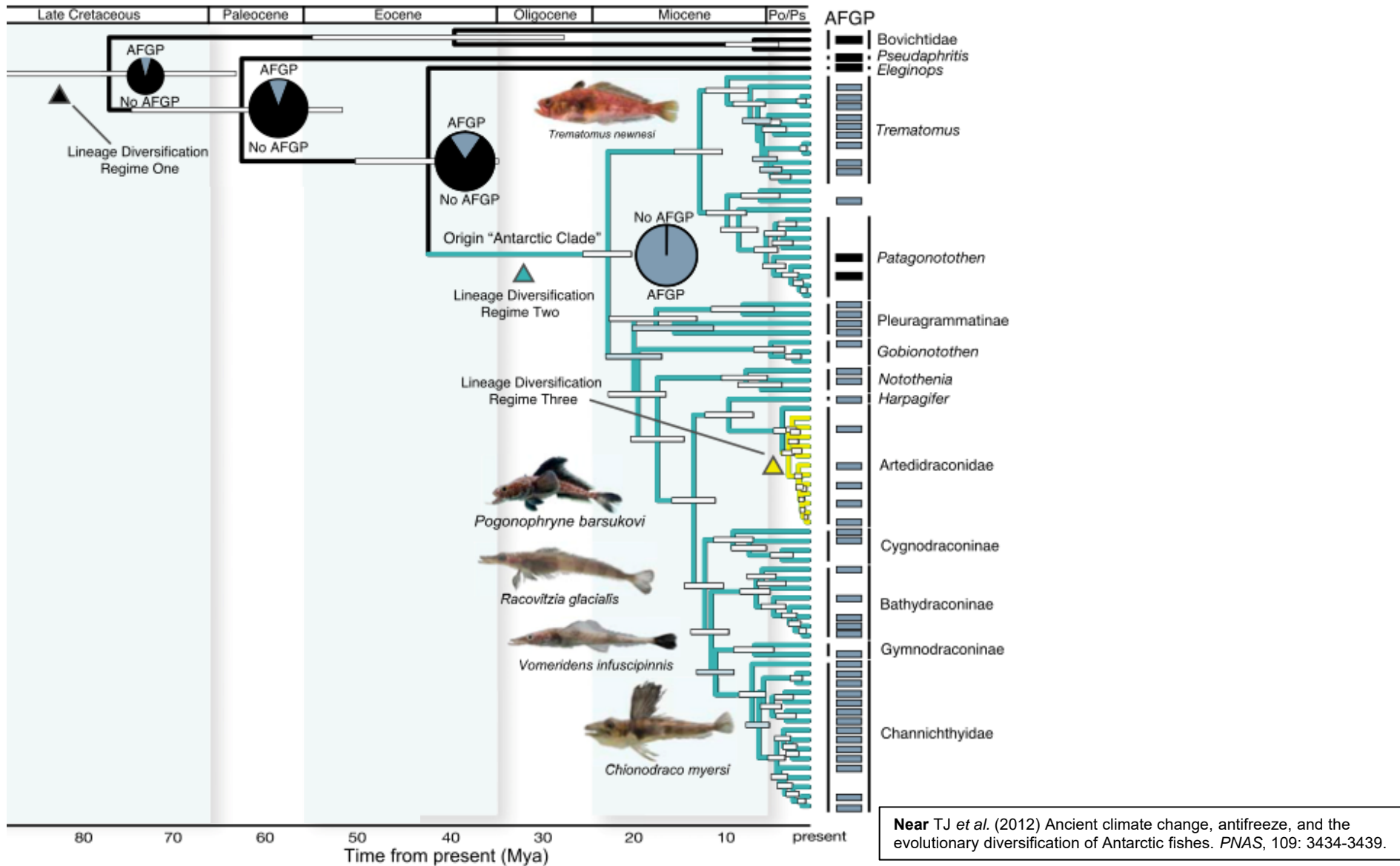
# Suborder Notothenioidei (Perciformes)



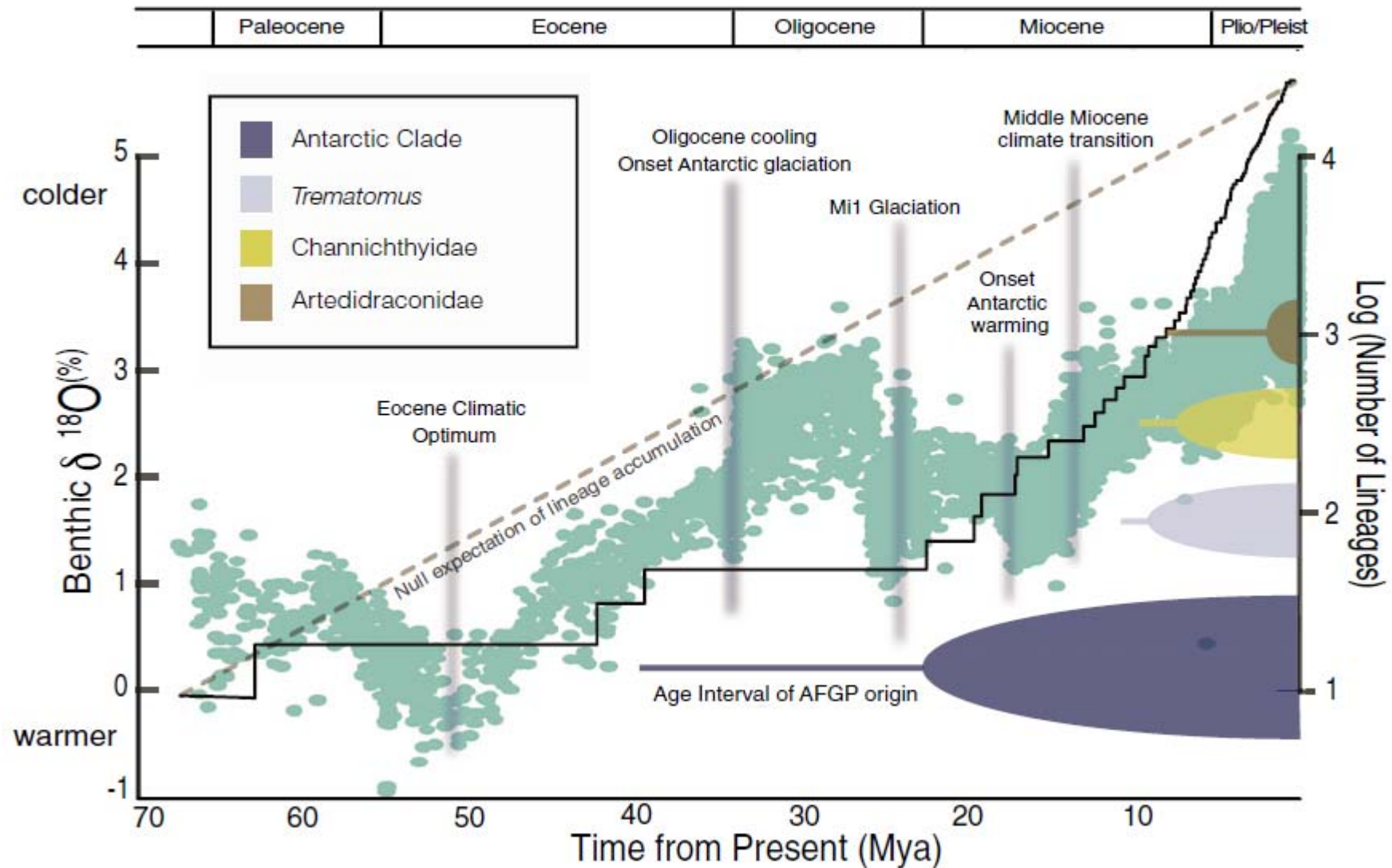
- Eastman JT (2005) The nature of the diversity of Antarctic fishes. *Polar Biol*, 28: 93-107.
- Lecointre G (2012) Phylogeny and systematics of Antarctic teleosts: methodological and evolutionary issues. In: *Adaptation and Evolution in Marine Environments - The Impacts of Global Change on Biodiversity*, Vol 1 (eds di Prisco G, Verde C), pp 97-117. Springer, Berlin.
- Patarnello T et al. (2011) How will fish that evolved at constant sub-zero temperatures cope with global warming? Notothenioids as a case study. *Bioessays*, 33: 260-268.

# Evolutionary history and adaptive radiation

Evolutionary history and dominance is linked to tectonic and paleo-climatic events



# Evolutionary history and adaptive radiation



Near TJ *et al.* (2012) Ancient climate change, antifreeze, and the evolutionary diversification of Antarctic fishes. *PNAS*, 109: 3434-3439.

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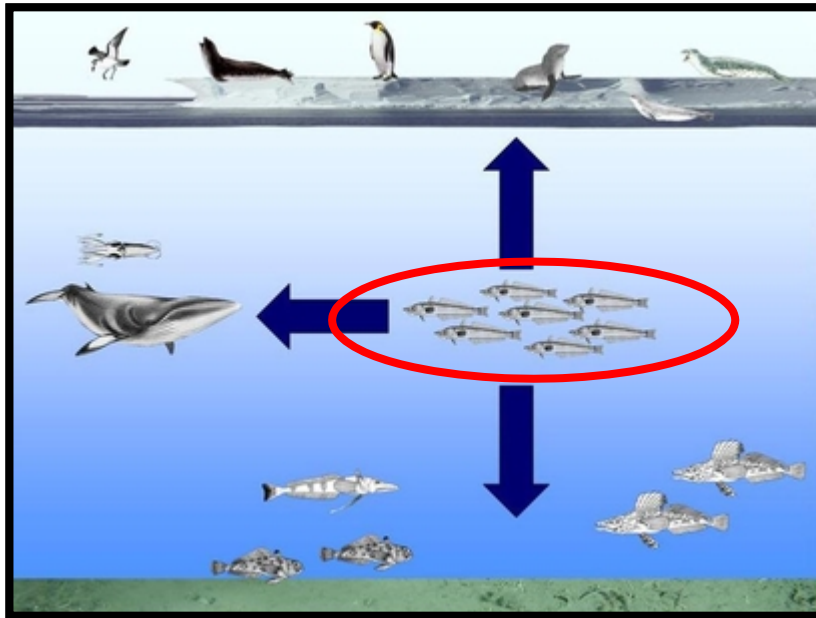
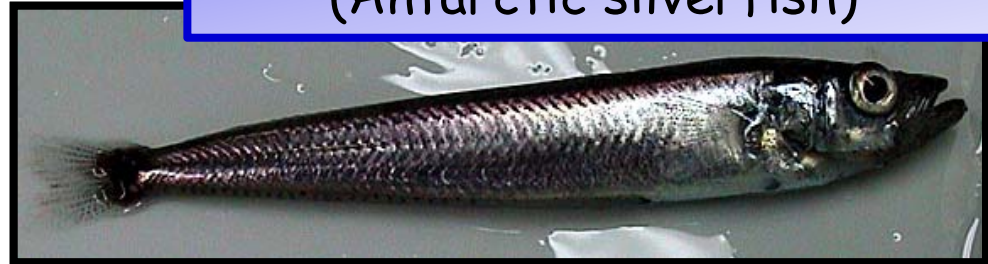
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# Population genetics: *Pleuragramma antarctica*

## *Pleuragramma antarctica* (Antarctic silverfish)



- circum-Antarctic distribution
- complete pelagic life-cycle
- dominant pelagic fish in many shelf areas (> 90% number, biomass)
- key role in the marine food web

- **La Mesa M, Eastman JT** (2011) Antarctic silverfish: life strategies of a key species in the high-Antarctic ecosystem. *Fish Fish*, 13: 241-266.
- **Vacchi M et al.** (2004) Early life stages in the life cycle of Antarctic silverfish, *Pleuragramma antarcticum* in Terra Nova Bay, Ross Sea. *Antarct Sci*, 16: 299-305.
- **Vacchi M et al.** (2012) A nursery area for the Antarctic silverfish *Pleuragramma antarcticum* at Terra Nova Bay (Ross Sea): first estimate of distribution and abundance of eggs and larvae under the seasonal sea-ice. *Polar Biol*, 35: 1573-1585.

# *P. antarctica*: genetic variability and population structure

*P. antarcticum* population structure along the **Antarctic Peninsula (AP)**

- ✓ microsatellite markers
- ✓ otolith chemistry



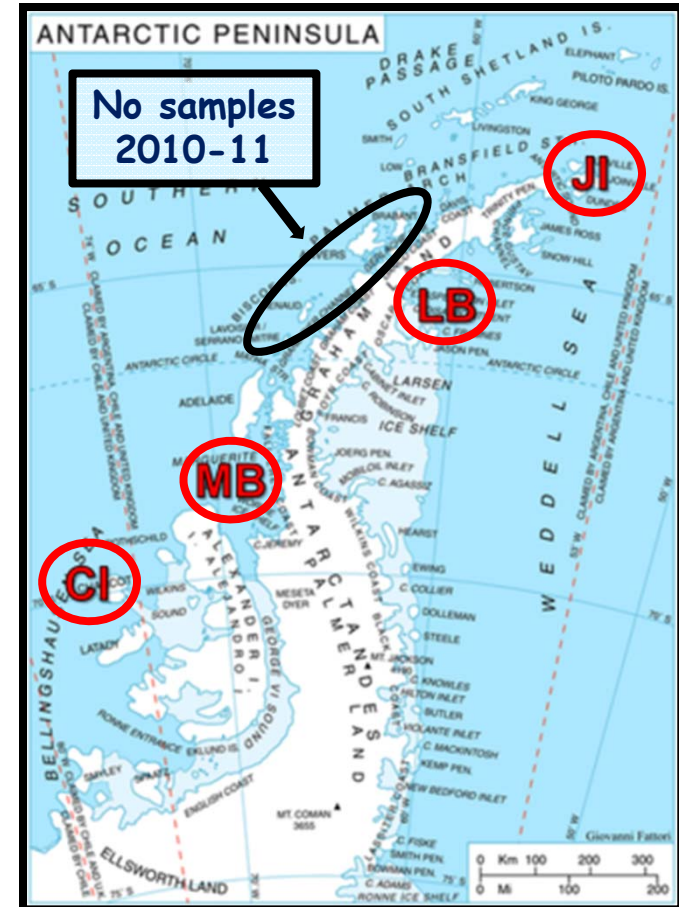
- Sea surface temperatures  $\uparrow$  by  $3^{\circ}\text{C}$  within the last 50 y
- Sea-ice melting
- Adélie penguins are  $\downarrow$  at almost all locations on the AP
- *P. antarcticum* has almost disappeared from their diet

- Ferguson J, et al. (2011) Connectivity and population structure in *Pleurogramma antarcticum*. WG-FSA-11/19, CCAMLR.
- Turner J, et al. (2005) Antarctic climate change during the last 50 years. *Int J Climatol*, 25: 279-294.
- Zazulie N, et al. (2010) Changes in Climate at High Southern Latitudes: A Unique Daily Record at Orcadas Spanning 1903-2008. *J Clim*, 23: 189-196.

# *P. antarctica*: genetic variability and population structure

9 population samples  
(562 individuals)

Site	Year	Campaign	N
Charcot Island	2010	NBP 10-02 <sup>a</sup>	60
Marguerite Bay	2001	SO GLOBEC-Cruise 1 <sup>c</sup>	28
	2002	SO GLOBEC-Cruise 3 <sup>c</sup>	49
	2010	NBP 10-02 <sup>a</sup>	60
	2011	LMG Cruise 11-01, Palmer LTER <sup>d</sup>	83
Joinville Island	2007	ANTXXIII/8AWI <sup>e</sup>	34
	2010	NBP 10-02 <sup>a</sup>	148
	2012	ANT XXVIII/4 AWI <sup>c</sup>	54
Larsen Bay	2007	ANTXXIII/8AWI <sup>e</sup>	46



# *P. antarctica*: genetic variability and population structure

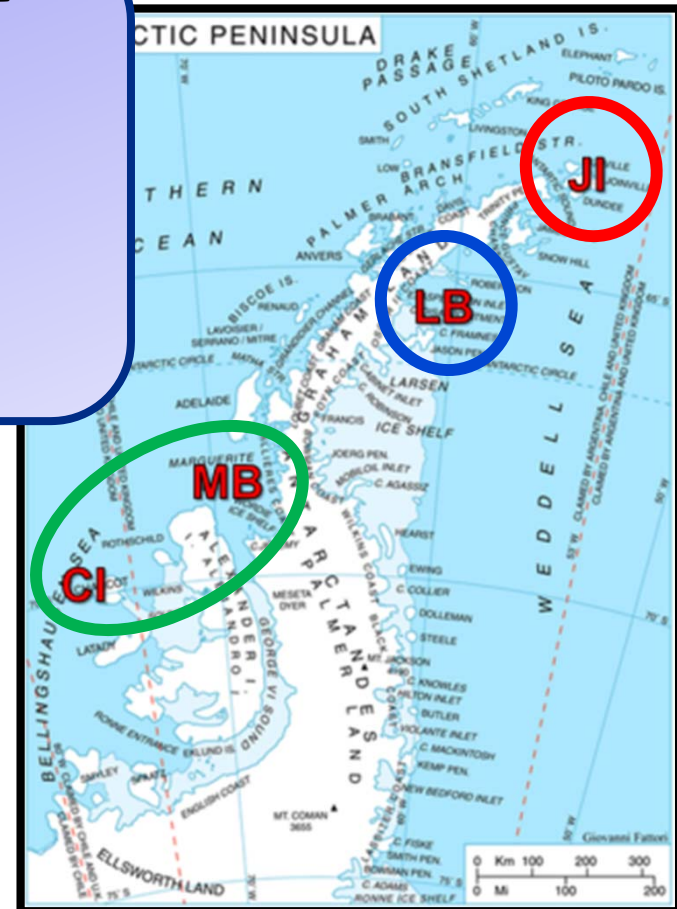
## Genetic variability

- no difference ( $N_a$ ,  $A_r$ ,  $H_{obs}$ ,  $H_{nb}$ ) across samples (one-way ANOVA,  $p > 0.05$ )

## Population structure

$F_{st}$  Index

- CI, MB → no difference both on a temporal (01-02-10-11) and on a geographic scale
- JI → no difference on a temporal scale (07-10-12)  
→  $F_{st}$  values JI vs CI-MB tend to ↑ with time:
- LB07 → differentiated from CI-MB  
(also from JI12 but not after Bonferroni correction,  $\alpha_{corrected}=0.005$ )

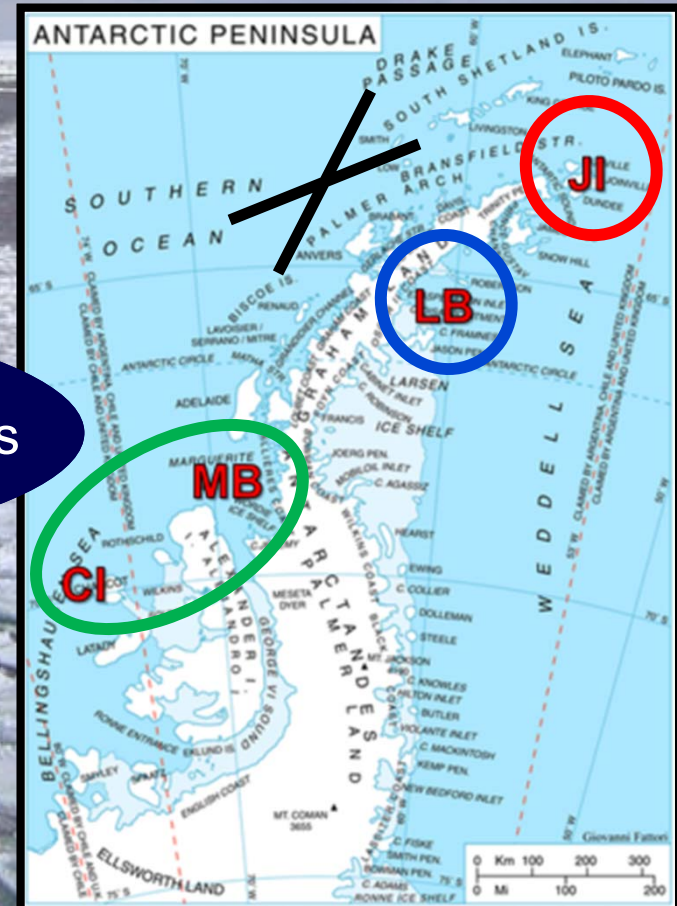


# *P. antarctica*: genetic variability and population structure

in summary...

- apparent **disappearance** from the central western AP
- **population fragmentation** may **increase** with time
- similar level of genetic variation  
→ differentiation is **recent**

*P. antarcticum* has been affected by climate change with possible cascading effects on the Antarctic marine food web



# Conclusions

The evolution of Antarctic fish genome was strongly driven by the sub-zero water temperature established in the Southern Ocean over million years.

The complex set of adaptations are often accompanied by 'irreversible' genomic losses or gene amplifications

On the micro-evolutionary scale, the observed habitat fragmentation strongly reduces population connectivity and consequently genetic variation

# Conclusions

These features, taken together with the unprecedented speed of rising temperatures, suggest that Antarctic fish might have little genetic potential to cope with global warming