



SCIENTIFIC MEETING

## EVOLUTION IN THE MARINE ENVIRONMENT

Tuesday 13 February 2007

The Meeting Rooms, The Zoological Society of London, Regent's Park, London NW1 4RY

**Chair: Professor Paul G Rodhouse**  
**Head of Biological Sciences Division, British Antarctic Survey**

### **Evolution in the Antarctic marine fauna**

*Dr Alex Rogers, Senior Research Fellow, Institute of Zoology, ZSL, London*

The Antarctic marine fauna is highly endemic and the diversity and abundance of taxonomic groups differs from elsewhere in the world. Such characteristics have resulted from evolution in isolation in an increasingly extreme environment over the last 100MY. Studies on Antarctic species represent some of the best examples of natural selection at the molecular, structural and physiological levels. Analyses of molecular genetics data are consistent with the marine fauna having been strongly influenced by geological and climatic cooling events over the last 70MY. Such events have resulted in vicariance driven by continental drift and the thermal isolation of the Antarctic and in pulses of species range contraction into refugia and subsequent expansion and secondary contact of genetically distinct populations or sister species during cycles of glaciation and glacial retreat. In some cases genetic studies have revealed that species defined by morphological characters are complexes of cryptic or sibling species. Climate change will cause changes in the distribution of many Antarctic and sub-Antarctic species through affecting population-level processes such as life-history and dispersal.

### **Detecting species in the oceans: the global use of DNA barcoding**

*Professor Gary R Carvalho, Molecular Ecology & Fisheries Genetics Laboratory, University of Wales Bangor, Bangor, Gwynedd, UK <http://biology.bangor.ac.uk/research/mefgl/>*

Species identification is the critical starting point of any research in marine biology. Conventional identification approaches based on phenotypic characters may be apparently straightforward. However there are various situations in which they may fail or have limited efficiency, such as cryptic species, inherently difficult taxonomic groups, or taxonomically ambiguous eggs and larvae. The discovery of new marine habitats and associated new species, increased threats to marine species from on-going environmental change and habitat disturbance make it increasingly important to develop rapid and robust ways of describing and cataloguing marine biodiversity. Molecular tools of universal implementation, such as the recently proposed DNA barcodes ("a rigorously standardized sequence of a minimum length and quality from an agreed-upon gene, deposited in a major sequence database, and attached to a voucher specimen whose origins and current status are recorded") can counter conventional limitations, providing a simple, yet robust system to

unambiguously identify not only whole individuals, but eggs, larvae and body fragments. International efforts are now coordinated by the Consortium for the Barcode of Life (CBOL) which includes more than 120 member organizations in 45 nations. It is closely allied to the Census of Marine Life, aimed at assessing the diversity, distribution, and abundance of marine life in the oceans -- past, present, and future. Here I introduce the concept of DNA barcoding and illustrate its potential in describing, monitoring and conserving marine species by reference to FISH-BOL, a CBOL-coordinated global effort to assemble DNA barcodes of all fishes by 2012.

## **Evolution of population genetic structure and local adaptation in the killer whale and bottlenose dolphin**

*Professor A. Rus Hoelzel, School of Biological and Biomedical Sciences, Durham University*

Dolphins (*Delphinidae*) are highly mobile, distributed worldwide, and represented by 35 mostly highly social species. In this presentation I focus on two species that we have studied in some detail. Our objective is to identify the evolutionary mechanisms that lead to differentiation among populations and speciation in a taxonomic group that has shown an extensive and relatively recent radiation of species. Our approach is to use molecular markers to assess extant and historical patterns of diversity and demographics. We find that habitat dependence is apparently structuring killer whale and bottlenose dolphin populations over geographic ranges that are well within easy dispersal range for these species, and suggest that differential learned foraging strategies may be key to this process. In a preliminary attempt to better understand the process of local adaptation to these habitats, we investigated variation at an immune system gene (the MHC, DQB locus). We found evidence for selection by heterozygote advantage or frequency dependence for cetacean species at this locus (comparing 29 species), and for differential local selection, perhaps related to differential pathogen environments, for the bottlenose dolphin and the killer whale. Together these data suggest the importance of local habitat patches, and the social facilitation of foraging to the evolution of population structure in these two species. Some data suggest that this could be common for various other dolphin species as well.

### **Further Reading:**

Natoli, A., Birkin, A., Aquilar, A., Lopez, A. & Hoelzel, A.R. (2005). Habitat structure and the dispersal of male and female bottlenose dolphins (*Tursiops truncatus*). *Proc. Royal Soc. B.* **272**:1217-1226.

Natoli, A., Peddemors, V. & Hoelzel, A.R. (2004). Population structure and speciation in the genus *Tursiops* based on microsatellite and mitochondrial DNA analyses. *J. Evol. Biol.* **17**:363-375.

Hoelzel, A.R., Natoli, A., Dahlheim, M., Olavarria, C., Baird, R.W. & Black, N. (2002). Low world-wide genetic diversity in the killer whale (*Orcinus orca*); Implications for demographic history. *Proc. Royal Soc. B.* **269**: 1467-1475.

Hoelzel, A.R. (in press). Evolution of population genetic structure in marine mammal species. In: *Population Genetics and Conservation*. Bertorelle, G., Bruford, M.W., Chemini, C., Hauffe, H.C. & Vernesi, C. (Eds). Cambridge: Cambridge University Press.