

## DNA barcoding at MEFGL (cont.)

Spiders - Spiders (Araneae) are ecologically relevant, being the dominant predators of insects, and are therefore important biodiversity indicators in natural and agricultural ecosystems. We are performing national spider barcoding studies according to a taxonomic framework and seek European partners to increase continental representation of taxa. In addition to providing a valuable ecological resource tool, molecular barcoding European spiders is predicted to uncover previously undescribed levels of molecular genetic diversity that exist across a diverse array of species, genera and families. This information will increase our understanding of the relationships between life history strategies and genetic diversity and assist in our understanding of taxonomic relationships among species.

In addition to the above projects, the SBS's wider Molecular Ecology and Evolution group are performing molecular barcoding on a range of venomous snake species. The latter activities facilitate species identification of medically important species to aid researchers in the fields of snakebite management, toxinology and systematics.



## Forensics

Forensic validation experiments conducted at Bangor University in conjunction with Wildlife DNA Services have demonstrated that the COI gene is an acceptable marker for use in forensic genetic casework. This now allows technical staff to use COI as an additional marker to corroborate sequence results generated using alternative mitochondrial genes such as *cyt b*. The uniform methodology and data submission protocols of barcoding studies provide a level of quality control important in forensic work that is seldom achieved when using alternative sequence search engines populated by data of questionable quality. Forensic investigations into the trade in endangered species and the persecution of protected species will benefit from the continued submission of sequence data of key target species from barcoding studies.

## DNA barcoding at Bangor University, some references:

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### Websites:

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Molecular Ecology and Fisheries Genetics Lab :

<http://biology.bangor.ac.uk/research/mefgl/>

other

FISH-BOL : [www.fishbol.org](http://www.fishbol.org) CBOL : <http://barcoding.si.edu/>

Canadian Centre for DNA Barcoding:  
<http://www.dnabarcoding.ca/>

## DNA BARCODING AT BANGOR UNIVERSITY



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## Presentation

The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL - <http://biology.bangor.ac.uk/research/mefgl/index.htm>) is a leading research division within Bangor University's School of Biological Sciences' (SBS) Molecular Ecology and Evolution Group. The MEFGL represents one of Europe's largest centres focusing on population and species diversity of aquatic animals, with additional activities on terrestrial reptile and invertebrate fauna. A central part of our work is the application of molecular markers such as microsatellites, single nucleotide polymorphisms, AFLPs and (Sanger and 454) sequence data to fundamental evolutionary and ecological questions relating to the origins, levels, distribution and ecological significance of genetic variation in wild populations. The MEFGL complements molecular genetic data with detailed ecological, behavioural and physiological information to facilitate examination of the underlying causes of individual, population or species diversity in time and space.

## DNA barcoding at MEFGL

In addition to a range of contemporary molecular ecological research directions, the MEFGL is involved in a number of DNA barcoding projects, including fish, crustacea, littoral meiofauna (Creer 2007, NERC funded), bryozoans, arachnids (Creer and Goodacre 2006) and venomous snakes (Creer 2005).

## Fish

MEFGL coordinates the European Regional Working Group for the Fish Barcode of Life initiative ([www.fishbol.org](http://www.fishbol.org)). In the scope of the European RWG we have current collaborations with partners in Italy, Malta, Poland, Portugal and within UK.

DNA barcoding of fish of the Antarctic Scotia Sea indicate priority groups for taxonomic and systematics focus. Our work on the suborder Notothenioidei includes families: Nototheniidae, Channichthyidae, Artedidraconidae and Bathydraconidae and has revealed high congruence between morphological and molecular classification, with COI providing effective species-level discrimination for most, though not all species.

## Fish (cont.)

We employed an extensive geographic sampling and also emphasize the utility of DNA barcoding in providing a valuable taxonomic framework for fundamental population studies through assigning life history stages (e.g. eggs and larvae) or other morphologically ambiguous samples (e.g. stomach contents) to parental species.



## Crustacea

Among crustaceans we have focused mainly in Decapoda, Amphipoda and Isopoda. Species diagnoses demand inspection of diverse morphological characters, some of which often show considerable variation. Sexual dimorphism and ontogenic variation further complicate identifications. Our work seeks to resolve such taxonomic ambiguities. We are particularly interested in bathyal species. Little is known about genetic variation on sufficiently large geographic and bathymetric scales to reveal patterns of population structure and differentiation. New interest in deep sea species richness has stimulated new contributions on global diversity and latitudinal trends. We apply DNA barcoding as a core research framework, which will complement taxonomy, phylogenetics and population genetics studies of shallow and bathyal crustaceans communities.



## Littoral meiofauna

Nematodes are the most abundant multicellular organisms on earth and in marine sediments they can make up between 50-90% of the multicellular fauna. Despite their abundance and pivotal role in ecosystem functioning, a current estimate of global nematode diversity (c. 1 million species) remains a matter of conjecture. This knowledge gap is the result of the small size and the apparent morphological similarity of nematodes that cause problems in the logistics and accuracy of species identification. We are currently using combinations of Sanger and 454 sequencing technologies to study meiofaunal molecular diversity at different spatial scales throughout Europe, in order to obtain putative estimates of global species richness and develop microarray, or phylochip identification tools.



## Bryozoa

Despite increasing threats to the marine environment, only a fraction of the biodiversity of the oceans has been described, owing in part to the widespread occurrence of cryptic species. Although DNA barcoding should be particularly useful in the sea, given the prevalence of marine cryptic species, the link between taxa identified through DNA barcodes and reproductively isolated taxa (biological species) has rarely been explicitly tested. In Bangor, we used an integrated framework comparing breeding compatibility, morphology and mitochondrial (COI) and nuclear (elongation factor-1-alpha) DNA sequence variation among globally distributed samples of the cosmopolitan marine bryozoan *Celleporella hyalina* (L.). Our results revealed that *C. hyalina* comprises numerous deep, mostly allopatric, genetic lineages that are reproductively isolated, yet share very similar morphology, indicating rampant cryptic speciation. The close correspondence between genetic lineages and reproductively isolated taxa in the context of minimal morphological change suggests that DNA barcoding will play a leading role in uncovering the hidden biodiversity of the oceans and that the sole use of morphologically based taxonomy would grossly underestimate the number of marine species.