

Guest Editorial

Antarctic Marine Biodiversity – a taxonomic crisis?

Taxonomic and species richness studies are particularly time-consuming when new, unexplored areas are investigated. As an example the recent ANDEEP I–III expeditions (2002–2005) to the bathyal and abyssal of the Weddell Sea and adjacent areas have increased the species numbers for Antarctic isopods from 371 to 956 and the identifications and species descriptions for many other groups have yet to be completed. For most Antarctic taxa no adequate taxonomic guides or keys are available and the current knowledge is in the heads of a small group of taxonomists around the world, of whom several are near to retirement. To save this most valuable knowledge for the future, taxonomists need to be encouraged to add their knowledge into databases and key-constructing software and to train the younger generation of biologist in the identification of species.

This is not just an Antarctic problem. Over the last decades the concern over the global loss of undisturbed habitats, the decline of charismatic species (e.g. whales or tigers), and the impacts of climate change on the biosphere have initiated international moves to measure the Earth's biodiversity, like DIVERSITAS, Species 2000, GBIF or the Census of Marine Life (CoML). In the Antarctic we are already trying to address the problem. The SCAR projects RiSCC and MarBIN have started to compile comprehensive databases on the species that live on and around the southernmost continent. The RiSCC biodiversity database is examining biodiversity patterns across all major groups for the entire Antarctic region in both terrestrial and limnetic ecosystems. Its counterpart is SCAR-MarBIN (www.scarmarbin.be), which compiles and manages information on Antarctic marine biodiversity and provides tools for the analysis of biogeographic patterns. Closely linked with SCAR-MarBIN is the current Census of Antarctic Marine Life (CAML), a sub-project of CoML.

Many funding agencies apparently assumed years ago that traditional taxonomy was unnecessary and that analysis of nucleic acids would provide all the information we need. DNA sequencing, which was first used to analyse phylogenetic relationships in Antarctic taxa, is now using bar coding gene loci (e.g. COI) to differentiate between problematic species, to discover cryptic species and to help to create lists of species numbers/species units. For example, CAML, starting its bar coding project in April 2007, has encouraged the research community to produce COI and 18S barcodes for the marine fauna collected on all the CAML-IPY cruises. The CAML barcodes not only require the molecular sequences for individual species but also detailed information on the sequenced specimen, including collection site, voucher specimen and images. The CAML barcodes are available through the Barcode of Life Database (BOLD) and their taxonomic and distribution information will be linked with SCAR-MarBIN.

While DNA bar coding had been seen as the future of taxonomy and morphological taxonomy was assumed to be obsolete, it has now been recognised that DNA bar coding has to be used alongside traditional taxonomy to be successful. This year's CAML-IPY campaign will generate a vast amount of new data on biodiversity and biogeography in the Antarctic. Species richness assessment of these samples will take years, assuming that we still have enough expert taxonomists willing and able to do the work. As useful as the DNA bar coding is, it is weak without the traditional taxonomy and the traditional taxonomy can greatly benefit and explore new areas with the DNA bar coding. For the future of research in Biodiversity we cannot afford to lose the traditional taxonomy but by combining old with new techniques we will be in a position to understand and use Biodiversity at a level we have never been able to achieve before. How can we make the funding agencies appreciate this point?

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