



**International Workshop on DNA  
Barcoding of Deep-Sea Organisms  
May 13th– 18th 2008**

German Centre for Marine  
Biodiversity Research

Senckenberg Research Institute  
Südstrand 44  
26382 Wilhelmshaven  
Germany

Contact phone: +49 (0)4421-9475-101



## Discussion Notes – Outcome for the CeDAMar community

By Gordon Paterson & Saskia Brix

### **What can a BOLI project do for CeDAMar?**

Access to support, certain types of equipment in some cases, training.

### **What can CeDAMar do for BOLI?**

Help BOLI reach their target of 50,000 species barcoded by 2010 by putting our species into BoLD, identify problematic areas. The bottleneck is to sample the amount of species – especially in the deep sea. CeDAMar is not running regular cruises, there are long time periods in between cruises. We can provide a lot of species, but the problem is that most species are undescribed and occur with sometimes a single individual only.

Perhaps CeDAMar can get a status like CMarZ as BOLI project?

*Discussion points:* certain research teams would be able to provide sequences to BoLD but not necessary species.

It is also clear that for some teams there is not the volume of material to get Guelph involved but perhaps the SI (more than 100 specimens and below 400 specimens). Dirk Steinke mentioned that it is not possible to do all barcodes in Guelph (CCDB). Thus, DNA barcoding needs to be decentralized.

CeDAMar has a project page on BoLD so people can use this as a platform where they can put their sequences. It would enable CeDAMar to keep track of how many sequences and species we contribute to BoLD.

There was discussion on the issues that different groups are either not using the target gene or were focused on a different objective. There were initiatives such as Sponge Barcoding Project. As a result several participants suggested that rather than try to fit their data into BoLD, it might be better to develop taxon specific sites.

The problem with BoLD is that it cannot handle other genes than CO I, e.g. ribosomal sequences. This is a problem with data of foraminiferans (Jan Pawlowski) or nematodes. This sequences would not pop up in the CeDAMar platform in BoLD, but are data useful for DNA barcoding.

Yes, CeDAMar can contribute to BoLD, but our own groups need to focus on taxon level first, then submit the data. BoLD as target came too late as CoML is ending in 2010. CeDAMar will continue. CeDAMar would need its own platform in BoLD to include all taxa and mt genes.

To support the development of taxon specific databases Gert Wörheide offered the data structure and scripts associated with the Sponge Barcoding Project database; adding that if some aspects of the functionality could be updated that this would be useful.

Gert Wörheide mentions the fact that FUNDS for DNA barcoding in his project are for preparing the specimens, but NOT for sequencing. There is enough money to go sampling or in the museum collection, for sequencing new/more money is needed.

### **What should CeDAMar do to support molecular initiatives?**

CeDAMar cruises collect a wide range of material much more than is worked up by the project. There were two aspects of this which were discussed:

- 1) communicating that a cruise was going out and that there may have been the opportunity to get material. The converse of this is where the cruises collect groups and are looking for an expert to help with the identification.
- 2) If material is to be collected what is the best way to fix and preserve for molecular methods? There are constraints on both aspects which the participants discussed, for example that the number of people on was limited so the degree they were able to respond to special requests for the sorting and preserving of material are extremely limited. Similarly there needs to be some understanding by those asking for material as to the need to respond in a reasonable time scale.

*Develop standardized protocols available on the website*

*Create a network for who is who and working with which specimens*

The participants suggested that the website listed up and coming cruises together with the PI and whether there was an opportunity to get material. Similarly a list of the researchers and their interests could also be gathered. Not only flag out that cruises are going out, also flag out which material can be taken. If this is advertised to the community, people have to commit to identifying instead of leaving the specimens sitting on the shelves waiting. And finally those with collections who had groups that they were seeking people to work up. A recommendation letter should be written including a summary of this workshop and send to CBOL to inform CBOL what is going on in CeDAMar.

*These suggestions were passed to the CeDAMar steering group*

In the discussion on methods it was felt that it would be useful to develop a page on the CeDAMar website where the best ways together with the simplest methodology of preserving different groups could be displayed and downloaded. In this way collecting could be tailored to the available resources without necessarily compromising viability for molecular analyses.

The other question which arose was one of collecting for the future. Barcoding may well currently focus on COI but it was clear that with the increasing pace of technological advance would mean that total genomics or similar perspectives would be the standard. It was therefore important that in gather material now it would be preserved in such a way as to be available for future studies.

*A survey of CeDAMar participants was suggested to gather the methods, solutions and options.*

Pedro Martinez posed the question – Do we know how stable and long material remains viable in the different preservative solutions? While many participants had experience of various solutions/methodologies, it was not clear that the reliability and longevity was known. This question would form the basis of a Master's project as well as a literature search.

For example, RNAlater frozen should stay forever, but we have not experience yet.

**How does CeDAMar molecular approaches and plans link to other CoML programmes?**

MarBOL is a nice idea and came out of CoML, but what does this mean for the future? After 2010?

Based on the molecular survey CeDAMar could collect information about sampling protocols and fixation of deep-sea invertebrates. Within CeDAMar we can create a network of people interested to contribute to MarBOL.

The other CoML programmes had different responses to the MarBOL programme, CoMARGE did not appear to be planning anything major to support BoL whereas CoSEAM was gearing up to do so. It was felt that CeDAMar should keep in contact with these other deep-sea programmes to see if a joint response and development of initiatives such as a database platform for depositing molecular data not destined for BoLD could be developed.

The steering group to discuss these with other programmes, particularly CoMARGE and CoSEAM