

## Participating Institutions and Researchers

### Coordination

IMAR – Instituto do Mar, Universidade Nova de Lisboa /  
Filipe Costa and M. Helena Costa

### Participants

- IO - Instituto de Oceanografia / Henrique Cabral
- IPIMAR - Instituto Português de Investigação Marítima/  
Antonina dos Santos
- IPM - Instituto Português de Malacologia / Gonçalo  
Calado
- Museu Nacional de História Natural (Museu Bocage)/  
Judite Alves
- Universidade dos Açores / Ana Cristina Costa
- Universidade do Algarve / Rita Castilho
- Universidade de Aveiro / Marina Cunha
- Universidade de Coimbra / João Carlos Marques
- Universidade de Lisboa / Maria Manuela Coelho
- Universidade do Minho / Fernanda Cássio

### Scientific Consultants

- Gary Carvalho / Bangor University, UK
- Paul Hebert / University of Guelph, Canada

### **Websites:**

Coordination: IMAR  
<http://www.imar.pt/>

Consultants' links:

Bangor University  
Molecular Ecology and Fisheries Genetics Lab  
<http://biology.bangor.ac.uk/research/mefgl/>

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

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

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### **Member of:**

  
CONSORTIUM FOR THE BARCODE OF LIFE

## **Research Network**

# **BARCODING AQUATIC LIFE PORTUGAL (BAL@PT)**



## **Coordination INSTITUTE OF MARINE RESEARCH (IMAR)**



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## Presentation

The research network Barcoding Aquatic Life – Portugal (BAL@pt) is a partnership of several Portuguese institutions which intends to build a regional database integrating taxonomic (morphological and molecular), biogeographic and ecological information on aquatic life. Currently BAL@pt involves research teams from 7 research Universities, the National Museum of Natural History (Museu Bocage), the national governmental agency in charge of marine and fisheries research (IPIMAR), and one scientific association (Portuguese Institute of Malacology). BAL@pt was given a formal status by way of a subscription of a memorandum of cooperation among members, and became a formal member of CBOL through its coordinating institution IMAR- Institute of Marine Research.

## Main Objectives

1-Implement and develop the Barcoding Initiative in Portugal. To follow up in the European and worldwide barcoding effort and to engage in international cooperative research.

2- Provide the scientific community and other prospective users with an up to date system for the identification of Portuguese aquatic species. To create a reference taxonomic library for the aquatic life, linking DNA barcodes with known species, archived as museum-voucher specimens.

3- Assist in the revision of the taxonomy of Portuguese aquatic life with the aid of molecular markers. To propose and test new species hypotheses using an integrative taxonomy approach. Detect and describe unknown species.

4- Share expertise, resources and data among scientific community and institutions involved in aquatic biodiversity research in Portugal and elsewhere. Provide advanced training for a new generation of specialized researchers with broad skills in aquatic biodiversity science, spanning conventional, ecological and molecular approaches.



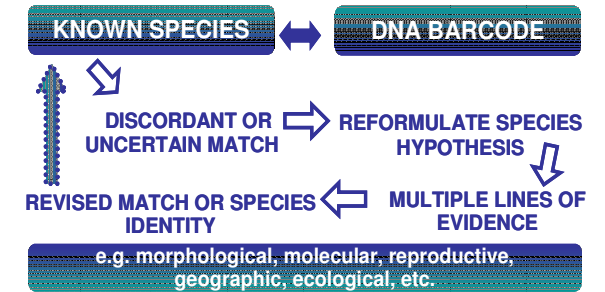
## Research plan

Our DNA barcoding methodology will involve: 1) extensive collection of specimens along the Portuguese mainland coast, offshore regions and archipelagos, 2) taxonomic identification and assembly of Reference Collections, 3) obtaining partial sequences (approximately 650 bp) preferably of the mitochondrial gene cytochrome c oxidase I (COI) from voucher specimens, 4) databasing and data analysis and 5) testing species hypothesis and revising current taxonomy when required.

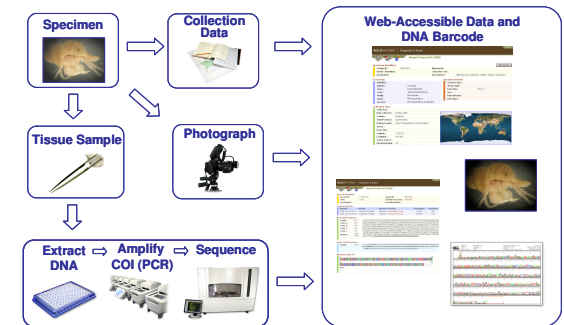
## Main target groups

We aim to cover most of the main groups of aquatic animals, from sponges to marine mammals, but also macroalgae and fungi. However most efforts to date have focused on fish, crustacea, molusca and annelida.

## WORKING HYPOTHESIS



## DNA barcoding analytical Chain



## Rationale and approach

Our basic premise is built upon the hypothesis of the occurrence of an unequivocal match between every known species and the DNA barcode obtained by reading an elected region of the genome; the rationale is that individuals of a species share very similar sequences, while the barcode arrays for different species are usually distinct. We will initially check every species for taxonomic congruence both within our database, and against other publicly available data (BOLD, GenBank). Failure to obtain an unambiguous match may result from insufficient resolution of the DNA barcode, or may reflect inaccurate species over-splitting by prior taxonomic efforts. However, ambiguities may also flag the presence of unrecognized species that were overlooked by conventional methods. In such scenarios we intend to follow a hypothesis-driven approach, testing our species hypothesis preferably against various sources of evidence. Resultant taxonomic revisions will ultimately undergo international peer-review.