



Biodiversity

LEAD: Javier Cristobo, Spanish Institute of Oceanography, Spain and Ute Hentschel, Helmholtz-Centre for Ocean Research (GEOMAR), Germany

Objectives

The main aim of this Work Package is to provide a complete assessment of the biodiversity contained within sponge grounds ecosystems of the North Atlantic.

In order to reach the aim the following objectives will be addressed:

- Identify, describe and classify all habitat-forming sponge species, their composition and structure in the study area.
- Investigate the diversity of sponge-grounds associated fauna.
- Investigate the diversity and function of microbial consortia associated with key sponge species.
- Develop a classification scheme for North Atlantic sponge ecosystems.

for pharmaceutical drugs and provide refuge for commercial fish.

The Work Package will explore sponge grounds as hotspots of biodiversity by studying fauna and microbiome in and out of these habitats.

What are the key knowledge gaps to address?

In terms of sponge biodiversity, scientists only know about 30% of the expected sponge species and this gap in knowledge is wider in the deep-sea sponge fauna and the currently known microbial biodiversity.

Expected major outputs

The Work Package will increase the number of known species and these will probably house many

Focus

The Work Package will study the biodiversity of the sponge ground ecosystems, including habitat-forming sponge species, their microbial biome and associated fauna as regards composition and structure, diversity, and function. A classification scheme for North Atlantic sponge ecosystems will be developed.

Why is this important?

Sponge grounds are reservoirs of biodiversity and high biodiversity ensures natural sustainability and health of ecosystems. Sponge grounds are a storehouse of novel chemical compounds with great potential



Sponge biodiversity from a June 2017 SponGES cruise
(Photo J. Cristobo / IEO)



TOP LEFT: *Asconema setubalense* beds in the Cantabrian Sea (Photo F. Sanchez/IEO)

TOP RIGHT: Associated fauna of carnivorous sponges (Photo: J. Cristobo / IEO)

ROV Liropus 2000 on board R/V Angeles Alvariño (Photo: J. Cristobo / IEO)

undiscovered microorganisms. The major expected outputs are:

- ⚙ Identification of ground structuring species;
- ⚙ A voucher-linked barcode library and a reference collection of the fauna associated with the North Atlantic sponge grounds;
- ⚙ Knowledge of the diversity and function of the microbiomes associated with key species; and
- ⚙ A classification scheme for North Atlantic sponge ecosystems.

Results achieved so far

In the first (and second) year of the project, samples are collected by different cruises in all case study areas, in order to identify the sponge grounds species, associated fauna, and the sponge-associated microorganisms. Preliminary protocols and standards related to sampling methodologies for data and specimen collection have been completed, including the main on-board procedures for collection, handling, fixation and storage of sponge, water and sediment

samples, in order to assist the partners during scientific cruises.

What methods/technologies/approaches are you using?

We employ modern technologies, for example ROVs or ROTV vehicles, on board ship to minimize the impact of sampling methods and collect the samples carefully for studies of genomics, transcriptomics, metabolomics, barcoding, etc, following the preliminary protocols and standards. We use cutting-edge, next-generation sequencing technologies in the laboratory to resolve patterns of sponge and microbiome diversity and function.

The EU-funded SponGES project will contribute to the sustainable management of deep-sea fisheries, and the protection of sponge-dominated vulnerable marine ecosystems in the North Atlantic through the collection of data and the development of knowledge on the vulnerability and threats as well as protection measures leading to a sustainable use of the deep-sea areas.



✉ info@deepseasponges.org
 🏠 deepseasponges.org
 📘 @DeepSeaSponges
 🐦 @DeepSea_Sponges