



MANAGING IMPACTS OF DEEP
SEA RESOURCE EXPLOITATION

Project acronym:	MIDAS
Grant Agreement:	603418
Deliverable number:	Deliverable 4.1
Deliverable title:	Database on reproduction and larval dispersal of benthic species from potential mining sites on the Mid-Atlantic Ridge, CCFZ, and Arctic gas hydrates
Work Package:	WP4
Date of completion:	30 May 2015



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**Database on reproduction and larval dispersal of benthic
species from potential mining sites on the Mid-Atlantic
Ridge, CCFZ, and Arctic gas hydrates**

Deliverable 4.1

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30 May 2015

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Summary

Understanding the life-cycle of organisms colonizing deep-sea habitats where mining activities might take place in the near future remains one of the most critical knowledge gaps that will need to be bridged if we want to be able to mitigate the impacts of resource extraction through the development of spatial management plans for example. The (re)colonization of impacted areas will greatly depend on the connectivity existing between populations, i.e. the ability of new colonists to travel from other areas, settle, grow and reproduce. The objective of this work was to gather all available data concerning reproductive biology and larval dispersal of species inhabiting areas which may be targeted by mining activities as defined in the MIDAS project: The Mid-Atlantic Ridge (MAR), the Clarion-Clipperton Fracture Zone (CCFZ) in the North Pacific, and Arctic gas hydrates. Most data gathered here concerns the MAR, since very few and no data are currently available for the Arctic gas hydrates, and the CCFZ, respectively. Species inhabiting hydrothermal vent sites on the MAR have been relatively well studied compared to species living in the other target areas of the MIDAS project. Nevertheless, reproductive or larval dispersal data are available for less than 15% of the MAR species, and in most cases, data are limited to a very low number of biological traits. None of the species inhabiting these sites has had its life-cycle fully characterized. In particular, time-series observations that are required to describe reproductive rhythms are only rarely available. The database highlights the amount of data that is still needed to be able to develop models simulating population connectivity and spatial management plans to mitigate mining impacts.

1. Introduction

With the growing interest in the potential for exploitation of deep-sea mineral resources, knowledge gaps are also pointed that will need to be bridged in order to develop management strategies to mitigate expected impacts on animal communities associated with the targeted resources. One of the most critical gaps identified concerns the life-cycle, reproductive and larval biology of endemic species of these habitats. Modeling approaches coupling biological and physical parameters are increasingly used to predict larval dispersal and species connectivity in order to inform spatial management plans. These modeling approaches often use many approximations, or even skip the input of biological parameters due to the lack of data available.

This database gathers current knowledge on reproductive and larval biology from deep-sea benthic species found in target areas which are within the focus of the MIDAS project: the Mid-Atlantic Ridge (MAR), the Clarion-Clipperton Fracture Zone (CCFZ), and the Arctic gas hydrates. However, since no data on reproductive and larval biology are available for species inhabiting the CCFZ and are very limited for the Arctic gas hydrates, most data are from vent sites and non-vent areas on the MAR. In addition, phylogenetically related species inhabiting similar habitats in other geographic regions have also been considered. In many taxa, reproductive traits such as gametogenesis mode are phylogenetically constrained, and knowledge from related species might provide meaningful proxies of biological traits relevant for modeling approaches.

2. Database creation

The database compiles data relative to reproductive and larval traits, larval settlement, as well as genetic connectivity, reviewed from the published literature, and occasionally incorporates master or thesis work.

The database consists of five sheets, four presenting data for species inhabiting habitats targeted by the mining activities, and the fifth giving details about the biological traits considered and methods employed in the original studies compiled in the database. Data for species colonizing active hydrothermal vents on the MAR, species from inactive or non-vent parts of the MAR, species from Arctic gas hydrates, and phylogenetically related species inhabiting similar habitats in geographic locations beyond MIDAS focus are presented within each of the four first sheets. Survey of reproductive and larval biology was also planned for the CCFZ initially, but to our knowledge, no data are yet available for species found in this area.

The database compiles biological traits which characterize species life cycle, larval dispersal, and provide relevant data to incorporate into models aiming at simulating connectivity and designing spatial management plans. Connectivity results from a suite of processes: (1) release of embryos or larval stages in the water column (i.e. reproductive output), (2) larval transport which depends on biological parameters (developmental mode, larval physiology and behavior) and physical parameters including hydrodynamics, (3) benthic settlement, and (4) growth and sexual maturation. Our database reflects these successive steps and groups biological traits within 3 main categories:

(1) Reproductive traits: sexuality, sex-ratio, reproductive rhythms at population level, size at first reproduction, gametogenesis mode, fertilization, spawning, fecundity, oocyte size, and sperm characteristics. Reproductive modes are described by sexuality, sex-ratio, fertilization and spawning behavior. Reproductive output, i.e. “how many, where and when” are offsprings released into the water column, is described and quantified through size at first reproduction and fecundity. Reproductive rhythms at population levels describe whether a species release larval stages continuously or not, and in case of discontinuous larval release, whether a periodicity (eg seasonality) exists. Reproductive rhythms are assessed very differently depending on authors and available samples. Most often authors look at the distribution of oocyte developmental stages within a more or less high number of mature individuals of the samples at a given period, or in best cases at different periods of the year. Spatial variation is rarely considered. Therefore, assessment of continuity often entails lots of extrapolation, leading to opposite conclusions whereas original datasets appears very similar. Oocyte size is reported here because it is often use as a proxy for larval development mode: small eggs are often related to extended larval development with larvae that need to uptake food from their planktonic environment, whereas large eggs are related with larval development where energy necessary for development comes entirely from the egg reserves and larvae do not have to feed. However, lecithotrophic development is not always associated with short larval life, and rather depends on larval metabolism which might be significantly reduced in deep-sea environments. Sperm morphological characteristics are used to estimate fertilization mode.

(2) Larval biology: larval developmental mode, larval size, planktonic larval duration (PLD), larval physiology, larval behavior, larval mortality. Direct observations of larval stages are rare. For a few species, they come from laboratory cultures obtained after *in vitro* fertilization. In addition, some larval stages have also been collected in situ. In that case, the challenge lies in the accurate identification of their adult counterparts. PLD is one of the most important parameter used in modeling approaches since it define the time during which a larvae can potentially travel, and may strongly influence larval dispersal distances.

(3) Settlement: recruitment period and settlement cues.

In addition to these traits which are directly relevant to the life cycle, general ecological traits including distribution range, habitat, local abundance and trophic ecology are also reported in order to evaluate species functional role and importance within the animal communities. Data available regarding species genetic connectivity are also added, in order to confront it with reproductive and larval biology traits.

In most cases, data comes from both spatially and temporally discrete sampling because of the difficulties and costs related with deep-sea work. In order to evaluate the degree of completeness of the data, information about geographic origin of the samples used, sampling period and methods used are also provided.

3. Results and concluding remarks

The MAR, and especially active vent sites, is by far the best studied of the MIDAS target areas (see D4.2). Even in that case, data on reproductive and larval biology are limited. Based on a relatively old estimate of the number of species inhabiting northern MAR vent sites (77 species, Desbruyères et al, 2001), our database highlights the low number of species for which reproductive data are available today : less than 15%. In most species, only a few biological traits have been described, and most often concern reproductive biology whereas larval biology traits mainly come from inferences rather than direct observation (eg. Egg size used as a proxy for larval developmental mode), and settlement remains largely unexplored (see Table 1).

Table 1: Current status of our knowledge on the life-cycle of vent species from the Mid-Atlantic Ridge. Green: good knowledge, including reliable assessment of temporal aspects; yellow: partial knowledge, observations exist on a few aspects; orange: weak knowledge often derived from inferences from other traits (eg: larval development mode inferred from egg size) without direct observation, red: no data available.

Species	Reproduction	Larval biology	Settlement	Genetic connectivity
<i>Bathymodiolus azoricus</i>	Green	Yellow	Yellow	Orange
<i>Bathymodiolus puteoserpensis</i>	Yellow	Orange	Red	Orange
<i>Lepetodrilus atlanticus</i>	Yellow	Orange	Red	Red
<i>Rimicaris exoculata</i>	Yellow	Orange	Red	Green
<i>Chorocaris chacei</i>	Yellow	Orange	Red	Orange
<i>Mirocaris fortunata</i>	Yellow	Orange	Red	Red
<i>Alvinocaris markensis</i>	Orange	Orange	Red	Orange
<i>Segonzacia mesatlantica</i>	Orange	Orange	Red	Red
<i>Bouvierella curtirama</i>	Green	Red	Red	Red
<i>Amathys lutzi</i>	Yellow	Red	Red	Red
<i>Branchipolynoe seepensis</i>	Yellow	Red	Red	Yellow
<i>Branchinotogluma sp.</i>	Yellow	Red	Red	Red

The main issue with the reproductive data gathered here is the lack of temporal series, which are required to fully assess reproductive rhythms, better evaluate species reproductive output, and obtain clues about the timing of larval presence in the water column. The only MAR species for which temporal series are available is the vent Bathymodiolin mussel *Bathymodiolus azoricus*. Seasonal reproduction has been demonstrated for individuals inhabiting the shallowest and most northern part of its known distribution range. Data on *B. azoricus* reproduction are also further supported by the data available for another well characterized related species, *Bathymodiolus childressi* from cold seeps in the Gulf of Mexico. The latter is the only species where larval development has been fully characterized using experimental laboratory cultures.

Besides the lack of temporal series, spatial variations in reproductive traits across habitat or geographical ranges have almost never studied. For a same species, populations inhabiting different part of the geographic range and experiencing different environmental conditions may exhibit differences in their reproductive output, and larval development might also be impacted (eg available in deep-sea holothurians).

Reproductive data from a given location may not be valid for the same species in a different part of its geographic range. Therefore, getting relevant data on the life cycle of species inhabiting areas targeted by future mining activities will require studying reproductive traits within these targeted areas, but also in other areas experiencing different local regimes (depth, productivity, currents...). Understanding the full life-cycle of all species cannot be achieved within a reasonable time delay. Efforts should therefore concentrate on model species representing major functional groups, with sufficient abundances and background knowledge to ensure relatively easy sampling and feasibility of more experimental approaches.

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