

ABSTRACT

„Knowledge based bioeconomy“ (KBBE) interlocks traditional academic topics like food research, agri- and aquaculture with new fields such as red, white, green and blue biotechnology to enhance important topics like medicine, health, nutrition as well as the merging of traditional chemical synthesis routes with biological approaches. One important part of KBBE is the integration of novel bio-derived catalysts, into biotechnological applications. To achieve this, it is crucial to have a variety of specialized biocatalysts at hand. Therefore, science is looking for new methods to identify novel enzymes to establish completely new and artificial production routes. Promising source for the discovery of new enzymes are metagenomes. Especially marine metagenomes offer an enormous potential as the ocean and seas cover not only more than 70% of the earth's surface, but also comprise an unlimited diversity of ecological niches. Unsurprisingly, Bacteria and Archaea in marine waters constitute a major fraction of global microbial biomass. Marine microorganisms have accordingly been used in the past as a source for novel enzymes, although many challenges exist when aiming at the exploration and exploitation of this biomass. To analyze the vast amount of genetic information within marine metagenomes, an efficient and powerful all-in-one function-linked screening system has yet to be found. To overcome these limitations, we want to develop a new screening platform for the fast and reliable all-in-one screening of metagenomes. We will introduce habitat guiding, as a preselection tool and develop an innovative approach that combines an in-vitro compartmentalization system with cell-free protein synthesis as function-based approach. Thus, our technology will improve the exploitation of the unique opportunities of marine microbiomes.

Topic:

- Metagenomes

Marine biomass:

- Microorganisms

Source of marine biomass:

- Microbiomes

Keywords:

Function-based metagenomics, habitat guiding, microfluidics, emulsion droplets, synthetic enzyme cascades

Total costs*: € 1.073.000

Funding granted*: € 1.032.000

Duration: 3 years (2018-2020)

** Exact amount may change after completion of national contracts*



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CONSORTIUM

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ABSTRACT

Organisms in the marine environment represent a largely unexploited source of highly valuable biomolecules. Due to the development of sequencing technologies in the last few decades, we are now able to access a vast amount of sequence information of metagenomes of cultivable and non-cultivable marine organisms. Unfortunately, our abilities to link such sequence information with function lags completely behind. The conventional system to annotate protein functions, e.g., annotation based on BLAST homology search, is very poor and often provides false predictions, in particular for classes of proteins for which biochemical characterization data has not been accumulated. Consequently, it is virtually impossible to identify novel proteins and enzymes based on sequence based screenings, only. Therefore, the goals of MarBioTech are to develop innovative tools and technologies to advance function-based searches in combination with sequence-based searches and to deliver valuable biomolecules of marine origin. Together with the innovative technology advancement, a wide range of existing marine resources including microbiomes of marine algae, jelly fish, and marine fish farms, among others, will be exploited by combining innovative function-, sequence-based and in vitro screenings for the identification of novel active high-value marine biomolecules. The target molecules will include enzymes involved in marine plastic degradation (PET esterases), fluorescent proteins for molecular medicine, novel highly active RNA polymerases as well as DNA nucleases for metagenome mining and molecular biology and quorum quenching (QQ) proteins to prevent biofilm formation.



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Topic:

- Biomolecules

Marine biomass:

- Microorganisms

Source of marine biomass:

- Microbiome of:
 - Algae
 - Medusozoa
 - Fish farms

Keywords:

Metagenomics, marine biodiversity, technology advancement, novel proteins and enzyme products

Total costs*: € 1.633.000

Funding granted*: € 1.515.000

Duration: 3 years (2018-2020)

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Mining the microbiomes from marine wood-digesting bivalves for novel lignocellulose depolymerizing enzymes

PROJECT FACTSHEET

CALL 3 | AUGUST 2017

ABSTRACT

Lignocellulose is a greatly undervalored biomass and methodologies to convert it to high-value products needs fortification. A critical step in biorefining is the enzymatic conversion of lignocellulose to soluble sugars and lignin. The cost and the efficiency of enzymes is far from optimal and new enzymes are needed to improve the efficiency and sustainability of lignocellulose depolymerization. Through META-MINE, we will exploit the process strategies of nature's own micro-biorefinery, the shipworm. Shipworms are voracious animals with respect to their appetite for wood. Their digestive system is especially intriguing. Wood engulfed by mechanical rasping is digested by enzymes secreted by a community of symbiotic bacteria located in the gill tissue. Current model systems for the study of cellulose degradation are highly complex (e.g. community driven anaerobe systems in ruminants and the intricate secreted enzyme systems of aerobic fungi), and challenging to analyze. The shipworm gill symbionts are specialists in lignocellulose degradation and perform this task by applying a perfected enzyme cocktail in a defined and physiochemically stable environment. Thus, by unravelling the contributions of the individual enzymes in the shipworm cocktail, we have the opportunity to take a leap forward in understanding the fundamental properties of enzymatic lignocellulose degradation. META-MINE will use the shipworms as a model system for a holistic study of marine lignocellulose degradation and mine the metagenomes for novel lignocellulose depolymerizing enzymes.

Topic:

- Lignocellulose degradation

Marine biomass:

- Symbiotic bacteria in shipworms

Source of marine biomass:

- Gill tissue of shipworms

Keywords:

Shipworm, lignocellulose-depolymerization, metagenomics

Total costs*: € 1.882.000

Funding granted*: € 1.711.000

Duration: 3 years (2018-2020)

** Exact amount may change after completion of national contracts*



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ABSTRACT

A growing interest exists in the development of new value chains based on protein-rich deboning residues from the meat and poultry industry. Herein, enzymatic hydrolysis is an attractive refinement process to achieve new products with market potential, but its breakthrough is prevented by the lack of suitable commercial enzymes able to access the recalcitrant bone components. Driven by industrial demands, the ProBone project focuses on streamlining discovery of valuable bone hydrolytic enzymes, by selectively prospecting the unique genes and proteins of the non-cultivable marine bone-degrading microbiome. Despite its resilience, bones are degraded by free-living bacteria as well as symbiotic microorganisms associated to bone-thriving invertebrates in the marine environment. This bone-degrading microbiome is, however, largely unexplored for its biotechnological potential. ProBone aims at delivering an innovative toolbox based on omics technologies and synthetic biology methods, to expedite discovery of active bone-degrading enzymes, and to accelerate the transition from discovery to end-user applications. An international consortium with recognized scientists of complementary expertise in marine biology, microbiology, bioinformatics and biochemistry, will apply and develop a refined computational workflow for gene discovery as well as ground-breaking improvements in recombinant expression and activity assessment. These developments are key to identify tailored enzymes for the emerging bio-based economy.



Gro Elin Kjæreng Bjerga, Project Coordinator
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Photo: Andreas R. Graven
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Topic:

- Bone-degrading enzymes

Marine biomass:

- Microorganisms

Source of marine biomass:

- Biobanks and repositories that are held within institutions/companies

Keywords:

Marine microbiome, bone-degrading, meta-omics, toolbox, enzymes

Total costs*: € 1.004.000

Funding granted*: € 940.000

Duration: 3 years (2018-2020)

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ABSTRACT

Marine eukaryotic protists offer a huge but currently underexploited reservoir of metabolic pathways with biotechnological potential. Given their unique adaptations through symbiosis, endosymbiosis and organelle acquisition, the ecofunctionalities of protists present a hitherto untapped source to discover novel metabolic pathways and bioactivities whilst bearing a high chance of discovering different activities compared to those identified in other marine sources. The PROMiSE experimental workflow employs a comprehensive set of Omics methods. This approach spans the encoded metabolic potential to identify biosynthetic gene clusters which in turn guide the targeted metabolite profiling, merged with discovery-based metabolomics. The goal is to target identified candidate compound classes and their pathway-related metabolites and conjugations dereplicated from the Omics information. By linking these methods back to the source cell through single cell Omics methods, PROMiSE offers a unique way to recognize functional gene clusters and to understand how metabolism is partitioned across ecosystems. The vertically integrated extraction and analyses procedure within PROMiSE are supported by a comprehensive array of cutting-edge in vitro and in vivo bioassays for reliably assessing biological activities by High-Content profiling and antibacterial screening. Analytical chemistry, including high resolution mass spectroscopy and nuclear magnetic resonance spectroscopy approaches, will be used to elucidate compounds found in the bioactive fractions, which will tie back the molecular data to identify relevant enzymes, pathways, and compounds.



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Topic:

- Protist Metabolome Screening

Marine biomass:

- Protists

Source of marine biomass:

- Biobanks and repositories that are held within institutions/companies

Keywords:

Marine protists, metagenomics, bioprospecting

Total costs*: € 1.494.000

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