Short Bibliography on current European Marine Biotechnology Research Activities

Deliverable 6.2 Work Package 6 Marine Biotechnology

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The Lead Partner responsible for Ocean Observation Work Package in the Atlantic Ocean Research Alliance Co-Ordination and Support Action is RANNÍS.

Disclaimer

Definition

The oceans have tremendous biodiversity with marine organisms having evolved to exist in the harsh conditions present in the oceans. Marine microbial ecology is the study of microbial marine organisms and their environmental impact, either as a source of knowledge, environmental monitoring, or the target of applications, through the use of cutting-edge techniques in biological technology and engineering.

Marine biotechnology is a tool for the study of marine microbial organisms and looks to this biodiversity and the coping mechanisms to develop new products e.g. medicines, enzymes, glues, cosmetics, artificial bone, biosensors, bioremediation, foods, biofuels, etc. The Atlantic Ocean is the second largest ocean on earth, extending to the poles and including the sub-tropics – its biodiversity is high encompassing a huge range of habitats.

Rationale

Identification of relevant European research activity is important as a start point to facilitate future collaboration for both sides of the Atlantic. Microbial ecology and Marine biotechnology are two different focus points of a similar theme. In this report they are mixed together.

Objective

The main objective of this short bibliography, which is non-exhaustive, is to list marine biotechnology research projects from Horizon 2020, EU collaborative projects (FP7) and other relevant European projects. These project have relevance to the AORA objectives and can contribute to present and future transatlantic research collaboration.

Contents

1. European Funded Projects

1.1. Horizon 2020

Title: **European Marine Biology Resource Centre preparatory phase 2**
Acronym: pp2EMBRC

Co-ordinator (organisation/affiliation, country): Centro de Ciencias do Mar do Algarve (Portugal).
Keywords/themes:
Duration: 14 months (From 2015-10-01 to 2016-09-30)

Link: Not available

Abstract/Description:

EMBRC is a distributed infrastructure of marine biology and ecology, encompassing aquaculture and biotechnology, exploiting the latest "omics", analytical and imaging technologies, and providing on site and remote scientific and technical services to the scientific community of the public and private sector. EMBRC successfully completed a preparatory phase in early in 2014 with the production of a business plan and a memorandum of understanding (MoU) signed by 9 countries. A host for its headquarters has been chosen and and an ERIC application is in preparation. Since only institutions from 5 MoU signatory countries went through the preparatory phase, the present proposal has as objectives: 1) to harmonize the access mechanism to the operational EMBRC-ERIC across all the partners, putting all the practical tools in place, including host contracts and single point online access platform, to enable EMBRC-ERIC to commence its access program; 2) to put in place practical guidelines towards the full implementation of the new European and international legislation and commitments on access and fair benefit sharing of the use of marine biological resources, thus providing clarity to future users of EMBRC-ERIC about their legal rights over obtained biological resources, and positioning itself globally as a broker between users and the supplying countries ; 3) to focus the smart specialization of the regions onto the opportunities marine biological resources offer for blue-biotech development and innovation, thus demonstrating the member states that EMBRC is a tool towards economic development of their maritime regions, and enticing them to sign the EMBRC-ERIC, and prioritize its sustained support, particularly from regions which are now underrepresented in EMBRC (Black and Baltic Seas). These activities will ensure that the beneficiary research communities can exploit the results obtained at EMBRC-ERIC facility from the start with the highest efficiency.

USA/CA Partners/Interactions: None.

Other Transatlantic Partners/Interactions: None.

Links: http://cordis.europa.eu/project/rcn/198826_en.html

Title: European Marine Biological Research Infrastructure Cluster to promote the Blue Bioeconomy
Acronym: EMBRIC

Co-ordinator (organisation/affiliation, country): UNIVERSITE PIERRE ET MARIE CURIE - PARIS 6, France.
Keywords/themes:
Duration: 48 months (From 2015 - 2019)

Link: http://www.embric.eu/

Abstract/Description:

Marine (blue) biotechnology is the key to unlocking the huge economic potential of the unique biodiversity of marine organisms. This potential remains largely underexploited due to lack of connectivity between research services, practical and cultural difficulties in connecting science with industry, and high fragmentation of regional research, development and innovation (RDI) policies. To overcome these barriers, EMBRIC (European Marine Biological Resource Infrastructure Cluster) will link biological and social science research infrastructures (EMBRC, MIRRI, EU-OPENSCREEN, ELIXIR, AQUAEXCEL, RISIS) and will build inter-connectivity along three dimensions: science, industry and regions. The objectives of EMBRIC are to: (1) develop integrated workflows of high quality services for access to biological, analytical and data resources, and deploy common underpinning technologies and practices; (2) strengthen the connection of science with industry by engaging companies and by federating technology transfer (TT) services; (3) defragment RDI policies and involve maritime regions with the construction of EMBRIC. Acceleration of the pace of scientific discovery and innovation from marine bioresources will be achieved through: (i) establishment of multidisciplinary service-oriented technological workflows; (ii) joint development activities focusing on bioprospection for novel marine natural products, and marker-assisted selection in aquaculture; (iii) training and knowledge transfer; (iv) pilot transnational access to cluster facilities and services. EMBRIC will also connect TT officers from contrasted maritime regions to promote greater cohesion in TT practices. It will engage with policy-makers with the aim of consolidating a perennial pan-European virtual infrastructure cluster rooted in the maritime regions of Europe and underpinning the blue bioeconomy.

USA/CA Partners/Interactions: None.

Other Transatlantic Partners/Interactions: None.

Links: http://cordis.europa.eu/project/rcn/198465_en.html

1.2 Seventh Framework Programme (FP7)

Title: Marine Microbial Biodiversity, Bioinformatics, Biotechnology

Acronym: Micro B3
Co-ordinator (organisation/affiliation, country): Jacobs University Bremen, Germany (Frank Oliver Glöckner).
Duration: 48 months (2012- 2016)
Link: https://www.microb3.eu

Abstract/Description:

The EU 7FP project Micro B3 aimed to develop innovative bioinformatic approaches and a legal framework to make large-scale data on marine viral, bacterial, archaeal and protists genomes and metagenomes accessible for marine ecosystems biology and to define new targets for biotechnological applications. Micro B3 built upon a highly interdisciplinary consortium of 32 academic and industrial partners comprising world-leading experts in bioinformatics, computer science, biology, ecology, oceanography, bioprospecting and biotechnology, as well as legal aspects. Micro B3 was based on a strong user- and data basis from ongoing European sampling campaigns to long-term ecological research sites. For the first time a strong link between oceanographic and molecular microbial research has been established to integrate global marine data with research on microbial biodiversity and functions. The Micro B3 Information System provided innovative open source software for data-processing, -integration, -visualisation, and -accessibility. Interoperability is the key for seamless data transfer of sequence and contextual data to public repositories. To underline the translational character of Micro B3, outreach and training activities for diverse stakeholders are ongoing as well as an Ocean Sampling Day to transparently make project results accessible and gain valuable user feedback.

Results Pertinent to Atlantic Ocean Research Alliance: Yes. Micro B3 launched The Ocean Sampling Day (OSD), a global scientific campaign to analyse marine microbial biodiversity and function, taking place during the summer solstice.

US/CA Partners/Interactions: None.

Other Transatlantic Partners/Interactions: None.

Links: http://cordis.europa.eu/project/rcn/101555_en.html

Title: Increasing Value and Flow in the Marine Biodiscovery Pipeline

Acronym: PharmaSea
Co-ordinator (organisation/affiliation, country): Katholieke Universiteit Leuven, Belgium (Peter de Witte).
Duration: 48 months (2012-2016)
Link: http://www.pharma-sea.eu/

Abstract/Description:

The PharmaSea project focuses on obstacles in marine biodiscovery research, development and commercialization and brings together a broad interdisciplinary team of academic and industry researchers and specialists to address and overcome these. The partners are ideally placed to demonstrate how to widen the bottlenecks and increase the flow of ideas and products derived from the marine microbiome towards a greater number of successes in a larger number of application areas. Despite the tremendous potential of marine biodiscovery, exploitation, particularly at a commercial scale, has been hampered by a number of constraints. These relate to access (physical and legal), genetics of the organisms, compound isolation, structure elucidation, early reliable validation of biological activity and best mechanisms of flow-through into exploitation. PharmaSea will solve these chronic bottlenecks by developing essential actions beyond the state of the art and linking them with best practice and appropriate pragmatic approaches. The robust pipeline structure established within PharmaSea will process a wide genetic basis including marine microbial strain collections held by partners and new strain collections from extreme environments (deep, cold and hot vent habitats) to produce new products with desirable characteristics for development by the SME partners in three accessible market sectors, health (infection, inflammation, CNS diseases), personal care and nutrition. The global aim of PharmaSea is to produce two compounds at larger scale and advance them to pre-clinical evaluation. To address relevant challenges in marine biodiscovery related to policy and legal issues, PharmaSea will bring together practitioners, legal experts, policy advisors/makers and other stakeholders, focusing on the feasibility of harmonising, aligning and complementing current legal frameworks with recommendations and ready to use solutions tailored to marine biodiscovery.

Result in Brief:

New drugs from the ocean depths

The world's oceans are home to more living organisms, especially microorganisms, than any other environment on the planet. However, successful exploitation of this exceptional resource has been limited, despite its enormous potential for harvesting unique biological compounds with benefits for all of humanity.

The purpose of the project 'Increasing value and flow in the marine biodiscovery pipeline' (PHARMASEA) is to discover new marine bacteria and novel compounds. In addition, the consortium will improve the effectiveness of the biodiscovery pipeline, thereby making bioresources attractive to industry.

Project partners will achieve their aim by processing genetic material from in-house collections of microbial strains, while seeking out new strains from extreme marine environments. These will be

used to develop new products for the pharmaceutical, food and nutrition, and cosmetic sectors. The main disease areas to be addressed are microbial infection, diseases of the central nervous system and inflammation.

By sampling some of the deepest parts of the ocean floor, PHARMASEA hopes to utilise microorganisms that are new to science. Deep ocean trenches are 'islands of diversity' with a unique chemistry and where evolution may have developed differently. Because so little of this extreme environment has been explored, PHARMASEA is breaking new ground.

The final goal of this exciting initiative is to produce two compounds from newly discovered microorganisms on a large scale. These compounds will be taken forward to pre-clinical evaluation for treating infection or diseases of the central nervous system. Other outputs will include a validated model biodiscovery pipeline, new chemometric tools, data mining techniques and data sets.

Furthermore, PHARMASEA will develop solutions to improving access to marine bioresources in different habitats and jurisdictions, and equitable sharing of the benefits from their exploitation. A toolbox will also be created to navigate legal aspects in order to simplify and speed up the marine biodiscovery process.

PHARMASEA is not just expected to have a major impact on scientific progress, it will also influence policy and enhance economic performance. It will also strengthen the competiveness of the European Research Area (ERA) by increasing technological know-how through interdisciplinary and international cooperation, thereby contributing to Europe's knowledge-based economy.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None.

Other Transatlantic Partners/Interactions: None.

Links: http://cordis.europa.eu/project/rcn/104338_en.html

Title: From sea-bed to test-bed: harvesting the potential of marine microbes for industrial biotechnology

Acronym: SeaBioTech
Co-ordinator (organisation/affiliation, country): University of Strathclyde (Brian McNeil).
Duration: 48 months (2012-2016)
Link: http://spider.science.strath.ac.uk/seabiotech/contact.htm

Abstract/Description:

SeaBioTech is a 48-month project designed and driven by SMEs to create innovative marine biodiscovery pipelines as a means to convert the potential of marine biotechnology into novel industrial products for the pharmaceutical (human and aquaculture), cosmetic, functional food and industrial chemistry sectors. SeaBioTech will reduce barriers to successful industrial exploitation of marine biodiversity for companies more accustomed to 'terrestrial' biotechnology. SeaBioTech directly addresses five key challenges to remove bottlenecks in the marine biodiscovery pipeline, leading to (1) improvements in the quality of marine resources available for biotechnological exploitation, (2) improvement in technical aspects of the biodiscovery pipeline to shorten time to market, and (3) developing sustainable modes of supply of raw materials for industry. The two last challenges centre on enabling activities to enhance the marine biodiscovery process: first, clarification of legal aspects to facilitate access to marine resources, their sustainable use, and their secure exploitation; second, to create an improved framework for access to marine biotechnology data and research materials. To achieve its goals, SeaBioTech brings together complementary and world-leading experts, integrating biology, genomics, natural product chemistry, bioactivity testing, industrial bioprocessing, legal aspects, market analysis and knowledge exchange. The expertise assembled within the consortium reflects the industry-defined needs, from the SME partners' initial definition of market and product opportunities to their ultimate proof-of-concept demonstration activities. SeaBioTech will have significant impact on research and technology, on innovation, on European competitiveness and on economic growth. It will provide a model to accelerate the development of European biotechnology into a world leading position.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions:

Links: http://cordis.europa.eu/project/rcn/104332_en.html

Title: Development of global plankton data base and model system for eco-climate early warning

Acronym: GreenSeas
Co-ordinator (organisation/affiliation, country): STIFTELSEN NANSEN SENTER FOR MILJOOG FJERNMALING, Norway.
Duration: 42 months (2011-2014)
Link: http://www.greenseas.eu/home

Abstract/Description:

GreenSeas shall advance the quantitative knowledge of how planktonic marine ecosystems, including phytoplankton, bacterioplankton and zooplankton, will respond to environmental and climate changes. To achieve this GreenSeas will employ a combination of observation data, numerical simulations and a cross-disciplinary synthesis to develop a high quality, harmonized and standardized plankton and plankton ecology long time-series, data inventory and information service. The focus will be on capturing the latitudinal gradients, biogeographical distributions and provinces in the planktonic ecosystem from the Arctic, through the Atlantic and into the Southern Ocean. It will build on historical data-sets, and ongoing multidisciplinary ocean planktonic ecosystem monitoring programs, enhanced where possible with an emphasis on the Southern Ocean. GreenSeas will also enhance international cooperative links with other plankton monitoring and analysis surveys around the globe. The heart of the GreenSeas concept is establishing a 'core' service following the open and free data access policy implemented in the Global Monitoring for Environment and Security (GMES) programme.

Using state-of-the-art web-based data delivery systems the 'core' service will make available both new and historical plankton data and information products along with error-quantified numerical simulations to a range of users. Connecting with 'downstream' services GreenSeas will moreover offer ecosystem assessment and indicator reports tailored for decision makers, stakeholders and other user groups contributing in the policy making process. Finally, knowledge transfer will be guaranteed throughout the project lifetime, while the legacy of the GreenSeas database web-server will be maintained for at least 5 years beyond the project lifetime.

Result in Brief:

Plankton monitoring for climate change

An EU project has collected data and improved models of plankton ecology in the Atlantic and Southern Oceans, with far-reaching effects on climate change modelling.

Plankton plays a crucial role in the marine ecosystem by assimilating carbon dioxide (CO2) and forming the base of the marine food web. To better understand climate change, researchers need a better grasp of how plankton influences ecological and biochemical processes in global oceans.

To achieve this goal, the GREENSEAS (Development of global plankton data base and model system for eco-climate early warning) project developed multiple simulation models of plankton ecology. Modelling included water colour measurements, nitrogen uptake and geographical distribution of the plankton in the Atlantic and Southern Oceans.

The GREENSEAS project team first collected historic data of plankton distribution in the Arctic, Atlantic, Nordic and Southern Oceans. The next step was to generate a database of the sea-air CO2 flux in the South Atlantic Ocean. Finally, they collected new data characterising the physical-chemical environment and phytoplankton community structure and productivity.

Modelling these parameters allowed scientists to generate simulations of phytoplankton behaviour in response to environmental changes. Minute changes in phytoplankton mass and distribution dictate significant changes in fish population. That in turn may require a major policy overhaul to protect fishing resources.

GREENSEAS developed new indicators for changes in planktonic ecosystems. Researchers also found that current proxies for productivity in plankton communities are not very accurate, suggesting that these should be recalculated.

Lastly, the project created a web portal for researchers and policymakers to access data and analysis on plankton activity in these oceans. The GREENSEAS project may contribute to improved climate change monitoring, which will improve decision making for human health, the environment and marine life.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: South Africa and Brazil

Links: http://cordis.europa.eu/project/rcn/97177_en.html

Title: BluePharmTrain

Acronym: BluePharmTrain

Co-ordinator (organisation/affiliation, country): WAGENINGEN UNIVERSITY, Netherlands.

Duration: 42 months (2013-2017)

Link: http://www.bluepharmtrain.eu/en/bluepharmtrain.htm

Abstract/Description:

Marine sponges harbour extremely diverse populations of microbes, and are world record holders for the production of a plethora of bioactive molecules. Previous studies, however, aiming at the growth of sponges or their associated microbes for the production of bioactive compounds to supply biological material for clinical trials, have been largely unsuccessful.

BLUEPHARMTRAIN is a multi-disciplinary alliance of 20 academic and industrial partners that will excel in research and training through integration of complementary expertise in cell biology, microbiology, natural product chemistry, genomics & transcriptomics (omics) and socio-economics. We will adopt cutting-edge omics technologies to give a new boost to the more traditional disciplines: microbial isolation, cell culture and natural product chemistry to go beyond the current scientific frontiers. For example, metagenomic and transcriptomic data will be applied to identify the metabolic potential and restrictions of -yet- uncultured microbes and will serve for the design of tailor-made cultivation conditions. In addition, heterologous expression of bioactive gene clusters and enzymes able to perform unusual modifications will serve as an alternative strategy to unlock the bioactive

potential of sponges. Thus we aim to develop an extensive technology platform that is applicable for obtaining a wide variety of bioactive compounds from distinct sponges and their microbes.

BLUEPHARMTRAIN will provide a complementary set of experimental and conceptual local and network-wide training modules and workshops to 15 young researchers. The recruited fellows will work towards personalized training plans to meet individual needs and interests, generating a critical mass of young researchers in the emerging field of blue biotechnology. The presence of a large consortium of versatile biotechnology, pharmaceutical and consultancy firms ensures a good balance between academic and transferable skills acquired by the fellows.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions:

Links: http://cordis.europa.eu/project/rcn/109793_en.html

Title: **Marine Metagenomics for New Biotechnological Applications**

Acronym: MAMBA

Co-ordinator (organisation/affiliation, country): BANGOR UNIVERSITY, United Kingdom.

Duration: 42 months (2009 - 2013)

Link: http://mamba.bangor.ac.uk/

Abstract/Description:

"The Project aims at the mining of individual enzymes and metabolic pathways from extremophilic marine organisms and the metagenomes from microbial communities from peculiar marine environments and consequent funnelling the new enzymatic reactions and processes towards the new biotechnological applications. Project builds up on the scientific and technological excellence of individual academic and industrial partners, and beyond that, on application of the state-of-the-art technologies for archiving, molecular screening for the activities (using a unique Surface Plasmon Resonance screening platform), protein structure elucidation, enzyme engineering and directed evolution and establishing new biotechnological processes (biocatalysis, synthesis of fine chemicals, etc.). Marine sampling hotspots to produce the metagenomic resources for their further exploration will cover the whole diversity of marine microbial life at its limits (hypersaline, low and high temperature, high pressure and low water activity conditions, etc.). Individual enzymes interacting with the substrates will be identified, and in case they are new, hyperexpressed and crystallized and their structures will be elucidated. Consequently, the most promising candidates will be scored against the chiral substrates of relevance for biocatalysis and their ability to perform in water-free systems will be evaluated, the directed evolution will be implemented to improve the performance, and specificity of the enzymes. A comprehensive bioinformatic survey throughout the whole tree of cellular life will reveal and suggest the new candidates homologous to the discovered new proteins, from other organisms to be cloned and assayed. The implementation of the set of new enzymes in the biotechnological processes for fine chemical synthesis and drug discovery will be conducted in a strong alliance with competent industrial partners."

Result in Brief:

Hundreds of new enzymes discovered

Marine microorganisms are a promising and still mostly untapped source of enzymes for commercial use. Now, researchers have developed a way to screen for enzyme activity, finding hundreds of new enzymes in the process.

Microorganisms, and particularly bacteria, represent a large portion of the genetic diversity on Earth. But scientists cannot grow most of these microorganisms in laboratory conditions, thus limiting our access to the enzymes (biological catalysts that speed up various reactions) they produce.

The EU-funded 'Marine metagenomics for new biotechnological applications' (MAMBA) project set out to develop and apply a new way to screen microorganisms for useful enzyme activity.

A high-throughput method was successfully devised at the start of the project. Samples were taken from various extreme marine locations and used to create 'expression libraries' — a well-established method for screening all expressed genes in a given sample of microorganisms.

These libraries were then screened directly for enzyme activity on specific enzyme targets known as substrates.

This novel approach identified more than 1 100 potential new enzymes, of which 600 were selected for more in-depth studies. Half of those were isolated to investigate further, and more than 40 new enzyme structures were elucidated.

These figures mean that MAMBA researchers effectively doubled the number of known enzymes that operate at extreme temperatures, high salinity and pH values. The protocols and screening platform used in the project have been commercialised, and several enzymes identified have been earmarked for commercial development. Exploration of the full scope of marine biodiversity is still at an early stage, but an important step in identifying the potential of microbial diversity has been made.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: Canada

Other Transatlantic Partners/Interactions:

Links: http://cordis.europa.eu/project/rcn/91262_en.html

Title: Bacterial Degradation of Marine Particles: Colonisation, Dispersal, and Impact on Vertical Export in the Ocean

Acronym BacPac

Co-ordinator (organisation/affiliation, country):

AGENCIA ESTATAL CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS, Spain.

Duration: 24 months (2012 - 2014)

Link:

Abstract/Description:

Sinking of organic particles from the ocean's productive surface layers is a key component in the biological carbon pump, and essential to carbon sequestration by the ocean. Its regulation needs to be comprehended in order to accurately determine the oceans' role in the global climate system. The impact of bacterial degradation on the fate of marine particles demands further study in order to significantly strengthen our understanding of oceanic carbon cycling. By investigating the prokaryotic community composition of suspended and sinking marine particles, the degradation activities of different prokaryotic groups, and colonisation of particles, BacPac will provide new knowledge elucidating the role of bacteria in vertical flux regulation.

The project will use state-of-the-art molecular tools (DGGE, ARISA, and 454-pyrosequencing) to determine the prokaryotic community in ambient seawater, on marine particles (zooplankton faecal pellets, algal aggregates and marine snow), and on sinking particles collected by sediment traps. The main sampling activities in the Mediterranean Sea will be supplemented by field collections from North-Norwegian and European Arctic waters. The project combines the researcher's expertise on vertical export and the host's expertise in marine microbial ecology in order to advance both disciplines.

BacPac's objectives are directly relevant to contemporary research in marine carbon cycling and microbiology, and will contribute to strengthening European scientific expertise in these fields. The proposed activities will advance both the scientific and complimentary skills of the researcher and will be an important step in his career development. The mobility (University of Tromsø, Norway, to the Marine Science Institute in Barcelona, Spain) will be beneficial to European research integration and will provide a network for future collaboration.

Result in Brief:

Marine bacteria and climate change models

Sinking particles of organic material are a key component of the biological carbon pump, which takes carbon from the atmosphere and deposits it in the deep sea. A detailed understanding of this phenomenon is needed for developing accurate models showing the ocean's role in climate change.

An EU-funded initiative was established to provide a better understanding of the factors controlling microbial diversity in the oceans. The BACPAC project investigated whether marine particles descending from the productive surface layers were colonised by the same communities of bacteria that are present in the surrounding water.

Studies were done on how efficiently these colonies broke down the particles and whether these patterns altered over time and space. These activities were conducted in the laboratory and in field sites in the North Atlantic and Arctic.

Results showed sinking particles are mainly colonised in the ocean's surface layers, where particle formation takes place. One of the most important factors of the sinking organic matter is faecal pellets produced by zooplankton grazing on microscopic plants (phytoplankton). The bacterial community is retained as the particles sink, thereby introducing new types of bacteria to the deep-sea environment.

Zooplankton–phytoplankton interactions were studied using the laboratory-reared copepod species Acartia grani. The aim was to determine whether the bacterial community in zooplankton faecal pellets stem from the diet or the gut of the consumers. This is an important question as the environmental conditions to which the pellet-associated bacteria are adapted affect the degradation rate of the pellets.

BACPAC also investigated variation in bacterial community composition associated with different zooplankton species in the western Mediterranean and eastern Atlantic Ocean. Large-sized zooplankton are able to vertically migrate between different ocean surfaces and depths and may contribute to the two-way exchange of different types of bacteria.

Preliminary results showed that zooplankton-associated bacterial communities generally had low species numbers compared to the surrounding water. However, it did include types of bacteria rarely found in marine environments. The studies also revealed that zooplankton feed on minute picocyanobacteria. These are extremely abundant in the ocean, but were traditionally considered too small to be grazed by most zooplankton.

The work conducted by BACPAC will be of direct benefit by providing new data on bacterial communities and their degradation of organic particles from the ocean's productive surface layer. This will provide valuable information for the successful development of biogeochemical models for describing the marine carbon cycle.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://cordis.europa.eu/project/rcn/103877_en.html

2. ERA-Net Marine Biotechnology projects

Title: Biorefinery and biotechnological exploitation of marine biomasses

Acronym Mar3Bio

Co-ordinator (organisation/affiliation, country): SINTEF Materials and Chemistry, Norway.

Duration: 36 months (2016 - 2018)

Link:
http://www.marinebiotech.eu/sites/marinebiotech.eu/files/public/Mar3Bio%20Project%20description%20ERA-MBT%20Call%201.pdf

Abstract/Description:

The marine biomasses to be used in Mar3Bio are brown algae and crustacean byproducts. These abundant but underexploited renewable biomasses have great potential for production of high value biomolecules. The current bottlenecks for a bio-refinery focusing on these raw materials are low yields, high energy consumption and incomplete spectrum of recovered biomolecules. Mar3Bio will tackle this by a multidisciplinary and intersectorial

R&D approach, and contribute to the development of efficient and sustainable bio-refinery processes for exploitation of the selected biomasses. The main objective is to advance technology beyond state-of-the-art to I) increase the yield and quality of the products arising from early process streams by optimizing the isolation and fractionation steps performed on the raw materials, and II) modify selected fractionated biomolecules to high value products. The

expected achievements will have great impact on the fulfilment of the ambitions of ERA-MarineBiotech.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://www.marinebiotech.eu/news-and-events/era-news/era-mbt-funds-six-projects-first-joint-call

Title: Enhanced biorefining methods for the production of marine biotoxins and microalgae fish feed

Acronym MarBioFEED

Co-ordinator (organisation/affiliation, country): Marine Institute, Ireland.

Duration: 36 months (2016 - 2018)

Link:
http://www.marinebiotech.eu/sites/marinebiotech.eu/files/public/MarBioFEED%20Project%20description%20ERA-MBT%20Call%201.pdf

Abstract/Description:

Shellfish production sites in the EU are prone to closures due to the accumulation of biotoxins, with over 26 EU regulated toxins requiring statutory monitoring. Further impacts are exerted on fish farming industries through the production of feed from contaminated shellfish. The focus of this proposal is to isolate large quantities of biotoxins using enhanced biorefining methods for the preparation of reference materials and to allow for research to be conducted on the effects of biotoxins on other important aquaculture industries. Further work will focus on enhanced production of microalgae as fish feed. Biotoxins will be sourced from contaminated shellfish, bulk algal culturing, harvesting of algal blooms in situ and enzymatic conversions. Biorefining processes will be enhanced through optimisation of algal culturing, the development and use of novel immunoaffinity and polymeric columns, reducing cost and increasing economic viability.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://www.marinebiotech.eu/news-and-events/era-news/era-mbt-funds-six-projects-first-joint-call

Title: Discovery and training of microbial biocatalysts for biomass conversion using moving bed technology (MBT)

Acronym MicroMBT

Co-ordinator (organisation/affiliation, country): UiT-The Arctic University of Norway, Norway.

Duration: 36 months (2016 - 2018)

Link:
http://www.marinebiotech.eu/sites/marinebiotech.eu/files/public/MicroMBT%20Project%20description%20ERA-MBT%20Call%201.pdf

Abstract/Description:

A culture collection of >100 genome sequenced marine bacteria from the Arctic region, and the Moving Bed Technology (MBT) will be used as tools to increase the value of marine rest raw materials. The bacterial isolates have been screened for biocatalyst activities (e.g., PUFA production, lipases, proteases), and hence represent an

excellent starting point for this project. Inspired by the RAS (Recirculating Aquaculture system) technology, the idea is to establish and optimize microbial communities on MBT biobeads. The bacterial communities will be specifically trained into microfactories for conversion of low value rest-raw material from the fish industry. The process will be analogous to RAS, where biofilters are used to convert waste into non-toxic products. Water and lipid phases from spent medium will be collected and screened for potential products. In summary, the robust MBT method will be

used in a completely new area, to convert cheap marine biomasses into new products.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://www.marinebiotech.eu/news-and-events/era-news/era-mbt-funds-six-projects-first-joint-call

Title: Novel Extraction Processes for mulTiple high-value compoUNds from selected Algal source materials

Acronym NEPTUNA

Co-ordinator (organisation/affiliation, country): National University of Ireland Galway, Ireland.

Duration: 24 months (2016 - 2017)

Link:
http://www.marinebiotech.eu/sites/marinebiotech.eu/files/public/NEPTUNA%20Project%20description%20ERA-MBT%20Call%201.pdf

Abstract/Description:

Novel enzyme-based extraction technologies will be applied to algal biomass derived from selected algal taxonomic groups including macroalgae (seaweeds), microalgae and cyanobacteria. Algal species will be chosen according to their potential to produce high bioactive levels which will be further enhanced by applying abiotic stresses. Algal extracts produced by enzymatic and traditional approaches will be tested for multiple applications, concentrating on

antioxidant and antimicrobial activities with applications in food, cosmetics, animal health (aquaculture) and personal/home care. Extracts that exhibit high activities will be chemically characterised to identify active components.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://www.marinebiotech.eu/news-and-events/era-news/era-mbt-funds-six-projects-first-joint-call

Title: The Seaweed Biorefinery – for high value added products

Acronym SeaRefinery

Co-ordinator (organisation/affiliation, country): Danish Technological Institute, Denmark.

Duration: 36 months (2016 - 2018)

Link:
http://www.marinebiotech.eu/sites/marinebiotech.eu/files/public/SeaRefinery%20Project%20description%20ERA-MBT%20Call%201.pdf

Abstract/Description:

SeaRefinery will develop eco-friendly chemical and enzymatic processing technologies to extract and purify high value-added components such as antioxidants, antimicrobial components and hydrocolloids from cultivated seaweed species (e.g. Saccharina latissima) in an integrated biorefinery. Bioactive compounds, e.g. phlorotannins, fucoidan, and laminarin, will be selectively tested for bioactivity. In addition, laminarin and marine proteins will be tested

in nutraceutical and selected food model systems. Alginate will be tested as additive for textile applications via coating and extrusion technologies. In order to maximise the value of the biorefinery feedstock (input) and derived products (output), we will grow monocultures on innovative textile cultivation substrates with high yield biomass production. Seasonal variation, replicated over two years, of the selected biomolecules will be a measuring tool for

harvesting the seaweeds with maximum contents of bioactive compounds.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://www.marinebiotech.eu/news-and-events/era-news/era-mbt-funds-six-projects-first-joint-call

Title: Thermophilic cell factories for efficient conversion of brown algae biomass to high-value chemicals

Acronym ThermoFactories

Co-ordinator (organisation/affiliation, country): Norwegian University of Science and Technology, Norway.

Duration: 36 months (2016 - 2018)

Link:
http://www.marinebiotech.eu/sites/marinebiotech.eu/files/public/ThermoFactories%20Project%20description%20ERA-MBT%20Call%201.pdf

Abstract/Description:

Brown algae biomass is a promising and challenging resource for industrial bioconversions, but there is a need to develop efficient cell factories to convert the constituent carbohydrates into high-value added products. In this proposal, four metabolically different environmental bacteria, inherently suitable to harsh process conditions, will be engineered for production of a number of industrially important platform and specialty chemicals, including 1,2-propanediol, cadaverine, propanol and lycopene. The project will implement and integrate systems biology and metabolic engineering, including rounds of model-driven metabolic optimization. Feedstock development and process engineering are important parts, to optimize fermentability of the algal hydrolysates, and ensure integration with downstream processing and product recovery. At the end of the project, use of all major carbohydrate fractions from brown algae through integrated processing will be demonstrated at small pilot scale.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://www.marinebiotech.eu/news-and-events/era-news/era-mbt-funds-six-projects-first-joint-call

1.4 European Research Council (erc)

Title: Functional redundancy of bacterial communities in the laboratory and in the wild

Acronym Redundancy

Co-ordinator (organisation/affiliation, country): IMPERIAL COLLEGE OF SCIENCE, TECHNOLOGY AND MEDICINE, United Kingdom.

Duration: 48 months (2013 - 2018)

Link:

Abstract/Description:

Understanding how species mediate ecosystem processes, such as energy and nutrient fluxes, is among the foremost challenges in ecology. Bacterial communities are pivotal for the functioning of the world's ecosystems. Although there have been great advances in describing the biodiversity of bacteria, little effort has been directed at understanding how differences in bacterial communities translate into differences in ecosystem functioning. The proposed research will develop a comprehensive framework to determine how bacterial species affect functioning while in complex mixtures of species. Once this baseline is obtained, it is possible to ask detailed questions about the 'functional ecology' of bacterial communities. Foremost among these is whether ecological processes (species sorting) are more important than evolutionary processes (adaptation) in establishing species roles in ecosystems. The research has implications for the fundamental understanding how ecological communities operate.

Result in Brief:

Mid-Term Report Summary - REDUNDANCY (Functional redundancy of bacterial communities in the laboratory and in the wild)

Bacteria underpin all ecosystems. However, while there are millions of bacteria in every pinch of soil, many are unknown to science, and their role in the ecosystem is poorly understood. One major challenge for microbial ecologists is to understand how changes to bacterial communities impact the surrounding ecosystem. This project has used a revolutionary new approach to improve our understanding of the link between bacterial communities and ecosystem functioning by developing methods for estimating interactions among bacteria in natural environments. We have been creating a 'living archive' of bacterial communities from across the UK. By testing these communities in a common environment in the lab, we have begun to understand how large numbers of bacterial species interact. Providing robust estimates of interactions among bacterial species is the first step in being able to predict how the community as a whole will influence the surrounding ecosystem. The first body of research from this project has shown that the strength of interactions diminishes during ecological succession as bacterial communities colonise a new environment.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://cordis.europa.eu/project/rcn/105887_en.html

Title: ABYSS - Assessment of bacterial life and matter cycling in deep-sea surface sediments

Acronym ABYSS

Co-ordinator (organisation/affiliation, country: ALFRED-WEGENER-INSTITUT HELMHOLTZ- ZENTRUM FUER POLAR- UND MEERESFORSCHUNG, Germany.

Duration: 48 months (2012 - 2017)

Link:

Abstract/Description:

"The deep-sea floor hosts a distinct microbial biome covering 67% of the Earth's surface, characterized by cold temperatures, permanent darkness, high pressure and food limitation. The surface sediments are dominated by bacteria, with on average a billion cells per ml. Benthic bacteria are highly relevant to the Earth's element cycles as they remineralize most of the organic matter sinking from the productive surface ocean, and return nutrients, thereby promoting ocean primary production. What passes the bacterial filter is a relevant sink for carbon on geological time scales, influencing global oxygen and carbon budgets, and fueling the deep subsurface biosphere. Despite the relevance of deep-sea sediment bacteria to climate, geochemical cycles and ecology of the seafloor, their genetic and functional diversity, niche differentiation and biological interactions remain unknown. Our preliminary work in a global survey of deep-sea sediments enables us now to target specific genes for the quantification of abyssal bacteria. We can trace isotope-labeled elements into communities and single cells, and analyze the molecular alteration of organic matter during microbial degradation, all in context with environmental dynamics recorded at the only long-term deep-sea ecosystem observatory in the Arctic that we maintain. I propose to bridge biogeochemistry, ecology, microbiology and marine biology to develop a systematic understanding of abyssal sediment bacterial community distribution, diversity, function and interactions, by combining in situ flux studies and different visualization techniques with a wide range of molecular tools. Substantial progress is expected in understanding I) identity and function of the dominant types of indigenous benthic bacteria, II) dynamics in bacterial activity and diversity caused by variations in particle flux, III) interactions with different types and ages of organic matter, and other biological factors."

Result in Brief:

Mid-Term Report Summary - ABYSS (ABYSS - Assessment of bacterial life and matter cycling in deep-sea surface sediments)

The deep seafloor covers more than 60% of the Earth's surface. Deep-sea surface sediments are dominated by bacteria in terms of abundance and biomass of life, and these bacteria play important roles in carbon and nutrient recycling. By remineralization they recycle nutrients back in to the water column, keeping oceans productive. While some bacteria also return a significant amount of sedimentary carbon in the form of CO2, others fix that CO2 and keep it in the deep ocean. However, the major drivers of bacterial community structure and the factors influencing organic matter recycling at the seafloor remain largely unknown. Of the approximately 2000 different types of bacteria per gram of deep-sea sediment, very few are known and hardly any are yet isolated for laboratory studies. The major goals of this project include the identification of: I) the identity and function of the dominant types of indigenous benthic bacteria, II) dynamics in bacterial activity and

diversity caused by variations in particle flux, III) interactions with different types and ages of organic matter, and other biological factors.

In the past two years, we have made significant progress in identifying the most abundant and cosmopolitan types of deep-sea bacteria in contrast to pelagic and deep subsurface environments, as well as their patterns of diversity and variation at regional and global scale (Jacob et al. 2013, Zinger et al. 2014, Ruff et al. in review, Bienhold et al. in prep.). With the targeted development of CARD-FISH probes we are now able to quantify key bacterial groups along environmental gradients and across different deep-sea regions. A few types of Gamma- and Deltaproteobacteria are found everywhere in the deep sea and seem to be key to the community activity due to their high abundance of a few million cells per gram of sediment. Current trials for single-cell genomics of these abundant deep-sea bacteria are underway to reveal their genomic potential and putative role in deep-sea ecosystem functioning. While the enrichment and cultivation of specific bacteria from deep-sea sediments remains a challenge, laboratory experiments at the community level have revealed varying responses of particular bacterial groups to different organic matter sources, which may help in defining their roles and conditions for future enrichment efforts. Field studies show that the deep-sea microorganisms respond instantly to surface-born processes by pelago-benthic coupling (Boetius et al. 2013). Results indicate an impact of changing organic matter quality on bacterial community structure and activity at the deep seafloor, with possible implications for future environmental scenarios. Whether pressure has a significant influence on these results is currently being evaluated based on a range of laboratory experiments. Furthermore, the analyses of samples from benthic lander incubations at the seafloor will help to test the response of bacteria to organic matter input at in situ conditions (e.g. with stable-isotope labeled algae), simultaneously allowing for the tracing of carbon uptake to higher trophic levels.

It remains largely unknown, which fraction of benthic deep-sea bacteria may originate from surface communities, e.g. through the transport on sinking particles. A first comparative characterization of bacterial communities from the pelagic, from sinking particles, and the seafloor, suggests distinct communities in the different environments, but also indicates overlap for certain groups that may be transported from the surface to the bottom and link the pelagic and benthic realms in terms of bacterial diversity. A detailed characterization of dissolved organic matter from sediment porewaters of the Central Arctic was achieved using high-resolution mass spectrometry (FT-ICR-MS). Distinct profiles were evidenced between different stations, indicating fresh and more degraded signatures of DOM in relation to environmental conditions, such as ice cover (Rossel et al. in prep.). Analyses are being expanded to mine data for relationships between specific compounds and bacterial diversity, e.g. using network analyses.

Furthermore, also some of the proposed ad hoc studies could already be addressed, including the investigation of temporal and spatial variations of microbial eukaryotic diversity in deep-sea sediments at the HAUSGARTEN observatory (Jacob et al. in prep.; Degen et al. in review). The team currently addresses the role of the Antarctic and Arctic sedimented ridges in the question of large scale diversity and functional gradients, including the role of dark CO2 fixation in deep sea environments.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://cordis.europa.eu/project/rcn/103849_en.html

Title: **Microbial Ecology of the DEep Atlantic pelagic realm**

Acronym **MEDEA**

Co-ordinator (organisation/affiliation, country): UNIVERSITAT WIEN, Austria.

Duration: 48 months (2011 - 2016)

Link:

Abstract/Description:

"The project aims at elucidating a major enigma in microbial ecology, i.e., the metabolic activity of prokaryotic communities in the deep sea under in situ pressure conditions, rather than under surface pressure conditions, as commonly done. Analysis of the global data set of prokaryotic abundance indicates that about 40% of prokaryotes reside in depth below 1000m depth with a phylogenetic composition different from that in surface waters. Using a recently fabricated high-pressure sampling and incubation system in combination with advanced tools to assess phylogenetic diversity, gene expression and single-cell activity, we will be able to resolve this enigma on a prokaryotic community level as well as on a phylotype level. This detailed knowledge on the distribution of the auto- and heterotrophic activity of deep-sea prokaryotes under in situ pressure conditions is essential to refine our view on the oceanic biogeochemical cycles, and to obtain a mechanistic understanding of the functioning of deep-sea microbial food webs."

Result in Brief:

Mid-Term Report Summary - MEDEA (Microbial Ecology of the DEep Atlantic pelagic realm)

In the MEDEA project, the microbial community composition and the metabolic activity of microbes in relation to the biogeochemistry in deep-water masses of the Atlantic are investigated. Particular focus is put on deciphering the metabolic activity of the microbes under in situ pressure conditions and to decipher the fraction of microbes which are adapted to the deep ocean conditions, i.e, the high hydrostatic pressure. To elucidate the microbial activity under in situ pressure conditions, a high pressure sampling and incubation system has been developed. During two research cruises in the Atlantic, it has been found that the metabolic activity under in situ pressure conditions is reduced by up to 80% compared to decompressed conditions. Currently, metagenomic and metaproteomic analyses are performed to determine whether there are genomic and proteomic features common to all bacteria and archaea adapted to the high pressure conditions of the deep sea.

The impact of the preliminary outcome of the MEDEA project for the marine carbon cycle is therefore, that deep-sea microbes are less active than commonly applied methods suggested. The implication of this study is therefore, that the reported imbalance between organic carbon supply and demand in the ocean is likely an artifact caused by not taking the hydrostatic pressure conditions into account when measuring deep-sea microbial activity.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://cordis.europa.eu/project/rcn/99425_en.html

Title: **From micro-scale interaction networks to ecosystem-level processes in microbial communities**

Acronym MINT

Co-ordinator (organisation/affiliation, country): EIDGENOESSISCHE TECHNISCHE HOCHSCHULE ZUERICH, Switzerland.

Duration: 60 months (2013 - 2018)

Link:

Abstract/Description:

What makes understanding the ecology and evolution of microbes such a unique challenge is the fact that, while the life of microbes unfold at scales of a few micrometers, their impact on ecosystems can be perceived at the scale of meters or kilometers. Our inability to map ecosystem-level processes to the micro-scale interactions that take place in microbial communities is one of the main obstacles hindering the development of mechanistic models that allow us to interpret microbial diversity and predict community dynamics. The overarching goal of this research project is to understand how the biotic interactions between microbes at the scale of micrometers impact microbial community structure and dynamics. By reconstructing the spatial structure and the interaction networks of microbial populations colonizing particles of a few tens of microns in diameter in aquatic environments, the proposed research will build mechanistic models that will serve to i) clarify the structure-function mapping of microbial 'species' in the environment, ii) understand microbial community assembly at the relevant physical scales iii) model how perturbations in the environment lead to micro-scale shifts in community structure and iv) elucidate how biotic interactions influence genome evolution in microbial communities. The results of this project will fill a fundamental gap in microbial sciences, allowing us to connect micro-scale population and community interactions to the global diversity and function of microbial communities.

Results Pertinent to Atlantic Ocean Research Alliance:

US/CA Partners/Interactions: None

Other Transatlantic Partners/Interactions: None

Links: http://cordis.europa.eu/project/rcn/110802_en.html