EUCONEXUS

Co-funded by the European Union

Compendium of Innovations 24–26

by Joint Master Progamme in Marine Biotechnology Students

Academic Research Integration

Academic Research Integration (ARI) is a research-based component of the EU-CONEXUS Joint Master Programme in Marine Biotechnology, where students collaborate on a shared, interdisciplinary research project.

Designed by professors from various specialisations, these projects offer students the opportunity to apply academic research and/or design skills in a practical context. Collaboration across different fields and institutions encourages transversality, allowing each student to contribute their expertise to a truly multidisciplinary joint effort.

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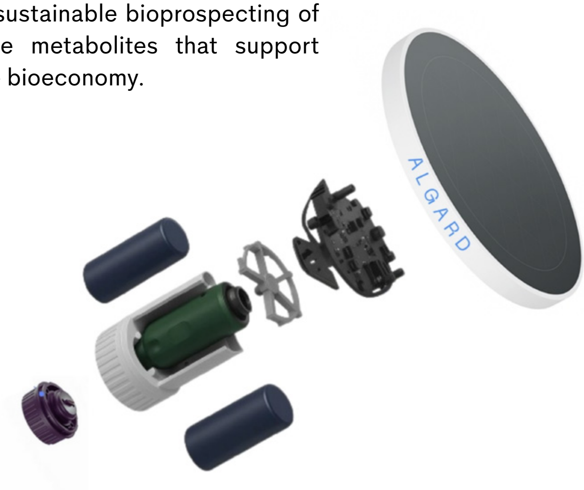
ALGARD

(AI-based ALGal bloom Alert, Response and Detection)

Introduction

Harmful algal blooms (HABs) are a threatening phenomenon for marine biodiversity, aquaculture productivity and coastal economies. Current monitoring tools hardly detect blooms at the strain level and fail to provide sufficiently early warnings, leading to delayed management actions and significant stock losses. ALGARD project aims at addressing this gap by developing a solar-powered underwater microcamera coupled with an advanced AI algorithm capable of real-time species identification, early bloom prediction and direct alerts to aquaculture operators.

In parallel, it builds a reference library linking algal strains to their biosynthetic gene clusters, opening new opportunities for the sustainable bioprospecting of bioactive metabolites that support the blue bioeconomy.



Methodology

36-month Project | TRL3 to TRL7

1. **AI Development:** Training deep learning algorithms on reference databases (CCAC, RRC) for automated cell classification, validated via microscopy and fluorescence.

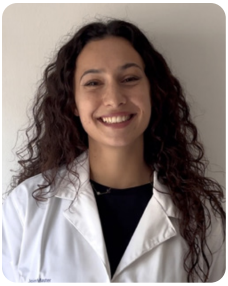
2. **Hardware Engineering:** Designing a solar-powered, autonomous underwater microcamera with microscopy-grade optics, active illumination, and anti-fouling systems.

3. **Field Validation:** Testing the system at 4 European pilot sites (Spain, Croatia, Greece) to evaluate performance across diverse real-world environmental conditions.

4. **Omics Analysis:** Isolating microalgal strains for Illumina genomic sequencing and antiSMASH bioinformatics to identify bioactive Biosynthetic Gene Clusters (BGCs).

Conclusion

The proposed technology aims to achieve high detection accuracy with at least 24-48 hours of warning time, enabling the anticipation of harmful algal blooms, reducing economic losses and allowing the harvesting of the biomass before it becomes a threat. At the same time it supplies industries with sustainably sourced raw material for nutraceutical, cosmetic and biofuel applications. Through the combination of aquatic monitoring, omics-based bioprospecting and stakeholder engagement, ALGARD will contribute to the sustainable protection of biodiversity and aquaculture, in line with Blue Economy and Horizon Europe priorities.



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GreenResilience

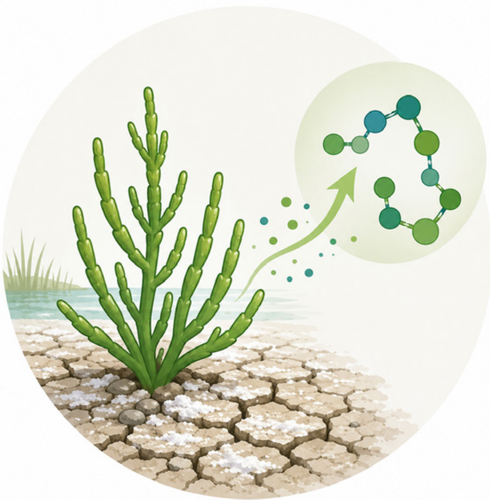
Decoding Nature to Fight Drought in Agriculture

Introduction

- Establish a sustainable, AI-integrated biotechnological pipeline that converts marine salt-marsh biodiversity into novel, climate-smart, market-ready biostimulants for drought resilience.

- Create a flexible, FAIR-compliant digital infrastructure (datasets, libraries, and computational tools) aligned with European Open Science Cloud (EOSC) principles.

- Validate the biostimulant candidates through multi-level testing, including in vitro assays, plant-based trials, and field testing in drought-prone regions across Europe, ensuring real-world efficacy.



Methodology

AI-Integrated Discovery Pipeline

1. **Peptide Generation:** Metagenomic sequencing of salt marsh eDNA combined with database mining (UniProt, MG-RAST) to identify peptide-decoding sequences and build a candidate library.
2. **In Silico Characterisation:** Profiling physiochemical properties (ProtParam), predicting bioactivity (PeptideRanker), and screening for signal peptides and functional domains (SMART, SignalP).
3. **In Silico Screening:** 3D structure prediction (PEP-FOLD/ColabFold), molecular docking with plant receptors (PyMOL/SwissDock), and AI modelling to predict Bacillus expression probability.
4. **Experimental Validation:** High-throughput bioactivity screening, Zea mays (corn) drought-stress assays, and peptide stability testing via HPLC and mass spectrometry.
5. **Peptide Optimisation:** Engineering top candidates using D-amino acids for protease resistance, PEGylation to extend half-life, and structural stapling to enhance bioactivity.
6. **Expression & Scale-up:** Codon optimisation for Bacillus, vector cloning, large-scale fermentation, and formulation delivery for downstream agricultural field trials.

Conclusion

Salt marsh communities, thriving under extreme salinity and water scarcity, possess unique biochemical strategies for stress tolerance. These strategies include the production of functional peptides with promising drought-mitigation properties (Hung et al. 2024).

By applying advanced environmental metagenomics, artificial intelligence (AI), and microbial engineering, GreenResilience unlocks these hidden resources and transforms them into practical agricultural solutions to fight droughts in agriculture.

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JELLYCAP

JELLYfish-based filters for CAPture of microfiber in wastewater from fashion industry

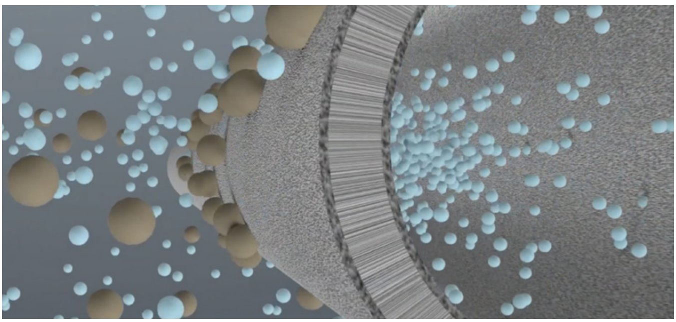
Introduction

Synthetic microfibers released from the fashion industry are a major environmental threat to aquatic ecosystems, with limited biodegradable filtration technologies currently available.

Global synthetic fiber production exceeded 68 million tons in 2020 and is projected to reach 145 million tons by 2030 (1). Early global estimates indicate that up to 35% of microplastics entering the environment originate from domestic textile laundering (2), highlighting the scale of the problem.

Conventional wastewater treatment systems are insufficient to capture these fibers, which ultimately end up in rivers and oceans.

JellyCap is an innovative technology that combines the natural adhesive characteristics of jellyfish mucus with artificial intelligence-based polymer design technology to create environmentally friendly microfiber capture filter media, thereby contributing to sustainable urban wastewater management.



Methodology

1. Mucus Collection & Characterization Jellyfish mucus is collected, purified and analyzed (proteomics, metabolomics and rheology) to identify adhesive components (3).

2. Omics & Feature Extraction Molecular and biochemical mucus traits are integrated into a feature set for modelling.

3. Machine Learning Optimization ML models predict polymer formulations with optimal adhesion, permeability and biodegradability. Jellyfish mucus and smart polymers. Sustainable filter reduces microfiber flow

4. Membrane Fabrication Top formulations are synthesized and combined with mucus to create prototype filter membranes (4).

5. Filter Testing Membranes are tested with microfiber-rich wastewater to measure capture efficiency, flow rate and fouling (5).

6. IterativeRefinementResultsarefedbackintoMLforimprovement, leading prototypes advanced to preliminary scale-up tests.

Conclusion

— Multi-omics dataset of jellyfish mucus identifying key adhesion molecules for microfiber capture.
— AI-designed biodegradable polymers optimized through molecular simulations.
— Prototype filter (>90% microfiber capture) inspired by mucus adhesion and designed for <12-month biodegradation.
— Pilot validation in real industrial wastewater streams with LCA + regulatory assessment.
— Exploitation plan, including stakeholder engagement, IP strategy and roadmap to market.

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MARINAID

AI-driven Bioprospecting of Marine Microbes for Novel Antibiotics and Antivirulence Compounds

Introduction

— Marine microbes hold vast untapped chemical diversity
— Rising antibiotic resistance outpaces current discoveries
— Traditional screening misses rare biosynthetic pathways
— AI accelerates detection of hidden metabolites
— Oceans provide unique bioactive chemical scaffolds

Methodology

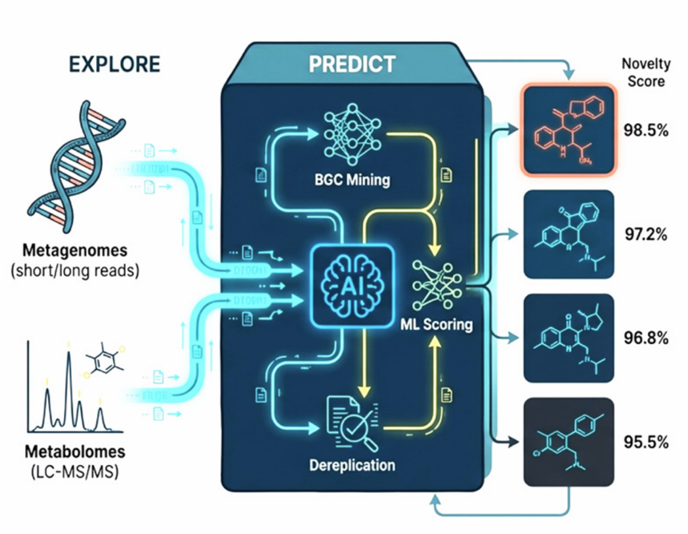
1. Combine genome mining tools (antiSMASH/MIBiG) with machine learning classifiers for activity prediction.

2. Use deep learning models to generate structural hypotheses for predicted metabolites.

3. Apply dereplication algorithms to avoid re-discovering known antibiotics.

4. Conduct targeted extraction, purification and bioassays on AI-selected marine microbes

5. Validate hits through LC-MS/MS, zone of inhibition tests and antivirulence assays



Conclusion

— AI clearly accelerates discovery from marine microbes by cutting unnecessary lab work. Early hits show potential for developing next-generation antibiotics and antivirulence candidates.

— The approach could scale across wider marine habitats and microbial collections. Future steps include structure optimisation, mode-of-action studies and toxicity screening.

— With refinement, this pipeline can form a long-term EU platform for AI-enabled blue-biotechnology drug discovery.

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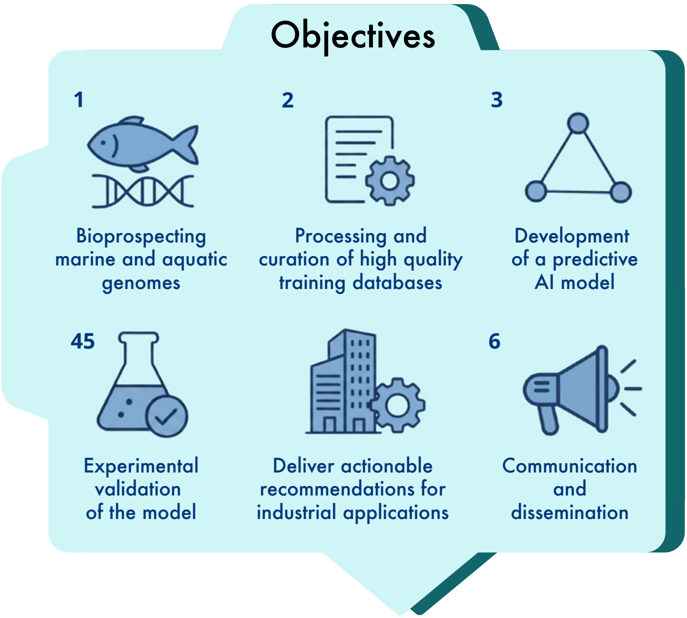
PROTEUS

Platform for Exploitation of marine bioprospected Resources using Omics and industry 4.0 Technologies for Engineered Utilisation Strategies

Objectives

1. Bioprospecting marine and aquatic genomes
2. Processing and curation of high quality training databases
3. Development of a predictive AI model
4. Experimental validation of the model
5. Deliver actionable recommendations for industrial applications
6. Communication and dissemination



Methodology

1. **Data:** Open source genomic databases, marine bioprospected data and active user input are integrated to produce high-quality training dataset for the Proteus AI.

2. **AI:** Trained on this data, Proteus will conduct highly accurate metabolic pathway matching and predictions, based on user imput and feedstock composition.

3. **AI recommendations:** Based upon a variety of selection criteria, Proteus will provide the user with a list of ranked potential pathways to transform the feedstock into valuable industrial compounds.

4. **Experimental validation:** Recommendations are tested via laboratory trials and the resulting data is integrated and processed into Proteus, further increasing it's effectiveness through reinforcement learning.

Results & Impact

1. Plug-and-Play AI platform.
2. Clear applications of marine biomass to biobased chemicals.
3. Push the European bioeconomy and support the Green Deal.
4. Publications and policy briefs.

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SEA CURE

Sustainable Exploration of the Marine Microbiome for CURES Using an Integrated AI-Platform for the Sustainable Discovery of Novel Anti-Neuroinflammatory Compounds

Introduction

Neuroinflammation is a key driver of neurodegenerative diseases, demanding novel therapeutics. Current discovery methods are slow and unsustainable. The SEA-CURE project pioneers an integrated AI-platform to efficiently discover and sustainably produce anti-neuroinflammatory compounds from marine microbiomes. Pilot data confirms our approach: we identified a lead metabolite, SEA-001, from a marine nudibranch. In silico analysis predicted strong binding to the NLRP3 inflammasome, which was validated by in vitro assays showing potent anti-neuroinflammatory activity and low cytotoxicity in human microglial cells. Building on this, the full project will ethically source samples to build genetic and chemical libraries. Our core AI will mine this data to predict biosynthetic gene clusters (BGCs) for bioactive compounds. The most promising candidates will be validated through heterologous expression and bioassays, with fermentative production ensuring a sustainable supply. SEA-CURE will deliver a validated discovery platform, de-risked therapeutic leads, and a framework for sustainable blue biotechnology.

Methodology

1. **Sample Curation:**

— Sample Collection:
Ethical sourcing of marine microbiome samples.

— Extraction:
Processing of natural extracts and chemical library creation.

— Metabolic Analysis: Compound identification and quantification via LC-MS.

2. **In Silico Process:**

— Molecular Docking: Simulating metabolite interactions with inflammatory targets.

— Molecular Dynamics: Analysing binding stability and molecular flexibility.

— ADMET Prediction: AI-driven screening of safety, toxicity, and metabolic profiles.

3. **In Vitro Process:**

— Pathway Discovery: Mapping metabolic routes to define the mode of action.

— Cellular Systems: Efficacy and cytotoxicity testing in human microglial models.

— Animal Models: Final biological validation in vivo to confirm therapeutic potential.

Conclusion

The SEA-CURE project successfully demonstrates a transformative, end-to-end pipeline for sustainable drug discovery. By integrating ethical marine bioprospecting with advanced multi-omics, artificial intelligence, and synthetic biology, we have overcome the critical bottlenecks of traditional biodescovery: speed, efficiency, and sustainability.

The project validates its core hypothesis, proving that AI can effectively prioritize novel anti-neuroinflammatory candidates from diverse marine microbiomes. The identification and preliminary validation of our lead compound, SEA-001, serves as a powerful proof-of-concept. Furthermore, the establishment of a scalable heterologous production process for such compounds ensures that promising discoveries are not hindered by supply limitations, paving the way for a new, eco-friendly model of natural product discovery.

In conclusion, SEA-CURE delivers not just a single therapeutic candidate, but a validated platform and a reusable framework. It marks a significant leap forward for EU research and innovation, directly contributing to a healthier society, a more competitive bioeconomy, and the principles of a circular, sustainable Blue Economy.

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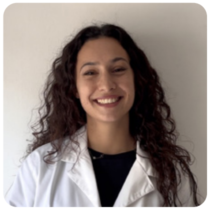
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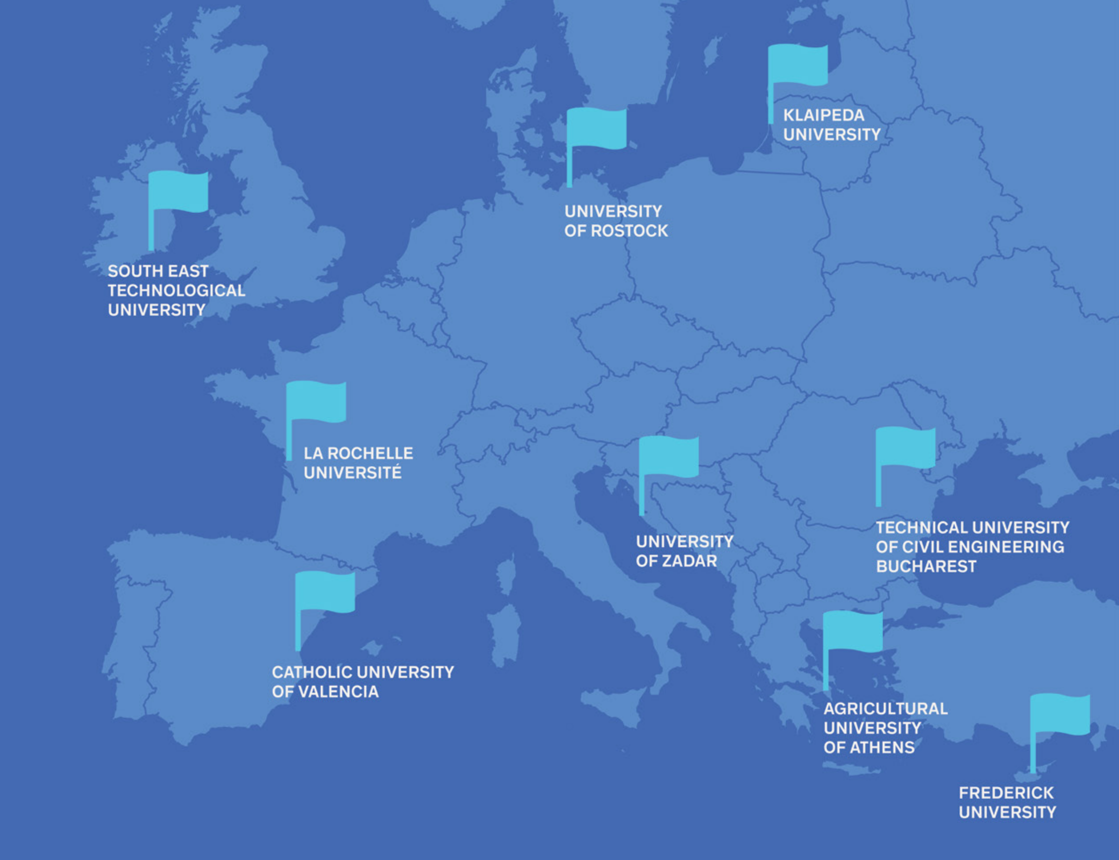

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