Chemical mediation of microbiome assembly in the kelp *Saccharina latissima*: from molecular mechanisms towards microbiome-informed kelp restoration

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Background: A largely overlooked aspect of kelp biology is that these organisms are holobionts, which means that their physiology and development rely, in part, on the complex metabolic interactions they have with their microbial partners. These interactions include nutrient exchanges, but also microbial gardening through compounds such as polyphenols or iodinated compounds, which may attract beneficial partners and protect against pathogens. These symbiotic bacteria, in turn, also produce signaling molecules and bioactive compounds that influence host development, morphogenesis and stress tolerance, and ultimately host fitness.

Despite increasing awareness of kelps as holobionts, restoration and management strategies still largely ignore the chemical and microbial side of kelp holobionts. Embracing this chemical and microbial aspect of kelps represents a great opportunity for designing more effective and resilient restoration strategies.

This interdisciplinary PhD project addresses this topic with methods spanning chemistry, microbiology, phycology, ecology and ocean management, and focuses on the model species *Saccharina latissima*, an important kelp found along the European coastline, although it is in decline in several locations. Particular attention will be given to one of its main bacterial symbionts, the genus *Granulosicoccus*, which is a recurrent and abundant member of the kelp microbiome. It is positively associated with host health and is suspected to play a regulatory role in algal biofilms.

Objectives: The aim of this PhD project is to understand how chemical interactions (host-bacteria and bacteria-bacteria), notably involving *Granulosicoccus*, contribute to microbiome assembly across life cycle stages and how they impact the fitness of the algal host species *Saccharina latissima,* especially in a restoration context. There are 4 main parts of the thesis, each with a specific sub-objective:

1) Characterize microbiome assembly and chemical profiles across kelp life stages and identify co-occurrence patterns.
2) Identify chemical compounds associated with shifts in microbial community composition, including potential signaling molecules or their inhibitors (e.g. quorum sensing).
3) Test how manipulation of the microbiota (inoculation with bacteria) and possibly also the chemical environment, affects host fitness and stress tolerance.
4) Monitor effects of microbiome manipulation and metabolite profiles in natural and restoration contexts, linking chemical interactions to field performance.

Methods: The project will implement methods from several different disciplines. In controlled laboratory conditions, *S. latissima* will be cultivated from spores through gametophytes to juvenile sporophytes under different microbial exposure regimes. These

include sterile-filtered seawater, natural seawater inocula, and targeted bacterial additions, notably *Granulosicoccus* strains. This design will allow assessment of horizontal microbiome transmission and identification of developmental windows during which microbiome composition is most plastic. Microbial community dynamics will be characterized using 16S and 18S rRNA metabarcoding of bacterial, archaeal, and eukaryotic associates. Host fitness will be quantified through growth measurements, photosynthetic efficiency assays, and controlled thermal stress experiments. These experiments will test whether specific microbiome configurations enhance tolerance to elevated temperatures, a key factor in kelp decline under climate change. This part of the project covers the disciplines of microbiology and algal physiology, the expertise of the UMR8227.
In parallel, algal exometabolites and surface-associated compounds will be analyzed using untargeted LC-MS/MS metabolomics. Through the integration of taxonomic and metabolomic datasets via multivariate statistics and network approaches, the project will identify chemical features that are correlated with specific microbial taxa, shifts in community structure or measurable changes in host performance. Particular emphasis will be placed on compounds that are potentially involved in quorum sensing, quorum quenching, and, more generally, microbial competition. The prospective student will benefit from the extensive expertise in natural product chemistry, metabolomics, and chemical ecology available within the MCAM team at the MNHN for this part of the project.

The mechanistic laboratory work will extend to mesocosm systems and field deployments, in collaboration with local aquaculture and restoration initiatives. Microbiome-manipulated juveniles will be deployed on kelp culture lines and in restoration-oriented trials using green gravel substrates. Success of establishment, growth, resistance to epiphyte colonization and microbiome stability will be monitored under semi-natural conditions. This translational component will link molecular mechanisms directly to applied ecosystem management. The prospective student will benefit from the expertise of UBS, which has ongoing projects in kelp restoration, as well as from the close collaboration planned with Dr. Jean-Charles Leclerc, a kelp ecologist at UMR7144 of the Roscoff Biological Station.

Expected Results: The project will clarify the importance of chemical mediation in structuring kelp-associated microbial communities and identify life stages that are particularly amenable to microbiome intervention. By correlating metabolomic signatures with microbiome composition and host fitness, it will generate hypotheses about key compounds that shape beneficial microbial assemblages, which may also have direct applications in kelp cultivation and restoration.
Experimental inoculations will test whether manipulation of specific bacterial partners durably enhances stress tolerance and performance during pilot cultivation and restoration experiments on kelp lines and in mesocosms, respectively. Even if probiotic approaches prove ineffective, defining these limits will provide valuable insight for this rapidly emerging field of research.

Conclusion: This PhD project bridges the fields of algal physiology, microbiology, natural product chemistry, microbial ecology, and restoration ecology. It spans from research at the molecular level all the way to applications in algaculture and restoration, which is relevant for Starfish Axis 03. By extension, it is furthermore relevant for Starfish Axis 05: kelp provides a number of key ecosystem services, so healthier kelp forests would directly result in societal benefits.