

FUNCTIONAL DIVERSITY OF ENDOSYMBIOTIC BACTERIA IN MARINE GREEN ALGAE

Kathryn Morrissey¹, Anne Willems² & Olivier De Clerck¹

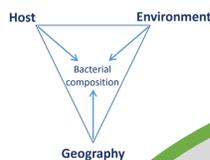
¹Phycology Research Group, Department of Biology, University of Ghent; ²Laboratory of Microbiology, Faculty of Sciences, University of Ghent

Siphonous green seaweeds, such as *Caulerpa*, are among the morphologically most complex algae and also among the most notorious invasive species in many parts of the world. Their ecological success has repeatedly been linked to their association with endophytic bacteria. However, little is known about their functional diversity as well as the principles underlying their assembly. To address how bacteria contribute to the ecological success of *Caulerpa*, a metagenomics and metatranscriptomic approach will be used to analyse the functional diversity of bacterial communities associated with both native and invasive species of *Caulerpa*.

CONCEPT

Bacterial Community structure

Algal-associated bacteria have been identified for many species of algae, including *Caulerpa*. Several factors influence the recruitment of certain bacterial groups. The host itself plays an important role as it's structure and functional requirements determine bacteria able to live with the algae symbiotically. Environmental factors and general geography are also forms of control in the assembly of bacteria. Temperature, light, salinity, wave action and available nutrients all have an effect on the bacterial community structure.



The Hologenome Theory

The host and its associated microbiome work cooperatively acting as a single entity, a "holobiont". The hologenome theory proposes that these organisms indeed coevolved together rather than independently from one another.

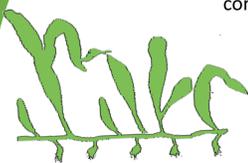
Caulerpa and its associated microbes form a community structure in which the bacteria and algae are dependent on each other for survival.

Essential interactions with microbes may contribute to the ecological success of the algae.



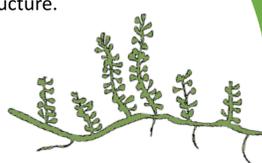
Native species vs. Invasive species – is there a link to the microbiome?

It has been suggested that invasive seaweed has a competitive advantage due to their bacterial community structure.



C. prolifera

VS.

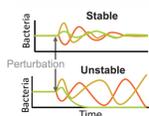


C. cylindracea

Could *C. cylindracea* have a microbial structure that allows it to be highly invasive? What functional diversity does the bacterial community provide enabling *C. cylindracea* to live in different environments?

Recovery and Stability

Abiotic stresses such as changes in temperature, nutrients, light and salinity all have an effect on the microbiome of an individual algae. Changes to this community structure can either be beneficial in which the algae recruits new bacteria to aid in recovery, or the degree of stress can cause an instability of the bacterial community structure within the host. In this case the algae cannot recover normal functioning and therefore dies.



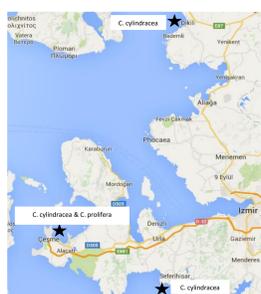
As a matter of Function

The principles of bacterial community assembly have not yet been defined. It has been proposed, however, that the bacterial groups recruited by the host depend more on the function they serve as opposed to species specificity. Studies show algal-associated bacteria have conserved functional diversity across different phylogenetically distinct individuals, whereas the bacterial species composition is highly variable.

EXPERIMENTAL PROCEDURE

Sampling

Three Sample sites were selected in Izmir, Turkey: Dikili, Çeşme & Seferihisar



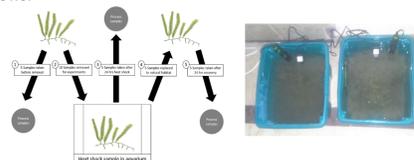
Five Sample units were collected from each site for natural population analysis. Seferihisar and Dikili were limited to only one species being present, whereas Çeşme had both *C. cylindracea* and *C. prolifera* growing naturally.



In situ Experiments

Nutrient experiments:
150g of fertilizer was added to the environment at two locations for both Çeşme and Seferihisar sites. Samples were taken weekly for two weeks after addition.

Temperature experiments:
Samples of both *C. prolifera* and *C. cylindracea* from Çeşme and Seferihisar respectively were heat shocked as follows:



After replacing the seaweed, samples were taken weekly for two weeks after heat shock.

Sample Processing

Samples were washed with sterile artificial seawater and then surface sterilized after swabs of the epiphytes were taken. Samples were frozen at -20°C. DNA will be extracted from frozen samples and metagenomics analyses will be performed to identify the bacterial communities present.



EXPECTED RESULTS

It is expected that a different bacterial community structure will be identified for each location and that each species will have their own unique assembly. We hope to observe initial changes in the bacterial community structure as a result of the abiotic stresses or changes simulated. Furthermore these preliminary results should indicate a potential recovery after abiotic stress. Additional experiments will be carried out in the laboratory as well as in situ to confirm our initial findings.