FUNCTIONAL DIVERSITY OF ENDOBACTERIAL BACTERIA IN MARINE GREEN ALGAE

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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 its 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.

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.

In situ Experiments

Nutrient experiments:
150 g of Nitrolan 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:

Sample Processing
Samples were washed with sterile artificial seawater and then surface sterilized after removal of the epiphytes. Samples were freeze-dried. DNA will be extracted from frozen samples and metagenomics analyses will be performed to identify the bacterial community 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.