

THE EFFECTS OF GRAZING ON THE MICROBIOME OF AN INVASIVE BROWN SEAWEED (*SARGASSUM MUTICUM*)

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The effects of grazing on terrestrial plants, and how they respond to the attack, have long been studied. It is now becoming clear that the entire holobiont (host genome+microbiome) has a role in induced resistance, through the production of secondary metabolism and/or by shifting bacterial community composition from “housekeeping bacteria” to “protective” microbes. Such mechanisms are poorly understood in macroalgae. Some studies have shown that grazers may have a preference for native seaweeds over invasive ones. *Sargassum muticum* is a successful invasive seaweed on European coasts where it has been present for over 40 years and its “ability to avoid predation” has been advanced as one of the reasons for this success. In this exploratory study, we used 16S amplicon sequencing and metagenomics to investigate how the microbiome of *S. muticum* shifts under grazing attack and how that is reflected in the structure and functional profile of associated bacteria. Preliminary results show that the bacterial community structure and predicted functions shift towards specific taxa that are related to secondary metabolite production and oxidative stress responses. With increasing algal aquaculture, a systems biology framework becomes important to understand the role of associated bacteria in seaweed establishment success. By understanding the mechanisms behind this community, it is possible that induced resistance of associated bacteria could be manipulated for biological management in aquaculture to replace chemical treatments.