



ENTANGLED LIFE: OCCURRENCE AND DIVERSITY OF SEAGRASS ASSOCIATED FUNGI BY AN ADVANCED METHODOLOGICAL APPROACH

PhD Student: Sara Frasca/ *Academic Tutor:* Prof. Luciana Migliore

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Fungi are ubiquitous eucaryotic organisms found in nearly every terrestrial and aquatic ecosystem. Fungi perform essential functions in ecosystems, being involved in nutrient cycling, and represent a key functional component. Therefore, understanding the structure and dynamics of fungal communities is important to monitor ecosystem functioning and maintenance of associated services. Many fungi are involved in symbiotic relationships. Commonly, terrestrial plants interact with above- and below-ground fungal symbionts that may influence responses and feedbacks to environmental changes. In fact, within the plant microbiota, mutualistic fungi (and bacterial symbionts) play a crucial role in plant adaptation, promoting growth, nutrient acquisition, and tolerance to abiotic or biotic stress. In terrestrial environment the influence of mutualistic fungi on plant growth and fitness is well-known, conversely, literature on fungal marine symbionts is scant. This is a significant lack of knowledge, considering the increasing human disturbance on the marine environment, especially in the coastal areas. In these areas, the ongoing loss of productive and critical ecosystems, like seagrass meadows, has been documented by several reports. Fungi represent an important component of seagrasses microbial communities, potentially pivotal for their long-term persistence. Consequently, fungal community structure and composition could give information about environmental stress as well as invasive capacity of seagrasses.

The aim of this PhD project is to analyse the leaf or roots/rhizome associated fungal communities of both the Mediterranean endemic *Posidonia oceanica* and the exotic *Halophila stipulacea* from different sites. To reach this goal will be necessary to set up a Next Generation Sequencing protocol (Illumina platform) a technique still needing to be defined on fungi, being the protocols and methods for fungal NGS still in its infancy. A new approach that will be tested is based upon the amplification of the ITS1 - 5.8S - ITS2 rDNA region. To establish a NGS protocols for the identification and analysis of fungal communities open new perspectives, not only in the application of microbial communities as a putative marker of seagrass conservation, together with already known data on associated bacterial communities and phenotypical/biochemical descriptors, but also is a further potential tool to identify biodegradation agents of cultural heritage, such as ancient or modern documents and artifacts. Last but not least, a model system and computational tools to accurately archive the seagrass biological and ecological data will be developed with GT50 S.r.l. company, to allow data comparison with time and across sites.