

Abstract

Many plants are unable to adapt to rapid environmental changes (e.g. salinity, drought, or limited nutrients) and may acquire assistance from microbes that have capacity to increase tolerance of host-plants in stress conditions. By having the right microbes for the condition, the plants are more resilient! Such microbes include endophytes that inhabit inner tissues of the plant without causing symptoms of disease in their host. This plant-endophytic association exists only when chemical equilibrium is maintained between both, making this mutualistic interaction even more unique. Moreover, some endophytes are able to actively or passively demonstrate beneficial effects by increasing plant resistance to biotic and abiotic stresses, as well as enhance nutrient uptake, photosynthesis and facilitate growth in many plants. Though, the endophytic microbiome may comprise a small portion of fungi (compared to bacteria) their contribution can be essential in the plants development. Thus, the main aim of this research is to decipher the community composition of endophytes in halophyte hosts from saline environments and reveal the potential functional capacity of fungal endophytes in host and non-host plants.

In general, plants such as halophytes possess several mechanisms to grow under salinity conditions i.e. ion exclusion, photosynthetic adaptation, ion compartmentalization and translocation at the cellular and tissue level. However, the question arises if their response to salinity could be affected by the soil type, changing climate conditions, growth stage of the plant etc. Hence, this study applied a whole transcriptome approach (*denovo* sequencing) and found the underlying gene response of obligatory halophyte *Salicornia europaea* that differed based on seasonality in comparison to the effects of salinization history at the two salt-affected sites. Further speculations led to *S. europaea*'s adaptability under unfavorable conditions, which may also be derived from their association with specific and unique endophytes inhabiting this halophyte. Accordingly, the next study

implemented metagenomic techniques to explore the endophytic microbiome (bacterial and fungal) in *S. europaea*, and observed contrasting data than that obtained from the results of the host's transcriptome expression. Significant differences with respect to the salinization history at the two sites were found to play a major role in shaping the endophytic assemblages, and there was no effect of seasonality and the halophyte organs (shoot and root). Additionally, the analysis depicts that the endophytic bacterial community influenced the fungal one but not the other way around. It was recognized that the endophytic fungal community in *S. europaea* was unique, concerning that the identified community structure were previously reported as plant pathogens or saprophytes in other plants, and it was interesting to analyze their potential functional traits in their host plant. Consequently, this study also assessed the culturable fungal endophytic diversity and the results showed that most of the isolated fungi belonged to Ascomycota (96%) including dematiaceous fungi and commonly known plant pathogens and saprobes. The fungal strains produced compounds required for plant growth promotion, nutrient exchange, and stress tolerance. Many showed enzymatic activities that are important for plant host colonization and protection from other plant pathogens. Different metabolic traits among similar fungal species isolated from both tested sites were particularly observed. Lastly, this study harnesses these endophytic fungal metabolic traits to examine their effectiveness and compatibility through endophyte inoculation in other non-host grass species. Two selected fungal strains were most effective in plant growth promotion and in increasing grass biomass.

In a future faced with increasing soil salinization, fungal endophytes as bioinoculants behave as a biological trigger to facilitate the plants growth and response to stress more rapidly and strongly as compared to the rhizosphere microbial associations of plants and this could provide continued protection in crops and a solution for crop production in non-cultivable soils.

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