# Perspectives for marine fungal research through the lens of spatial metatranscriptomics

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## Résumé

Macroalgae live in association with microorganisms that influence the development, defense or growth of their hosts or growth of their hosts. The interweaving of these relationships has led to the concept of the holobiont, which encompasses, as a unit of functional biology, the host and its associated microbiota (bacteria, archaea, fungi). The interactions between algae and their microbiota play a central role in the health of the host. Global warming is causing a rise in temperature and an increase in atmospheric concentrations in the oceans, affecting the performance and survival of marine habitats such as algae. The direct or indirect effects of these changing environments on the associated microbiota remains enigmatic. Model species such as Laminaria digitata or Saccharina latissimia whose holobiont is known to consist of fungal and bacterial species (Ihua et al. 2019, Tourcheroche et al. 2019). The approach described extends recent efforts (Giacomello et al. 2017) by capturing information not only from the host and its colonizing prokaryotic microorganisms but also from its colonizing eukaryotic ones, thus achieving to retrieve spatial information from three different coexisting organisms simultaneously. Spatial Metatranscriptomics captures fungal, bacterial and host signals from a tissue section while preserving their spatial structure and thus enabling integrated network analysis of gene expression by the host and its microbiota. The application of spatial metatranscriptomics the holobiont of an algal model species has the potential to identify new fungal protein clusters as well as novel fungal metabolic pathways.

**Mots-Clés:** marine fungi, macroalgae, transcriptomics

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