
Deciphering molecular cross-talks during kelp-endophyte interactions

Catherine Leblanc^{*1}, Miriam Bernard¹, Xing Qikun¹, Nadia Collet¹, Sylvie Rousvoal¹,
Erwan Corre², and Akira Peters³

¹Sorbonne Université, CNRS, Integrative Biology of Marine Models, Station Biologique de Roscoff –
CNRS : UMR8227 – France

²Sorbonne Université, CNRS, ABIMS, Station Biologique de Roscoff – CNRS : FR2424 – France

³Bezhin Rosko, Santec – Bezhin Rosko – France

Abstract

Kelps are important primary producers in temperate to cold northern hemisphere shores and key species in the formation of coastal marine habitats. As sessile organisms, these large brown algae are able to actively respond to external biotic stress by regulating transcription and metabolic pathways in order to cope with various associated micro- and macroflora. In kelps, small endophytic filamentous algae are known to invade stipes and fronds. For instance, the endophyte *Laminarionema elsbetiae* is highly prevalent in European populations of the sugar kelp, *Saccharina latissima*, but has also been found occasionally in *Laminaria digitata*. The presence of algal endophytes coincides with morphological changes in the hosts- such as dark spots, galls, twisted stipes and deformation of the blades. However, little is known about the molecular and chemical bases of this interaction, its physiological impacts on the hosts and its ecological role. To get further insight into host-endophyte interactions, we set-up an experiment to monitor the impact of the endophyte on growth of laboratory-grown kelp sporophytes. First results revealed that co-cultivation of *L. elsbetiae* does not induce strong oxidative responses of its main host *S. latissima*, neither affect its growth. On the contrary, growth of the occasional host *L. digitata* decreased significantly when co-cultured with the endophyte within less than a week. The molecular detection of endophytes associated with the kelp tissue by qPCR showed a lower prevalence in *L. digitata*, suggesting that defence reactions against *L. elsbetiae* were triggered in *L. digitata*, but not in *S. latissima*. Large-scale transcriptomic analysis of endophyte-induced early responses in both kelp species will help us to decipher the molecular and metabolic cross-talks during kelp-endophyte interactions.

*Speaker