
Diversity patterns of the microbiota associated to *Laminaria digitata*, a kelp with an iodine defense metabolism

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Abstract

The microbiota of the seaweed holobiont plays an important role in host health and physiology and it is affected by interactions with the host. The kelp *Laminaria digitata* possesses a unique defense metabolism, associated with the production of toxic iodine compounds. *L. digitata* gradually concentrates iodine in its tissues depending on age, thallus areas, and season. Iodine is highly concentrated in the peripheral cell layers, creating specific niches for the associated microbiota during iodovolatilisation. This microbiota is thus expected to vary along the alga according to these characteristics. Here, we investigate (*i*) the acquisition mode of the associated microbiota of *L. digitata*, (*ii*) the stability of the microbiota according to different maturation stages of the sporophyte, (*iii*) correlations between fluctuations of the microbiota according to varying concentrations in iodine in the algal tissues. The associated microbiota of cultivated and harvested wild plantlets, blade and stipe samples from four wild adult *L. digitata* sporophytes was determined using metabarcoding. Analyses of the microbial community composition and structure showed that the microbiota from the field plantlet was different from the laboratory plantlet but similar to the blade, and the four stipe samples strongly clustered together. This suggested (*i*) an environmental acquisition of the associated microbiota; (*ii*) the relative stability of a core microbiota at the kelp blade surface, and (*iii*) an associated microbiota specific to the thallus area. In the context of *L. digitata*'s defense metabolism, cross-kingdom interactions in the kelp holobiont may determine the composition and the distribution of the associated microbiota.

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