
Preliminary metabolomic approach on structure of the bacterial community of the marine diatom *Haslea ostrearia*

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Résumé

The marine diatom *Haslea ostraria* produces a water-soluble blue-pigment named marenine of economic interest. But the lack of knowledge of the ecological conditions, under which this microalga develops in its natural ecosystem, more especially bacteria *H. ostrearia* interactions, prevents any optimization of its culture in well-controlled conditions.

The structure of the bacterial community was analyzed by PCR-TTGE before and after the isolation of *H. ostrearia* cells recovered from 4 localities, to distinguish the relative part of the biotope and the biocenose and eventually to describe the temporal dynamic of the structure of the bacterial community at two time-scales.

The differences in genetic fingerprints, more especially high between two *H. ostrearia* isolates (HO-R and HO-BM) showed also the highest differences in the bacterial structure as the result of specific metabolomics profiles. The non-targeted metabolomic investigation showed that these profiles were more distinct in case of bacteria-alga associations than for the *H. ostrearia* monoculture

Here we present a Q-TOF LC/MS a metabolic fingerprinting:

- to investigate differential metabolites of axenic versus non axenic *H. ostrearia* cultures.

- to focus on the specific metabolites of a bacterial surrounding associated with the activation or inhibition of the microalga growing.

The Agilent suite of data processing software makes feature finding, statistical analysis, and identification easier. This enables rapid transformation of complex rawdata into biologically relevant metabolite information.

Mots-Clés: *Haslea ostraria*, co, culture, microalgae, marine diatom, TTGE, high resolution mass spectrometry, untargeted metabolomics

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