

Preliminary metabolomic approach on the bacterial structure community of Haslea ostrearia Florence Mondeguer¹*, Alexandra Lépinay^{2,3}, Hervé Capiaux⁴, Vincent Turpin², Thierry Lebeau³

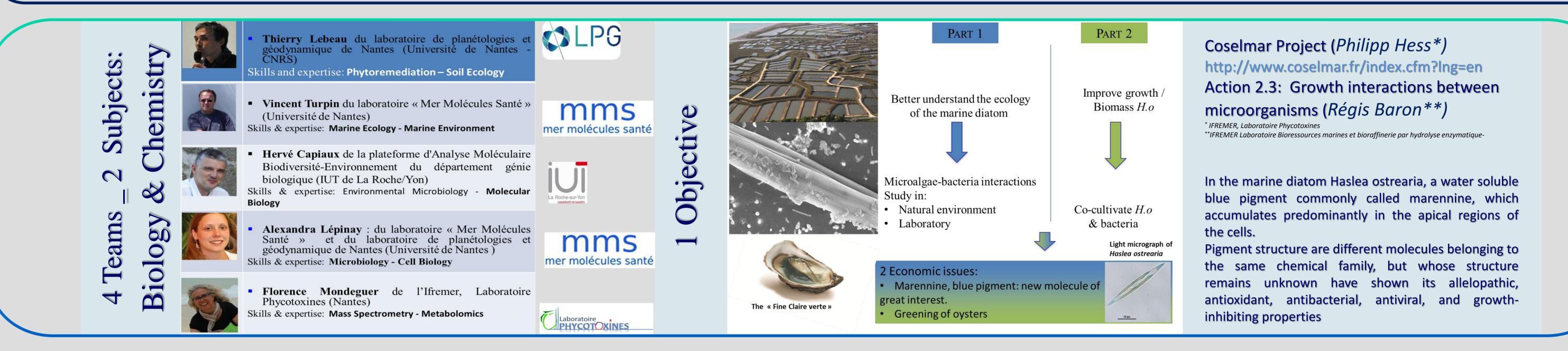
¹Ifremer, Laboratoire Phycotoxines, 44311 Nantes Cedex3, France florence.mondeguer@ifremer.fr ² MMS EA 2160, Faculté Sciences et Techniques, Université de Nantes - 44322 Nantes Cedex, France E vincent.turpin@univ-nantes.fr E-mai ² MMS EA 2160, Faculté Sciences et Techniques, Université de Nantes - 44322 Nantes Cedex, France alexandra.lepinay@univ-nantes.fr E-mai ³ UMR LPGN 6112 CNRS, Université de Nantes - 44322 Nantes Cedex, France thierry.lebeau@univ-nantes.fr E-mail ⁴Plateforme d'Analyse Moléculaire Biodiversité-Environnement- 85035 La Roche sur Yon, France herve.capiaux@univ-nantes.fr E-mai

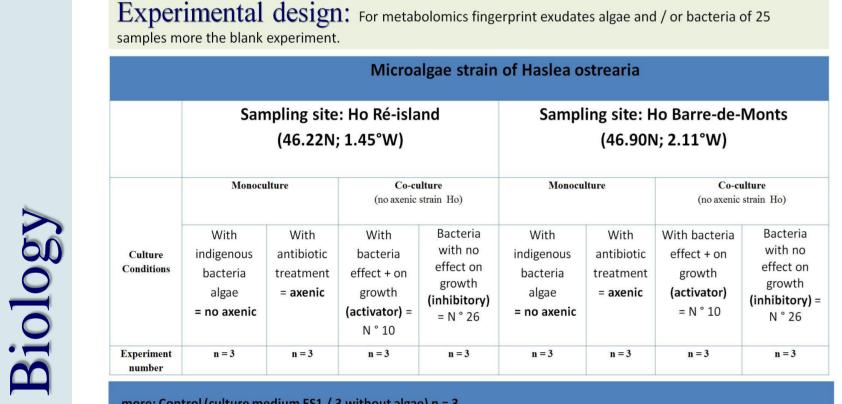
Keys Words: Haslea ostrearia, marine diatom, co-culture microalgae, bacterial community, TTGE, High Resolution Mass Spectrometry, untargeted metabolomics

Introduction:

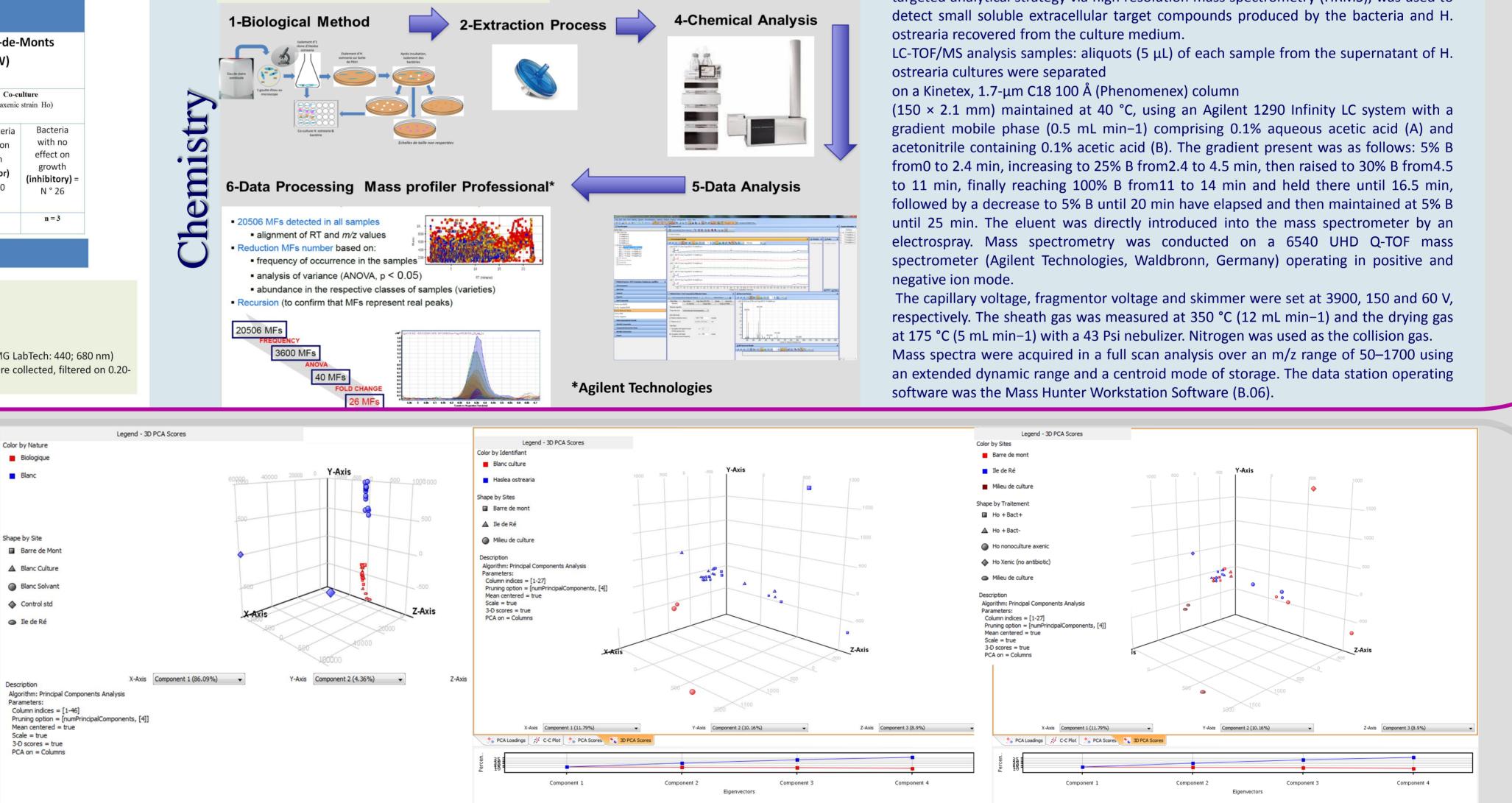
Haslea ostrearia (HO) produces a water-soluble, blue-green pigment, called marennine, with proven economic benefits (as a bioactive compound used to green oysters, which improves their market value). The structure of the bacterial community was analyzed by PCR-TTGE before and after the isolation of H. ostrearia cells recovered from 4 localities, to distinguish the relative part of the 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 from Ile de Ré and Barre de Mont (HO-R & HO-BDM) 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.





Metabolomics Workflow



Barre de Mont, Co-cultu

Frequency with cut-off percentage: 100.0 156 entities

Untargeted metabolomic profiling UHPLC-ESI-QToF, through implementing a nontargeted analytical strategy via high resolution mass spectrometry (HRMS), was used to

pre: Control (culture medium ES1 / 3 without algae) n = 3

Material and Methods:

• Algae and co culture bacteria algae were grown in wells plate, six days at 3 · 103 cells mL-1

n = 3

- Daily monitoring of algal growth (2 times per day) by measuring the fluorescence of chlorophyll (BMG LabTech: 440; 680 nm) • After 6 days of culture (during the exponential growth stage), 200 μL of the culture supernatant were collected, filtered on 0.20-
- μm PTFE membrane filters and frozen at-80 °C prior to fingerprint acquisition.

n = 3

Here we present a Q-TOF LC/MS metabolomic fingerprinting approach

- 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 raw data into biologically relevant metabolite information.

This comprehensive study analyzes and search compounds of interest by focusing on the following comparisons. HO-R and BM clones separated and the removing effect of ES medium 1/3 is done 1.Co-culture inhibitory HO-bacterium vs. activating co-culture HO-bacterium growth of HO

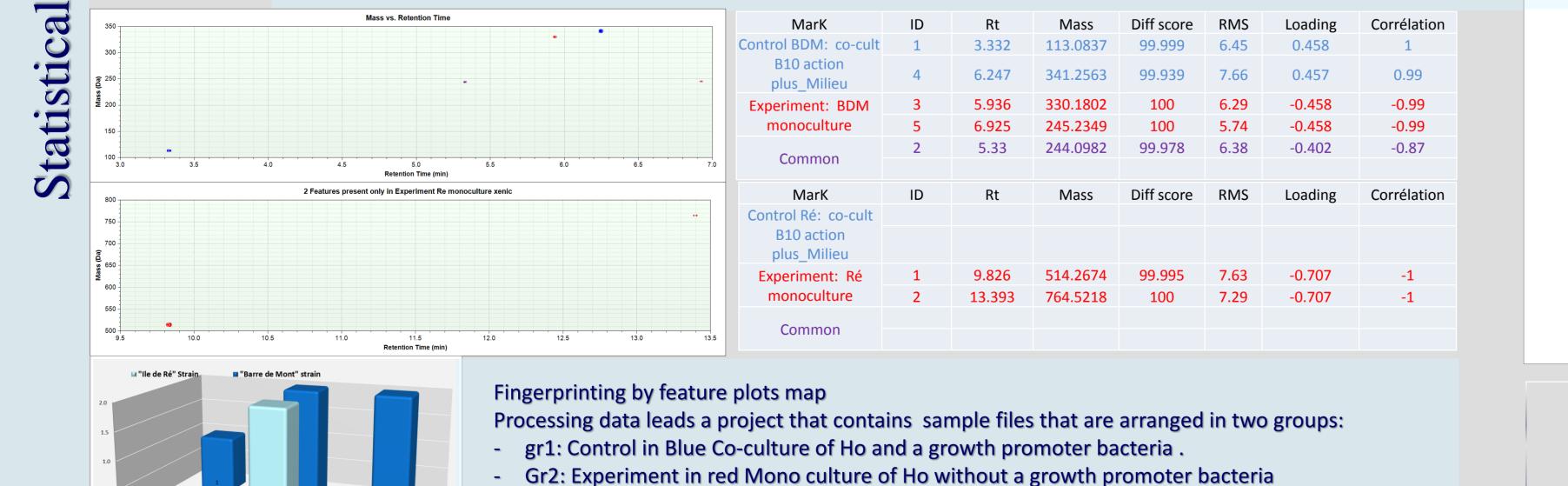
2. Monoculture xenic vs. HO-activating bacteria co-culture

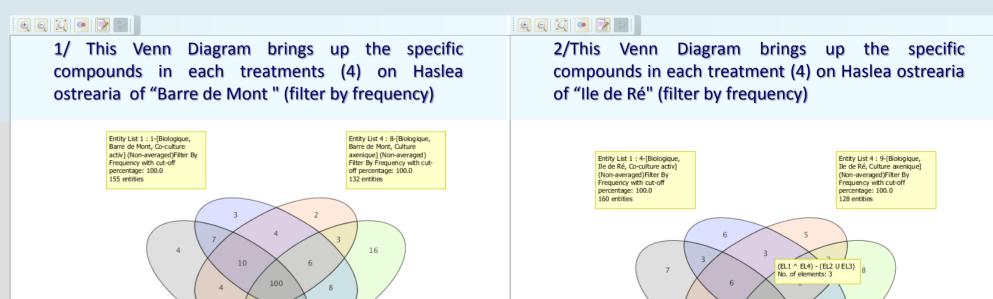
n = 3

3. Monoculture xenic vs. inhibiting HO-bacteria co-culture

parameters.

Specific B10 Bacteria action plu

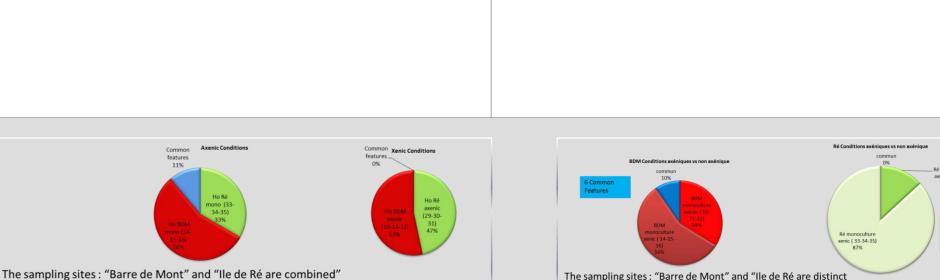




ntity List 3 : 6-[Biologique arre de Mont, Monocultu

(Non-averaged)Filter By Frequency with cut-off percentage: 100.0

Results Best



tes : "Barre de Mont" and "Ile de R

Entity List 2 : 5- [Biolog Ile de Ré, Co-culture in (Non-averaged)Filter By Frequency with cut-off percentage: 100.0 155 entities

n cut-off percentage: 100

More informations with these References:

Lepinay Alexandra, Capiaux Hervé, Turpin Vincent, Mondeguer Florence, Lebeau Thierry (2016). Bacterial community structure of the marine diatom Haslea ostrearia. Algal Research, 16, 418-426. http://doi.org/10.1016/j.algal.2016.04.011

Created method set to features (or compounds) finding, alignment, normalization, and filtering

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