



## Using metabolomics to highlight biomarkers of (non)-exposure of mussels and oysters to phycotoxins

Valentin Derrien, Justine Massias, Axel Raux, Amélie Derrien, Killian Guyomard, Lionel Dégremont, Virginie Le Razavet, Florence Mondeguer, Yann Guitton, Damien Réveillon

### ► To cite this version:

Valentin Derrien, Justine Massias, Axel Raux, Amélie Derrien, Killian Guyomard, et al.. Using metabolomics to highlight biomarkers of (non)-exposure of mussels and oysters to phycotoxins. *Analytics* 2022, Sep 2022, Nantes, France. 2022. hal-04321042

**HAL Id: hal-04321042**

**<https://hal.science/hal-04321042>**

Submitted on 4 Dec 2023

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Valentin Derrien<sup>1,2</sup>, Justine Massias<sup>2</sup>, Axel Raux<sup>2</sup>, Amélie Derrien<sup>3</sup>, Killian Guyomard<sup>4</sup>, Lionel Dégremont<sup>5</sup>, Virginie Le Razavet<sup>4</sup>, Florence Mondeguer<sup>1</sup>, Yann Guitton<sup>2</sup>, **Damien Réveillon<sup>1\*</sup>**

<sup>1</sup>Ifremer, PHYTOX, laboratoire METALG, F-44000 Nantes, France; <sup>2</sup>Oniris, INRAE, LABERCA, 44300 Nantes, France; <sup>3</sup>Ifremer, Unité Littorale, Laboratoire Environnement Ressources - Bretagne Occidentale, F-29185 Concarneau, France; <sup>4</sup>Ifremer, EMMA, Plateforme Mollusques Marins de Bouin, F-85230 Bouin, France; <sup>5</sup>Ifremer, ASIM, F-17390 La Tremblade, France

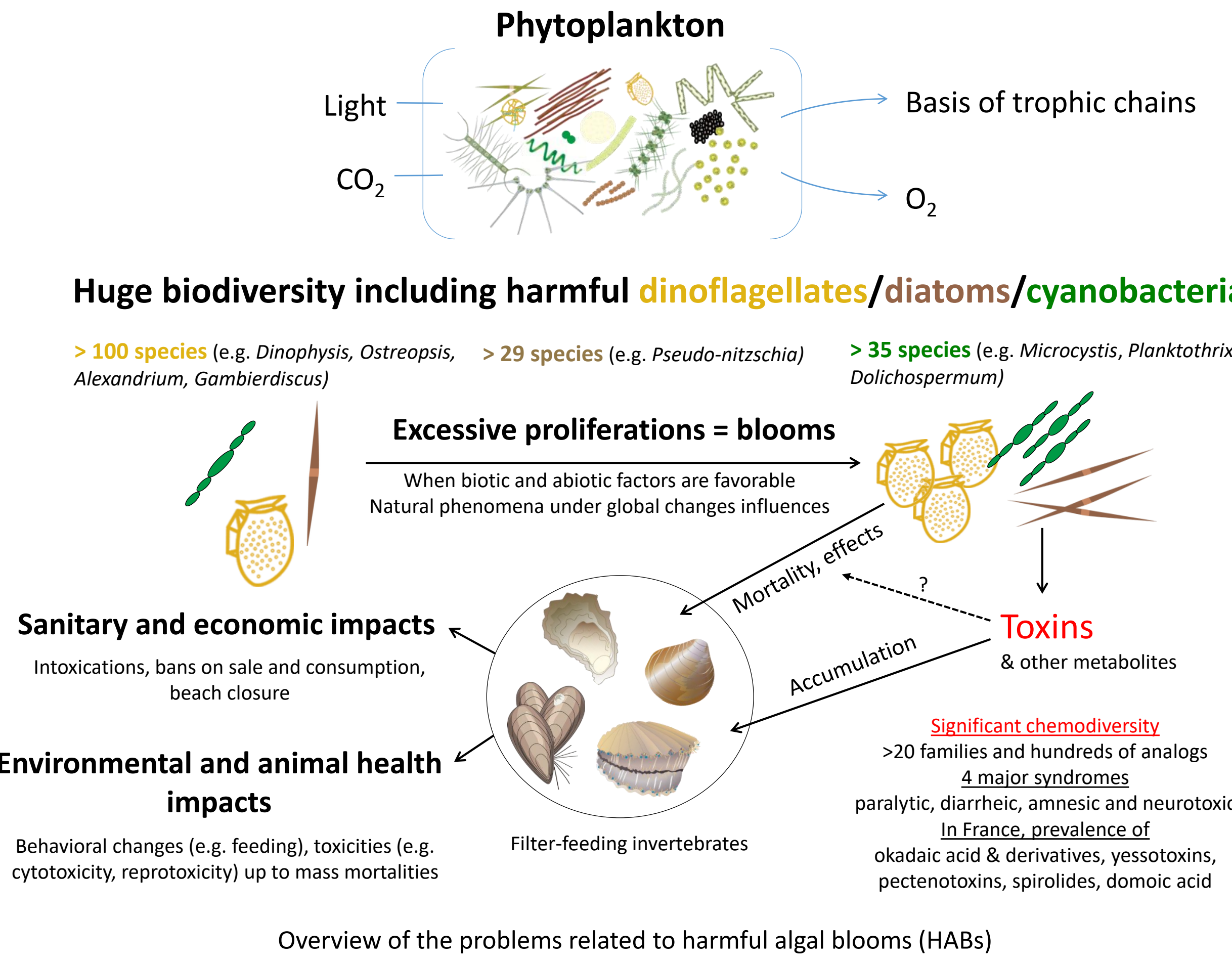
## Context

- Some micro-algae species produce toxins that can cause food poisoning in humans through the consumption of contaminated shellfish
- Monitoring programmes have been implemented to protect the consumers → quantification by targeted analyses using LC-MS/MS
- Alternatively, we could try to consider the consequences of a contamination by phycotoxins on the global metabolite expression of bivalves to find biomarkers of exposition or non-exposition → **metabolomics?**

**Objectives:** Innovate for the assessment of shellfish safety via a double approach: metabolomics + molecular network  
Highlight **biomarkers** characteristic of a (non)-exposure of bivalves to phycotoxins

**Strategy:** Use the latest generation of high resolution mass spectrometers and bioinformatic tools, in collaboration with the metabolomic platform of a leading partner in food chemical safety (**LABERCA**).

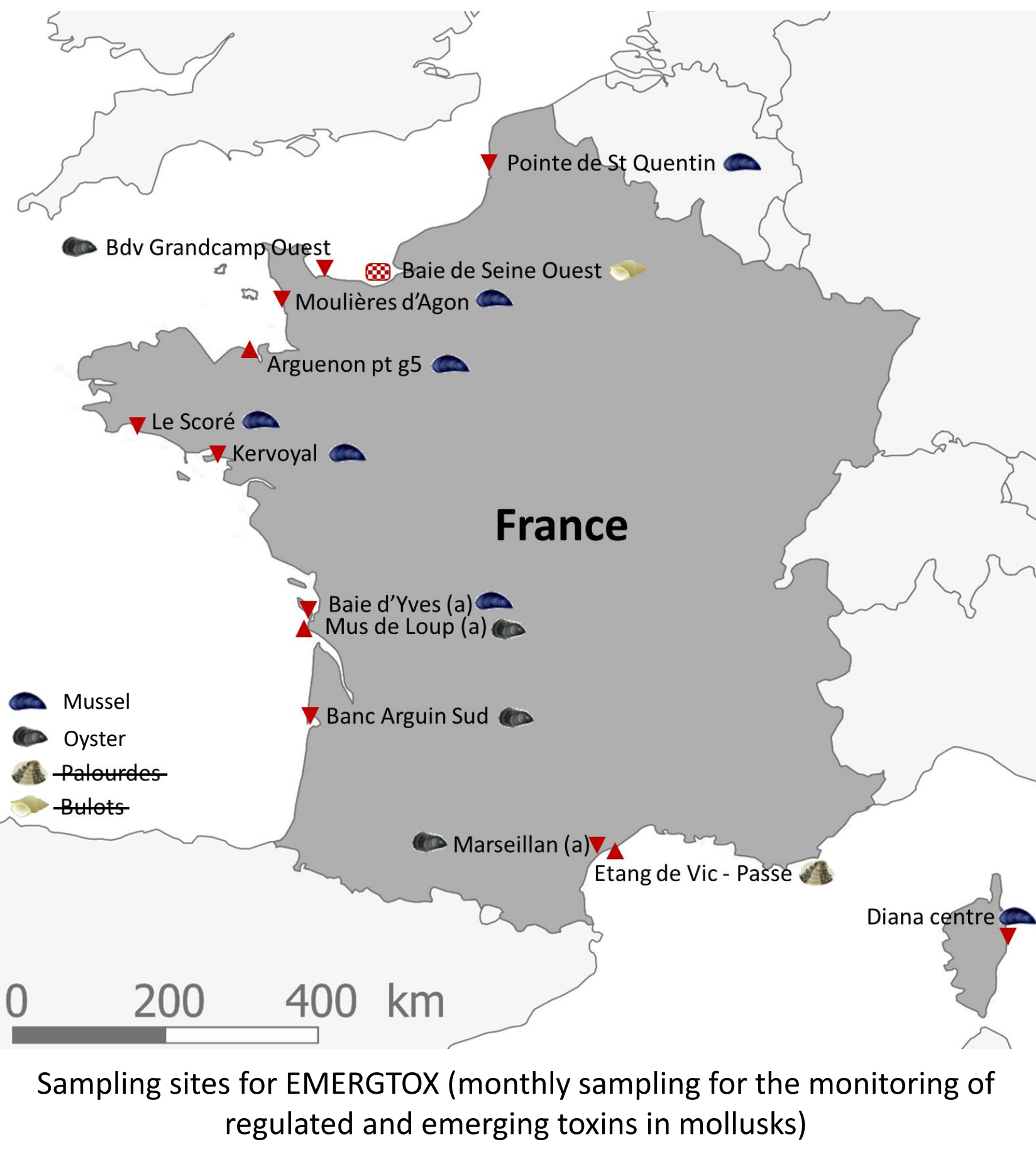
**Background:** Based on preliminary results suggesting metabolites characteristic of non-exposure in mussel (Mondeguer et al., 2012, **Ifremer** - **LABERCA** collaboration) and on the implementation of a monitoring method based on biomarkers obtained from untargeted metabolomics by **LABERCA**



Overview of the problems related to harmful algal blooms (HABs)

## Metabolomic approach

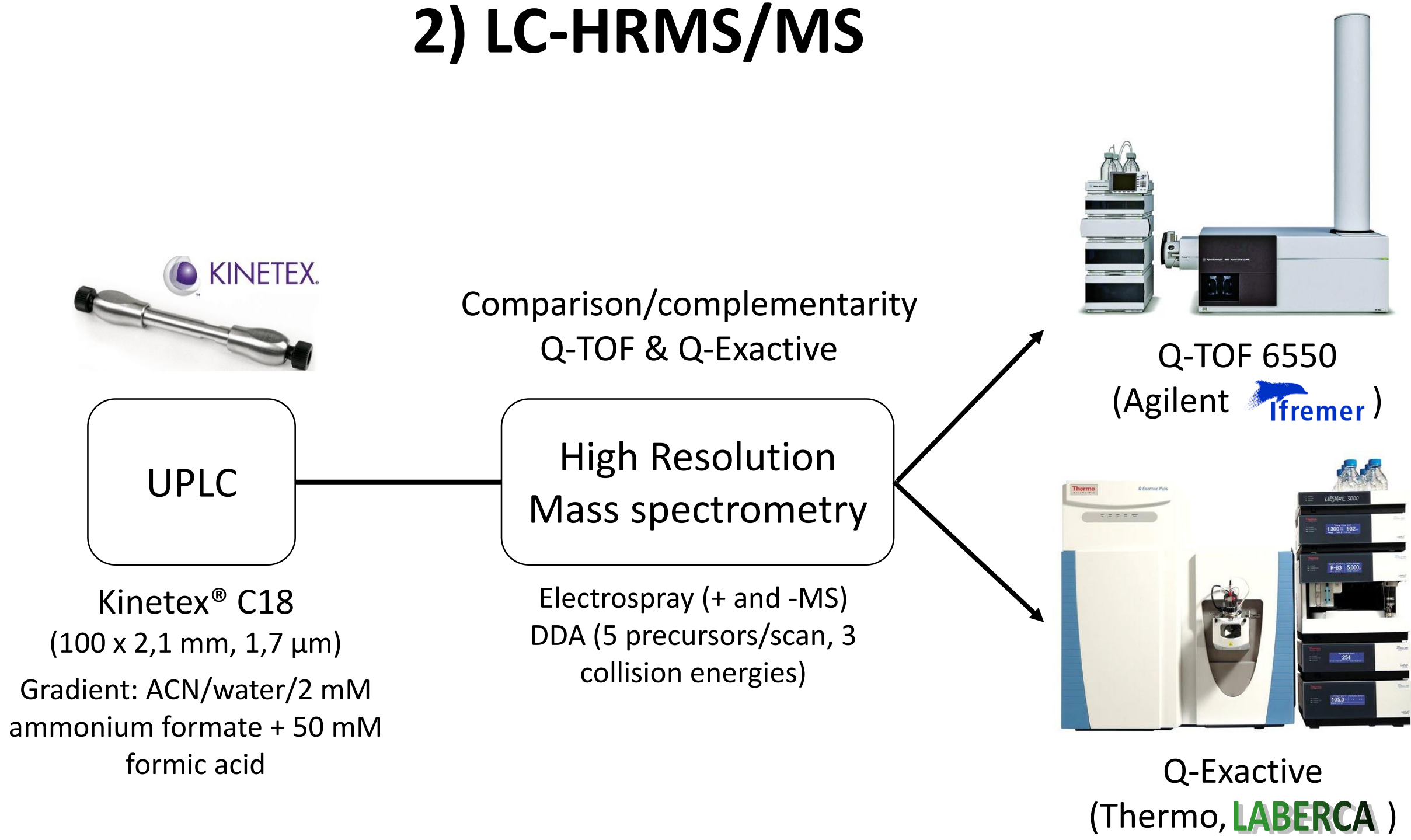
### 1) Samples and experimental design



- Samples available from:**
- EMERGTOX monitoring programme:
  - 459 bivalves harvested between 2018 and 2021 (73%)
  - Metadata: quantification of 44 phycotoxins
- Organisms maintained in controlled conditions at the experimental platform of Bouin (= “**healthy**”)
- Experimental design:**
- Healthy** vs. **contaminated** (all toxins considered)
- ≥ 1000 µg/kg for
  - ≥ 200 µg/kg for
- Characteristic of natural contaminations
- Trying to consider the *in situ* physiological status (resting, sexual maturation, spawning, fattening)

Selection of 50 and 45 (Filtered MeOH extracts of digestive glands)

### 2) LC-HRMS/MS



- Untargeted metabolomics (following the guidelines of Broadhurst et al., (2018))**
- Analytical and extraction process blanks, quality controls
  - Standard reference materials (4 IS spiked in all samples + mix of 10 phycotoxins)
  - Appropriate order of analysis (randomized for samples)
  - Data-dependant analysis

### 4) Statistical analyses and selection of ‘biomarkers’

Supervised orthogonal partial least squares – discriminant analyses (OPLS-DA) were constructed (and validated by permutation tests) using the classes **healthy** and **contaminated**.

### 3) Data processing

