Microbial balance and triggering of recent mussel mortality events in France: Is there a link?

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DE LA TRANSITIO

ÉCOLOGIQUE ET SOLIDAIRE

1-Context

Since the spring of 2014, the mussel farming of Charente-Maritime and Vendée has experienced an unprecedented crisis; mass mortality events of blue mussel (M. edulis) have affected livestock areas, decimating up to 100% of production in some farming areas (Béchemin et al., 2015). In this context, the MORBLEU research project (DPMA-Ifremer agreement) was initiated to explore potentially aggravating factors, associated or correlated with mortality of mussels.

5-Bacterial diversity during the initiation of mortality (2015)



- Monitoring of bacterial communities (through an NGS metabarcoding approach) confirms that this period of initiation of the mortality phenomenon is also marked by changes in bacterial equilibrium (Figure 3).
- Additionally to a decline in taxonomic richness, the relative abundances of the most dominant

2-Objective

- Rapidly after the first mortality events in 2014, search for infectious agents in moribund mussels revealed, among other things, the presence of bacteria capable of inducing mortalities (Bechemin et al., 2015).
- The aim of this work is to support the hypothesis that these episodes can be linked to an evolution of microbial communities (water column and mussel microbiota).

3-Evolution of mortalities of blue mussels



FIGURE 1: Evolution of spring mortality rates at different stations of Charentais Sounds

The historical of zootechnical monitoring of the Charentais Sounds mussel farming areas (Remoula and Mytilobs networks) shows that the spring mortality episodes of mussels encountered since 2014 are abnormally high, particularly at the Filière station (Figure 1).

Abu

FIGURE 3: Winter and spring evolution of the relative abundance of OTUs (operational taxonomic unit, 16S rRNA gene) and classes of bacteria at the Filière station in 2015.

bacterial taxa (OTU) decline in favor of more confidential taxa.
A decrease in the relative abundances of the class of *Alphaproteobacteria* in favor of *Flavobacteria* class is shown.

6-Evolution of the environment of the Breton Sound

Dim 1 (42.75%)

FIGURE 4: Results for the compromise of the Partial Triadic Analysis (PTA); from 2000 to 2016, years in color correspond to years with high

- Discrimination of years based on indices of phytoplankton diversity and general climatic descriptors (atmospheric temperatures and cumulative rainfall) makes possible to group the years with high level of mortality.
- This group of years is characterized, in winter and spring, by weather rather hot and rainy, and diversity indices rather

Whatever the year, the initiation of this phenomenon of mass mortality of mussels occurs initially on the sector of the long-line mussel culture farms in Breton Sound, the most marine area of Charentais Sounds.

4-Phytoplankton diversity at the time of mortality initiation

- Particular events of the microbial dynamic (taken from phytoplankton flora readings of the Rephy network) occur during the (estimated) periods of onset of mortality, both in 2014 and 2015 and 2016 (Figure 2).
- A simultaneous decline in indicators of phytoplankton biodiversity (generic richness and equitability) then appears relatively concomitant with the initiation of the phenomenon of

level of mortality.

low (Figure 4).

7-Conclusion

- Although there is a relative simultaneity between certain events of the microbial dynamics (imbalances) and the first spring mussels mortalities, no causal link between these two elements is currently established.
- Our observations contribute to the hypothesis of a microbial origin (pathogenic bacteria) responsible for the spring mortality of mussels, among those advanced since the emergence of the phenomenon.
- Whatever the temporal window of observation (seasonal, or medium-term historical), a link between the evolution of microbial balances and the spring mortality of mussels gets clear.
- If causal links existed, in addition to the fact that an organism or a group of organisms could be identified as responsible for mortality (seasonal dimension), the emergence of this phenomenon could have its origin in the evolution of Microbial communities of shellfish ecosystems under the action of more global constraints (historical dimension in the medium-term, such as warming change). The holistic approach carried out in the MORBLEU project will contribute to describe potential links between dynamic equilibrium of the planktonic microbial communities and "health" of mussel

FIGURE 2:Winter and spring evolution of diversity (Generic richness and equitability) at the Station "Filiere" from 2014 to 2016

mortality (Travers et al., 2016).

Data and processing

Data sources

- Mussel mortality : Remoula and Mytilobs recordings (Ifremer Networks / Quadrige)
- Meteorology (atmospheric temperature and precipitation) : Chassiron station (Météo-France / Synop)
- Phytoplankton abundances from the REPHY network (Ifremer / Quadrige)
- eDNA metabarcoding (NGS) of prokaryotic plankton (16S rRNA gene) analyzed as part of the MORBLEU 2015 project

Data processing

- The diversity indices (Richness and Equitability) are calculated on the basis of the aggregated phytoplankton abundances at the genus level.
- The years 2000 to 2016 are discriminated by a partial triadic analysis based on environmental variables (climate and diversity) : matrix (years X variables) repeated from February to June, forming the cube of data analyzed.

livestocks.

Acknowledgments

Our thanks go to Alexandre Brunet, James Grizon, Jean Luc Seugnet, Patrick Soletchnik and Delphine Tourbiez for their support in the Morbleu project.

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