

Exploring cryptic Labyrinthulomycetes (Stramenopiles) diversity in *P. olseni*-infected clam populations along the French Atlantic Coast

Elisa Chailler¹, Morgan Perennou², Sarah Itoïz², Héliaz Le Bayon¹, Morgan Smits¹, Evelyne Derelle², Adeline Bidault², Nelly Le Goïc², Philippe Soudant², Aurélie Chambouvet¹

1 Sorbonne Université, UMR 7144, Station Biologique de Roscoff, Place Georges Teissier, 29680 Roscoff, France.

2 Univ Brest, CNRS, IRD, Ifremer, LEMAR, Plouzané, France.

Introduction

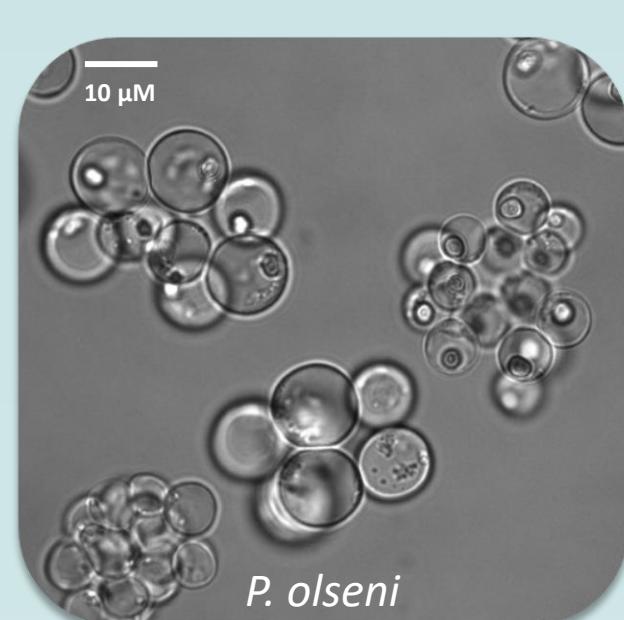


Manila clam (*Ruditapes philippinarum*)

- Imported to Europe in 1972 for aquaculture purposes
- Found along the French Atlantic coast

Host to several phyla of micro-eukaryotic organisms, including *Perkinsus olseni* (Alveolata):

- Exotic unicellular parasite introduced in Europe in 1972
- OIE-listed, causing clam mortalities in Portugal and Spain



What is the diversity of micro-eukaryotic organisms associated with *P. olseni* infected manila clams?

We will use a culture-dependant approach to explore this diversity

Results

1. Culture and DNA extraction using *Perkinsus* broth media

7 and 6 cultured strains belonging to the Labyrinthulomycetes were obtained following a sampling campaign in Arcachon Bay respectively in 2018 and 2022.

Labyrinthulomycetes (Stramenopile) are protists, mostly saprophytes but some are parasitic (QPX, MCPX). Their diversity is greater than currently described.

2. Genetic characterization of associated eukaryotic culture

3. Exploring the presence of underdescribed clusters of Labyrinthulomycetes along latitudinal French coastline

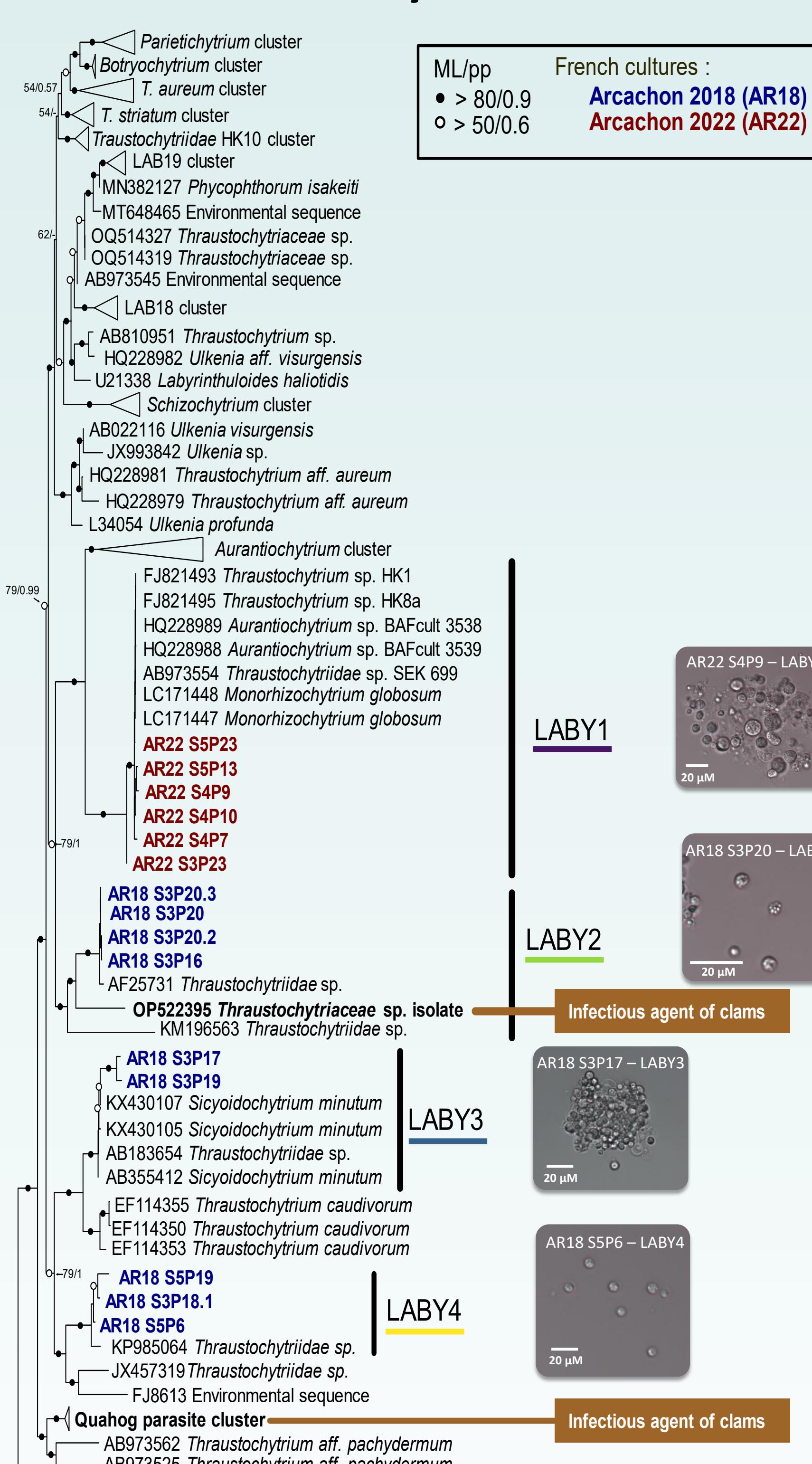


Fig 1: ML phylogenetic tree of Labyrinthulomycetes SSU rDNA focusing on groups recovered from cultured clam tissues samples. The phylogeny is estimated from a masked alignment consisting of 115 taxa and 1,112 characters. ML bootstrap (1,000 pseudoreplicates) and Bayesian posterior probability (1,000,000 generations) values are added to each node. 4 sequences were used as outgroup (*Oblongichytrium* sp., *Amphitrema wrightianum*)

Methodology

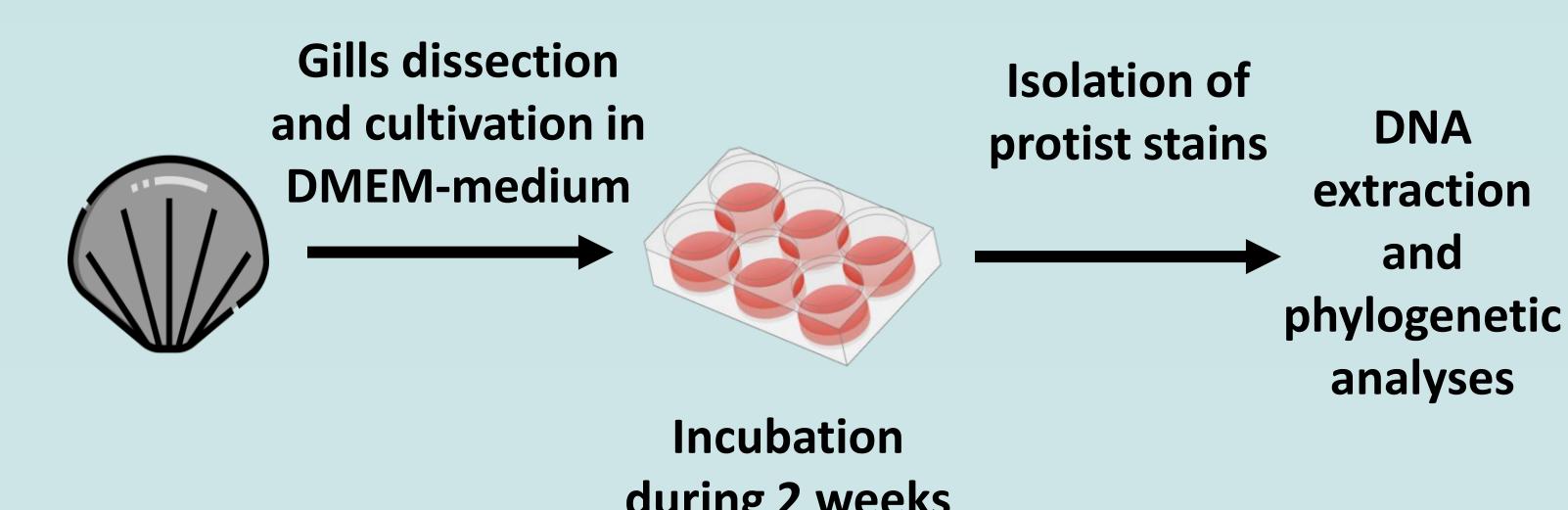
1. Sampling where *P. olseni* is recurrent

50 clams harvested per site in the Arcachon Bay, 63 in Brest and 46 in Noirmoutier (France)

Site	<i>P. olseni</i> prevalence
Brest	38%
Noirmoutier	35%
Lanton (Arcachon)	60%
Piquey (Arcachon)	68%
Andernos (Arcachon)	80%

Table 1: Prevalence of *P. olseni* in 3 sampling sites in Arcachon Bay in 2022, in Brest and Noirmoutier in 2023

2. Culture and DNA extraction using *Perkinsus* broth media



4. Exploring the presence of underdescribed clusters of Labyrinthulomycetes along latitudinal French coastline

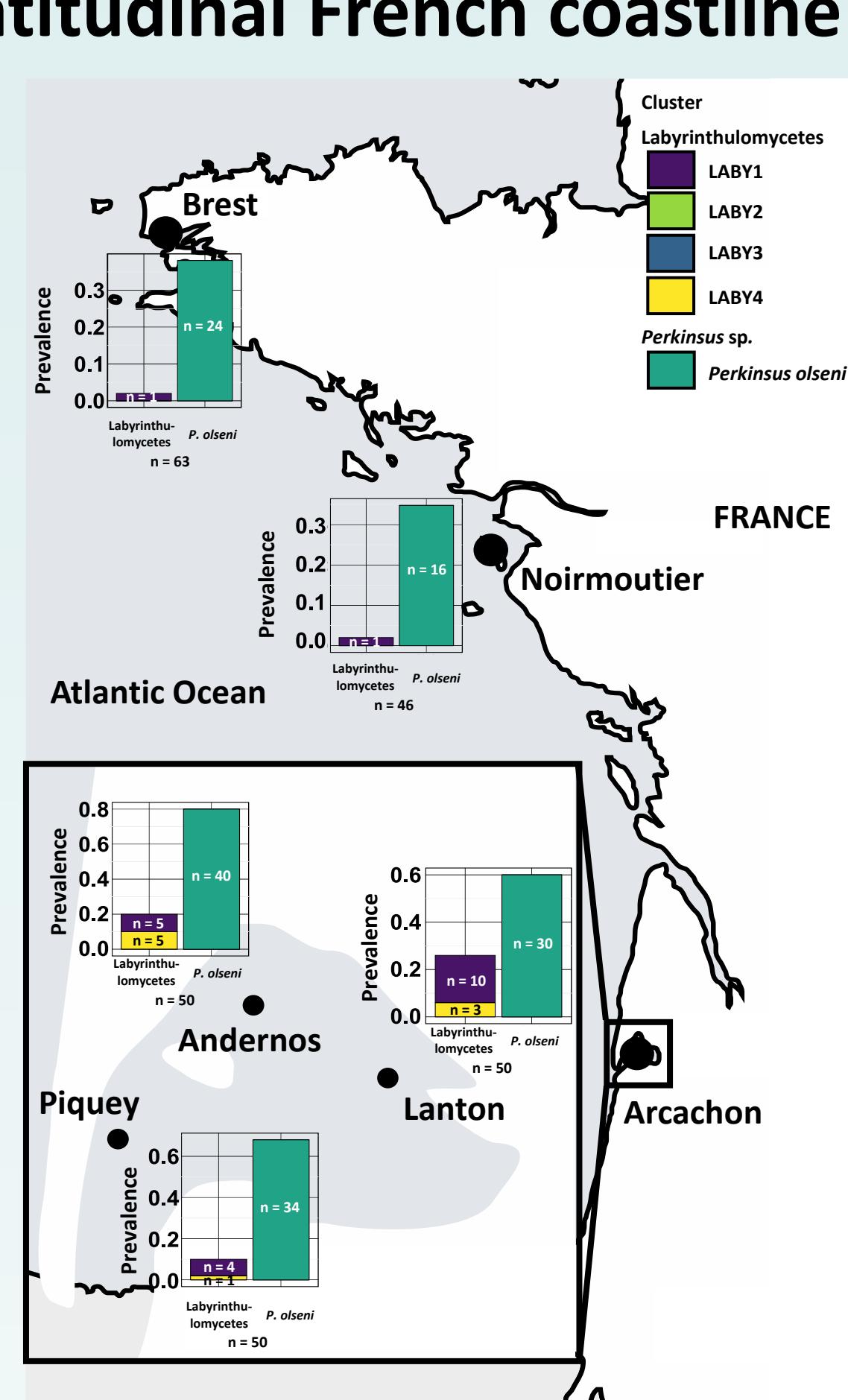
Search for Labyrinthulomycetes in a total of 259 clam samples from 3 sites (Brest, Noirmoutier and Arcachon) using specific primers

Targeted cluster	Primers	Sequence (5'→3')
LABY1 group	LABY1_F	GGGCGGCATTATTAGATT
	LABY1_R	GCACCGCCGATCGCTA
LABY2 group	LABY2_F	TGGAGATGAAGCAATCCTGC
	LABY2_R	CCACCAACTAAAGAACGGCCA
LABY3 group	LABY3_F	TTTTTGTGGCGCGC
	LABY3_R	GCGCGCGGGTCAATTAA
LABY4 group	LABY4_F	AAGCGGAACCTCGGAAACG
	LABY4_R	TGCACTGTGGCAACCAA

Table 2: Specific primers designed and used in this study.

Conclusion and Perspectives

- Presence of unexpected Labyrinthulomycetes communities associated to *P. olseni* infected manila clams
- The majority of Labyrinthulomycetes species found along the French Atlantic coast belongs to LABY1 group
- No detection of genetic signature belonging to LABY3 and LABY2 groups
- The prevalence and diversity of Labyrinthulomycetes is more important in Arcachon Bay, where *P. olseni* is more prevalent



References

- Azevedo, C., & Corral, L. (1997). Some ultrastructural observations of a thraustochytrid (Protoctista, Labyrinthulomycota) from the clam *Ruditapes decussatus* (Mollusca, Bivalvia). *Diseases of Aquatic Organisms*, 31, 73–78. <https://doi.org/10.3354/dao031073>
- Burge, C. A., Kim, C. J. S., Lyles, J. M., & Harvell, C. D. (2013). Special Issue Oceans and Humans Health: The Ecology of Marine Opportunists. *Microbial Ecology*, 65(4), 869–879. <https://doi.org/10.1007/s00248-013-0190-7>
- Honda, D., Yokochi, T., Nakahara, T., Raghukumar, S., Nagakiri, A., Schaumann, K., & Higashihara, T. (1999). Molecular Phylogeny of Labyrinthulids and Thraustochytrids Based On the Sequencing of 18S Ribosomal RNA Gene. *Journal of Eukaryotic Microbiology*, 46(6), 637–647.
- Leyland, B., Leu, S., & Boussiba, S. (2017). Are Thraustochytrids algae? *Fungal Biology*, 121(10), 835–840. <https://doi.org/10.1016/j.funbio.2017.07.006>
- López-García, P., Rodríguez-Valera, F., Pedrós-Alio, C. (2001). Unexpected diversity of small eukaryotes in deep-sea Antarctic plankton. *Nature*, 409, 603–607. <https://doi.org/10.1038/35054537>
- Medlin, L., Elwood, H. J., Stickle, S., Sogin, M. (1988) The characterization of enzymatically amplified eukaryotic 16S-like rRNA-coding regions. *Gene*, 71 (2), 491–499. [https://doi.org/10.1016/0378-1199\(88\)90066-2](https://doi.org/10.1016/0378-1199(88)90066-2)
- Pan, J., del Campo, J., & Keeling, P. J. (2017). Reference Tree and Environmental Sequence Diversity of Labyrinthulomycetes. *Journal of Eukaryotic Microbiology*, 64(1), 88–96. <https://doi.org/10.1111/jeu.12342>
- Scanlan, P. D., & Marchesi, J. R. (2008). Micro-eukaryotic diversity of the human distal gut microbiota: qualitative assessment using culture-dependent and -independent analysis of faeces. *The ISME Journal*, 2 (12), 1183–1193. <https://doi.org/10.1038/ismej.2008.26>
- Stokes, N., Ragone Calvo, L., Reece, K., & Burreson, E. (2002). Molecular diagnostics, field validation, and phylogenetic analysis of Quahog Parasite Unknown (QPX), a pathogen of the hard clam *Mercenaria mercenaria*. *Diseases of Aquatic Organisms*, 52, 233–247. <https://doi.org/10.3354/dao052233>