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# Agricultural uses, continental inputs and temporal dynamics of eukaryotic taxa in a marine critical transition zone of the Petit Cul-de-Sac Marin (Guadeloupe)

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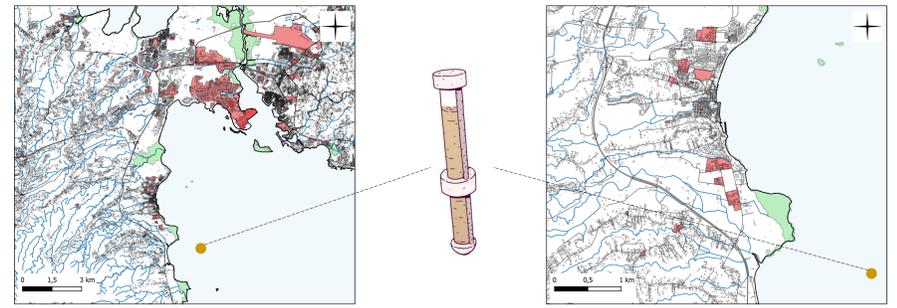
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## Context

First studies by Pierre Sabatier and colleagues\* (co-funded by the OHM Littoral Caraïbe, APR 2018 and 2019) analyzed core sediments from both Guadeloupe and Martinique (French West Indies), and showed that the widespread use of a non-specific systemic herbicide (glyphosate) at the turn of the 21<sup>st</sup> century has induced an unprecedented rise in soil erosion and a major release of persistent chlordecone pesticides that were trapped in banana field soils since their ban in the late 1990s'.

\* Sabatier *et al.* (2021) Evidence of Chlordecone Resurrection by Glyphosate in French West Indies. *Environ. Sci. Technol.* **55**, 2296-2306.



Map of sampling location in the Petit Cul-de-Sac Marin (Guadeloupe, French West Indies)

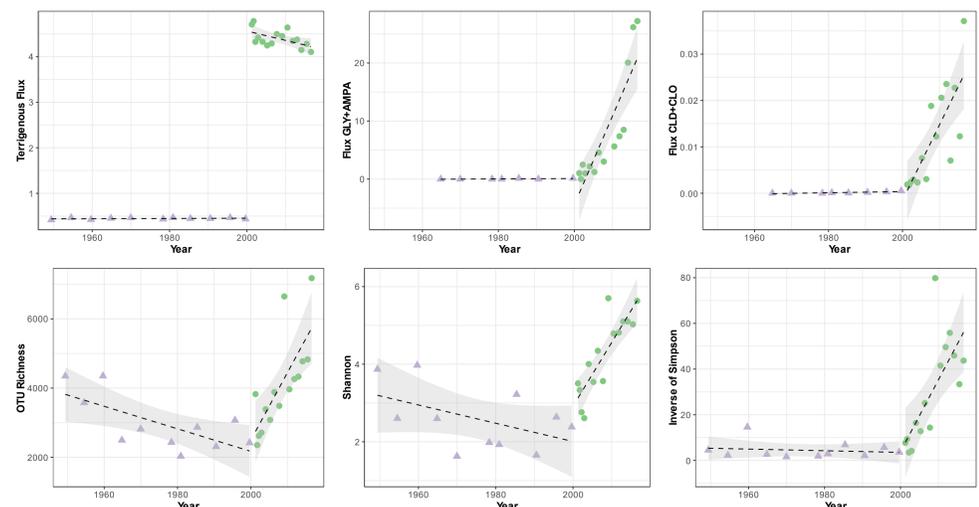
■ Marine core sediment ■ Industrial & transportation areas ■ Mangroves ■ Dwelling houses

## Influence of the sedimentation rate and other environmental factors on diversity indices

A sediment core was collected in the Petit Cul-de-Sac Marin, which is surrounded by the highest industrial and commercial areas and correspond to the most densely populated area of Guadeloupe (French West Indies). The core was sampled according to change in sedimentation rate, every 6 cm for the upper 70 cm (11 samples) corresponding to the period 2001-2017 which is characterized by a fast sedimentation rate (FSR), every 2 cm between 70 and 100 cm (15 samples) corresponding to the period 1950-2000 which is characterized by a slow sedimentation rate (SSR).

The environmental DNA samples were extracted and a single DNA library was prepared by amplifying the V7 region of the 18S rRNA gene. After sequencing of bar-codes and filtering processes we obtained 3,615,742 reads that correspond to 41,081 eukaryotic operational taxonomic units (OTUs; cutoff 95%) that were taxonomically assigned using the PR2 eukaryotic database.

We found that only 9,414 (22.9%) were shared between the two periods, suggesting important differences in community composition. Regarding the *alpha* diversity, both OTU richness and diversity (Shannon index and inverse of Simpson index) were significantly higher in the FSR samples than in the SSR samples. *Beta* diversity analyses further confirmed that the FSR and SSR eukaryotic communities were different.



Differences in the evolution of sedimentological data, herbicide and insecticide fluxes, and alpha diversity indices of a core archive from a marine critical transition zone

## Long-term impacts on the eukaryotic diversity

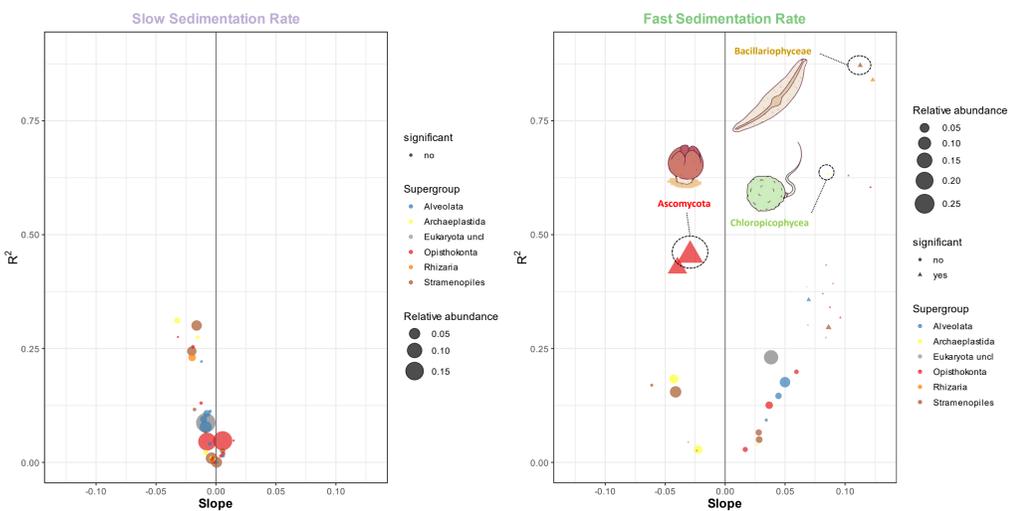
For the most abundant 33 classes of eukaryotic organisms, we separately performed analyses of their relative abundance, *alpha* diversity (i.e., diversity within a particular area) and *beta* diversity (i.e., diversity between areas) for both the slow sedimentation rate (SSR, years 1950-2000) and the fast sedimentation rate (FSR, years 2001-2017) periods.

Regarding the relative read abundances (see Figure), we found significant positive trends (i.e., this relative abundance was increasing over time) over the FSR period for Bacillariophyceae (Stramenopiles), Chloropicophyceae (Archaeplastida), Coccidiomorpha (Alveolata), Gastrotricha (Opisthokonta) and unclassified Cercozoa (Rhizaria) and significant negative trends for Ascomycota (Opisthokonta) and unclassified Fungi (Opisthokonta). For these same classes and more generally for some unclassified classes, there was non-significant temporal change in relative abundance during the SSR period, suggesting a relative stability over the second half of the 20<sup>th</sup> century.

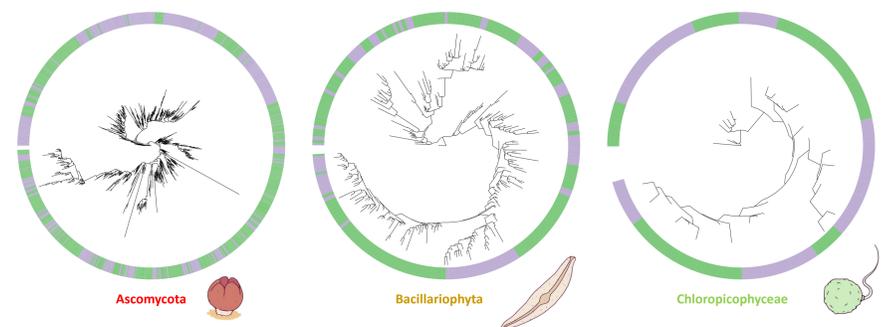
Regardless of the *alpha* diversity metrics tested, we found many more significant trends during the FSR than during the SSR period. The measures of community dissimilarity calculated for each period between a date and the first date of this period, revealed significant positive slopes, indicating that over time, eukaryotic communities tended to be more dissimilar. Moreover, *beta* diversity analyses revealed increasing changes in community composition during the FSR period compared to the SSR period.

To better understand variations in specific eukaryotic classes, we performed deeper analyses on three eukaryotic groups among the coastal biomes that presented: different temporal patterns of variation and with different ecological roles. We choose Ascomycota (Opisthokonta, Fungi) as member of the carbon decomposer community as well as Bacillariophyta (commonly known as diatoms) and Chloropicophyceae (Archaeplastida) as members of the carbon fixing organisms.

For these three classes of organisms we found a non-random and clumped phylogenetic pattern for the FSR- and SSR-specialists, suggesting adaptations of these species to two different ecological niches characterized by distinct physico-chemical parameters.



Temporal evolution of the relative abundance of the major eukaryotic classes



Maximum-likelihood phylogenetic tree of specialist OTUs

## Conclusion

The geographical isolation of island ecosystems favors the appearance of specific communities with patterns and environmental characteristics that make them particularly sensitive to human disturbance. Here, we carried out temporal analyses on the abundance and *alpha* and *beta* diversity of eukaryotes from a sediment core that presented two distinct periods characterized by a shift in sedimentation regime and a constant gradual increase in marine glyphosate and chloredecone fluxes. We could capture the ongoing temporal changes in assemblage composition in a way that probably reflects the ecological processes and the ecosystem functions that are involved. Overall, our results show a correlation between concentration of pollutants from agricultural usages, modifications of the land erosion processes and compositional reorganizations over the two last decades in a critical transition zone located close to the most anthropized area of Guadeloupe.

