Marine microbes on the rise over two decades: potential invasions in the NW Mediterranean?

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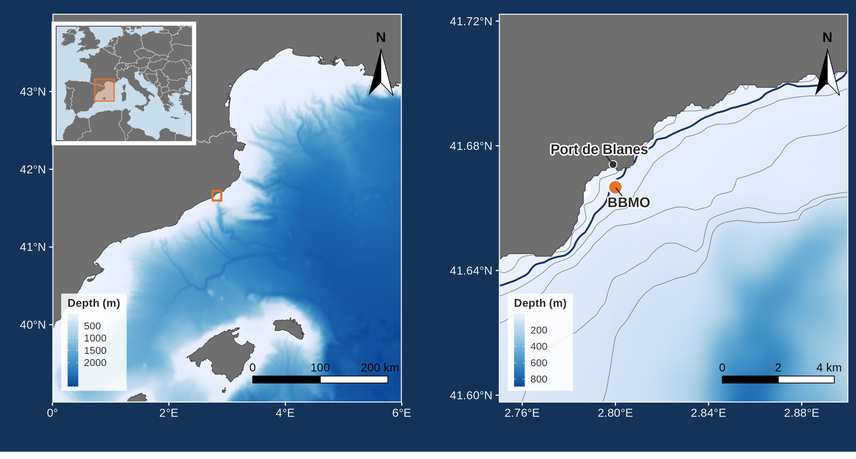


INTRODUCTION

The Mediterranean hosts numerous biological invasions, yet potential invasions within its microbiome have rarely been monitored. Identifying microbial invasions is particularly challenging because a sustained increase in abundance may reflect range distribution modification, recruitment from the local rare biosphere or seed bank, or the introduction and establishment of a non-indigenous microorganism. Here, we investigate microorganisms showing increasing trends in abundance over 20 years at the LTER Blanes Bay Microbial Observatory (BBMO). Taxa displaying clear increasing trends are identified as candidate microbial invaders, whose origin and invasion status require further investigation.

OBJECTIVES

1. Detect microbial taxa with significant increasing trends over two decades and characterise these candidates.
2. Test whether the signal is supported across datasets and statistical routes.
3. Deliver a priority list of the most robust candidates.

METHODOLOGY

Four datasets from the same DNA extracts
Monthly surface picoplankton (0.2–3 µm)

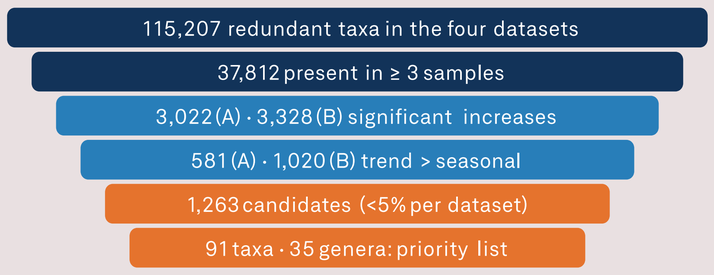
rRNA gene (prokaryotes and protists):
- 16S ASV (V4–V5), 18S ASV (V4): 265 samples, 2001–2023
- mTAGs (shotgun metagenomes): 232 samples, 2004–2023

Marker genes (prokaryotes):
- mOTUs (shotgun metagenomes): 232 samples, 2004–2023

Filters and statistical routes (fixed a priori)
Taxa present in ≥3 samples are tested.

Candidate: increasing trend (FDR ≤ 5%) and trend variance > seasonal variance, tested on the same taxa by route **A** (STL + seasonal Mann–Kendall) and route **B** (Bayesian dynamic GAM, mvgam).

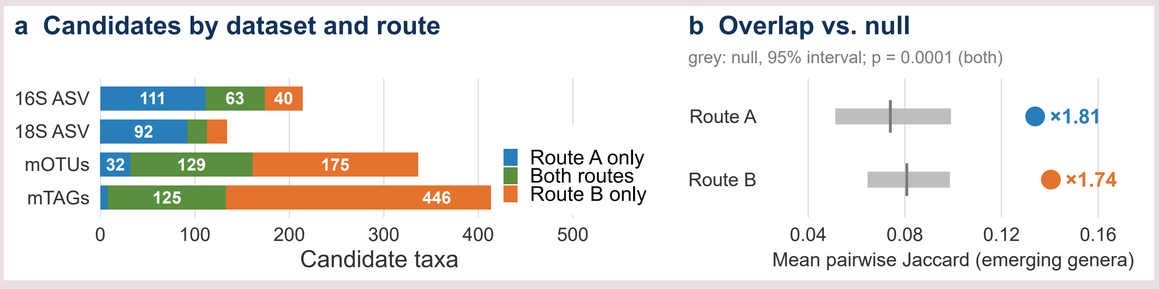
Robust genus: candidate in ≥2 datasets; cross-dataset overlap tested against random genera of similar abundance (abundance-stratified null).



RESULTS

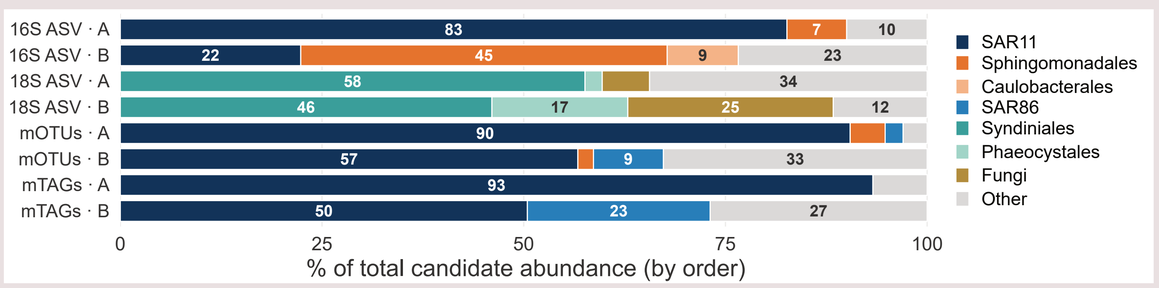
1 Candidates and cross-dataset support

Route **A** finds more candidates in the amplicons, route **B** in the metagenomes. Candidate genera are shared between datasets **nearly twice as often as expected by chance**.



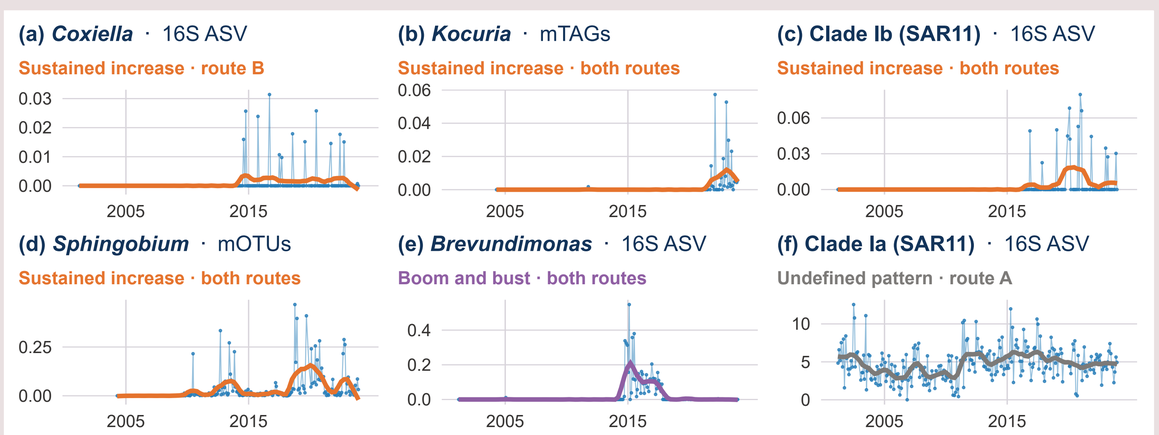
2 Who are they?

Route **A** candidates are dominated by SAR11 lineages (83–93% of their abundance); route **B** gives more weight to **Sphingomonadales** (45% in 16S ASV).



3 Trajectories compatible with arrival or range modification

Visual classification of all 1,263 trajectories: **28% show a sustained increase** (orange trend line), a trajectory compatible with, but not diagnostic of, invasion or range modification; **21% boom and bust**; **51% undefined**. Dots, relative abundance (%); thick line, STL trend.



4 Who are the priority candidates?

91 taxa in 35 genera form the priority list. Each row is a genus (unfamiliar names are explained in brackets); each dataset column is split into route **A** (left dot) and route **B** (right dot). Dot size: number of taxa; Colour: share of variance explained by the increasing trend. Genera are ranked from strongest to weakest signal within each group.

CONCLUSIONS

Potential invasions?

A small set of marine microbes, supported across datasets, is clearly on the rise. Trends alone cannot tell an invasion from a range modification or a rare-biosphere bloom: these are candidates, not proven invaders yet.

On the rise, but few
<5% of the taxa tested show significant increasing trends over two decades.

Cross-dataset support
27% of candidate taxa are found by both routes, and 12–15% of candidate genera in ≥2 datasets, more than expected by chance.

SAR11 is not one story
Much of the signal lies in SAR11 lineages, which may be recruited from the rare biosphere, modify their range or invade.

91 priority candidates
91 taxa (35 genera) are the candidates to follow; 13 genera are supported by ≥2 datasets and both routes

Acknowledgements & funding. We thank Clara Cardelús and all members of the LTER-BBMO sampling team (http://bbmo.icm.csic.es). This work has been supported by the project ALIEN-OCCICAT (EFA 149/03), a Catalonia–Occitanie cross-border project on early detection and monitoring of non-native marine species, co-funded 65% by the European Union through the European Regional Development Fund (ERDF) under the Interreg VI-A Spain–France–Andorra Programme (POCTEFA 2021–2027). BBMO sequencing has also been supported by the projects MINIME (PID2019-105775RB-I00, MICINN, Spain) and MAORI (PID2022-136281NB-I00, MICINN, Spain). We thank Sergio González-Motos and David Pere Arnal-Borràs for their help with the STL decomposition.