Fungal diversity in an oxygen minimum zone of the Tropical Pacific Ocean revealed by Illumina sequencing

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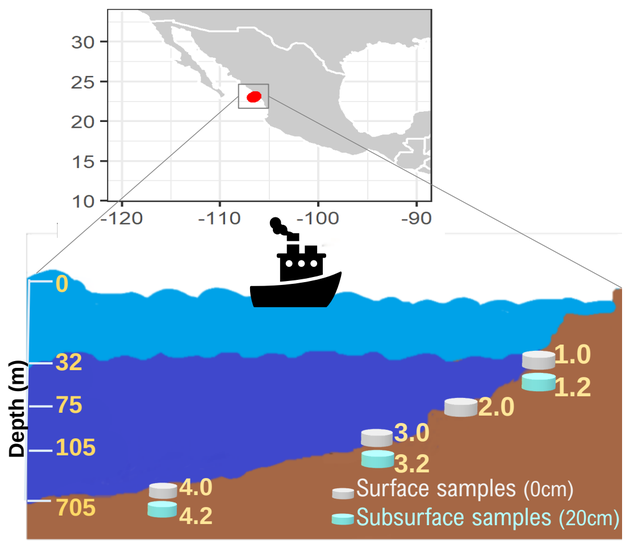
Introduction

Fungi contribute to denitrification pathways in oxygen minimum zones (OMZ). These organisms produce nitrous oxide (N_2O) that is a potent atmospheric greenhouse gas that contributes to global warming. Recently, fungi have been accounted for 18-22% of total N_2O production in water column[1] in the North Pacific, denoting their importance in the marine ecosystem. Despite their ecological relevance fungi are little explored in OMZ. Overall, *Ascomycota* and *Basidiomycota* are the most abundant groups with the occurrence of numerous uncultured lineages. The Arabian Sea is the best explored region, whereas little is known about the Pacific Ocean (the largest OMZ in the world).

We evaluated fungal diversity and community composition in sediment samples collected in 4 stations along a transect from the coast to the open ocean in the OMZ of the Mexican Tropical Pacific, using a metabarcoding approach.

Methods



1. **DNA extraction (sediment)**
   PowerSoil Kit®

2. **Illumina MiSeq secuencing**
   - ITS1 Region
   - Paired-end (2×300)
   - 25,000 reads/sample

3. **Bioinformatics analysis**
   DADA2 Amplicon Sequencing. Exactly. Version 1.18
   unite community

4. **Diversity analysis: α and β**
   vegan, ggplot2, iNEXT

Results

Fig 1. Relative abundance of fungal phyla

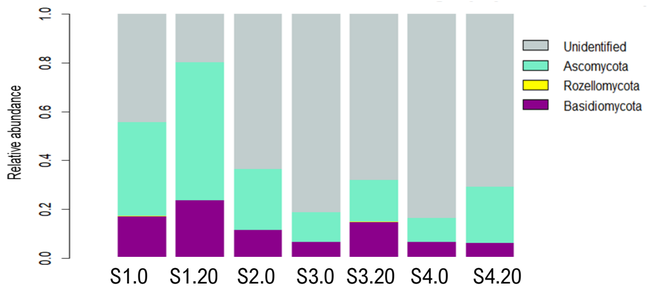


Fig 2. Shannon Index

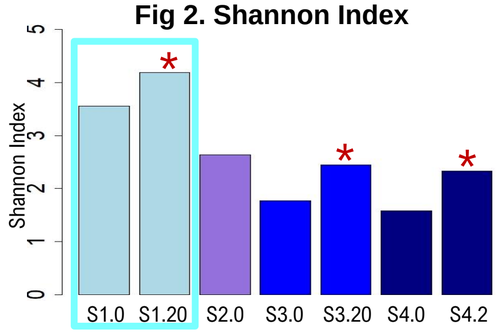


Fig 3. Bray-Curtis dissimilarity

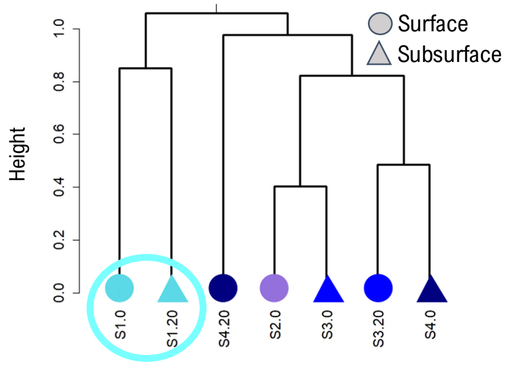
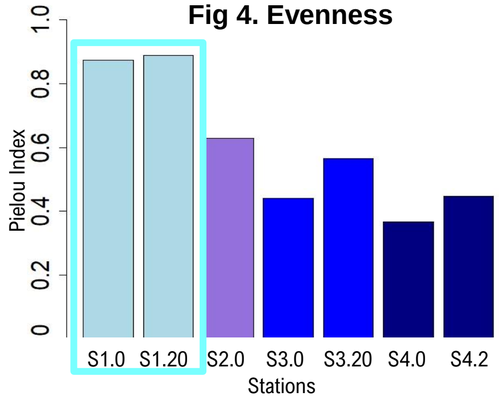


Fig 4. Evenness



Discussion

- We obtained 353 fungal amplicon sequence variants (ASV).
- *Ascomycota* was the most abundant phylum *(Fig. 1).*
- The high abundance of *Fungi* spp. confirms the occurrence of OMZ endemic unculturable phylotypes *(Fig.1).*
- *Penicillium* spp., *Paraphaeosphaeria* spp. and *Trichoderma* spp. were the most abundant species.
- We observed higher Shannon values *(Fig. 2)* in relation to reports for the Eastern Tropical Pacific[2], suggesting that this system is more diverse.
- The subsurface samples were more diverse than surface samples (*Fig. 2* * *y 3*), probably due to heterogeneous environmental conditions at that temporal scale.
- Sampling sites were clustered into 2 groups: near-shore and off-shore (*Fig. 3*). Higher diversity and evenness were observed in near-shore samples *(Fig. 4),* probably due to the greater accumulation of terrestrial organic matter in the coast.

Conclusion

Our results evidenced **high fungal diversity** in little-explored OMZ of the Tropical Pacific Ocean, with the phylum *Ascomycota* and novel uncultured phylotypes as dominant elements. We identified greater diversity levels in **near-shore** and in **subsurface** sediment samples, perhaps because of the accumulation of organic matter in these sites.

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References: 1. DOI: 10.3390/jof7030218;
2. DOI: 10.3389/fmicb.2020.575207