

Metagenomic insights into variability of microbial diversity and functions in the oxygen minimum zone of the Eastern Tropical Pacific Ocean



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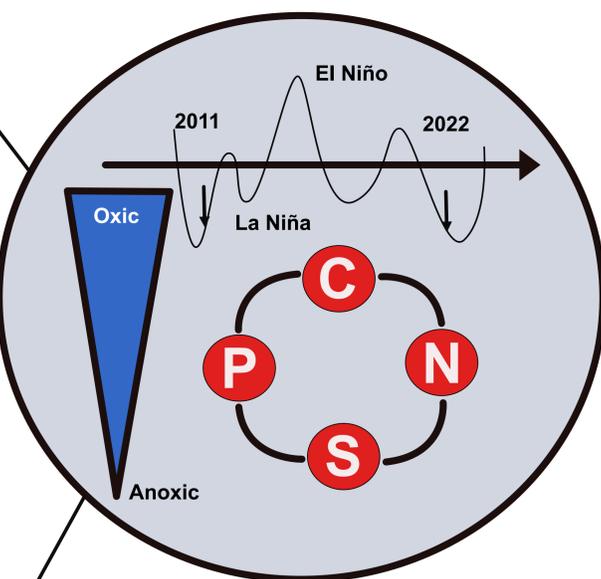
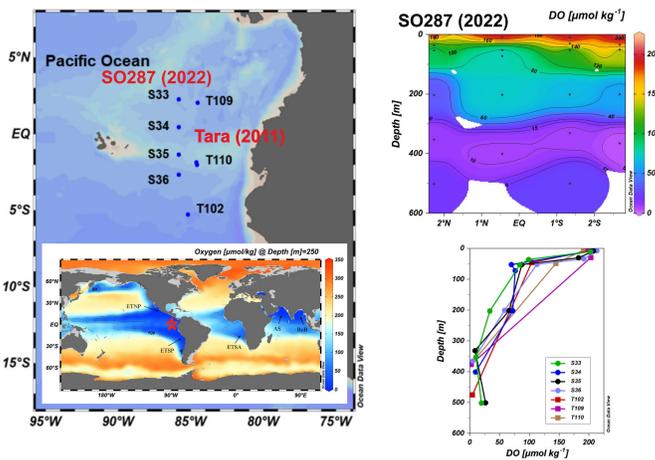
1 Introduction

Oxygen minimum zones (OMZs) expand in the ocean and may significantly affect the microbial process which drive major biogeochemical cycles of carbon, nitrogen, sulfur, phosphorus in the ocean [1]. The Eastern Tropical Pacific Ocean (ETP) bears one of the largest perennial OMZ in the present ocean and is strongly influenced by the recurring climate pattern (alternating cold and warm phases) known as El Niño Southern Oscillation (ENSO) [2]. However, little is known about how microbial diversity and functions in biogeochemical cycles might shift in associated with oxygen variability and ENSO events.

The Pacific OMZs:

- harbors the largest OMZs and one of the four major eastern boundary upwelling system
- predicted to expand while their core waters - where oxygen is lowest - would shrink [3]
- a major hotspot N-loss via microbial activity [4]
- a significant N₂O and CO₂ source to the atmosphere [5]
- a site with seasonally occurring coastal sulfur plumes [6]

3 Study Site



2 Aim of study

Aim 1: Microbes' response towards possible future ETP OMZ expansion

- a systematic analysis of the spatial variations of microbiological processes along the dissolved oxygen (DO) gradient: from well-oxygenated to suboxic (5µM)
- microbial community: Archaea and Bacteria
- microbiological processes: carbon-nitrogen-sulfur-phosphorus cycles
- link to physiochemical factors (Nutrient, DO, N₂O)

Aim 2: Effect of ENSO events on microbes

Comparison of microbial community and functions:

- Our dataset SO287 (2022) (S33 - S36) vs Tara Ocean dataset (2011) (T109, T110, T102)
- three depths: surface (<10m), below surface (<50m) and oxygen minimum waters
- Sampled from similar stations under similar La Niña conditions

6 Microbial composition (2011 vs 2022)

	T102.1	T109.1	T110.1	T109.2	T102.2	T110.2	T102.3	T109.3	T110.3
Proteobacteria: Alphaproteobacteria	15	15.1	16.1	15.5	12.2	17	23.4	30.9	16.5
Proteobacteria: Gammaproteobacteria	13	12.2	12.9	11.1	12.2	12.3	5.6	5.9	8
Bacteroidota: Bacteroidia	10.9	13.7	12	13.3	12.6	9.6	0.3	0.3	4.2
Cyanobacteria: Cyanobacteria	3.8	5.5	4.4	4.9	6.4	4.3	5	4.4	4.4
Actinobacteriota: Acidimicrobia	2.9	1.6	1.8	1.9	2	3.1	7.4	7.4	7.5
Marinimicrobia: Marinimicrobia	2.5	3.2	3.5	2.8	3.6	10.8	2.2	2.4	4.8
Thermoplasmata: Poseidonia	0	0	0	0	0.1	0.1	18.5	9	7.7
Thermoproteota: Nitrospinae	0.1	0.3	0.3	0.1	0.4	0.8	0.5	7.1	7.2
SAR324: OC60‑12	2.6	3.3	1.1	4	2.4	1.1	2.3	2.4	1.9
Verrucomicrobiota: Verrucomicrobiae	0.7	0.5	0.6	0.6	1.9	0.6	0.7	0.7	0.7
Firmicutes_A: Clostridia	0.5	0.4	0.5	0.5	1.6	0.5	0.5	0.6	0.6
Firmicutes: Bacilli	0.5	0.4	0.5	0.5	1.6	0.5	0.5	0.6	0.6
Actinobacteriota: Actinomycetia	0	0	0	0	0.3	0.6	0.5	0.6	0.7
Nitrospina: Nitrospina	0	0	0	0	0	0	2.1	1.6	0.9
Chloroflexota: Dehalococcoidia	0.1	0.1	0.1	0.1	0.2	0.1	1	1	1.1
Remaining taxa (569)	2.6	1.8	1.9	2	4.1	2.1	5.4	5.6	5.3

Tara (2011) vs SO287 (2022) Archaeal and Bacterial community

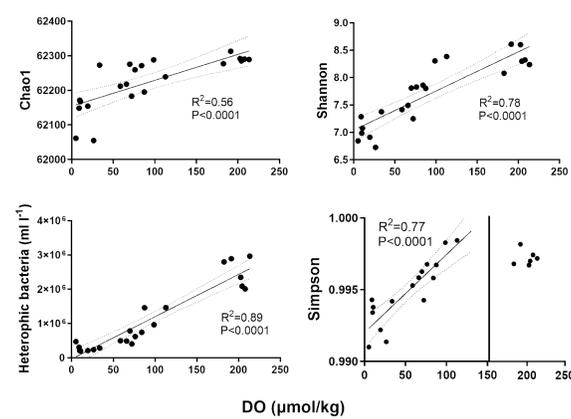
	S33.1	S34.1	S35.1	S36.1	S33.2	S34.2	S35.2	S36.2	S33.3	S34.3	S35.3	S36.3
Proteobacteria: Alphaproteobacteria	24.9	26.7	26.7	26.8	26.7	26.7	26.7	26.7	13.4	19.9	21.4	21.8
Proteobacteria: Gammaproteobacteria	11.3	11.7	10.2	12.1	6.5	11.7	12.4	10.8	11.3	16.4	16.8	16.6
Thermoplasmata: Poseidonia	6.5	11.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4
Bacteroidota: Bacteroidia	13.2	11.9	12.9	12.2	13.6	10.8	11.4	10.9	13.1	11.8	4.5	6.4
Marinimicrobia: Marinimicrobia	1.6	1.9	1.6	1.2	1.7	1.3	1.4	1.1	2.3	3.1	3.1	3.1
Cyanobacteria: Cyanobacteria	3.8	4.7	5.1	3.6	4.8	3.7	4.5	10.1	5.4	5.8	5.8	5.8
Thermoproteota: Nitrospinae	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1
Actinobacteriota: Acidimicrobia	1.9	2.2	4.8	2.9	3.4	3.8	2.1	8.2	7.6	4.2	3.9	3.4
Verrucomicrobiota: Verrucomicrobiae	3	2.5	2.4	3.5	1.6	5.9	4.2	1.6	6.1	3.1	5.7	5.6
Actinobacteriota: Actinomycetia	3.7	3.6	4.3	3.7	3.7	3.9	5	3.2	3.7	2.6	3.1	2.9
SAR324: OC60‑12	0.2	0.2	0.4	0.2	1.1	0.4	0.1	3.6	4.4	2	1.1	3.7
Firmicutes_A: Clostridia	4	3	2.8	2.7	2.6	2.1	3.2	2.4	3.3	1.9	3.1	2.3
Firmicutes: Bacilli	3	2.1	1.8	1.8	1.9	1.4	2.1	1.8	1.7	1.4	2.2	1.7
Chloroflexota: Dehalococcoidia	0.4	0.4	0.2	0.3	0.2	0.2	0.6	0.4	0.2	0.4	0.8	3.2
Nitrospina: Nitrospina	0	0	0	0	0	0	0.5	0.2	0.1	0.9	1.2	1.6
Remaining taxa (569)	10.8	8.6	10.6	8.2	6.9	7.2	9.3	6.7	6.6	5.4	6.5	7.6

Same: Top groups, total number of taxonomy in class and family levels.

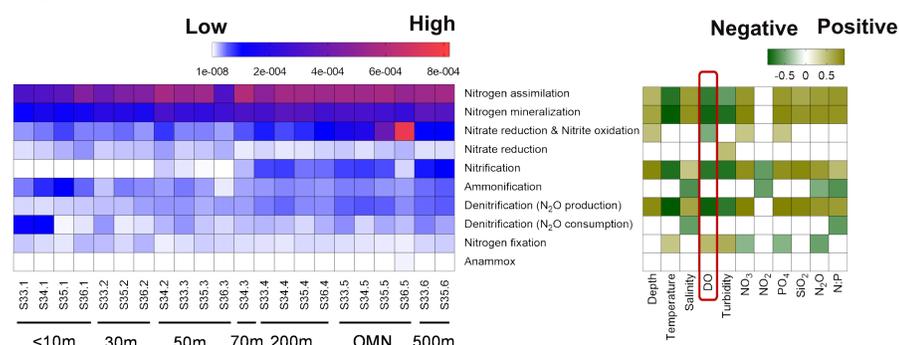
Main difference:
 Tara (19-45%) > SO287 (9-31%): Alphaproteobacteria (SAR11 clade)
 SO287 (2-19%) > Tara (2-11%): Poseidonia (Archaea)

4 Microbial diversity (SO287, 2022)

Microbial diversity and abundance (cell counts) decrease along the decline of oxygen.



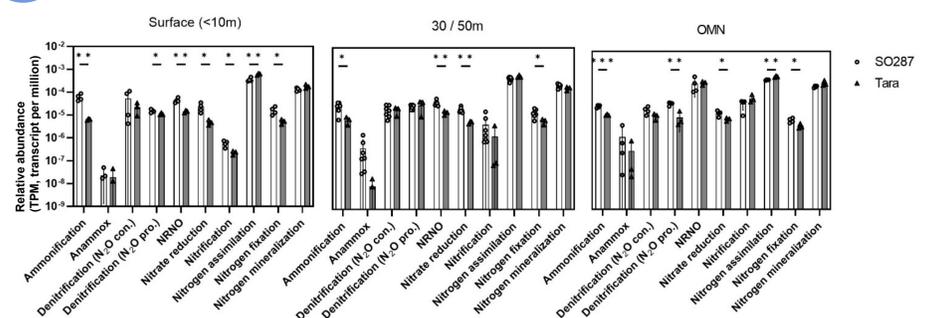
5 C-N-S-P pathways (SO287, 2022)



Example: nitrogen metabolisms: relative abundance of each nitrogen pathway in metagenomes and their correlation with physiochemical parameters (p<0.05, |r|>0.5)

Oxygen decreases: nitrogen fixation ↓; nitrogen assimilation / mineralization, nitrate reduction and nitrite oxidation, nitrification, denitrification (N₂O production) ↑

7 C-N-S-P pathways (2011 vs 2022)



Example: nitrogen metabolisms: Tara (2011) < SO287 (2022) (e.g., DNRA, denitrification (N₂O production), nitrogen fixation, nitrate reduction)

8 Conclusion

Impact of ENSO events: SO287 (2022) VS Tara (2011)

- No taxonomic difference, but different relative abundance of a few groups (e.g., Alphaproteobacteria - SAR11 clade)
- More potential nitrogen metabolisms in SO287 (2022)

Impact of possible future OMZ expansion: Oxygen variability in SO287 (2022)

- Oxygen declines, microbial diversity and abundance ↓, while nitrogen related metabolisms ↑
- Some other conclusions that are not shown here:
- Different microbial function groups: different range of oxygen sensitivity (e.g., 80, 12µmol/kg)
- Microbial Community ≠ Microbial Function