# Characterization of microzooplankton communities in a polluted coastal area integrating high-throughput sequencing and microscopy



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#### Study area



#### Multidisciplinary and integrative approach

- Environmental variables: T, S, nutrients, Chl a
- Microzooplankton sampling and composition analysis:

Niskin bottles (3-200 um) Surface waters – frozen filters Metabarcoding 18S v9



CalVET net (50-200 um) Vertical hauls, bottom to surface – etOH Microscopy





Metabarcoding COI, 18S v4 (work in progress)

#### **Environmental variability**



#### Microzooplankton relative abundances identified by microscopy



Taxa with abundance <1% were grouped in Others.

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Significant differences between zones: Coast <20 m bottom depth Offshore 20-60 m bottom depth

#### Microzooplankton relative abundances identified by 18S v9



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#### Microzooplankton relative abundances identified by 18S v9



Taxa with abundance <1% were grouped in Others.



Surface waters: No significant differences between zones

#### **Environmental variability**



## Summary

- Summer stratification prevented bottom pollution spreading to the surface
- Environmental variables and microzooplankton community structure variability were driven by stratification and pollution
- Both surface and water column samples were dominated by dinoflagellates, but different species
- Need to account for mismatch between metazoans contribution to metabarcoding reads and microscopic counts

Work in progress...

- Comparison of CalVET samples metabarcoding with microscopy
- Separated protozoans and metazoans data analysis

### Acknowledgements



This work was funded by the Consejería de Economía, Innovación y Ciencia de la Junta de Andalucía, project MICROZOO-ID (P20\_00743)



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