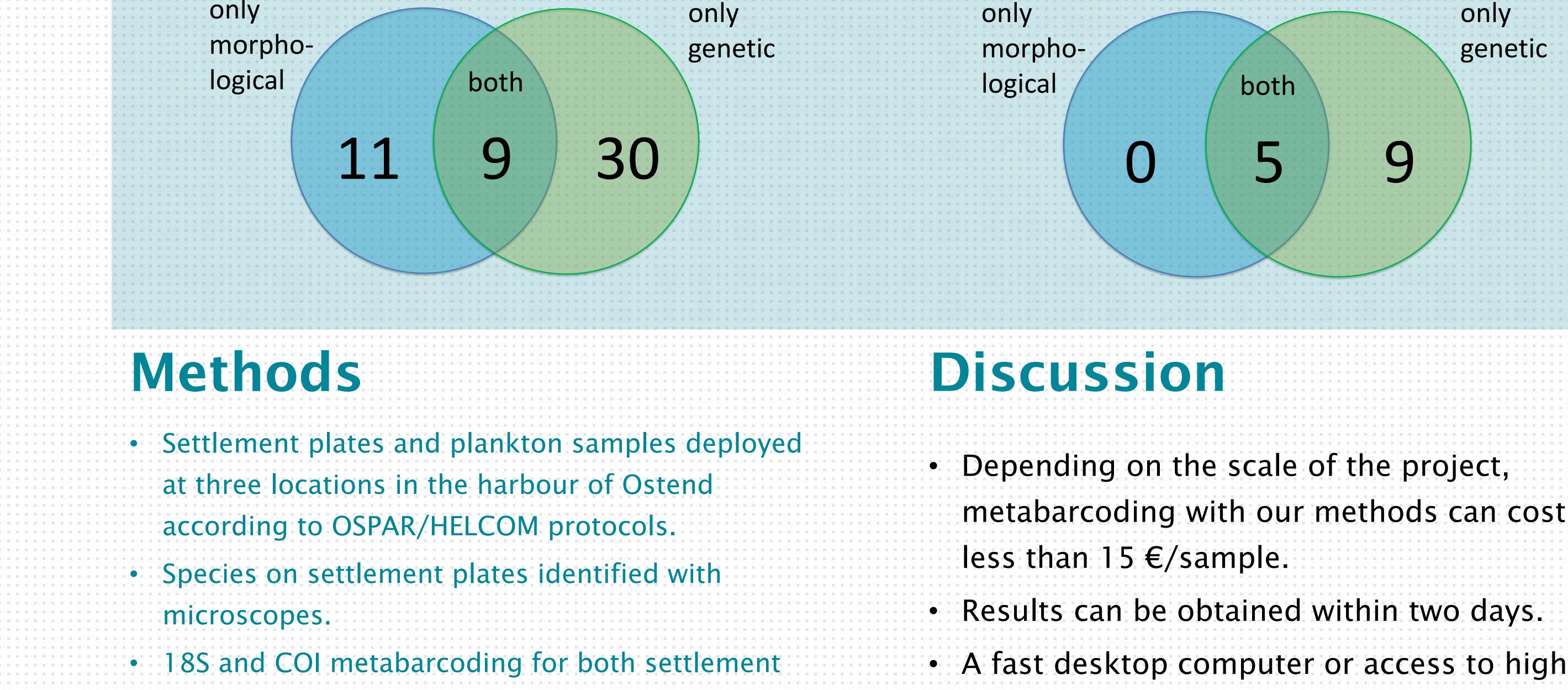
Time and cost efficient DNA-based monitoring of marine non-indigenous species in the harbour of Ostend (Belgium) using nanopore sequencing

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Results identification of all species

identification of nonindigenous species



plates and plankton samples.



We used nanopore technology to generate long 18S and COI reads (about 650-700 base pairs) to allow species level identification (at 99 % identity cut-off)

Nanopore sequences are inherently noisy. We

performance cluster is needed to run the

OPTICS algorithm

Conclusion

Genetic techniques are more sensitive, more accurate and more efficient than traditional analyses with microscopes.

But unfortunately they still do not work for all species. We are not yet ready to put the microscope aside, but eventually we will.

corrected errors using a density based clustering algorithm (OPTICS) as implement in *ashure* (Baloğlu et al. 2021 Methods in Ecology and Evolution). We did not yet publish our bioinformatics pipeline. Please contact PIH for early access.

Vlaams Instituut voor de Zee vzw

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