Environmental DNA reveals marine biodiversity in human-impacted and invaded ecosystems

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Impacts on biodiversity, such as environmental alterations, are generally considered potential threats to human health, particularly in areas involved in food production activities. However, the empirical evidence presented in our study, based on the quantification of marine biodiversity using environmental DNA (eDNA), suggests that this relationship may be context-dependent, particularly where production activities may contribute to bioremediation processes.

Our case study concerns a coastal area in northwestern Sardinia characterized by the presence of an oyster farm (*Crassostrea gigas*) in a region altered by colonization by *Caulerpa* sp., a genus known for its negative effects on biodiversity.

Our sampling involved the filtration of seawater through membranes in proximity to the farm and in a control site. eDNA was analysed using metabarcoding of the 18S rRNA gene and sequencing on an Illumina platform. The raw reads were subsequently processed through a bioinformatic pipeline including quality control, filtering, denoising/clustering, and taxonomic assignment, down to species level where possible.

Biodiversity recorded at the station close the farm is significantly higher than at the control site, both in terms of species richness and evenness.

By analyzing the ecology of the identified species, we speculated on the rule of oyster filter-feeding activity, which may enhance local environmental conditions and increase biological diversity. This pattern is interpreted in relation to a possible filtering effect exerted by the farmed organisms within the cultivation area and in the immediately surrounding zones.

Further investigations are required to verify these patterns and clarify the underlying mechanisms; however, this study encourages reflection on the potential role of compatible anthropogenic activities in modulating biodiversity and contributing to bioremediation processes in marine ecosystems.