

Integrating molecular methods into long-term plankton observations.

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Over the last fifteen years, molecular genetics has rapidly advanced the rate of plankton species discovery in the oceans and the advent of high-throughput DNA sequencing has revealed a vast level of diversity previously unknown. As the use of genetics is more accepted, should we consider its routine use for reporting plankton species to national government and European bodies? Most long-term ecological research sites (LTERS) that report plankton still use microscopy-based species identification that favours the identification of larger organisms over smaller ones. This is done for continuity even though there is awareness that microscopy methods are insufficient to monitor all plankton diversity. Several LTERs are now additionally using molecular method to augment the species they find as there is a need for this information from a variety of stakeholders, most notably for four of the descriptors of the new MSFD legislation. However there are several obstacles in integrating molecular methods into established plankton time-series. We conducted a literature survey and a questionnaire from marine molecular ecologists, many who also carry out microscopic surveys, to find out the benefits and challenges of integrating molecular identification methods into routine long-term observations.

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