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***Genetic monitoring of open ocean biodiversity: an evaluation of DNA metabarcoding for processing continuous plankton recorder samples***

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The Continuous Plankton Recorder (CPR) has been used to characterise zooplankton biodiversity along transects covering hundreds of thousands of kilometres in the Southern Ocean CPR survey. We investigated the potential to use DNA metabarcoding (DNA-based species identification of mixed samples using high-throughput sequencing) as a tool for rapid collection of taxonomic data from CPR samples. In our study, zooplankton were collected on CPR silks along two transects and identified using standard microscopic methods and by sequencing a mitochondrial COI marker. DNA increased the number of metazoan species identified and provided high resolution taxonomy of groups problematic in conventional surveys (e.g. larval echinoderms and hydrozoans). Metabarcoding also generally produced more detections than microscopy, but this sensitivity may make cross-contamination during sampling a problem. In some samples, the prevalence of DNA from large plankton such as krill masked the presence of smaller species. Overall, the genetic data represents a substantial shift in perspective, making direct integration into current long-term time-series challenging. We discuss a number of hurdles that exist for progressing this powerful DNA metabarcoding approach from the current snapshot studies to the requirements of a long-term monitoring program. Given the continually increasing efficiency of DNA metabarcoding, it is almost certain this approach combined with underway sampling will play an important role in characterising the status and trends of key species in future Southern Ocean monitoring programs.