mtDNA enrichment from preserved samples for meta-genomic skimming

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Genetic assays become increasingly common in biodiversity monitoring programs. An often used tool is metabarcoding of multi-species samples. The core of this concept is to amplify (using polymerase chain reaction: PCR) and to sequence a short piece of the genome. A common issue with this approach is that the primers do not perform equally well in different phylogenetic groups, making it difficult to quantify the relative abundance of species in bulk. Sequencing all available DNA in a sample without prior PCR would circumvent this problem, but such high-throughput sequencing can still be expensive. A cost-effective middle-way is to enrich mitochondrial DNA (mtDNA) using differential centrifugation and to sequence meta-mitogenomes. Successful mtDNA enrichment has been demonstrated on fresh samples, but access to such material is often difficult in marine sciences, where samples are collected on research vessels, often in remote corners of the world. We therefore tested a protocol that starts from frozen samples and samples preserved in EtOH and DESS. Our results show that freezing does not substantially impede mtDNA enrichment, making meta-mitogenomics an attractive method for marine biodiversity assessment.

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