Marine Benthic Necromass: Discriminative detection of detrital DNA in Mid-Arctic Ridge sediments

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The magnitude to which the benthic necromass nucleic acid fraction, DNA specifically, may affect environmental sequencing surveys is a critical question that has received little attention. The reasons for this neglect are i) DNA is generally believed to have a short molecular half-life, ii) extracellular DNA represents dissolved C, N and P which should be readily metabolized by active microbial community fractions and iii) despite some potential preservation, oxidative and hydrolytic events over decades to millennia should damage the molecule beyond minimal sequencing integrity. The scarcity of microbial viability methods for complex environmental samples further confounds this issue. We interrogated fresh Arctic sediments for the presence of detrital DNA using Propidium Monoazide, a photo-active DNA interchelating dye impermeable to intact prokaryotic membranes. This approach employs membrane integrity, a prerequisite for chemiosmotic potential and ATP production, as a viability metric. We report statistically significant (P_{val}=0.003) extracellular 16S rRNA gene loads in shallow Artic sediments with no detectable extracellular gene loads in horizons deeper than 10 cm. Furthermore, we report that initial entombment may disproportionally affect mortality rates of prokaryotic domains as infered from higher proportions of Bacterial extracellular 16S rRNA genes relative to those of Archaea in shallow horizons. Thus, extracelluar DNA is preserved in the Arctic benthos albeit further scrutiny is required to elucidate its ecological significance and spatial-temporal distribution.