Advances in molecular methodologies and the application and interpretation of molecular methodologies for macrofauna classification – Their relevance to environment assessment and monitoring

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In order to understand possible impact of future exploitation of deep-sea mineral resources, baseline studies of macrofauna species composition and species ranges are required. It is important to notice that we need this data for two purposes; (i) describe the impacted areas in terms of species lists (this is fauna "classification" and answer the question "who lives there?"); and (ii) use select species to understand the resilience to impact provided by the ability to recolonize from refuges such as the planned APEI's. While some biodiversity data is available for ecosystems at deep-sea hydrothermal vents (massive sulphides) and deep-sea mounts (manganese crusts), very little is known of the biodiversity at abyssal fields (and not limited to the CCZ). At abyssal basins elements of macrofauna exhibit a very high diversity of small species at low abundances. The lack of species records (not a single benthic polychaete species is so far recorded from the CCZ) has persisted despite a large number of scientific cruises to the central east Pacific Ocean during the last forty years. There are probably multiple reasons for this. One of the most abundant macrofauna groups, the polychaetes, consists of soft bodied animals that break into small fragments when sediment samples are treated in a standard way and bulk fixed on board research vessels. Only through careful (and immediate) extraction from the sediment by expert taxonomists, samples will allow for detailed morphological examination and extraction of high grade DNA. But also with good quality samples that are now starting to accumulate from the CCZ, with excellent morphology and associated DNA sequence data, major challenges remains in achieving lists of species for the specific area studied, data that are required to assess species range sizes and population connectivity.
Connectivity at spatial and temporal scales can be studied either by comparing community structure or by assessing population genetic data for selected species for which required samples sizes are available. Since the species concerned here are "non model" species, using standard genetic markers such as mitochondrial and ribosomal genes, is justified. These genes are also by far the most widely sampled for most taxa, and data is readily available at Genbank. After collecting data from select species where samples of reasonable sizes can be achieved from the spatial scales that are asked for (100's of km's), standard population genetics parameters can be calculated, such as Fst, and population structure visualized using e.g. haplotype networks.
Other methods to assess biodiversity range from analyses of tracks or "lebenspur" in the sediment surface to use of DNA fragments dispersed in the environment (eDNA). To produce species lists, both methods require a database where the analysed DNA or specific track pattern is matched with a species name. To answer specific questions with limited explanation power, such as "did the activity change the diversity?" these methods may prove usefull also without a matching database. However, much basic research regarding, *e.g.* the spatial distribution of eDNA, remains before the methods can be used.