Theme session C

Microbes to mammals: metabarcoding of the marine pelagic assemblage

Conveners: Ann Bucklin (USA), Rowena Stern (UK), Katja Metfies (Germany)

Session description

Molecular approaches are revolutionizing analysis and assessment of marine pelagic assemblages and enabling simultaneous detection of diversity from microbes to mammals. Emerging results indicate that global estimates of pelagic diversity will markedly increase with more accurate detection of rare, cryptic and introduced species, as well as higher resolution of time/space patterns. As high-throughput DNA sequencing (HTS) becomes more accessible and less expensive, use of metabarcoding (i.e., large-scale taxonomic identification of complex environmental samples via analysis of orthologous DNA regions) may be expected to expand into numerous applications in ocean research, monitoring, and management and may be critically important in allowing rapid detection and description of the impacts of climate change on pelagic biodiversity and biogeography.

Among the challenges remaining for reliable and routine application of metabarcoding are evaluation and comparison of results using different genes and gene regions; impacts of degraded DNA (e.g., environmental DNA and DNA recovered from gut contents); and continued development of taxonomically comprehensive reference databases for all gene regions. A particular need is to move metabarcoding applications from identification and detection of taxa to their quantification in terms of abundance and/or biomass.

Despite the remarkable promise of metabarcoding in yielding new understanding and appreciation for global patterns of biodiversity, it is critically important to maintain expertise and capacity in morphological taxonomy across the many groups represented in the marine pelagic assemblage.

The 10 oral presentations focused on diverse topics within the overall goal of the theme session:

Prospects for using metabarcoding for ecosystem monitoring and assessment. The session began with an introduction to the session by Ann Bucklin (USA), which was based upon the planned invited talk by Naiara Rodriguez-Ezpeleta (ES), who was unable to attend due to travel challenges. Several potential applications of metabarcoding for ecosystem monitoring and management were described, including calculation of biotic indices and detection of introduced invasive species (Abstract #250). Kelly Goodwin (USA) continued this focus in her talk (Abstract #447) on inclusion of DNA sequencing into an ecosystem observing program in the Southern California Bight (USA).

Environmental DNA (eDNA) analysis: The revolutionary use of eDNA for assessing biodiversity of pelagic ecosystems was called out by two exceptional talks. Luke Thompson (USA) presented comprehensive and compelling results from the Earth Microbiome Project (Abstract #230), describing a massive metagenetic survey. Natalie Sawaya (USA) then presented her research using eDNA metabarcoding to assess biodiversity in the Florida Keys National Marine Sanctuary (Abstract #449). This outstanding talk won the ICES award for the Best Presentation from an Early Career Scientist!

Comparison of morphological and metabarcoding analyses: A third talk using eDNA metabarcoding analysis also elucidated another focus of the theme session to compare metabarcoding results with morphological and optical analyses of the same samples; the talk prepared by Annette Govindarajan (USA; presented by Ann Bucklin) described a comparative morphological-molecular study of coastal zooplankton diversity (Abstract #441).

Prospects for metabarcoding analysis of species-level biodiversity for metazoans. Ongoing efforts to improve the accuracy and resolution of metabarcoding biodiversity assessment were presented in a talk prepared by Jennifer Questel (USA; presented by Ann Bucklin) on use of different gene markers for metabarcoding analysis of zooplankton biodiversity of the Pacific-Arctic Chukchi Borderlands region (Abstract #160). Hayley DeHart (USA) described efforts to improve taxonomic resolution of metabarcoding results by preparation of reference DNA sequence databases for two marker genes (mtCOI and 18S rRNA) for Arctic zooplankton (Abstract #437).

Metabarcoding analysis of trophic interactions and pelagic food-web dynamics. Ángel F. González (ES) presented a talk for Lorena Olmos-Pérez (ES) that described successful efforts to characterize diet composition and variability of different species of cephalopod larvae using metagenomics (Abstract #75). Another study described by Heidi Yeh (USA) used metabarcoding to characterize prey choice and selectivity of the copepod Calanus finmarchicus in the Gulf of Maine, NW Atlantic Ocean (Abstract #183).

Applications for time-series collections and long-term ocean observation: This theme session focus was brought to light by the last talk by Ann Bucklin (USA) on metabarcoding analysis of zooplankton diversity in time-series collections from an Ecosystem Monitoring (EcoMon) Survey of the NW Atlantic of the US continental shelf (Abstract #409).

Conclusions & recommendations:

Metagenetic analysis (also called metabarcoding) is revolutionizing the analysis of marine biodiversity due to the promise of rapid detection and description of the impacts of climate change on marine ecosystems. Importantly, applications of metabarcoding for ecosystem observation will require that metabarcoding approaches are validated, ground-truthed, and standardized. Such integrative morphological and molecular taxonomic approaches can then provide a foundation for monitoring and management of the pelagic realm. In particular, standardized biodiversity indices based on molecular (metagenetic or metabarcoding) analysis, can be used for assessment, management, and monitoring of pelagic ecosystems, including targeted contributions for quantifying the effects of climate change and evaluating the role of structural and functional diversity in marine ecosystems, consistent with the Marine Strategy Framework Directive (MSFD) and related ICES strategic scientific and advisory goals.