

ICES/PICES 6ZPS 2016/ Session S8 New technologies and approaches in zooplankton trophic studies

Molecular techniques for identifying zooplankton gut contents and quantifying feeding

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One of the challenges in teasing apart planktonic food webs is both identifying and quantifying the prey consumed in situ. In situ consumption rates of copepods are traditionally measured by bottle incubation with natural plankton or extrapolation of laboratory-derived functional curves to the field. Other approaches include use of various biomarkers to provide information on prey consumed. A recent approach has been the use of prey DNA in the guts of zooplankton to identify prey consumed. This approach, with universal PCR primers and predator-specific PCR blockers, provide a high degree of taxonomic specificity in identifying the prey consumed. Contemporary sequencing techniques have greatly increased the amount of sequence data ( $10^6$  amplicons) over older clone library techniques ( $10^2$  amplicons). Use of quantitative PCR and species-specific primers makes it possible to quantify the amount of DNA of individual prey species present in the zooplankton guts. While these approaches appear promising, there is much work needed to further validate the methods. We will discuss some initial results and areas requiring further work.

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