

## Theme Session F

### Complexity and structure of planktonic foodwebs: who really eats whom?

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Feeding and avoiding being eaten are fundamental processes that govern the structure and function of pelagic ecosystems. This is a broad and complex topic, but it must be better understood in order to predict how planktonic food webs may respond to global change. Warming may drive predator/prey and grazer mismatches by changes in relative timing of their life cycles; shifting biogeographical boundaries may alter prey selection and impacts of grazing; predicted smaller body sizes of zooplankton may result in mismatches in predator/prey and grazer size ratios. After decades of zooplankton research, there are many and diverse viewpoints on the controls and impacts of trophic relationships in planktonic foodwebs, including several different paradigms. Among these are: 1) predator/prey size ratios are key in structuring food webs; 2) metazoans can switch from eating bloom-forming species (e.g. diatoms) to eating their main competitor (e.g. protists), thus stabilising the food web; and 3) nutrient stress (i.e., food quality) may determine grazing pressure on phytoplankton. Clearly, a more holistic framework is needed for understanding trophic relationships throughout the planktonic food web. Key to success will be the coordinated use of diverse approaches (modelling, experimentation, direct observation) and techniques (molecular, stable isotopes) to reveal changing predator/prey and grazing relationships.

The session attracted 15 contributions (10 oral and 5 poster presentations) and brought together scientists from 9 nationalities. It was a pleasure to see, and interesting to learn of, such a wide variety of techniques that are currently being used on a global scale from both East to West and North to South to look at food web structure. These ranged from laboratory feeding studies using single species to an assessment of field-based meroplankton feeding on natural assemblages, and from quantitative PCR (qPCR) of gelatinous zooplankton to modelling of herring populations. The session was ordered such that the topic of the presentations progressed through the food web from the microbial loop to herring and capelin fisheries. The wide range of trophic levels, the novel use of techniques seen in the presentations, and the size of the audience were deemed marks of success demonstrating the importance and broad appeal of the session topic for the ICES community.

#### **Some prominent themes of the session included:**

**Diversity:** Theme session presenters recognised the importance of coordinated analysis of both the diversity of potential prey in the pelagic assemblage and the diversity of prey items in predator guts in order to yield more accurate and comprehensive understanding of prey choice and selectivity (F:04, F:12, F:13, F:14). In the northern Barents Sea, recently observed changes in the copepod community have been reflected in the feeding preferences of pelagic fish (F:01). In the Gulf of Riga, statistical analysis revealed that changes in the phytoplankton species composition clearly affected the growth of zooplankton species (F:13). As well as understanding prey composition, it is equally important to accurately identify the predator; this was demonstrat-

ed by two field studies through the successful use of molecular techniques (F:12, F:14).

**Increasing knowledge of trophic pathways:** A number of trophic linkages and pathways remain under-studied. The use of new approaches – beyond microscopic examination of predator gut contents – has helped us understand what's really being eaten. The application of analytical flow cytometry in feeding studies of zooplankton larval stages of decapods, bivalves and copepod nauplii (F:04, F:12) and heterotrophic nanoflagellates (F:15) has proved a useful technique to enumerate organisms (e.g., heterotrophic bacteria and marine cyanobacteria) that are too small to decipher using traditional gut content analysis. The use of fatty acids as biomarkers has been adopted to expand traditional stomach content studies and has provided complementary information on the importance of the trophic linkages between different zooplankton groups and mesopelagic fish around Iceland (F:09). The trophic link between proto-zooplankton and ichthyoplankton was demonstrated by a laboratory study which showed how the presence of algae and protists could enhance early feeding and thus higher growth and better condition in Atlantic herring larvae; this study highlighted the importance in the field for the timing of first-feeding by fish to coincide with algal spring blooms (F:02). The use of molecular techniques such as Polymerase Chain Reaction (PCR) & quantitative PCR (qPCR) were presented during the session as valuable tools to analyse prey of meroplankton (F:04, F:12) and fish (F:10), including especially prey groups which may remain undetected by traditional techniques. The development and optimisation of qPCR protocols was presented to characterise the trophic importance of gelatinous zooplankton in fish gut contents (F:10); this paper addressed the need to re-evaluate the overall significance of gelatinous organisms as prey sources, since this trophic pathway will create an alternative pathway of energy and elements in planktonic food webs.

**Impact on predator performance:** The analysis of food web dynamics becomes increasingly complex when we consider predator-prey linkages and carbon fluxes together with numerical, physiological and/or behavioural responses of the predator to differing prey characteristics and/or environmental conditions. These topics were addressed by both experimental and field studies during the session. The impact of food abundance on growth performance is theoretically straight forward; but empirical observations, especially in the field, remain complex and require further attention. A combined approach of feeding experiments using the natural plankton community and the estimation of metabolic rates revealed a highly food-limited environment for copepod nauplii in the oligotrophic gyres of the South Atlantic (F:12). Not only instantaneous but also past food limitation alters the metabolic performance of a predator as shown by starvation experiments using herring larvae (F:02). Next to prey abundance, its quality can also effect food web interactions. Nutrient limitation of algae influences not only the reproductive success of copepods but also their feeding selectivity, probably based on a chemosensory mechanism, and may thus also alter *in situ* carbon flow (F:07). These food quality effects show a clear interaction with prey abundance. Furthermore, food texture may have a significant impact on digestibility and assimilation efficiency, thus leading to an over- or underestimation of different prey items (F:10). A combined field and modelling approach revealed that nutrient inflow alters the whole food web structure, probably by changing growth conditions not only for phyto- but also for zooplankton (F:08). The abundance of non-prey taxa can influence the digestive capacity, protein biosynthesis and feeding activity of fish larvae, as shown by comparisons of herring larvae performance between clear and green water conditions (F:02). This highlights the importance of match-mismatch not

only with prey abundance and quality, but also with optimal environmental feeding conditions.

**Food web response to environmental drivers:** Environmental drivers affect the structure of planktonic food webs. The challenge is to understand and predict how and to what extent such changes will occur. An increase in sea surface temperature has resulted in a shift in certain zooplankton species northwards, changing the biomass of prey available in polar regions (F:11). Such temperature increases may also affect the phenology of plankton, which may lead to a mismatch between predators and prey. During the session, the topic of environmental drivers and the consequences of change were examined through both modelling and molecular techniques. The size spectrum of stable isotopes was shown to complement those of biomass in the synthetic description of food web properties and demonstrated that the trophic structure in central regions of the oceans is relatively homogeneous. Atmospheric nitrogen inputs affect stable isotopes and trophic structure of plankton and were shown to be associated with fewer trophic levels (F:06). Using a combination of both field and modelling results can provide valuable insights into the plankton community response to anthropogenic pressures and increase our understanding of trophic pathways (F:03, F:08, F:06). Given the potential disruption of planktonic food webs due to global change it will be important to incorporate food web processes into future assessment of fish stocks.

**Conclusions and recommendations:** Theme Session F reflected a wide variety of traditional and emerging techniques (e.g. biochemical and molecular; PCR, qPCR) that are currently under development and being adopted in marine ecology. The application of such novel approaches has yielded new insights into understanding the structure and complexity of planktonic food webs. Methods presented demonstrated their high potential to (1) accurately determine species diversity, which is essential for understanding ecosystem functioning and (2) enhance understanding of linkages between trophic levels within the plankton community. However, it became apparent that no method alone, either traditional approaches or new techniques, will be able to unravel the complexity of pelagic food web interactions. A multi-disciplinary approach is essential. As a cautionary note, it is not sufficient to assume that an organism is being eaten just because it is available to be eaten; therefore, inclusion of one or more techniques to assess feeding and/ or trophic linkages is crucial. We highly recommend that ICES continue to investigate, encourage and integrate research efforts focused on the dynamics, diversity, and function of planktonic food webs that use a combination of traditional and novel (molecular, biochemical) techniques in conjunction with modelling.