

Probing the Microbial Food Web of Lake Erie: Status and Changes.

Mohi Munawar(munawarm@dfo-mpo.gc.ca) ,I.F. Munawar, H. Van Stam and M. Fitzpatrick. Department of Fisheries and Oceans Canada, Great Lakes Laboratory for Fisheries and Aquatic Sciences, P.O. Box 5050, 867 Lakeshore Rd., Burlington, ON L7R 4A6.

Not much is known about the microbial food web structure and interactions in Lake Erie with the exception of phytoplankton which is well established. Fisheries and Oceans Canada has maintained a long term and lakewide database of Lake Erie phytoplankton and primary productivity since the early 1970's which permitted the assessment of the impact of the invasion of zebra mussels. Generally a shift from Diatoms to Green Algae was apparent. An overview of the carbon-14 size fractionated primary productivity data revealed that small sized organisms such as autotrophic picoplankton (<2 μ m) and nanoplankton (2-20 μ m) were the dominant size components of phytoplankton productivity. On the other hand, net plankton (>20 μ m) contributed the least to productivity, especially in the eastern basin. Significant structural and functional differences were observed for the three basins.

Although the microbial loop and its function is well established in marine ecosystems, little is known about the microbial plankton of the Great Lakes in general and Lake Erie in particular. Microbial surveys were initiated in Lake Erie on a lakewide basis in 1992, continued during 93-94 as a part of the Lake Erie trophic transfer (LETT). Microbial parameters such as bacteria, autotrophic picoplankton, heterotrophic nanoflagellates and ciliates were evaluated across the lake by means of epifluorescence-DAPI and quantitative Protargal Staining (QPS) techniques. In conjunction with the phytoplankton analysis by the standard Uthermohl technique, carbon-14 size fractionated primary productivity experiments were also conducted. These surveys have provided insight into the microbial foodweb structure of Lake Erie for the first time. The availability of this new microbial data has opened new frontiers of research and modelling in enhancing our understanding of the microbial food web dynamics and its linkage to fisheries about which very little is known.