**Methods**

*Field Sampling*

Sampling occurred in all three basins of Lake Erie in 2014, as part of the Cooperative Science and Monitoring Initiative (CSMI). We conducted monthly sampling of benthic macroinvertebrates, zooplankton, and water quality as well as seasonal sampling of fish and fish diets. Sample locations were designed to capture the west to east gradient and capture the nearshore to offshore gradient. Samples included in this study were collected in May and September, referred to here as spring and autumn, respectively.

This work was conducted from the Research Vessel Muskie (United States Geological Survey, Lake Erie Biological Station), a 70’ LOA, purpose-built research vessel with a mono-hull and twin propellers. Fish were captured using a four-seam, three bridle, bottom trawl, with a fishing circle that was 200 meshes by 12-cm mesh size. The body of the net transitions from a mesh size of 12-cm to 6-cm and was constructed of polyethylene. The cod end liner was constructed of knotless dyneema mesh with a stretched mesh size of 14-mm. The head rope length was 11.2-m and the foot rope length was 14.2-m. To accommodate hard bottom substrate, the sweep was designed with 8” rubber discs interspersed between 2-3/8” rubber discs in a configuration called a “rubber cookie sweep”, known to be successful for trawling for squid on glacial moraines in the north Atlantic. The bridle length was 36.6-m overall with a junction between the top and middle bridle at 18.3-m. Prescribed trawling time was 10 minutes at a target speed of 3 knots.

For each trawl sample, fish were sorted by species and size mode (determined by eye) and each species-size group were weighed in aggregate. From each catch, a subsample (n=5) from each species-size group was measured for individual lengths and weights (using a motion compensating scale with accuracy of 0.2-g). Total count was calculated by dividing the aggregate weight by the mean individual weight. Fish were immediately placed in a Shuttle™ Ultra-Low (Stirling Ultracold, Division of Global Cooling, Inc.) freezer after processing.

Zooplankton were collected with vertical net tows taken from just above the bottom to the surface using a 0.5-m-diameter bongo plankton net (150-μm mesh). The volume of water filtered was measured by positioning a TSK ® (Tsurumi-Sikie-Kosakusho Co., Ltd.) flowmeter in the mouth of the net. Zooplankton were concentrated and transferred to a sample bottle, narcotized with Alka-Seltzer®, and preserved with a 10% solution of phosphate buffered formalin.

Benthic macroinvertebrates were collected at each site using a ponar grab sampler (area = 0.046 m2). Samples were washed through a 500-μm mesh sieve and retained material was preserved with 95% ethanol containing Phloxine B dye.

At each site, a YSI® 6600 series multiparameter sonde was used to provide water-column measurements. Attached sensors measured depth, temperature, and dissolved oxygen availability.

*Laboratory analyses*

To determine zooplankton abundance and composition, the sample was added to a know volume of water, subsampled with a Hensen-Stempel pipette, and at least 200 organisms were counted and identified (Brooks 1959, Wilson and Yeatman 1959, Balcer et al. 1984) for each sample. To count large predatory cladocerans (e.g. *Bythotrephes longimanus* and *Leptodora kindti*), the whole sample was rinsed through a 150-μm sieve and all individuals were identified and counted. For each sample, prey lengths of up to 20 individuals of each species were measured to the nearest 1-μm using a Nikon SMZ-U stereoscopic zoommicroscope (7.5-75x magnification) eyepiece reticle. Prey length was converted to dry mass using mass-length regressions (need to cite). The mean dry mass of an individual of each prey type was determined for each site and multiplied by the number of each prey type at each site to determine dry-biomass contribution of each species in an individual location (Hyslop 1980). All invertebrates from zooplankton samples were identified to the lowest possible taxonomic level.

Macroinvertebrates from Ponar samples were rinsed through a 500-μm sieve and placed in a white enamel pan and picked, counted, and identified to family using a low power magnifier lamp (1.5x magnification). Chironomidae were further separated into pupae and larvae. For each sample, prey lengths of up to 10 individuals of each prey type were measured to the nearest 1-μm using a Nikon SMZ-U stereoscopic zoommicroscope (7.5-75x magnification) eyepiece reticle. Prey length was converted to dry mass using mass-length regressions (need to cite). The mean dry mass of an individual of each prey type was determined for each site and multiplied by the number of each prey type at each site to determine dry-biomass contribution of each prey type in an individual location (Hyslop 1980). All benthic macroinvertebrates were identified to the family taxonomic level.

In the laboratory, fish were thawed, total length (to the nearest +1-mm, TL) and weight (to the nearest +0.1-g wet mass) were measured, stomachs were removed, and the entire fish (minus stomach contents) was dried at 60 °C for 72 hrs or until a constant mass was obtained (to the nearest +0.001 g). For Emerald Shiners, which do not have a true stomach, the contents were removed from the esophagus through the second bend in the S-shaped digestive tract (Persson 1982).

To determine diet composition, all large prey (e.g. Chironomidae pupae and larvae, *Bythotrephes*, *Leptodora*) from each stomach were identified and counted. Mesozooplankton (e.g. Copepoda, Cladocera) were identified and counted from each stomach, so that at least 200 individuals were counted. For stomachs that contained more than 200 mesozooplankton, the sample was divided into equal aliquots and individually processed until a subsample containing 200 individuals was counted. For each stomach, prey lengths of up to five individuals of each prey type were measured to the nearest 1-μm using a Nikon SMZ-U stereoscopic zoommicroscope (7.5-75x magnification) eyepiece reticle. Prey lengths were then converted to dry mass using published mass-length regressions for each prey type (Pothoven et al. 2000a, 2001; Pothoven and Vanderploeg 2004). The dry mass of partially digested organisms were assumed equal to the mean individual mass of measured organisms. Total counts of each prey type from fish stomach were multiplied by the representative mean weight for that prey type and then summed to obtain the total biomass of each invertebrate group in the diet. All invertebrates from stomach contents were identified to the family taxonomic level. Diet composition was expressed as percent of total dry food mass.

Whole-body energy density was used as an index of fish condition. To determine energy density, the dried carcass was ground with a mortar and pestle to produce a homogenized sample. Subsamples were pressed into pellets containing a mean dry homogenate weight of 0.16 g (range: 0.06-0.23) and a mean spike weight of 0.17 g (range: 0.09-0.31). All samples were spiked with calorimetric grade benzoic acid to ensure complete combustion. Pellets were then combusted in a Parr 6400 automatic isoperibol calorimeter that was standardized with benzoic acid. Combustion samples were pressed into pellets containing a mean dry tissue weight of 0.16 g (range: 0.06-0.23) and a mean spike weight of 0.17 g (range: 0.09-0.31). Energy density is reported on a wet weight basis.

*Data analyses*

To determine prey selectivity, we used Vanderploeg and Scavia’s (1979) selectivity coefficient, W’, calculated as:

W’i = (ri / pi) / ri / pi);

where relative prey abundances in the environment (p) and diet (r) were expressed in numbers and ri / pi) was the maximum value of (ri / pi). Prey abundances were calculated based on the number of each prey in the environment or diet for each respective season and basin. The selectivity coefficient, W’, varies between 0 (no ingestion of a prey type) to 1, the W’ value for the most preferred prey type(s), i.e. the prey type(s) with the maximum value of (ri / pi). Prey abundance that was absent in diets but present the environment were eliminated from the analysis.