2000-03

General Schedule

(Say, 1829). Living specimens of Eastern Pondshell mussels were found at 10 of the 18 survey sites and comprised 3.87% of the total sample of 1008 living mussels found. New locality records for living Eastern Pondshell, Creek Heelsplitter, Squawfoot, Fluted-Shell, Paper Pondshell, and Cylindrical Papershell were also established. Supported by ODNR Division of Natural Areas and Preserves.

2:30 THE EVOLUTIOIN OF SIMULTANEOUS HERMAPHRODITISM IN THE FRESHWATER MUSSEL GENUS *TOXOLASMA* (BIVALVIA: UNIONIDAE). Angela M. Fetty (Walter R. Hoeh), Kent State University, Dept. of Biological Sciences, Kent OH 44242. Afetty7013@aol.com

Taxa that are reproductively variable have provided biologists with the ability to test mechanisms of evolutionary change. North American freshwater mussels, a primarily dioecious taxon, are an exceptionally useful study group for investigating mating system transitions (e.g., from dioecy to simultaneous hermaphroditism [SH]). Studies of unionid genera consisting of both dioecious and hermaphroditic species offer significant opportunities for increased comprehension of the ecological, genetic, historical, and morphological factors involved in the origin and maintenance of SH. The freshwater mussel genus *Toxolasma* currently contains eight recognized species: *T. corvunculus, T. cylindrellus, T. lividus, T. mearnsi, T. parvus, T. paulus, T. pullus,* and *T. texasensis* (*T. parvus* is the only hermaphroditic species). Species delineation and interspecific relationships within *Toxolasma*, currently based on morphological data sets, are questionable and have hindered the examination of mating system transitions in this genus. The goal of this project is to use phylogenetic analysis of DNA sequence data (from the cytochrome *c* oxidase subunit I [COI] gene) to (1) estimate the evolutionary relationships among multiple populations representing the species within *Toxolasma* and (2) use this estimate to infer the minimum number of mating system transitions that occurred within *Toxolasma*. The estimation of the phylogenetic relationships among the species within *Toxolasma* is a necessary first step toward gaining an understanding of the events that led to the origin of SH in this genus. To date we have extracted total DNA, PCR amplified a portion of the COI gene, gel purified the PCR products, and ran sequencing reactions for both strands of the PCR products. We have sequence from 42 individuals, representing 42 populations.

2:45 INFLUENCE OF ZEBRA MUSSELS, *DREISSENA POLYMORPHA*, ON PHYTOPLANKTON PHOTOSYNTHESIS IN LAKE ERIE. Robert T. Heath, X. Gao, H. Wang, and V. Mattson, Kent State University, Dept. Biological Sciences, Kent OH 44242. rheath@kent.edu

Although much attention has been given to investigation of population- and community-level effects of zebra mussels (ZM, *Dreissena polymorpha*), relatively little attention has been given to ecosystem-level effects of this non-indigenous mollusc. Here we report the possible effects of these molluscs on photosynthetic capabilities dependent on the physiological responses of phytoplankton in the western basin of Lake Erie. Phytoplankton were collected in 8L carboys from the 1 m stratum 9 km west of Rattlesnake Is. and 2 km north of Niagra Reef, a region with a silty sediment and relatively unpopulated by ZM. Fifteen ZM (1.3 to 1.7 cm in length) collected from rocks near Green Is. were washed, and placed in some carboys (exptl.) and not in others (control); carboys were incubated under laboratory conditions approximating ambient light and temperature. After 24 hours, photosynthetic parameters a, the photosynthetic potential, P_{opt}, the optimum photosynthesis per µg chlorophyll, and b, the photoinhibition coefficient for the phytoplankton in the carboys was determined in a "photosynthetron" that controls temperature at ambient T and varies light intensity of photosynthetically active radiation from 0 to 700 µE sec^{-1} m^{-2}. We found that in the presence of ZM, P_{opt} and α significantly declined, while b increased. This indicates that the presence of ZM may decrease the photosynthetic responses of phytoplankton communities they encounter not only by decreasing the number of phytoplankton but also by altering their physiology. This study was supported by Lake Erie Protection Fund Grant Nos. 97-18 and 98-09.

3:00 SELECTIVITY OF FISH SIZE AND SPECIES COMPOSITION FOR THREE TRAP NET DESIGNS. Daniel E. Shoup, Robert E. Carlson and Robert T. Heath, Kent State University, Dept. of Biological Sciences, Kent OH 44242. dshoup@kent.edu

Trap nets of varying design are commonly used to assess fish populations, but the effect of design on selectivity is not well known. This study compared both the size distribution and species composition of fish caught by trap nets with dimensions differing only in mesh size (0.6 cm delta mesh, 1.3 cm or 2.5 cm square mesh for small, medium, and large nets respectively) and throat size (3.8, 7.6 or 12.7 cm square respectively). Two nets of each mesh/throat size shared a 9 x 1.2m lead. Each net in the pair also had one 3 x 1.2 m wing. Nets were set on the bottom along the 2 m contour in Sandy Lake, Portage Co., Ohio. Nets were sampled 25 times between July 4, 1999 and August 20, 1999. All fish caught were identified and enumerated. On 14 dates, the total lengths were also recorded. There were significant differences in the minimum, mean, and maximum size of fish caught by the different mesh/throat sized trap nets. Large mesh/throat nets had significantly larger total catch per unit effort (CPUE) than small mesh/throat nets. Some species-specific CPUE's also differed between some net sizes. We conclude that data from trap nets with different mesh and throat sizes should not be directly compared with each other, and that multiple net mesh/throat sizes should be utilized when a more complete picture of fish size and abundance is desired. This research was supported in part by Sigma Xi, The International Research Society.

3:30 GENETIC STUDIES OF POPULATION STRUCTURE IN THE LAKE STURGEON OF THE GREAT LAKES. Tara Rose, Ted M. Cavender, Brian Mark and Paul A. Fuerst, Ohio State University, Dept. of Evolution, Ecology and Organismal Biology, Columbus OH 43210. Rose.256@osu.edu

Information about the genetic population structure of the lake sturgeon, *Acipenser fulvescens*, in the Great Lakes, is critical to adequate management of this locally endangered fish. Questions concerning the degree of population differentiation, and the similarity of populations are relevant in making decisions concerning possible restocking or supplemental stocking of populations. Genetic differences between localities within the lake sturgeon population have been examined using RAPD (Randomly Amplified Polymorphic DNA) analysis and microsatellite locus comparison. A set of fish representing several localities throughout the Great Lakes has been analyzed. These localities include the Wolf River and Menominee River from Wisconsin, the Sturgeon River and the St. Clair River and Lake Erie. Population distances based on allele sharing and allele frequency were determined and population relationships analyzed using UPGMA cladograms. The RAPD studies show substantial differences between localities, and an East-West component of overall differentiation. The analysis of these data by cladistic methods shows that genotypes are shared between some populations. An analysis of the same localities using microsatellite DNA shows a similar clustering of populations. The data should be expanded with additional populations and more loci to confirm the preliminary findings. The results suggest that transplantation of stock must be undertaken with care. (We thank the Wisconsin, Michigan and Ohio DNRs for assistance in collecting material and the USFWS, Ohio Sea Grant and the National Science Foundation for partial support of the work reported here).

3:45 MICROSATELLITE ANALYSIS OF FORMALIN TREATED LAKE ERIE STURGEON TO DETERMINE THE GENETIC VARIABILITY FOLLOWING A POPULATION CRASH. Julie L. Maybruck, and Paul Fuerst, Ohio State University, Dept of Molecular Genetics, Columbus OH 43210. Maybruck.2@osu.edu

Populations of the Lake sturgeon, *Acipenser fulvescens*, suffered a severe reduction in numbers when the value of sturgeon flesh and caviar was realized in 1860. By the end of the 19th century, the population in Lake Erie alone was reduced by 80%. A decline of this magnitude suggests that a population bottleneck may have occurred. To assess this possibility, a temporal genetic study examining the genetic variation of Lake Erie sturgeon is being conducted. Formalin treated specimens collected throughout the 20th century were obtained from The Ohio State University Museum of Biodiversity. These samples represent part of a larger study to determine if a population bottleneck has occurred. Difficulties in obtaining DNA from formalin have been reported. For example, Giorgi et al. (1994) found that formalin fixation caused DNA sequence changes. These results were confirmed by a study conducted in our lab, indicating that sequence comparisons are unreliable. However, no insertions or deletion events were observed in the mitochondrial analyses conducted in our lab nor were they reported by Giorgi et al. in their study of formalin treated nuclear DNA. Since microsatellite allele difference occur by changes in size but not in sequence, microsatellite DNA analysis of formalin fixed material was investigated. It was first necessary to determine the reliability of the microsatellite data from formalin treated specimens. A comparative study of microsatellite data between matched ethanol fixed and formalin treated samples from the same individuals was conducted. The banding patterns of ethanol and formalin treated samples from the same individual were found to be the same. Allele sizes were not changed. Microsatellite analysis appears to be a reliable and more appropriate technique for the analysis of the formalin treated specimens. Results using this method will be presented. (Supported by funds from the Ohio Sea Grant College Program).

4:00 EFFECTS OF PREY AVAILABILITY ON LARVAL GIZZARD SHAD (*DOROSOMA CEPEDIANUM*) PREY SELECTIVITY. David W. Paul, Maria J. Gonzalez and Amina I. Pollard. Wright State University, Dept. of Biological Sciences, 3640 Colonel Glenn Hwy, Dayton OH 45435-0001. dpaul@ehstech.com

The objective of this study was to compare prey selectivity by larval gizzard shad in a hypereutrophic reservoir (Acton Lake, Ohio) between years with different zooplankton composition (1996 and 1997). Zooplankton abundance was higher in 1996 than 1997. Rotifers dominated the zooplankton community (48.28% in 1996 and 92.31% in 1997) when larval gizzard shad were present in the lake. The proportion of cladocerans and small copepods was higher in 1996 (31.6%) than 1997 (6.7%). Mean density of larval gizzard shad was lower in 1996 (2.2 ind/m^3, max 10.4 ind/ m^3) than in 1997 (7.4 ind/m^3, max 35.6 ind/m^3). We calculated Chesson's Prey Selectivity Index on three larval fish sizes (< 10.5 mm TL, 10.6-15.0 mm TL and >15.1 mm TL). In 1996, larval gizzard shad <10.5 mm TL positively selected for nauplii, *Asplanchna sp., Polyarthra sp.* and *Synchaeta sp.* The medium size-class 10.6-15.0 mmTL selected cyclopoids, nauplii and *Asplanchna sp.* Larvae greater than 15.1 mmTL positively selected for *Daphnia parvula*, cyclopoids, nauplii and *Asplanchna sp.* In 1997 larvae <10.5 mm TL positively selected for cyclopoids, *Asplanchna sp , Brachionus angularis, Polyarthra sp.*, and *Synchaeta sp.* The medium size class selected for *Asplanchna sp., Polyarthra sp.*, and *Synchaeta sp.* Large larvae selected strongly for *Brachionus angularis* and *Asplanchna sp.* Our results suggest that rotifers, which are commonly excluded from studies of feeding preference, may be important food sources of gizzard shad throughout larval life stages, in particular, when the availability of cladocerans and copepods is low.