Under Heisen and States and State

MOLLUSK CONSERVATION SOCIETY

WALKERANA VOLUME 16 NUMBER 1 MARCH 2013

Pages 21-28

Effect of small dams on freshwater mussel population genetics in two southeastern USA streams.

Erin Abernethy, Erin McCombs, Lynn Siefferman, & Michael Gangloff



WALKERANA The Journal of the Freshwater Mollusk Conservation Society

©2013 ISSN 1053-637X

Editorial Board

CO-EDITORS

Gregory Cope, North Carolina State University Wendell Haag, U.S. Department of Agriculture Forest Service Tom Watters, The Ohio State University

EDITORIAL REVIEW BOARD Conservation

Jess Jones, U.S. Fish & Wildlife Service / Virginia Tech James Layzer, Tennessee Cooperative Fisheries Research Unit, Tennessee Tech University

Ecology

Ryan Evans, Kentucky Department of Environmental Protection, Division of Water Michael Gangloff, Appalachian State University Catherine Gatenby, White Sulphur Springs National Fish Hatchery Caryn Vaughn, Oklahoma Biological Survey, University of Oklahoma

Freshwater Gastropods

Paul Johnson, Alabama Aquatic Biodiversity Center Jeff Powell, U.S. Fish & Wildlife Service, Daphne, Alabama Jeremy Tiemann, Illinois Natural History Survey

Reproductive Biology

Jeff Garner, Alabama Division of Wildlife and Freshwater Fisheries Mark Hove, Macalester College/University of Minnesota

Survey/Methods

Heidi Dunn, Ecological Specialists, Inc. Patty Morrison, U.S. Fish & Wildlife Service Ohio River Islands Refuge David Strayer, Cary Institute of Ecosystem Studies Greg Zimmerman, Enviroscience, Inc.

Systematics/Phylogenetics

Arthur Bogan, North Carolina State Museum of Natural Sciences Daniel Graf, University of Wisconsin-Stevens Point Randy Hoeh, Kent State University

Toxicology

Thomas Augspurger, U.S. Fish & Wildlife Service, Raleigh, North Carolina Robert Bringolf, University of Georgia John Van Hassel, American Electric Power Teresa Newton, USGS, Upper Midwest Environmental Sciences Center

EFFECT OF SMALL DAMS ON FRESHWATER MUSSEL POPULATION GENETICS IN TWO SOUTHEASTERN USA STREAMS

Erin Abernethy

Department of Biology, Appalachian State University 572 Rivers St., Boone, North Carolina 28608 U.S.A.

current: Odum School of Ecology, University of Georgia 140 E. Green St., Athens, Georgia 30602 U.S.A.

email: efabernethy@gmail.com

Erin McCombs, Lynn Siefferman, Michael Gangloff

Department of Biology, Appalachian State University 572 Rivers St., Boone, North Carolina 28608 U.S.A.

ABSTRACT

The global imperilment of freshwater mussels is strongly linked to widespread habitat destruction by dams, but more subtle mechanisms by which dams impact mussels are not well studied. For example, dams fragment populations in free-flowing reaches, potentially leading to low survival probability due to genetic effects, but few studies have addressed the genetic effects of fragmentation on mussel populations. We examined patterns of genetic variation in the mitochondrial CO1 and ND1 genes in populations of two mussel species that were fragmented by >175 y old small dams. We found that only a few rare haplotypes were restricted to reaches either upstream or downstream of the dams, and an array of genetic parameters showed little differentiation among upstream and downstream reaches. These results can be interpreted in one of two ways. First, gene flow across these dams may remain high, resulting in little genetic fragmentation. Alternatively, the apparent lack of population differentiation could be a historical artifact of high, pre-dam gene flow, and the genetic markers we used may not yet reflect relatively recent population isolation.

KEY WORDS stream; dam; conservation; biodiversity; invertebrates

INTRODUCTION

Dams are responsible for many freshwater mussel population declines and extinctions (Williams et al., 1992; Neves et al., 1997; Vaughn & Taylor, 1999). Streams are impacted by dams through alterations in habitat, modifications in river hydrology and temperature, and blocked migration routes of host fishes (Watters, 1996; Lessard & Hayes, 2003; Graf, 2006). These effects may reduce freshwater mussel distribution, egg fertilization, infection of host fishes, and juvenile settlement particularly downstream of large dams (Fisher & LaVoy, 1972; Layzer & Madison, 1995; Moles & Layzer, 2008). Small dams (<5 m) also have negative effects, but mussel density, species richness, and growth rates can be higher immediately downstream of small dams compared to other parts of some watersheds (Gangloff et al., 2011; Singer & Gangloff, 2011). Dam age and height, stream physiochemistry, and watershed land use may be key factors responsible for the observed benefits of these small dams (Gangloff et al., 2011). In contrast to the effects of dams on physical stream habitats, more subtle effects such as genetic population fragmentation are not well known for mussels.

Genetic evidence for population fragmentation by dams has been documented in highly mobile fishes such as white-spotted charr (Salvelinus leucomaenis) and bull trout (Salvelinus confluentus) (Neraas & Spruell, 2001; Yamamoto et al., 2004) and in less mobile fishes such as logperch darters (Percina caprodes; Haponski et al., 2007). Conversely, populations of other fishes, including greenside darters (Etheostoma blennioides) and black redhorse (Moxostoma duquesnei), as well as crayfishes, showed no genetic differentiation between populations upstream and downstream from dams (Haponski et al., 2007; Reid et al., 2008, Hartfield, 2010). The few studies of mussel genetic population structure provide similarly mixed results, but none show evidence of reduced gene flow or isolation by dams. Populations of several mussel species showed little or no detectable genetic population structure despite the presence of dams that separate these populations (Berg et al., 1998; Grobler et al., 2006; Szumowski et al., 2012), but other populations show evidence of significant structure apparently unrelated to recent dam effects (Hughes et al., 2004; Elderkin et al., 2008; Grobler et al., 2011). These studies suggest that dam-induced genetic effects on aquatic organisms are highly situation-specific and may depend on factors such as dam porosity, the number and proximity of dams within a river system, and the mobility and life history of species. In addition, because mussels are dependent on fish hosts and host fish use varies among species, genetic structure of mussel populations is highly influenced by differences in mobility and life history traits among fish species.

In this study, we examined the genetic structure of Elliptio arca and Elliptio complanata populations located upstream and downstream from two >175 y old small dams that impound short reaches of the streams (< 2 km). Elliptio arca is endemic to the Mobile Basin and has declined substantially, making it a species of high conservation concern (Mirarchi et al., 2004). Primary fish hosts of E. arca are darters (Haag & Warren, 2003). Darters are known for their low mobility that can be greatly reduced or blocked by stream barriers (Warren & Pardew, 1998; Schaefer et al., 2003). Elliptio complanata is widespread in Atlantic slope drainages and is considered stable (Williams et al., 1993). Elliptio complanata is reported to use members of the Centrarchidae, Percidae, and Fundulidae as host fishes, but recent evidence suggests that American eels (Anguilla rostrata) may also be an important host (Lellis, 2001; Cummings & Watters, 2004). Juvenile eels are able to climb wet dam faces directly, and adults can move short distances over-land, allowing them to circumvent stream obstructions such as dams (Sorensen & Bianchini, 1986; Tesch, 2003). We predicted that if the dams are acting as barriers for these two mussel species and their host fishes then we should find unique haplotypes restricted to reaches either upstream or downstream from the dams, low gene flow values, population structuring values that suggest no interbreeding, and statistically significant genetic differentiation values.

METHODS AND MATERIALS

We studied genetic diversity in *Elliptio arca* (Alabama Spike) in Sandy Creek, a third-order tributary of the Tallapoosa River (Mobile River Basin), in east-central Alabama, and *Elliptio complanata* (Eastern Elliptio) in the upper Tar River (Pamlico River Basin), a fourth-order stream in north-central North Carolina (Fig. 1). Both of the study streams drain largely forested catchments in rural, sparsely-populated sections of the southern Appalachian Piedmont and are fragmented by historic mill dams (height <5 m), which impound short reaches of the streams (<2 km).



FIGURE 1

Mussel collection sites on Sandy Creek, Chambers Co., Alabama, and the Tar River, Granville Co., North Carolina. On both streams, site 1 is upstream of the mill dam impoundment, site 2 is immediately downstream of the dam, and site 3 is 0.5 km (Sandy Creek) or 5.0 km (Tar River) downstream of the dam. On Sandy Creek, the darkened area in the stream channel upstream of site 2 represents the mill dam impoundment; darkened areas downstream of site 2 are artifacts of the map and do not represent impoundments.

Sandy Creek is impounded by Jones Mill Dam (c. 1836) in Chambers County, Alabama, and the Tar River is impounded by Gooch Mill Dam (c. 1797) in Granville County, North Carolina. Both dams are structurally intact and do not have obvious routes for upstream fish passage. The sluiceways that powered the millworks of both dams are now sediment-filled and have not been operational for at least 50 y. Water moves over the top of these dams, except in periods of low flow, and seasonal high flow events create substantial flow over the dams. We collected mussels in free-flowing reaches upstream, immediately downstream, and farther downstream of the dams (Fig. 1). Large populations of the study species exist in all of these reaches (Gangloff et al., 2011; McCormick, 2012).

We excised fresh tissue (adductor muscle) in the lab and stored it in TE buffer in a -20°C freezer. We sampled adductor muscle to reduce the possibility of sampling male mitotypes, because unionid reproductive tissues can exhibit doubly uniparental mtDNA inheritance (Breton et al., 2007). Any male mitotypes that were sequenced were omitted from the data set. DNA was extracted using a Qiagen DNeasy[®] kit and animal tissue extraction protocol and stored in a -20°C freezer. We examined fragments of the mitochondrial NADH dehydrogenase 1 (ND1) and cytochrome c oxidase 1 (CO1) genes. These markers were chosen due to their widespread use in freshwater mussel phylogenetic and phylogeographic studies (Serb & Lydeard, 2003; Campbell et al., 2005, 2008; Elderkin et al., 2008).

Approximately600basepairsoftheCO1geneand700 base pairs of the mitochondrial ND1 gene were amplified with polymerase chain reaction (PCR) using available primers (Serb et al., 2003; Campbell et al., 2008). PCR product was then sent to Retrogen, Inc. (San Diego, CA) for sequencing with an ABI 3730 DNA Analyzer (Applied Biosystems, Grand Island, NY). Forward and reverse sequences were compiled and edited in Sequencher (Gene Codes Corporation, Ann Arbor, Michigan) and aligned in MEGA5 (Tamura et al., 2011). CO1 and ND1 sequences for each specimen were concatenated in order to create a single sequence for each individual and one haplotype network for each species. TCS was used to construct haplotype networks (Clement et al., 2000). Reference individuals in these haplotype networks are concatenated Elliptio arca sequences from the Black Warrior Drainage (GenBank Accession Number AY655093) and the Coosa Drainage (AY654995) and Elliptio complanata from the Connecticut River (AY158780) and the James River (EU448173; Serb et al., 2003; Campbell et al., 2005; M. Gangloff et al., unpublished data). Individual sequences within our dataset that represented unique haplotypes (when not concatenated) were uploaded to GenBank (Accession numbers KC708454 - KC708480). DnaSP was used for population genetics analyses (Rozas et al., 2003).

We computed several standard population genetics statistics, including nucleotide diversity, haplotype diversity, population structuring, gene flow, and genetic differentiation. Nucleotide diversity (π) is defined as the mean number of nucleotide differences between any two sequences and was calculated using equation 10.5 from Nei (1987). Values of nucleotide diversity range from 0 (low) to 0.2 (high) in animals (Daniels et al., 2002; Marko, 2004). Haplotype diversity (H_d) reveals haplotype richness within a subpopulation and was calculated using equation 8.4 from Nei (1987). Values of haplotype diversity range from 0 (low) to 1 (high) in animals (Barber et al., 2002; Cross et al., 2007). The population structure statistic (Fst) calculates the genetic variation among subpopulations, with values ranging between 0 and 1, with values closer to 1 suggesting less interbreeding (Hudson et al., 1992, equation 3). Gene flow (N_m) is an estimate of the effective number of migrants exchanged between subpopulations per generation (Hudson et al., 1992, equation 4). Values between 0 and 1 are considered low and those greater than 1 high. Negative F_{st} and N_m values are a result of more diversity within subpopulations than between populations. Genetic differentiation (S_{nn}) determines the probability of haplotype recovery from the same location (Hudson, 2000). Values near 1 are indicative of highlydifferentiated populations, and values near 0.5 suggest populations are panmictic.

RESULTS

The population of *E. arca* in Sandy Creek had eight haplotypes, two of which were found only upstream of the dam (haplotypes 3 and 4) and two were found only downstream (haplotypes 2 and 8; Fig. 2A). Two of the most common haplotypes were found in all three reaches (haplotypes 1 and 5), and two were shared between only two reaches (haplotypes 6 and 7). Nucleotide diversity was low for all populations, ranging from 0.00179 to 0.00196, and haplotype diversity was relatively high, ranging from 0.68 to 0.79 within reaches (Table 1). Population structuring was low ($F_{st} = 0.00683$), and gene flow between reaches was high ($N_m = 72.69$). Genetic differentiation was closer to 0.5 than to 1 ($S_{nn} = 0.38$), suggesting that *E. arca* populations separated by Jones Mill Dam are one panmictic population.

The population of *E. complanata* in the Tar River had nine haplotypes, one of which was found only upstream from the dam (haplotype 6) and two were found only immediately downstream of the dam (haplotypes 2 and 4; Fig. 2B). Three of the most common haplotypes were shared between all three reaches (haplotypes 1, 5, and 7), and three haplotypes were shared between the upstream reach and at least one downstream reach (haplotypes 3, 8, and 9). Nucleotide diversity was also low in this species, ranging from 0.01011 and 0.01047, and haplotype diversity was high, ranging from 0.69 to 0.83 (Table 1). Population structuring was low ($F_{st} = -0.06181$), and gene flow was high between the three

populations ($N_m = -8.59$). Genetic differentiation was closer to 0.5 than to 1 ($S_{nn} = 0.31$), suggesting that *E. complanata* populations separated by Gooch Mill Dam are one panmictic population.



FIGURE 2

Parsimony network of mtDNA haplotypes for the concatenated CO1 and ND1 genes in (A) *Elliptio arca* and (B) *Elliptio complanata*. Each pie chart represents a unique haplotype with connecting lines representing one nucleotide difference (step) between haplotypes, except where otherwise noted. Observed haplotypes are labeled with an identifying number followed by the number of individuals having that haplotype (N). Colors represent the proportion of individuals from each reach having a particular haplotype (white, upstream of the dam; grey, immediately downstream of the dam; black, farther downstream of the dam; see Fig. 1). Pie charts with only one color are haplotypes unique to a particular reach. See Methods for information about reference individuals.

DISCUSSION

We found no strong evidence of genetic isolation in either *Elliptio arca* or *E. complanata* as a consequence of stream fragmentation by mill dams. Although we did observe unique haplotypes upstream (3 out of 17 haplotypes) and downstream (4 out of 17 haplotypes) from both dams, this small number of unique haplotypes does not conclusively suggest that isolation is occurring (Grobler et al., 2006; Perrin et al., 2008). If occurring, isolation would also be evident from low gene flow, high population structuring values, and significant genetic differentiation parameters (Hamilton, 2009).

Because evidence for isolation is weak, either unidirectional or bidirectional gene transfer may be occurring across these small dams. Downstream gene transfer for both species could happen easily by sperm drift or during high flow events when infected host fishes are washed over the top of mill dams. Upstream gene transfer is more difficult to envision, especially for E. arca. Darters, host fishes for E. arca, are known for their low mobility that can be greatly reduced or blocked by stream barriers (Schaefer et al., 2003). Darters would have a difficult time moving upstream over Jones Mill Dam during the flooding events when there is substantial flow over the dam. On the other hand, the American eel, a likely host fish for E. complanata in the Tar River, is well-known for its ability to circumvent stream obstructions such as dams (Sorensen & Bianchini, 1986; Tesch, 2003). This ability provides a plausible mechanism for upstream movement of glochidia and gene flow. Although eels were not found by recent surveys at Gooch Mill Dam, they have been found upstream of other small mill dams in the Tar River (J. Holcomb, unpublished data). Other potential host fishes for E. complanata present at Gooch Mill Dam, Lepomis cyanellus, Lepomis gibbosus, Lepomis macrochirus, and Micropterus salmoides, would likely have a difficult time getting upstream of Gooch Mill Dam (Ellis, 1974; J. Holcomb, unpublished data). In contrast to downstream gene flow, upstream dispersal is probably less frequent and highly context-specific, and we are unable to propose mechanisms of upstream gene flow for *E. arca* in Sandy Creek. Nevertheless, the distribution of unique haplotypes and other genetic measures do not support a primarily downstream mode of gene flow in either population.

Although we found no evidence of genetic isolation or unidirectional gene flow, a number of factors need to be considered when assessing the extent to which populations upstream and downstream of the dams are isolated. More rapidly evolving genetic markers such as microsatellites might detect population structure that was not evident from mtDNA, which may not show evolutionary changes over the 177-216 year existence of these dams and the relatively small number of mussel generations during this time. Similarly, because population sizes of both species remain large at all of our sites, they may retain a large percentage of historical genetic diversity such that our measures reflect signatures of former, pre-dam gene flow rather than contemporary gene flow (see Grobler et al., 2011). Our relatively small sample size may also have limited our ability to detect rare haplotypes or other patterns of genetic variability and structuring in these populations. Future work could take advantage of non-lethal DNA collection techniques such as viscera, mantle, and foot swabbing to allow increased sample size without sacrificing more individuals (Henley et al., 2006).

Our study provides a first look at the extent to which small dams might fragment freshwater mussel populations. Dams are a pervasive component of stream ecosystems with > 2.5 million small dams in the United States (National Research Council, 1992), and stream fragmentation by dams poses serious demographic risks to isolated populations in addition to potential genetic consequences (Morita & Yamamoto, 2002; Schick & Lindley, 2007). Dam removal projects are an increasingly important tool for re-establishing biological connectivity and ecosystem function and may provide benefits to numerous aquatic species, but they may also have substantial negative short-term impacts (Stanley et al., 2002; Stanley & Doyle, 2003; Sethi et al., 2004). In Sandy Creek and the Tar River, dense, species-rich mussel assemblages occur immediately downstream from these dams (Singer & Gangloff, 2011; McCormick, 2012). Although more research is needed to determine patterns and mechanisms of gene flow, the lack of strong evidence for genetic isolation in our study suggests that, at least in the short-term, removing Jones and Gooch mill dams should be considered low priority objectives relative to other habitat restoration projects in these watersheds.

ACKNOWLEDGEMENTS

We thank Byron Hamstead, Rachael Hoch, Ray Kessler, and Megan McCormick for assisting with mussel collections. Molecular work was greatly aided by the guidance of Dr. Eva Gonzales. This project was funded by Appalachian State University's Office of Student Research and Biology Department and a State Wildlife Grant to Dr. Michael Gangloff and Lynn Siefferman through the North Carolina Wildlife Resources Commission.

LITERATURE CITED

Barber, P.H., Moosa, M.K. & S.R. Palumbi. 2002. Rapid recovery of genetic diversity of stomatopod populations on Krakatau: temporal and spatial scales of marine larval dispersal. *Proceedings of the Royal Society* B 269: 1591-1597.

- Berg, D.J., Cantonwine, E.G., Hoeh, W.R. & S.I. Guttman. 1998. Genetic structure of *Quadrula quadrula* (Bivalvia: Unionidae): little variation across large distances. *Journal of Shellfish Research* 17: 1365-1373.
- Breton, S., Beaupre, H.D., Stewart, D.T., Hoeh, W.R. & P.U. Blier. 2007. The unusual system of doubly uniparental inheritance of mtDNA: isn't one enough? *Trends in Genetics* 23: 465-474.
- Campbell, D.C., Johnson, P.D., Williams, J.D., Rindsberg, A.K., Serb, J.M., Small, K.K. & C. Lydeard. 2008. Identification of 'extinct' freshwater mussel species using DNA barcoding. *Molecular Ecology Resources* 8: 711-724.
- Campbell, D.C., Serb, J.M., Buhay, J.E., Roe, K.J., Minton, R.L. & C. Lydeard. 2005. Phylogeny of North American amblemines (Bivalvia, Unionoida): prodigious polyphyly proves pervasive across genera. *Invertebrate Biology* 124: 131-164.
- Clement, M., Posada, D. & K.A. Crandall. 2000. TCS: a computer program to estimate gene genealogies. *Molecular Ecology* 9: 1657-1659.
- Cross, M.A., Collins, C., Campbell, N., Watts, P.C., Chubb, J.C., Cunningham, C.O., Hatfield, E.M.C. & K. MacKenzie. 2007. Levels of intra-host and temporal sequence variation in a large CO 1 sub-units from *Anisakis simplex* sensu stricto (Rudolphi 1809) (Nematoda: Anisakidae): implications for fisheries management. *Marine Biology* 151: 695-702.
- Cummings, K.S. & G.T. Watters. 2004. Mussel/host data base. http://128.146.250.63/Musselhost/ [15 February, 2013]
- Daniels, S.R., Stewart, B.A. & P.A. Cook. 2002. Congruent patterns of genetic variation in a burrowing freshwater crab revealed by allozymes and mt DNA sequence analysis. *Hydrobiologia* 468: 171-179.
- Elderkin, C.L., Christian, A.D., Metcalfe-Smith, J.L. & D.J. Berg. 2008. Population genetics and phylogeography of freshwater mussels in North America, *Elliptio dilatata* and *Actinonaias ligamentina* (Bivalvia: Unionidae). *Molecular Ecology* 17: 2149-2163.
- Ellis, J.E. 1974. The jumping ability and behavior of green sunfish (*Lepomis cyanellus*) at the outflow of a 1.6 ha pond. *Transactions of the American Fisheries Society* 103: 620-623.
- Fisher, S.G. & A. LaVoy. 1972. Difference in littoral fauna due to fluctuating water levels below a hydroelec-

tric dam. Journal of the Fisheries Research Board of Canada 29: 1472-1476.

- Gangloff, M.M., Hartfield, E.E., Werneke, D.C. & J.W. Feminella. 2011. Associations between small dams and mollusk assemblages in Alabama streams. Journal of the *North American Benthological Society* 30: 1107-1116.
- Graf, W.L. 2006. Downstream hydrologic and geomorphic effects of large dams on American rivers. *Geomorphology* 79: 336-360.
- Grobler, P.J., Jones, J.W., Johnson, N.A., Beaty, B., Struthers, J., Neves, R.J. & E.M. Hallerman. 2006. Patterns of genetic differentiation and conservation of the slabside pearlymussel, *Lexingtonia dolabelloides* (Lea, 1840) in the Tennessee River drainage. *Journal of Molluscan Studies* 72: 65-75.
- Grobler, J.P., Jones, J.W., Johnson, N.A., Neves, R.J. & E.M. Hallerman. 2011. Homogeneity at nuclear microsatellite loci masks mitochondrial haplotype diversity in the endangered fanshell pearlymussel (*Cyprogenia stegaria*). Journal of Heredity 102: 196-206.
- Haag, W.R. & M.L. Warren. 2003. Host fishes and infection strategies of freshwater mussels in large Mobile Basin streams, USA. *Journal of the North American Benthological Society* 22: 78-91.
- Hamilton, M.B. 2009. *Population Genetics*. John Wiley & Sons, West Sussex, UK.
- Haponski, A.E., Marth, T.A. & C.A. Stepien. 2007. Genetic divergence across a low-head dam: a preliminary analysis using logperch and greenside darters. *Journal of Great Lakes Research* 33: 117-126.
- Hartfield, E.E. 2010. Consequences of low-head dams on crayfish distribution and gene flow in Alabama streams. *Thesis, Auburn University*, Auburn, Alabama, USA.
- Henley, W.F., Grobler, P.J. & R.J. Neves. 2006. Noninvasive method to obtain DNA from freshwater mussels (Bivalvia: Unionidae). *Journal of Shellfish Research* 25: 975-977.
- Hudson, R.R. 2000. A new statistic for detecting genetic differentiation. *Genetics* 155: 2011-2014.
- Hudson, R.R., Slatkin, M. & W.P. Maddison. 1992. Estimation of levels of gene flow from DNA sequence data. *Genetics* 132: 583-589.
- Hughes, J., Baker, A.M., Bartlett, C., Bunn, S., Goudkamp, K. & J. Somerville. 2004. Past and present patterns of connectivity among populations of four

cryptic species of freshwater mussels *Velesunio* spp. (Hyriidae) in central Australia. *Molecular Ecology* 13: 3197-3212.

- Layzer, J.B. & L.M. Madison. 1995. Microhabitat use by freshwater mussels and recommendations for determining their instream flow needs. *River Research and Applications* 10: 329-345.
- Lellis, W.A. 2001. Freshwater mussel survey of the Delaware Water Gap National Recreation Area: qualitative survey. *Report to the National Park Service*. US Geological Survey, Wellsboro, PA.
- Lessard, J.L. & D.B. Hayes. 2003. Effects of elevated water temperature on fish and macroinvertebrate communities below small dams. *River Research and Applications* 19: 721-732.
- Marko, P.B. 2004. 'What's larvae got to do with it?': disparate patterns of post-glacial population structure in two benthic marine gastropods with identical dispersal potential. *Molecular Ecology* 13: 597-611.
- McCormick, M. 2012. Counterintuitive effects of small dams on freshwater mussel assemblages. *Thesis, Appalachian State University*, Boone, North Carolina, USA.
- Mirarchi, R.E., Garner, J.T., Mettee, M.F. & P.E. O'Neil. 2004. *Alabama wildlife. Volume 2. Imperiled aquatic mollusks and fishes.* University of Alabama Press, Tuscaloosa, Alabama.
- Moles, K.R. & J.B. Layzer. 2008. Reproductive ecology of *Actinonaias ligamentina* (Bivalvia:Unionidae) in a regulated river. *Journal of the North American Benthological Society* 27: 212-222.
- Morita, K. & S. Yamamoto. 2002. Effects of habitat fragmentation by damming on the persistence of stream-dwelling charr populations. *Conservation Biology* 16: 1318-1323.
- National Research Council. 1992. *Restoration of aquatic ecosystems: science, technology, and public policy*. National Academies Press, Washington, DC.
- Nei, M. 1987. *Molecular evolutionary genetics*. Columbia University Press, New York, New York.
- Neraas, L.P. & P. Spruell. 2001. Fragmentation of riverine systems: the genetic effects of dams on bull trout (*Salvelinus confluentus*) in the Clark Fork system. *Molecular Ecology* 10: 1153-1164.
- Neves, R.J., Bogan, A.E., Williams, J.D., Ahlstedt, S.A. & P.W. Hartfield. 1997. Status of aquatic mollusks in the southeastern United States: a downward spiral of diversity. Pp. 43-85. [In:] Benz, G.W. & D.E. Collins (eds.). Aquatic fauna in peril: the southeastern

perspective. Lenz Design and Communications, Decatur, Georgia.

- Perrin, W.F., Wursig, B.G. & J.G.M. Thewissen. 2008. *Encyclopedia of marine mammals*. Academic Press, Burlington, Massachusetts.
- Reid, S.M., Wilson, C.C., Mandrak, N.E. & L.M. Carl. 2008. Population structure and genetic diversity of black redhorse (*Moxostoma duquesnei*) in a highly fragmented watershed. *Conservation Genetics* 9: 531-546.
- Rozas, J., Sanchez-DelBarrio, J.C., Messeguer, X. & R. Rozas. 2003. DnaSP, DNA polymorphism analyses by the coalescent and other methods. *Bioinformatics* 19: 2496-2497.
- Schaefer, J.F., Marsh-Matthews, E., Spooner, D.E., Gido, K.B. & W.J. Matthews. 2003. Effects of barriers and thermal refugia on local movement of the threatened leopard darter, *Percina pantherina. Environmental Biology of Fishes* 66: 391-400.
- Schick, R.S. & S.T. Lindley. 2007. Directed connectivity among fish populations in a riverine network. *Journal of Applied Ecology* 44: 1116-1126.
- Serb, J.M., Buhay, J.E. & C. Lydeard. 2003. Molecular systematics of the North American freshwater bivalve genus Quadrula (Unionidae: Ambleminae) based on mitochondrial ND1 sequences. *Molecular Phylogenetics and Evolution* 28: 1-11.
- Serb, J.M. & C. Lydeard. 2003. Complete mtDNA sequence of the North American freshwater mussel, *Lampsilis ornata* (Unionidae): an examination of the evolution and phylogenetic utility of mitochondrial genome organization in Bivalvia (Mollusca). *Molecular Biology and Evolution* 20: 1854-1866.
- Sethi, S.A., Selle, A.R., Doyle, M.W., Stanley, E.H. & H.E. Kitchel. 2004. Response of unionid mussels to dam removal in Koshkonong Creek, Wisconsin. *Hydrobiologia* 525:157-165.
- Singer, E. & M. Gangloff. 2011. Effect of a small dam on freshwater mussel growth in an Alabama USA stream. *Freshwater Biology* 56: 1904-1915.
- Sorensen, P.W. & M.L. Bianchini. 1986. Environmental correlates of the freshwater migration of elvers of the American Eel in a Rhode Island brook. *Transactions of the American Fisheries Society* 115: 258-268.
- Stanley, E.H. & M.W. Doyle. 2003. Trading off: the ecological effects of dam removal. *Frontiers in Ecology and the Environment* 1: 15-22.

- Stanley, E.H., Luebke, M.A., Doyle, M.W. & D.W. Marshall. 2002. Short-term changes in channel form and macroinvertebrate communities following lowhead dam removal. *Journal of the North American Benthological Society* 21: 172-187.
- Szumowski, S.C., Boyer, S.L., Hornbach, D.J. & M.C. Hove. 2012. Genetic diversity of two common freshwater mussel species, *Lampsilis cardium* and *Quadrula pustulosa* (Bivalvia: Unionidae), in a large federally protected waterway (St. Croix River, Minnesota/ Wisconsin, U.S.A.). *American Malacological Bulletin* 30: 59-72.
- Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & S. Kumar. 2011. MEGA5: Molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution* 28: 2731-2739.

Tesch, F.W. 2003. The eel. Blackwell, Oxford, UK.

Vaughn, C.C. & C.M. Taylor. 1999. Impoundments and the decline of freshwater mussels: a case study of an extinction gradient. *Conservation Biology* 13: 912-920.

- Warren, M.L. & M.G. Pardew. 1998. Road crossings as barriers to small-stream fish movement. Transactions of the *American Fisheries Society* 127: 637-644.
- Watters, G.T. 1996. Small dams as barriers to freshwater mussels (Bivalvia, Unionoida) and their hosts. *Biological Conservation* 75: 79-85.
- Williams, J.D., Fuller, S.L.H. & R. Grace. 1992. Effects of impoundment on freshwater mussels (Mollusca: Bivalvia: Unionidae) in the main channel of the Black Warrior and Tombigbee Rivers in western Alabama. Bulletin of the Alabama Museum of Natural History 13:1-10.
- Williams, J.D., Warren, M.L., Cummings, K.S., Harris, J.L. & R.J. Neves. 1993. Conservation status of freshwater mussels of the United States and Canada. *Fisheries* 18: 6-22.
- Yamamoto, S., Morita, K., Koizumi, I. & K. Maekawa. 2004. Genetic differentiation of white-spotted charr (Salvelinus leucomaenis) populations after habitat fragmentation: spatial-temporal changes in gene frequencies. *Conservation Genetics* 5: 529-538.

TABLE 1

Nucleotide diversity (π), haplotype diversity (H_d), population structuring (F_{st}), gene flow (N_m), and genetic differentiation (S_{nn}) for the concatenated genes (CO1 and ND1) in *Elliptio arca* and *Elliptio complanata*. Reaches represent populations in the vicinity of mill dams on Sandy Creek, AL, (*E. arca*) and the Tar River, NC, (*E. complanata*). The upstream reaches were upstream of the mill dam impoundments, the mill dam reaches were immediately downstream of the dams, and the downstream reaches were 0.5 km (Sandy Creek) or 5.0 km (Tar River) downstream of the dams (see Fig. 1).

Species	Reach	n	π	H_d	F_{st}	N_m	Snn
Elliptio arca	Upstream	14	0.00186	0.79			
	Mill dam	12	0.00179	0.68			
	Downstream	16	0.00196	0.72			
	Overall	42	0.00188	0.73	0.00683	72.69	0.38
Elliptio	Upstream	17	0.01047	0.76			
complanata	Mill dam	14	0.01011	0.83			
	Downstream	13	0.01036	0.69			
	Overall	44	0.00993	0.75	-0.06181	-8.59	0.31



THE JOURNAL OF THE FRESHWATER MOLLUSK CONSERVATION SOCIETY



©2013

FMCS 2013-2015 Officers

President Patricia Morrison Ohio River Islands NWR 3982 Waverly Road Williamstown, WV 26187 patricia_morrison@fws.gov

President Elect Teresa Newton USGS 2630 Fanta Reed Rd. LaCrosse, WI 54603 tnewton@usgs.gov

Secretary Greg Zimmerman EnviroScience, Inc. 6751 A-1 Taylor Rd. Blacklick, Ohio 43004 gzimmerman@enviroscienceinc.com *Treasurer* **Heidi L. Dunn** Ecological Specialists, Inc. 1417 Hoff Industrial Park O'Fallon, MO 63366 636-281-1982 Fax: 0973 **Hdunn@ ecologicalspecialists.com**

Past President Caryn Vaughn Oklahoma Biological Survey University of Oklahoma 111 E Chesapeake St. Norman, OK 73019 cvaughn@ou.edu

WALKERANA The Journal of the Freshwater Mollusk Conservation Society

OUR PURPOSE

©2013

The Freshwater Mollusk Conservation Society (FMCS) is dedicated to the conservation of and advocacy of freshwater mollusks, North America's most imperiled animals. Membership in the society is open to anyone interested in freshwater mollusks who supports the stated purposes of the Society which are as follows:

1) Advocate conservation of freshwater molluscan resources;

2) Serve as a conduit for information about freshwater mollusks;

3) Promote science-based management of freshwater mollusks;

4) Promote and facilitate education and awareness about freshwater mollusks and their function in freshwater ecosystems;

5) Assist with the facilitation of the National Strategy for the Conservation of Native Freshwater Mussels (Journal of Shellfish Research, 1999, Volume 17, Number 5), and a similar strategy under development for freshwater gastropods.

OUR HISTORY

The FMCS traces it's origins to 1992 when a symposium sponsored by the Upper Mississippi River Conservation Committee, USFWS, Mussel Mitigation Trust, and Tennessee Shell Company brought concerned people to St. Louis, Missouri to discuss the status, conservation, and management of freshwater mussels. This meeting resulted in the formation of a working group to develop the National Strategy for the Conservation of Native Freshwater Mussels and set the ground work for another freshwater mussel symposium. In 1995, the next symposium was also held in St. Louis, and both the 1992 and 1995 symposia had published proceedings. Then in March 1996, the Mississippi Interstate Cooperative Research Association (MICRA) formed a mussel committee. It was this committee (National Native Mussel Conservation Committee) whose function it was to implement the National Strategy for the Conservation of Native Freshwater Mussels by organizing a group of state, federal, and academic biologists, along with individuals from the commercial mussel industry. In March 1998, the NNMCC and attendees of the Conservation, Captive Care and Propagation of Freshwater Mussels Symposium held in Columbus, OH, voted to form the Freshwater Mollusk Conservation Society. In November 1998, the executive board drafted a society constitution and voted to incorporate the FMCS as a not-for-profit society. In March 1999, the FMCS held it's first symposium "Musseling in on Biodiversity" in Chattanooga, Tennessee. The symposium attracted 280 attendees; proceedings from that meeting are available for purchase. The second symposium was held in March 2001 in Pittsburgh, Pennsylvania, the third in March 2003 in Raleigh, North Carolina, the fourth in St. Paul, Minnesota in May 2005, the fifth in Little Rock, Arkansas in March 2007, the sixth in Baltimore, Maryland in April 2009, the seventh in Louisville, Kentucky in 2011, and the eighth in Guntersville, Alabama in 2013. The society also holds workshops on alternating years, and produces a newsletter four times a year.

FMCS SOCIETY COMMITTEES

Participation in any of the standing committees is open to any FMCS member. Committees include:

Awards Environmental Quality and Affairs Gastropod Distribution and Status Genetics Guidelines and Techniques Information Exchange - Walkerana and Ellipsaria Mussel Distribution and Status Outreach Propagation and Restoration

TO JOIN FMCS OR SUBMIT A PAPER

Please visit our website for more information at http://www.molluskconservation.org

Or contact any of our board members or editors of WALKERANA to talk to someone of your needs. You'll find contact information on the back cover of this publication.