M.L. 2013 Minnesota Aquatic Invasive Species Research Center Subproject Abstract
For the Period Ending December 31, 2018

SUBPROJECT TITLE: MAISRC Subproject 9.2: Population genomics of zebra mussel spread pathways, genome sequencing and analysis to select target genes and strategies for genetic biocontrol.
SUBPROJECT MANAGER: Dr. Michael McCartney
AFFILIATION: University of Minnesota, Minnesota Aquatic Invasive Species Research Center
MAILING ADDRESS: 2003 Upper Bufford Circle, Skok Hall 135
CITY/STATE/ZIP: St. Paul, MN 55108
PHONE: (612) 626-1412
E-MAIL: mmccartn@umn.edu
WEBSITE: www.maisrc.umn.edu
FUNDING SOURCE: Environment and Natural Resources Trust Fund (ENRTF)
LEGAL CITATION: M.L. 2013, Chp. 52, Sec. 2, Subd. 06a

SUBPROJECT BUDGET AMOUNT: $380,318
AMOUNT SPENT: $380,318
AMOUNT REMAINING: $0

Overall Subproject Outcome and Results

Since arriving in Duluth Harbor in 1989, zebra mussels have infested more than 150 inland lakes and 17 rivers and streams in MN, with rising ecologic and economic costs. Efforts to block new invasions must be focused strategically on major sources of spread. To help achieve this, we used direct, forensic-like analyses to genetically identify waters from which mussels were carried to infest MN lakes. Using our new genome sequences and methods, we genetically classified mussels from more than 70 water bodies, with more than 6,000 DNA markers per mussel (compared to 9 markers/mussel in Subproject 9.1) – providing significantly increased clarity in the analysis. We found that lakes in the Detroit Lakes, Brainerd and Alexandria regions form large, unique genetic clusters found nowhere else. Additionally, mussels from the Mississippi and St. Croix Rivers, Lake Superior, and Lake Minnetonka (4 highly-likely source waters) are distinguishable from the clustered invasions with 6,000 genomic markers, but with our previous analysis of 9 markers, they were not. More research is needed across a larger, more regional landscape to determine the original sources of zebra mussels into Minnesota, but results reinforce the management message that prevention can work – there is no genetic information to support the hypothesis of a “super spreader” lake. Early and high profile infestations of zebra mussels appear to have been contained (e.g. Lake Millle Lacs). However, vectors that are moving mussels locally within lake-rich regions, need to be identified and blocked.

For the first time, we sequenced the entire zebra mussel genome, using state of the art technology that allowed mapping of genes to chromosomes with great confidence. We sequenced and measured expression of genes in tissues that control shell formation, byssal thread attachment, and survival in high temperatures—each are strong candidates for targeted gene modification. The results include a publicly accessible genome: a powerful tool for invasion biology and biocontrol researchers in Minnesota and worldwide.

Subproject Results Use and Dissemination

The results from this project were regularly communicated in presentations to public and professional audiences. McCartney delivered a total of 14 public presentations on research activities and outcomes at non-scientific meetings and events, and authored or co-authored a total of nine presentations on results of this work at professional conferences, meetings, and invited seminars, including talks at the University of MN Duluth, University of Montana Flathead Lake Biological Station, Montana Fish Wildlife and Parks, and the University of Iowa. As intended in the dissemination plan, outreach was accomplished at local, state and national levels with public talks in Douglas, Hubbard, Itasca, Meeker, Otter Tail, and Stearns Counties in MN, two in Wisconsin, two in Montana and one in Iowa. Media attention on this project was high and resulted in three print news items, including two front-page feature articles in the Minneapolis Star Tribune. A highlight was two podcasts by Montana Public Radio in which both the population genomics of spread and the genome sequencing projects were covered in detail. Our research was regularly communicated in newsletter articles posted on the MAISRC website. Information about the zebra mussel genome project in the form of a white paper, written originally for a professional audience of scientists and managers in multiple disciplines (Activity 3), but accessible to members of the public with some background in AIS[1]. Two publications are in process (titles below)—one in revision[2] and the other to be submitted soon. Two other manuscripts are in preparation, one on invasion genomics (Activity 1), and the other reporting on sequencing and analysis of the zebra mussel genome (Activities 2 and 3). All Next Generation Sequence data from Activities 1 and 2 will be publicly available in the MAISRC Data Repository at the University of Minnesota or the National Center for Biotechnology Information database.

[1] McCartney, M.A., Mallez, S., Gohl, D. and K. Beckman (2018) The zebra mussel genome project: developing a new resource for invasion biology and biocontrol research. A white paper available from the author.

[2] McCartney, M.A., Mallez, S., Gohl, D. and K. Beckman (in revision) Genome projects in invasion and conservation genetics research programs. *Conservation Genetics*

Mallez, S. and McCartney, M.A. (in prep) Moving zebra mussels into the 'omics' era: SNPs from NGS-based genotyping outperform microsatellites in discerning invasion sources. *Ecology and Evolution*