

Zebra Mussel Genetic Biocontrol and Genomic Surveillance

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University of Minnesota Genomics Center
5/21/2026



Towards Developing Genetic Biocontrol Tools in Zebra Mussels

MAISRC Subproject 9

Zebra mussel genome project

2017-2019



Mike McCartney

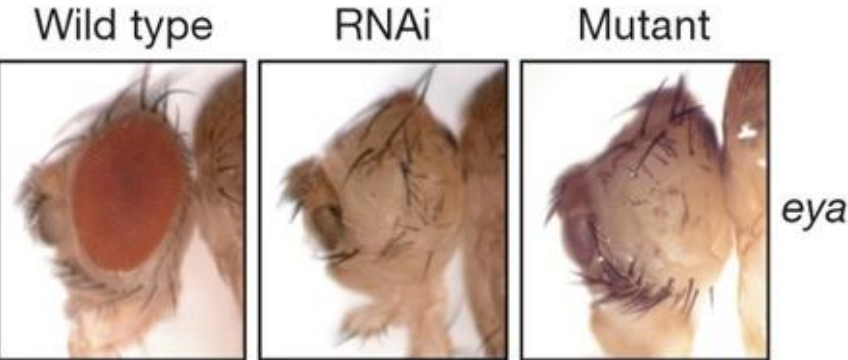


How Do You Genetically Manipulate An Organism You Can't Robustly Cultivate?



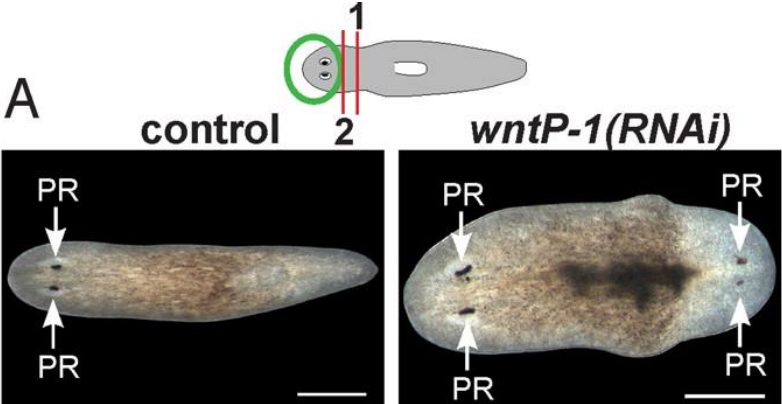
RNA Interference is a Versatile Tool for Manipulating Gene Expression

Drosophila



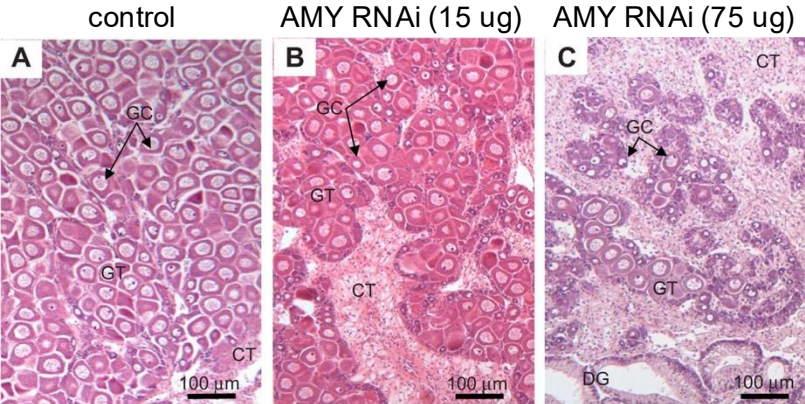
Dietzl et al. 2007. *Nature*.

Planarians



Petersen and Reddien 2009. *PNAS*.

Oysters



Huvel et al. 2015. *J. Exp. Biol.*

Humans

FDA Approves Patisiran, First-Ever RNA Interference Therapeutic Approved for Clinical Use

ASGCT Oligonucleotide and RNAi Therapeutics Committee - August 16, 2018

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2020-2022

2023

MAISRC Subproject 36
RNA-interference screens for
zebra mussel biocontrol target
genes



Scott Ballantyne
UWRF



2024-2028

SERDP Project RC23-3845
RNA interference (RNAi) for
targeted control of invasive
zebra mussels



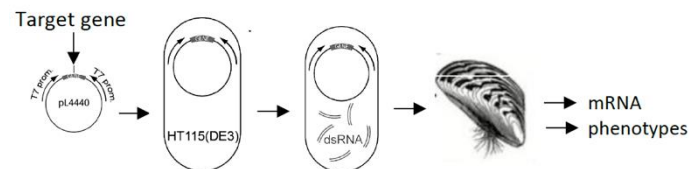
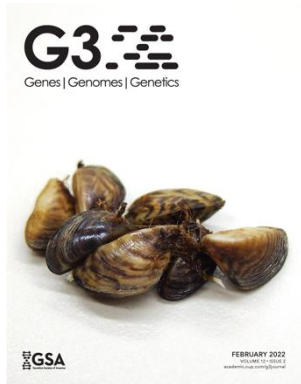
Cathy Richter
USGS CERC



Katy Klymus
USGS CERC



Thea Edwards
USGS CERC



Engineering Microbes to Express RNAi Triggers



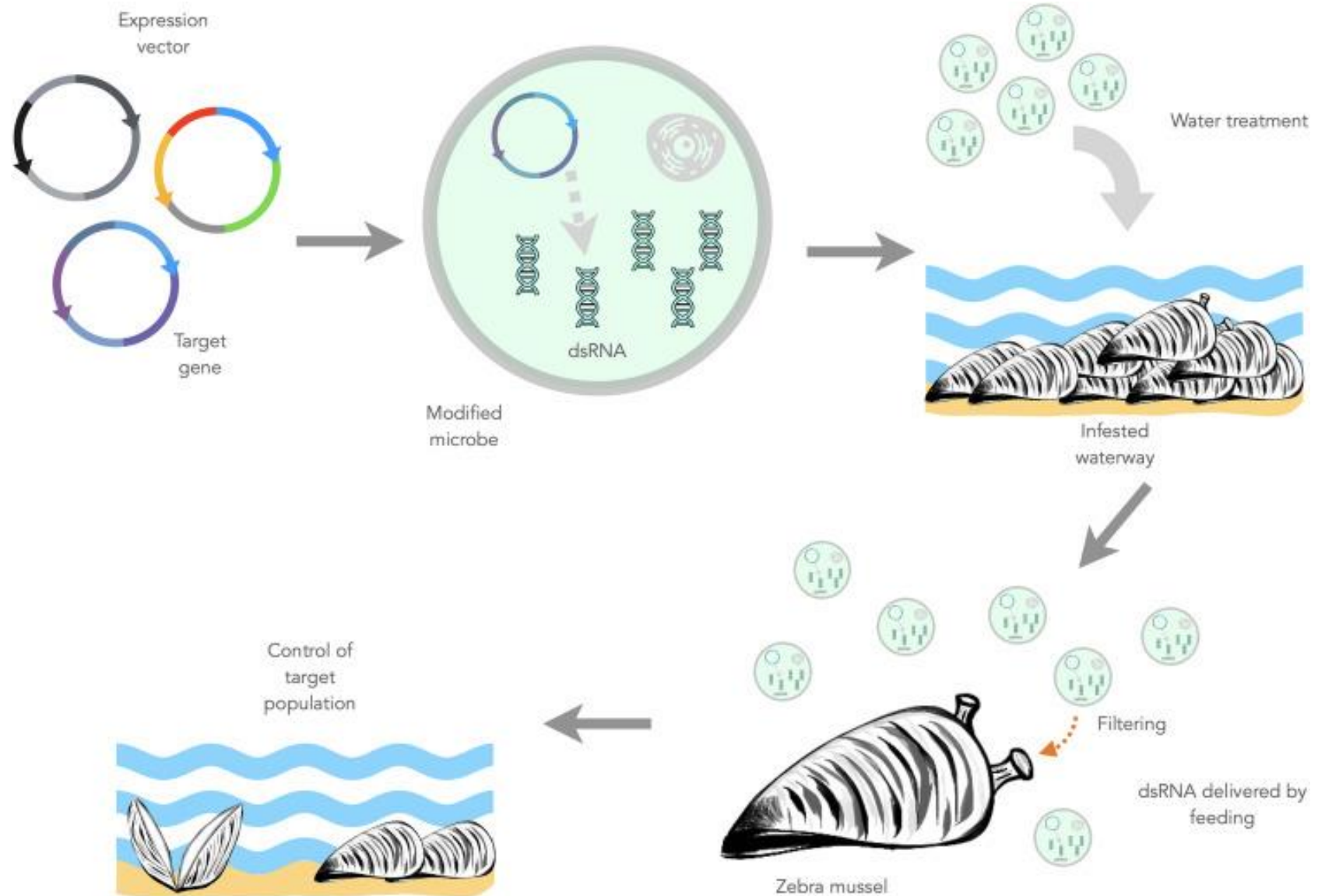
Scott Ballantyne



Lindsey O'Brien



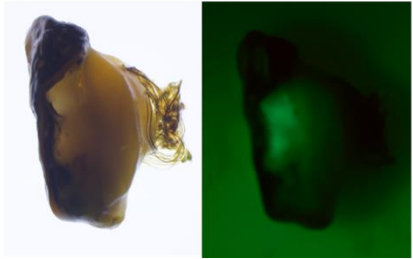
Victor Hernandez
Elizarraga



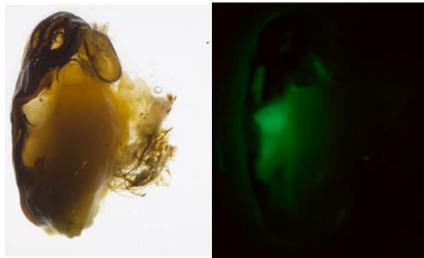
Knock-Down of Zebra Mussel Gene Expression by RNAi

Injection

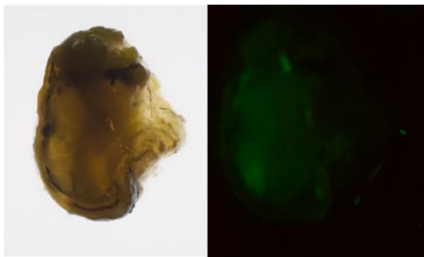
Injection control (Calcein)



Injection dsRNA

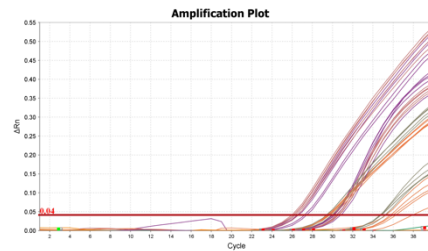


No injection

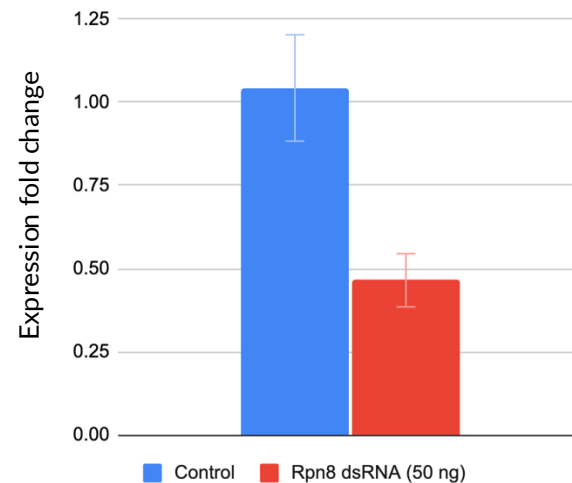


→
RNA
Extraction

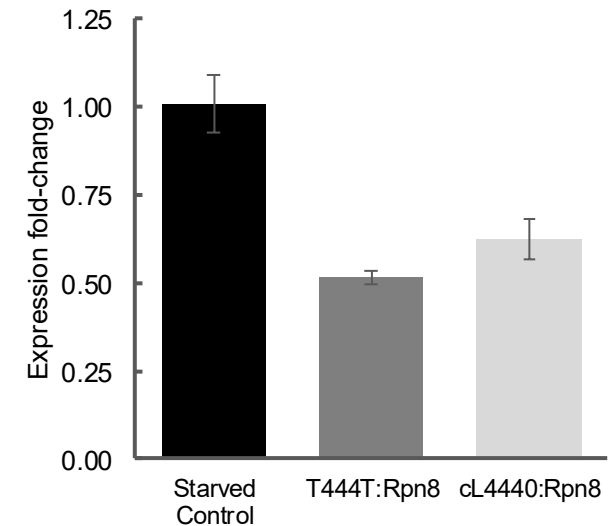
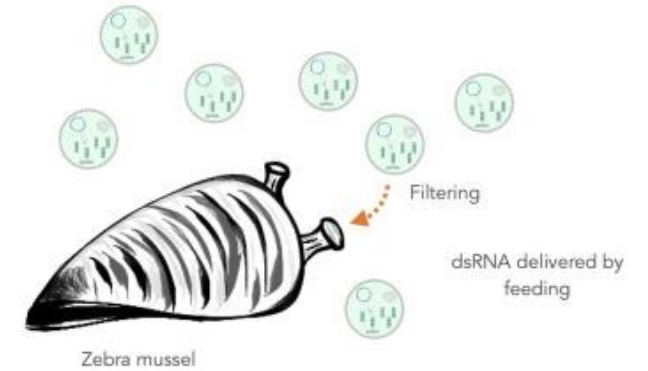
RT-qPCR



Rpn8 dsRNA



Feeding



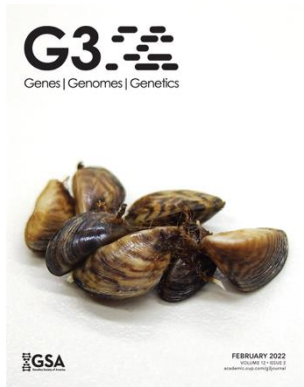
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RNA-interference screens for zebra mussel biocontrol target genes

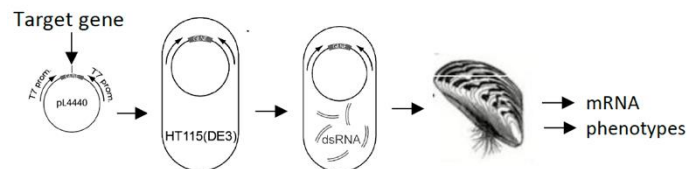


Scott Ballantyne
UWRF



2024-2028

SERDP Project RC23-3845
RNA interference (RNAi) for targeted control of invasive zebra mussels



USGS G25AP00161-00
Genomic Surveillance of Zebra Mussel Populations Using Genotyping by Sequencing

2025-2028



Alex Bajcz
MAIRSC



Cathy Richter
USGS CERC



Katy Klymus
USGS CERC

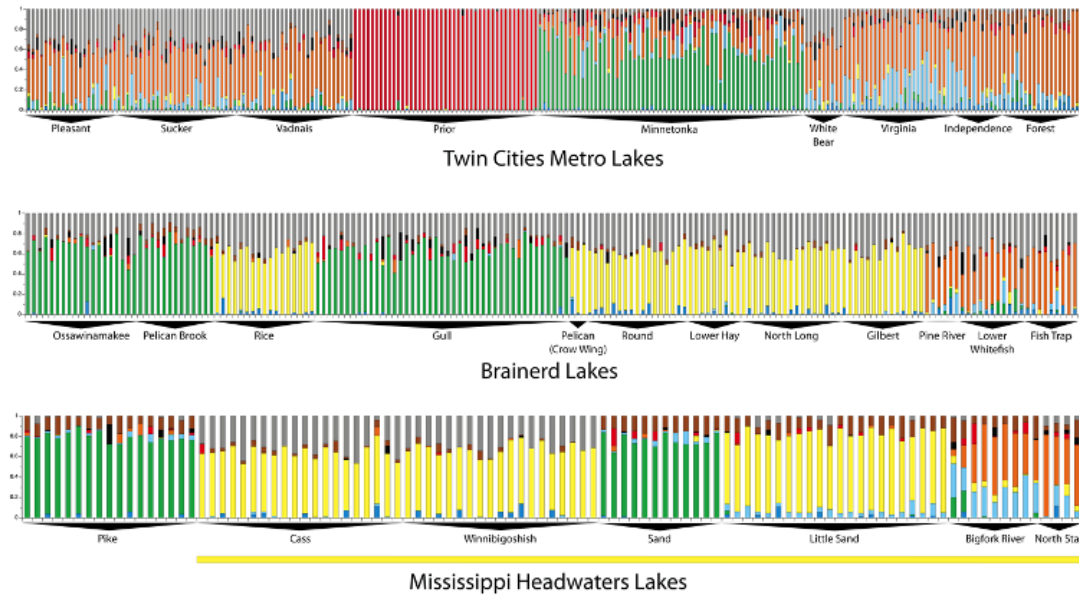


Thea Edwards
USGS CERC

Genomic Surveillance to Infer Invasion Pathways



Zebra mussel genomic surveillance



McCartney *et al.* 2025. *Scientific Reports.*



Mike McCartney



Alex Bajcz
MAIRSC



Victor Hernandez
Elizarraga



GENOMICS CENTER

MINNESOTA AQUATIC INVASIVE SPECIES RESEARCH CENTER **Mussel Strains** **GENOMICS CENTER UNIVERSITY OF MINNESOTA**

Filter & generate results
Use these filters to restrict the outputs generated. The filters are cumulative; only records satisfying all filters will be retained.

Filter by invasion year
Select invasion year range: 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020

Filter by watershed
Filter by search string
Filter by state
Filter by county
Filter by waterbody
Filter by scenario ranking
Reset filters
Regenerate outputs

Connections between source and destination waters
Map Table
Each arrow on the map shows a possible infestation history connection between two waterbodies (or sites within larger waterbodies) according to a statistical model. Each arrow points from the "donating" waterbody to the "receiving" waterbody. Black arrows show the most likely scenarios according to the model; the second-most likely scenarios are in gray. Arrow line width is proportional to the relative evidence for a given scenario, according to the model; thicker lines have greater evidence. Sometimes, the model believes two waterbodies contributed significantly to the population of a single receiving waterbody (admixture). Such scenarios are shown via dashed lines. Click any line to see more information about that prospective connection. The same data are available in tabular form in the second tab.

Ancestry plots
Graphs Table
Each bar shows the genetic profile of one individual geotyped from a given site (x-axis). Colors represent distinct genetic clusters (Qs). These Q values (q1 to q9) distill thousands of markers in the genome into nine ancestry categories. Only the top three per individual are shown; the rest are shown in gray. Taller colored segments indicate stronger genetic affinity with a given cluster. Similar bar patterns indicate genetic similarity between individuals and sites. The same data are available in tabular form in the second tab.

Download graphs as PDF

<https://z.umn.edu/MusselStrains>



Acknowledgements



The UMGC Innovation Lab



The University of Minnesota Genomics Center

Collaborators

UMGC

Lindsey O'Brien
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