Fifteen years of studying the Texas hornshell: what we know, and what that means

David J. Berg & Kentaro Inoue
Department of Biology
Miami University
bergdj@miamioh.edu
Warm winters
Good football
Miami University

Cold winters
Bad football
Collaborators

Brian Lang  Kentaro Inoue  Todd Levine
THE BIG QUESTION
(in ecology)

Why are organisms where they are, and why aren’t they where they aren’t?

• Contemporary conditions
• Historical conditions
• Human activity
THE BIG QUESTION
(in conservation)

What factors cause populations to decline or disappear?

• Environmental challenges
• Demographic challenges
• Genetic challenges
**Popenaias popeii**
Texas hornshell

- Endemic to Rio Grande & Gulf coastal drainages
- Isolated/fragmented populations

Historic records and current distribution are marked on the map.
Black River, New Mexico

Crevice

Rock shelf

Undercut bank
Objectives

- Describe “habitat” use
- Understand demography
- Characterize genetic structure
- Inform conservation efforts of NMDGF
Methods

• Identify ecological hosts and habitat use
• Estimate population size and change
• Partition genetic variation
Study sites:
Black River, southeast NM

- Single species system
- 14 km-reach of the stream
- Closed-population

Mark-and-recapture sites
Laboratory trials

• 24 of 33 species were hosts
• 17 native, 7 introduced species

HOST GENERALIST
Host Identification
> 99% of glochidia carried by:

River carpsucker (Carpiodes carpio; 84%)

Gray redhorse (Moxostoma congestum; 12.9%)

Red shiner (Cyprinella lutrensis; 2.5%)

Levine et al. 2012
Mussel Demography
Mark-and-recapture

- Surveyed from 1997 to 2012
  - Three sites; two microhabitats (riverbanks and river channels)
  - Tested hydrological cycles on demographic parameters
- Program MARK
  - Recapture probability
  - Survival
  - Finite rates of population growth ($\lambda$)

Inoue et al. 2014
Distance Sampling

- Shallow habitats (every 250 m)
- Deep habitats (every 500 m)

<table>
<thead>
<tr>
<th>Sampling Sites</th>
<th>Depth (m)</th>
<th>Area (m²)</th>
<th>Total (m²)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Shallow sites</td>
<td>236,500.3</td>
<td>84.1</td>
<td>281,167.1</td>
</tr>
<tr>
<td>Deep sites</td>
<td>44,666.8</td>
<td>15.9</td>
<td></td>
</tr>
</tbody>
</table>

Inoue et al. 2014
Mussel Demography

- Recapture probability higher in river channels (80% vs. 70%)
- Survival similar between habitats

- Avg. annual survival = 98.6%
- $\lambda = 0.999$ (range = 0.988 – 1.064)

- Black River in 2012
  
  N = 48,006 individuals (95% CI: 28,849-74,127)
  
  60% in “good” habitat, 40% in “bad” habitat

Inoue et al. 2014
Mussel Demography

Minimum monthly discharge (m³/s)

Survival

Mean monthly discharge (m³/s)

Inoue et al. 2014
Genetic Analyses

- mtDNA sequences
  COI (~ 800 bp)
  - haplotype diversity

- Microsatellites
  20 loci
  - population genetic structure
  - Approximate Bayesian computation (divergence time, \( N_e \), habitat connectivity)

Inoue et al. 2015
Genetic Variation – COI sequences

- 34 haplotypes
- “star” pattern
- 1 BR haplotype

Black River (n = 146)
Rio Grande (n = 10)
Devils River (n = 3)
Rio Grande (n = 58)

Inoue et al. 2015
Genetic Variation – 18 microsatellites

Inoue et al. 2015
Group 1

Black River

Parameters Median 95% credible interval
Black River $N_e$ 5870 (3654 – 9,210)
Rio Grande $N_e$ 70,300 (41,600 – 91,900)
Divergence Time (yr) 80,270 (21,093 – 168,210)

$F_{st} = 0.246$

Inoue et al. 2015

Group 2

Devils River

Rio Grande
Conclusions

1. Three fish species are the ecological hosts
   Manage hosts

2. Black River population is stable but threatened by declining discharge
   Ensure minimum flow, monitor demography

3. Black River and Rio Grande are genetically distinct
   Manage as separate units

Levine et al. 2012. Freshwater Biology 57: 1854-1864 (Corrigendum 57: 2762)
Next Steps

1. Population viability analysis (in progress)

2. Re-introduction into Delaware River (in progress)

3. Genetic/genomic analyses of additional populations (in preparation)

Ultimate Goal:

Quality habitat supporting demographically robust populations with sufficient genetic variation