

# Environmental DNA Methods for Detecting Species at Risk Fish

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Environmental Assessments & Approvals



National Research  
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# Introduction

- Species at Risk (SAR) detection historically required conventional surveys
- Environmental DNA (eDNA) as a rapid SAR surveillance method is gaining traction in research, but is not widely used in other sectors
- **eDNA:** DNA shed or released in a habitat used to infer species detection/no detection

# Introduction

- Advantages for targeted SAR assessments:
  - Time & cost savings (esp. large areas)
  - Improved accuracy & repeatability
  - Covert, rare or patchily distributed species
  - Multi-season monitoring
  - Historic vs. recent signal detection (sediment)
  - Metabarcoding communities

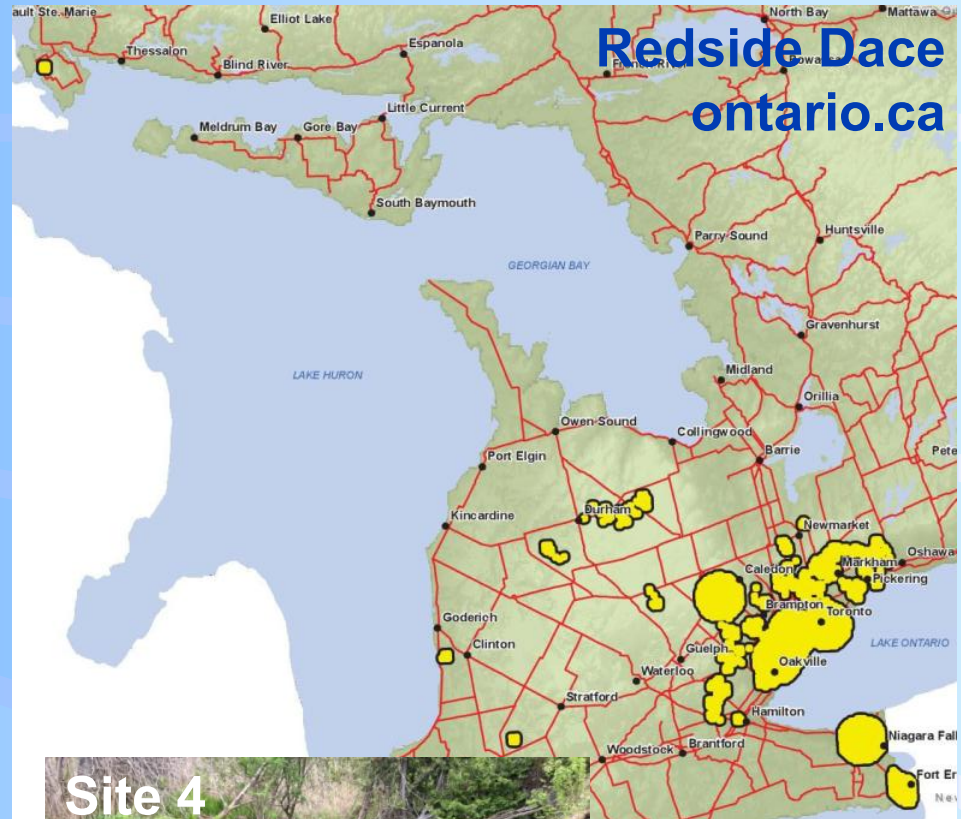
# Introduction

- Four-year study to develop eDNA protocols for SAR assessments in environmental consulting
- Five focal SAR in Ontario:
  - Blanding's Turtle (THR)\*
  - Little Brown Myotis (END)
  - Silver Shiner (THR)
  - Redside Dace (END)
  - Lake Sturgeon (END)
- Agency engagement (foster support)

**\*Tarof *et al.* (Submitted to eDNA)**

# Introduction

- Occupy pools in shallow streams
- Live to ~4yrs old
- Males spawn annually in gravel riffles at 2-3yrs old (mid May-early June)
- Shed scales



# Introduction

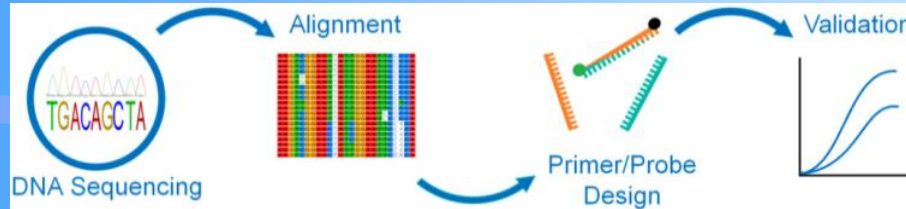
- Live at bottom of large rivers and lakes for  $\geq 100$  yrs
- Males spawn at 12-20 yrs old on benthic rock every 2-3 yrs (mid May-late June)
- Do not shed scales



# Introduction

- **Question:** Do eDNA methods work well for fish with distinctly different ecologies and life histories?

# Methods



## 1. Highly specific TripleLock™ mtDNA assay design



## 2. Sampling regime (year, site & biological replicates)

## 4. Triplicate qPCRs



## 3. Fieldwork & eDNA extraction

# Methods



- Used published/agency field data to ID pos. & neg. sites
- Sampled fall 2018, spring & summer 2019
- Discrete sampling (2018); equidistant or continuous sampling along 1-5km transects (2019)
- Collected environmental metadata
- Validated markers (low LOD, high qPCR efficiency)

# Methods

<b>SAR</b>	<b>Sites</b>	<b>N-Size (Water)</b>	<b>Total Water Volume (L)</b>	<b>N-Size (Benthic)</b>
RD	6	126	374.9	8
LS	7	113	501.5	6
Neg.	2, 4	19	30.3	4
<b>Totals:</b>	<b>17</b>	<b>258</b>	<b>906.7L</b>	<b>18</b>

Sampling: Surface/at Depth (& Benthic in 2018 only)  
Amplified mtgenome, excluding all other taxa

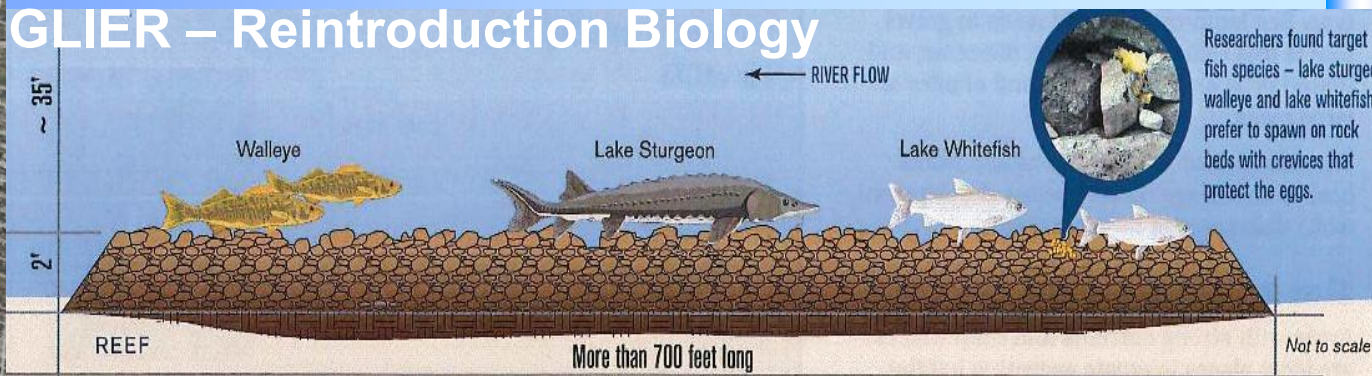
# Methods

## Predictive Software™ – Water Volume & Where?

Site 6 (2019)



GLIER – Reintroduction Biology



- Predictive analysis:
  - 10L water total (32.9L collected)
  - 5-10m depth
  - 1.2 $\mu$ m pore size
  - Accuracy: 99.5%
  - Survey Power: 99.4%

# Results – Redside Dace

## Detected from Water at 67% of Sites

Site	Region	Detected	
		2018	2019
1	S. Ont.	N	-
2	S. Ont.	N	-
3	S. Ont.	Y	N
4	S. Ont.	Y	Y
5	S. Ont.	-	Y
6 <sup>a</sup>	S. Ont.	-	Y
2 Neg. Sites	S. Ont.	N	-

<sup>a</sup>Research Station/Hatchery

Mean per sample detection rate:  $0.64 \pm 0.35$

# Results – Redside Dace

Mean ± SE (n)

	Positive	Negative	t ( $\chi^2$ ) <sup>a</sup>	P
DO (mg/L)	143.7 ± 46.1 (26)	0.6 ± 0.7 (2)	4.99	<0.0001*
Temp (° C)	13.2 ± 1.9 (26)	16.5 ± 3.8 (2)	-2.13	0.04
pH	8.4 ± 0.3 (28)	8.3 ± 0.3 (2)	0.60	0.55
TDS (ppm)	415.7 ± 63.1 (28)	247.8 ± 84.6 (2)	3.10	0.004*
Turbidity (NTU)	2.1 ± 0.9 (28)	3.9 ± 4.2 (2)	-0.73	0.47
Depth (cm)	54.6 ± 139.8 (29)	22.8 ± 4.5 (2) (29)	(0.23)	0.63
Flow (m/s)	0.4 ± 0.3 (28)	0.1 ± 0.1 (2)	(2.82)	0.09

Comparisons based on positive sites where species was detected

<sup>a</sup>Non-parametric Mann-Whitney test (non-normal distribution)

\*Significant after Bonferroni correction, (Bonferroni P = 0.007)

# Results – Lake Sturgeon

## Detected from Water at 57% of Sites

Site	Region	Detected	
		2018	2019
1	C. Ont.	N	N
2	C. Ont.	Y	N
3	S. Ont.	N	-
4	S. Ont.	N	-
5 <sup>a</sup>	S. Ont.	-	Y
6	S. Ont.	-	Y
7 <sup>a</sup>	S. Ont.	-	Y
4 Neg. Sites	S. Ont.	N	-

<sup>a</sup>Research Station/Hatchery

**Mean per sample detection rate:  $0.67 \pm 0.36$**

# Results – Lake Sturgeon

**Mean ± SE (n)**

	<b>Positive</b>	<b>Negative</b>	<b>t (<math>\chi^2</math>)<sup>a</sup></b>	<b>P</b>
DO (mg/L)	20.3 ± 39.9 (11)	58.9 ± 69.2 (4)	-0.97	0.35
Temp (° C)	19.3 ± 6.2 (11)	12.9 ± 4.8 (4)	1.39	0.19
pH	8.0 ± 0.3 (11)	7.2 ± 1.4 (4)	1.65 <sup>b</sup>	0.29
<b>TDS (ppm)</b>	143.9 ± 66.4 (11)	263.8 ± 53.1 (4)	-3.36	<b>0.005*</b>
Turbidity (NTU)	5.0 ± 2.6 (11)	2.0 ± 3.4 (4)	0.73 <sup>b</sup>	0.55
<b>Depth (cm)</b>	634.9 ± 323.0 (11)	46.6 ± 50.3 (4)	(6.81)	<b>0.009</b>
<b>Flow (m/s)</b>	0.4 ± 0.3 (11)	0.1 ± 0.1 (4)	(2.10)	<b>0.055</b>

<sup>b</sup>Welch's ANOVA (heteroscedastic variance)

\*Significant after Bonferroni correction, (Bonferroni P = 0.007)

# Discussion

- Target eDNA was detected from water for both species at ~2/3 of positive sites
- No detection - benthic substrate, negative sites
- Results suggest detection is related to:

	<u>RD</u>	<u>LS</u>
○ Higher DO	√	
○ Cooler water	√	
○ Higher TDS	√	√
○ Water flow rate, depth	?	?

# Discussion

- Potential for predictive software™ to refine sampling regime and improve detection
- Remarkable success detecting rare fish species
  - Site 6 (Lake Sturgeon)
    - 51km long
    - Up to 6km wide
    - 3-15m deep
    - Water residence time of 21hrs

# Conclusions

- eDNA SAR detection offers exciting new opportunities for environmental consulting
- Sampling regime considerations:
  - Species' life history & ecology of eDNA
  - Equidistant/continuous sampling
  - Metadata to characterize eDNA environment
  - Flow dynamics & bathymetry data may strengthen sampling designs