Detecting historical population structure among highly impacted White Sturgeon populations of the Upper Columbia River

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Acispenseriformidae – Sturgeon and paddlefish

27 Species in the Northern Hemisphere
White Sturgeon

- Largest fish in North American freshwater

To 6 m in length - 880 kg - over 100 years old
White Sturgeon – Life history

- Slow growing – In upper Columbia River females mature at about 30 years and males at about 20 years.
- Spawns every 4 to 5 years.
- Females lay 100,000 to 1,000,000 eggs.
- Eggs sink to bottom and hatch in about 1 week
- After hatching larvae drift downstream until they reach suitable habitat.
- Feed on invertebrates and fishes.
White Sturgeon - Range

- Alaska to California and is found in lakes and rivers as well as brackish and marine waters.
In Canada only in British Columbia

Currently six recognized populations
Range in Western British Columbia
Range in Eastern British Columbia
White Sturgeon - Human Use

- Commercial, Native and recreational fisheries.

Commercial catch statistics Fraser River, 1880 to 1993. (Figure from Echols 1995).
White Sturgeon – other impacts
White Sturgeon

- All harvest in British Columbia banned since 1994.
- Catch and release fishery allowed in Lower Fraser River

Some sport fishing activities involve research - impact of catch and release not understood.
White Sturgeon – Population Status

All populations have declined from historical levels

Lower Fraser - 47,000
Mid-Fraser – 3,700
Upper Fraser – 850  Endangered
Nechako – 571      Endangered
Kootenay – 760     Endangered
Upper Columbia – 1500  Endangered

Endangered = facing imminent extirpation or extinction  
(data from Golder 2006, Irvine et al. 2007)
Historically fish had access to over 600 km of river/lake habitat

Now river impounded by 4 major dams
Keenlyside dam completed in 1968
Keenlyside dam - HLK

185 megawatts
Waneta Dam completed in 1954
Waneta Dam

450 megawatts
Brilliant Dam completed in 1944
Brilliant Dam

145 megawatts
Grand Coulee Dam completed in 1942
Grand Coulee Dam

6800 megawatts
After completion of Keenlyside dam in 1968 widespread recruitment failure.....
Changes in WS size composition = recruitment failure beginning ~ 1970
Spawning occurs but juveniles are not being recruited into the population - cause uncertain
White sturgeon – recovery initiative started 2001

First recovery plan produced in 2002 collaboration between govt, communities, USA and Canada.
UCR currently considered as one population
Five principle habitat areas within the Upper Columbia Recovery Area. **AR – HLK – BRL – WAN - ROOS**

(Hildebrand et al., 1999)
Population Structuring?

- Knowing population units important for determining cause of recruitment failure and for management and recovery planning.

- How can we gain insight into population structure, historical and contemporary?

- Genetics can provide insight.
Defining the Question.

“In the approximately 10,000 years since colonization, did white sturgeon in this region segregate into reproductively isolated populations?”
Defining the Question.

If there was genetic structure could we detect it given change to water flows and potential blockage of migration routes and behaviour?
White Sturgeon – genome

- Octoploid nuclear genome
- 250 chromosomes
- Nuclear genetic markers such as microsatellites - usually highly variable (require large samples) can be difficult to score and analyse in complex genomes.
Mitochondrial genome—haploid, easy to analyse.

PCR amplification
Avoiding complex
Repeated region.

First we sequenced region and did
Restriction Fragment Length
Polymorphism analysis in silico.

Chose three restriction enzymes.

SfcI, Hsp92II, MseI
Restriction Fragment Length Polymorphism

old technique for ancient fish

DNA extraction > PCR > enzyme digestion > gel electrophoresis

\( SfcI \quad + \quad Hsp92II \quad + \quad MseI \quad = \quad 9 \text{ haplotypes} \)
Kootenay Lake population was almost monomorphic for haplotype 2 and this distinguished this group from the others.
Genetic structure **suggested** between other sites but….

Work was done with samples of mixed age catch location was not well defined…

How was age of the fish affecting the results?

Could we use catch location data to more rigorously define the samples?

Roosevelt fish?
Recruitment failure began around 1970.

Pre- and post- recruitment failure fish are present in the system.

Habits of older fish more likely to reflect historical life history i.e. population structure.

Approach: remove post dam fish from genetic analysis
Settling up the analysis. Age of fish.

Define pre-recruitment failure fish as those born prior to 1968.

Ageing done by fin ray analysis as per Brennan and Cailliet 1989.

If fin ray information was lacking:

\[ \text{Age} = 0.0006 \times FL^2 + 0.0862 \times FL + 3.9914 \]

Application of this criteria resulted in the removal of 102 fish from the analysis.
Setting up the analysis.
Use Tagging and recapture data to define sample location—evaluated for HLK, BRL, WAN.
Tagging and recapture
Tagging and recapture
Recapture and read.
Tagging and recapture - stats
Database maintained by UCWSRI

- From 1993 to 2006. 607 fish - 802 captures.
- 270 fish captured more than once.
- 249 fish were caught exclusively within one zone.
- Equal captures in multiple locations occurred for 22 fish.
Tagging and recapture – assignment to high use area evaluated for **HKD**, **BRL**, **WAN**.

- Fish assigned to area most frequently captured
- Fish with equal number of detections pooled and randomly split
- Fish with detections that could not be evenly split were removed.
Results of Capture data

84% of subsequent detections in same locations (p<0.001)
Tagging and recapture

- 84% of subsequent detections in same location (p<0.001)
- 92% HLK
- 64.5% BRL (lower fidelity may be due to low water in summer)
- 93.4% WAN
Sonic telemetry – evaluated for HKD, BRL, WAN, ROOS.
Sonic telemetry
Sonic telemetry
Sonic telemetry
Sonic telemetry- stats

- 73 fish were monitored for 1.5–4 years between 2002 and 2007
- 40,278 location x day detections
Sonic telemetry—assignment to high use area evaluated for **HKD, ROOS, WAN, BRL.**
Results of telemetry data

90 % of subsequent detections in same locations (P<0.001)
Results of telemetry data

90% of subsequent detections in same locations (P<0.001)
Sonic telemetry

- 90% of subsequent detections in same locations (P<0.001)
- 94% - HLK
- 98% - BRL
- 95% - WAN
- 95% - ROOS
### Haplotype frequencies

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- Most of the signal coming from haplotypes 2, 3 and 4.
- AR and HLK have more 3 than 2.
- KL has less diversity than all others.
Haplotype frequencies
Pairwise differentiation test KL ($\alpha = 0.05$).

Can we reject the null hypothesis of genetic homogeneity?

$H_0$ samples are the same

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KL differentiated from all others.

$F_{ST}$ range from 0.1 to 0.46 $P < 0.05$
Bonnington Falls –
Historical obstacle to fish passage.
Pairwise differentiation test $KL \quad \alpha = 0.05$

Can we reject the null hypothesis of genetic homogeneity? $H_o$ samples are the same

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$F_{ST}^{KL-BRL} = 0.1 \quad P < 0.05$

BRL differentiated from KL
Brillant dam
BRL and KL linked by downward migration.
## Pairwise differentiation – AR and HLK

Can we reject the null hypothesis of genetic homogeneity?

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\[ F_{ST} = 0.0 \]

AR and HLK samples not different.
AR and HLK samples not different.

HLK dam broke up a population that spawned up river.

Spawing observed in HLK.
Pairwise differentiation – AR and HLK

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AR and HLK unique population (sample size of WAN may be limiting test)

\[ F_{ST} 0.09 \text{ to } 0.46 \ P<0.05 \]
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**ROOS different than all but WAN.**

$F_{ST}$ range from 0.02 to 0.23
ROOS, WAN Unique population?

Contraction of habitat may have caused mixing or introgression of mitochondrial DNA haplotypes prior to recruitment failure but old habits retained.
Haplotype frequencies to calculate genetic distance
Overall genetic structure – CSE distance
Overall genetic structure
Overall genetic structure
Overall genetic structure

Due to habitat contraction?
Interpretations:

• Genetics when combined with other approaches is very powerful.

• When fish dispersed to different areas within the region after initial colonization, genetic divergence occurred.

• Before the dams were built, AR and HLK fish could were one population that spawned above the HLK dam.
Interpretations

ROOS and WAN - Contraction of habitat may have caused mixing or introgression of mitochondrial DNA haplotypes prior to recruitment failure but old habits retained.

BRL linked to KL by unidirectional migration.
Overall Interpretation

• Even in severely disrupted habitats with declining populations fishes may retain genetic structure and habits.

• Genetics here used to detect homogenization, disruption and unidirectional migration.

• Such information will be useful as a basis for future study and design of recovery plans.
Acknowledgements

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• Jason McLellan for samples and telemetry data.

• Glenn Cooper, Kathryn Clark, Chantal Rajotte for lab expertise.
Thank you….Questions?