

**M.W. Thorn and Y.E. Morbey - Egg size and the adaptive capacity of early life history traits in Chinook salmon (*Oncorhynchus tshawytscha*)**

Three Chinook salmon populations were used:

- 1) Credit River – located in the northwestern section of Lake Ontario, Canada (43°34'39.58"N, 79°42'8.57"W). Adults were captured on 01 October 2012 using electrofishing.
- 2) Sydenham River – located in the southern Georgian Bay basin of Lake Huron, Canada (44°33'34.36"N, 80°56'39.49"W). Adults were captured from 22 September – 06 October, 2012 using a fish trap built into the Mill Street Dam in Owen Sound, Ontario.
- 3) Pine River – located in the southern Georgian Bay basin of Lake Huron, Canada (44°13'10.12"N, 79°57'24.84"W). Adults were captured from 19-27 September 2012 using seine and dip nets.

**File: Eggsize\_Femalesize.csv**

File Contents – female length and egg diameter for all individual females used in the study. Missing data is denoted using “NA”.

Dataset Variables

dam: unique female identification code

pop: population identification code (C: Credit River, N: Pine River, S: Sydenham River)

dia: mean egg diameter (mm) from a sample of 25 eggs

fl: fork length (mm)

**Files: T1\_Growth.csv, T2\_Growth.csv, T3\_Growth.csv**

File Contents – family level trait data for each population/treatment (T1: 6.5°C treatment; T2: 9.4°C treatment, T3: 15.2°C treatment). Family means for hatch length, swim-up length, juvenile length, and yolk sac volume were calculated using individual level data from each family. Yolk sac conversion efficiency, hatch to swim-up growth, and swim-up to juvenile growth are derived measures from family mean data. Missing data is denoted using “NA”. Note: no juvenile traits were measured in the 15.2°C treatment.

Dataset Variables

dam: identification code for the female used to create the family

sire: identification code for the male used to create the family

pop: population identification code (C: Credit River, N: Pine River, S: Sydenham River)

dia: mean egg diameter (mm) of the female used to create the family

hatch\_sl: mean standard length measured at hatch (mm)

yvol: mean yolk sac volume measured at hatch (mm<sup>3</sup>)

swim\_sl: mean standard length measured at swim-up (mm)

juv\_sl: juvenile length measured at the juvenile stage (mm)

ysce: yolk sac conversion efficiency (mm/mm<sup>3</sup>)

hs\_grow: hatch to swim-up growth rate (mm/degree day)

sj\_grow: swim-up to juvenile growth rate (mm/degree day)

### **Files: T1HatchData.csv, T2HatchData.csv, T3HatchData.csv**

File Contents - individual level hatch length and yolk sac volume data for each family/population/treatment (T1: 6.5°C treatment; T2: 9.4°C treatment, T3: 15.2°C treatment). Missing data is denoted using “NA”.

#### Dataset Variables

sire: identification code for the male used to create the family

dam: identification code for the female used to create the family

pop: population identification code (C: Credit River, N: Pine River, S: Sydenham River)

sl: standard length measured at hatch (mm)

yvol: yolk sac volume measured at hatch (mm<sup>3</sup>)

cup: identification code for the individuals derived from a specific egg container

dia: mean egg diameter (mm) of the female used to create the family

### **Files: T1SwimData.csv, T2SwimData.csv, T3SwimData.csv**

File Contents - individual level swim-up length data for each family/population/treatment (T1: 6.5°C treatment; T2: 9.4°C treatment, T3: 15.2°C treatment).

#### Dataset Variables

sire: identification code for the male used to create the family

dam: identification code for the female used to create the family

pop: population identification code (C: Credit River, N: Pine River, S: Sydenham River)

sl: standard length measured at swim-up (mm)

dia: mean egg diameter (mm) of the female used to create the family

**Files: T1TermData.csv, T2TermData.csv**

File Contents - individual level juvenile length data for each family/population/treatment (T1: 6.5°C treatment; T2: 9.4°C treatment, T3: 15.2°C treatment).

Dataset Variables

sire: identification code for the male used to create the family

dam: identification code for the female used to create the family

pop: population identification code (C: Credit River, N: Pine River, S: Sydenham River)

sl: standard length measured at the juvenile stage (mm)

dia: mean egg diameter (mm) of the female used to create the family

**File: Trait\_Haldanes.csv**

File Contents – pairwise phenotypic divergence rates calculated using Haldanes for each temperature/trait combination before and after controlling for the effects of egg size. Traits that were not related to egg size or had an egg size x population interaction were excluded.

Dataset Variables

temp: factor indicating the temperature treatment (low: 6.5°C treatment; medium: 9.4°C treatment, high: 15.2°C treatment)

trait: factor indicating the trait used to calculate the divergence rate (hatch: hatch length, yvol: yolk sac volume, swim: swim-up length, juv: juvenile length, he\_grow: hatch to swim-up growth rate; yce: yolk sac conversion efficiency)

pair: factor indicating the two populations used to calculate the divergence rate (CP: Credit-Pine; CS: Credit-Sydenham; SP: Sydenham-Pine)

raw: factor indicating if the divergence rate was calculated before (Y) or after (N) controlling for egg size

hald: the calculated divergence rate in Haldanes