Influence of changing lake temperatures on coregonine embryogenesis at local to global scales

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**ABSTRACT:**

**INTRODUCTION:**

Aquatic ecosystems present unique and difficult challenges for biodiversity conservation because of the diverse array of habitats and the numerous socio-economic benefits they provide (Halpern et al. 2015, Langhans et al. 2019). Lakes are one of the most sensitive natural resources to climate change (Woolway et al. 2020). Climate change can alter lake physical and chemical characteristics and has biological consequences for lake ecology and metabolism (Adrian et al. 2009, Williamson et al. 2014), yet the broader impacts of climate-derived changes in lake dynamics remain unclear (Shatwell et al. 2019). However, the responses of many lake populations are projected to be inadequate to counter the speed and magnitude of climate change, leaving groups vulnerable to decline and extinction (Hoffmann and Sgrò 2011).

Lakes are warming at an unprecedented rate on a global scale (Austin and Colman 2007, O’Reilly et al. 2015, Woolway et al. 2017). Conversely, water temperature change is not projected to rise steadily across regions, seasons, or lake types (O’Reilly et al. 2015, McCullough et al. 2019). The greatest seasonal increase in water temperature of seasonally ice-covered lakes is projected to take place during the spring (Schindler et al. 1990, Winslow et al. 2017), and the greatest seasonal increase in air temperature will be during winter in northern Europe and North America (Christensen et al. 2007). Changes in spring conditions and increases in the frost-free season can prolong annual growing seasons with warmer summers, longer autumns, shorter ice-cover duration, and rapid spring water warming (Meehl et al. 2007). Temperature is considered an abiotic master factor for aquatic ecosystems, as changes in water temperature directly alter the physical and chemical properties of water and affect phenological and reproductive events, metabolic rates, growth, and survival of aquatic organisms (Brett 1979, Little et al. 2020). The effects of climate change on lake fishes are predicted to lead to declines in cold-water species (Fang et al. 2004, Mackenzie-Grieve and Post 2006, Jacobson et al. 2010, Herb et al. 2014) and increases in warm-water species (Lehtonen 1996, Chu et al. 2005, Sharma et al. 2007, Van Zuiden et al. 2016) as the climate warms (Comte et al. 2013, Hansen et al. 2017). ﻿Fundamental questions for evolutionary and conservation biologists in a global change context include how lake fishes will respond to rising water temperatures and what mechanisms will be involved in the process.

Freshwater whitefishes, Salmonidae Coregoninae (hereafter coregonines), are of great socio-economic value (Ebener et al. 2008b, 2008a, Lynch et al. 2015, 2016). Coregonines are also considered to be critically sensitive to the effects of climate change because they are cold, stenothermic fishes (Stockwell et al. 2009, Elliott and Bell 2011, Jeppesen et al. 2012, Isaak 2014, Jonsson and Jonsson 2014, Karjalainen et al. 2015, 2016b). Species that possess narrow optimal ranges, live near their thermal limits, or develop over long periods at cold temperatures are at-risk under warming climate scenarios as temperature can have strong effects on embryos (Blaxter 1991, Pepin 1991, Ficke et al. 2007, Lim et al. 2017). Coregonine fisheries worldwide have experienced population declines due to highly variable and weak year-class strengths (Anneville et al. 2015; Myers et al. 2015; Nyberg et al. 2001; Vonlanthen et al. 2012). The reason for declining recruitment is unknown, but winter conditions appear to play a role in recruitment success (Karjalainen et al. 2015; Karjalainen et al. 2016; Marjomäki et al. 2004; Nyberg et al. 2001). Coregonines generally spawn during late fall, embryos incubate over winter, and begin hatching in late spring (Karjalainen et al. 2000, Stockwell et al. 2009). Spawning adults, embryos, and larvae are exposed to a variety of thermal conditions throughout this long period of reproduction and incubation. At least some coregonines, however, have the ability to adapt to temperature changes within the limits of phenotypic plasticity and through genetic adaptive changes (Karjalainen et al. 2015, 2016).

Life history traits in fishes can vary across latitudes and the driving selective force for this variation is size-dependent winter mortality in young-of-the-year (Conover and Present 1990, Yamahira and Conover 2002, Chavarie et al. 2010). ﻿Such size-dependent winter mortality results in a strong and increasing selection pressure towards fast-growing fishes with increasing latitude. Year-class strength of most fish species, including coregonines, is thought to be established prior to the end of the first season of growth, with the first few weeks after hatching especially critical (Hjort 1914, Cushing 1990, Ludsin et al. 2011, 2014, Karjalainen et al. 2015, 2016). The response of coregonines to environmental change at the embryonic and larval stages are expected to play an important role in population persistence (Myers 1997, Karjalainen et al. 2000) and have major implications on ecosystem health as coregonines contribute significantly to ecosystem function and energy transfer (Gamble et al. 2011, Muir et al. 2014, Stockwell et al. 2014, Karjalainen et al. 2015). Large-scale experimental evolution studies may aid in understanding the response of coregonines to changing environments (Hoffmann and Sgrò 2011). Coregonines occur broadly across northern latitudes and are an ideal group to identify how cold-water fishes may adapt to climate-driven shifts in environmental parameters, such as water temperature.

We experimentally analyzed the reaction norms of early-life stage coregonines to changing winter thermal regimes across broad latitudinal gradients. We hypothesized that coregonine populations across latitudes will have differential responses to changing winter conditions. Evolutionary differences to varying climates may be driving thermal resilience during embryonic and larval stages. High-latitude populations which experience lower water temperatures and shorter growing seasons are expected to (1) have prolonged incubation periods across all temperatures, (2) have lower embryo survival as temperature increases, and (3) exhibit a smaller size-at-age across all temperatures than populations at lower latitudes. We also hypothesized that a greater magnitude of seasonal fluctuations and water temperature variation will result in lower-latitude populations having a stronger parental response (*i.e.,* heritability) to changing temperatures due to stronger selection towards thermal plasticity. Understanding the adaptive capacity of coregonine populations will be critical to determining which populations may survive and which may perish as thermal conditions continue to change.

**METHODS:**

Study Sites and Collections

We used a cross-lake, cross-continent, cross-species approach to evaluate the responses and thermal tolerances of coregonine embryos and larvae to changing thermal regimes. Wild-caught populations of cisco in Lake Superior (USA/Canada) and Lake Ontario (USA/Canada), and vendace and European whitefish in Lake Konnevesi (Finland; Figure 1) were sampled using live-capture gear. Adult field collections occurred during coregonine spawning periods for Lake Ontario and Lake Superior. On Lake Konnevesi, adults were collected prior to spawning and stored in an aquaculture pool with water fed directly from the lake until spawning was initiated. A single laboratory in North America (University of Vermont (UVM), USA) and Europe (University of Jyväskylä (JYU), Finland) conducted all sampling, fertilization, and experimental work for populations on each continent.

The term population is used in many ways. For the sake of clarity, our operational use of a population is to represent a single species within a single lake (*e.g.,* cisco in Lake Superior).

Fertilization and Incubation

Eggs and milt were stripped from dams and sires from each population and artificially fertilized under a blocked, nested full-sib, half-sib fertilization design (Figure 2) to create a maximum of 48 full-sibling families nested within half-siblings per population (Table X). This fertilization design was used to maximize the amount of genetic variation and minimized the potential loss of multiple families if a dam or sire produced poor quality gametes, compared to a full-factorial design. Pairing was performed by dividing the adults used in the experiment into three or four fertilization blocks. A single block consisted of four sires each paired to three unrelated dams, where all offspring of a given dam were full siblings. Fertilizations were performed block by block to ensure germ cell survival.

Approximately 200 eggs per dam were fertilized by approximately 10 μl of milt from each sire in the block. After the addition of milt, water was added to activate the germ cells and gently mixed for one minute. The embryos were rinsed 2-3 times until the water was clear. Water used during fertilizations was reconstructed freshwater (OECD ISO 6341:2012) to standardize the chemical properties of the water used among populations and between labs. Embryos were transported in coolers either by shipping overnight for Lake Superior or driven same day for Lake Ontario. A temperature logger recorded air temperature inside the cooler during transport (Lake Superior: mean = 2.80°C, sd = 0.21°C; Lake Ontario: mean = 3.28°C, sd = 0.37°C). No embryo transport was required for Lake Konnevesi. Demographic data (*e.g.,* total length and weight) were collected on adults.

Fertilization success was determined by haphazardly taking 10 embryos from each family and assessing under microscopy within 72-hours post-fertilization (Oberlercher and Wanzenböck 2016). If fertilization was low (<30%), the family was removed from the experimental setup. Embryos from successfully fertilized families were individually distributed into 24-well cell culture microplates and incubated in 2 ml of reconstructed freshwater. Reconstructed freshwater was used during incubation to maintain sterility, prevent bacterial growth in the wells, and eliminate the need for harsh fungicide treatments on the embryos. A total of 36 embryos per family were used for Lake Konnevesi and 48 embryos per family for Lake Ontario and Lake Superior. Families were randomly distributed across three or four microplates (*i.e.,* 12 eggs per family per microplate and two families per 24-well microplate). Microplates from each species and population were incubated at constant temperatures of 2.0, 4.5, 7.0, and 9.0°C and randomly placed in climate-controlled chambers at UVM (Memmert® IPP260Plus) and climate-controlled rooms at JYU (Brand). Forced airflow was used in both the climate-controlled chambers and rooms to ensure equal air circulation around the microplates. All microplates were covered to prevent excessive evaporation. Microplate orientation and position were rotated weekly to eliminate any temperature heterogeneity within the chambers and rooms. Water temperatures were recorded hourly with loggers (HOBO® Water Temperature Pro v2 at UVM and Escort iMini at JYU) and daily mean water temperatures calculated. Incubations took place in the dark, with the exception of short maintenance periods. Microplates were checked weekly for dead eggs and the eye-up stage. During the hatch period, microplates were checked on a two-day cycle for newly hatched larvae. All newly hatched larvae were photographed for life-history and morphological traits.

Statistical Analyses

All statistical analyses were performed in R version 4.0.3 (R Core Team 2020).

*Life-history and Morphological Traits*

Embryo survival (ES) was estimated as the percent of embryos surviving between the eye-up and hatch stages. Incubation period was assessed by two variables: the number of days from fertilization to hatching (DPF) and the sum of the degree-days (ADD). Total length-at-hatch (LAH; mm) and yolk-sac volume (YSV; mm3) were measured from five individuals per family at, or as close as possible to, 50% hatching for each family. YSV was calculated assuming the shape of an ellipse (Blaxter 1963):

where a = length of the yolk sac (mm) and b = height of the yolk sac (mm).

Embryo survival was analyzed as a binomial response variable, and incubation period, LAH, and YSV at hatching as continuous response variables. Early embryo mortality induced from fertilization failure produced inequalities in the number of offspring among families and an unbalanced design. The sample size for incubation period is a function of ES and subsequently resulted in an unbalanced design. Therefore, binary data (*i.e.,* ES) were analyzed with binomial generalized linear mixed-effects models (LMM) and normally distributed data (*i.e.,* DPF, ADD, LAH, and YSV) were analyzed with restricted maximum likelihood LMMs with the lme4 package (Bates et al. 2015). Population and incubation temperature were included as fixed effects and sire, dam, family (sire and dam combination), and fertilization block as random effects. Because embryos were raised independently, the replication unit in the statistical models is the individual embryo. All traits were examined for population and incubation temperature effects in addition to individual parental effects (dam and/or sire effects), fertilization block, and all possible interactions with backward, stepwise effect-selection using the buildmer package (Voeten 2020). The maximal model for each trait was selected by comparing a model including or lacking the term of interest to the reference model based on changes in log-likelihood, Akaike information criterion, Bayesian information criterion, and change in explained deviance. The mixed-effects model output does not produce significance values for model effects; therefore, significance for population, incubation temperature, interaction effects, and any random-effects selected were determined using a likelihood ratio test between the maximal model and reduced models with the model effect of interest removed. Lake Superior and Lake Ontario (hereafter Great Lakes region (GLR)) were fit independently from Lake Konnevesi (hereafter Finland region (FIR) to eliminate any confounding factors between continents and among species.

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*Heritability*

In addition to population-level effects, life-history and morphological traits were analyzed for heritability. The variance components and heritability estimates were assessed using non-parametric bootstrapping to address unbalanced family sizes. ﻿We generated a bootstrap sample by resampling, with replacement, the individuals within each family, population, and incubation temperature treatment until the number of observations in the original sample was reproduced for each of the traits. Individuals were resampled to account for within-family variation and ensure that the genetic effects were not overestimated (Neff and Fraser 2010). From the resampled data, the phenotypic variance was partitioned into random effects for sire (VS), dam (VD), sire:dam (VS:D), fertilization block (VBlock), microplate (VPlate), and residual (VE) variance components using mixed-effects models with the fullfact package (Houde and Pitcher 2019) for each population and incubation temperature treatment. The resampling and variance calculations were repeated 10,000 times.

Under our fertilization design, the variance among half-sib families (VS) represents one-fourth of the additive genetic variance (VA) and can therefore be used to estimate VA and the narrow-sense heritability (h2; hereafter heritability), assuming that epistasis is negligible (Lynch and Walsh 1998). Additive genetic variance was calculated as four times the sire component of variation: . Dominance, or non-additive, genetic variance (VI) was calculated as four times the sire:dam component: . Total phenotypic variance (VP) was portioned into additive genetic variance, dominance variance, fertilization block variance, and residual variance: . Heritability was calculated as the ratio of additive genetic to total phenotypic variance for each population and incubation temperature treatment: . Heritability was estimated for each bootstrap resample and the bias-corrected mean and standard error was determined from the empirical bootstrapped distributions.

**RESULTS:**

Incubation Water Temperatures

Water temperature during incubations were maintained near the target incubation temperature for 2.0°C and 7.0°C for both labs. Incubation water temperature at 4.5°C and 7.0°C were lower than the target incubation temperature at JYU, but not at UVM (Table 1).

Spawning Adults

Total lengths and fresh mass of spawning adults used for gamete collection varied widely among populations. Lake Konnevesi vendace were notably smaller than all other populations. The remaining populations varied less in size, but Lake Konnevesi whitefish were smaller than Lake Superior cisco and Lake Ontario cisco (Table 2).

Life-history and Morphological Traits

*Embryo Survival*

The likelihood-ratio test found a significant interaction effect between ES in population and incubation temperature for both GLR (*P* < 0.001, χ2 = 198.56, 3 df) and FIR lakes (*P* < 0.001, χ2 = 52.94, 3 df; Table 3) and do not allow for main effect interpretation. The significant interaction suggested that different temperatures affect ES differently between the populations within each region. ﻿The effect of population depended on temperature because the ﻿differences in ES among populations were more pronounced at higher temperatures. ES was highest among all populations at 2.0°C. LO-Cisco had the highest ES up to 7.0°C and then decreased rapidly at 9.0°C. LS-Cisco and LK-Vendace ES was less variable across all temperatures, but less than LO-Cisco. ES in LK-Whitefish was lowest among populations and consistently decreased as temperature increased (Figure 2).

*Incubation Period (DPF)*

The likelihood-ratio test found a significant interaction effect between DPF in population and incubation temperature for both GLR (*P* < 0.001, χ2 = 1,113.95, 3 df) and FIR lakes (*P* < 0.001, χ2 = 157.91, 3 df; Table 3) and do not allow for main effect interpretation. The significant interaction suggested that different temperatures affect DPF differently between the populations within each region. ﻿The effect of population depended on temperature because the ﻿differences in DPF among populations were more pronounced at colder temperatures. DPF was highest for all populations at 2.0°C and decreased as temperature increased. Higher-latitude populations (*i.e.,* LK-Vendace and LK-Whitefish) had longer incubation periods compared to lower-latitude populations (*i.e.,* LS-Cisco and LO-Cisco) across all temperatures (Figure 2).

*Incubation Period (ADD)*

The likelihood-ratio test found a significant interaction effect between ADD in population and incubation temperature for both GLR (*P* < 0.001, χ2 = 160.60, 3 df) and FIR lakes (*P* < 0.001, χ2 = 440.18, 3 df; Table 3) and do not allow for main effect interpretation. The significant interaction suggested that different temperatures affect ADD differently between the populations within each region. The effect of population depended on temperature because the ﻿differences in ADD among populations were more pronounced at higher temperatures. ADD was highest for all populations at 7.0°C and decreased as temperature increased and decreased. Higher-latitude populations (*i.e.,* LK-Vendace and LK-Whitefish) had larger differences in incubation periods across temperature compared to lower-latitude populations (*i.e.,* LS-Cisco and LO-Cisco; Figure 2).

*Length-at-Hatch*

The likelihood-ratio test found a significant interaction effect between LAH in population and incubation temperature in FIR lakes (*P* = 0.031, χ2 = 8.85, 3 df; Table 4) and do not allow for main effect interpretation. The significant interaction suggested that different temperatures affect YSV differently between the populations. Both temperature (*P* < 0.001, χ2 = 592.28, 3 df) and population (*P* < 0.001, χ2 = 443.20, 1 df; Table 4) main effects were significant in GLR lakes. All pairwise population and temperature comparisons for both GLR lakes were significant (*P* < 0.001). All populations showed a decrease in LAH as temperature increased. LO-Cisco had the largest LAH across all temperatures. LK-Vendace had a large difference in LAH and were significantly smaller compared all other populations.

*Yolk-sac Volume*

The likelihood-ratio test found a significant interaction effect between YSV in population and incubation temperature for both GLR (*P* < 0.001, χ2 = 36.50, 3 df) and FIR lakes (*P* < 0.001, χ2 = 157.91, 3 df; Table 4) and do not allow for main effect interpretation. The significant interaction suggested that different temperatures affect YSV differently between the populations within each region. YSV was highest for all populations at 9.0°C and decreased as temperature decreased. LK-Vendace had a large difference in YSV and were significantly smaller compared all other populations. Excluding LK-Vendace, YSV dropped more rapidly as temperature decreased at higher-latitude populations (i.e., LK-Whitefish) compared to lower-latitude populations (*i.e.,* LS-Cisco and LO-Cisco; Figure 3). The difference in YSV between GLR populations decreased as temperature increased.

Heritability

**TABLES:**

Table 1. Mean water temperatures (°C) with standard deviations (in parentheses) during embryo incubations at the University of Vermont (UVM) and the University of Jyväskylä (JYU).

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  | Incubation Temperature Treatment | | | | | | |
| Laboratory | 2.0 |  | 4.5 |  | 7.0 |  | 9.0 |
| UVM | 2.0 (0.5) |  | 4.4 (0.2) |  | 6.9 (0.2) |  | 8.9 (0.3) |
| JYU | 2.2 (1.5) |  | 4.0 (0.7) |  | 6.9 (0.5) |  | 8.0 (0.6) |

Table 2. Mean total l­engths (TL; mm) and fresh mass (FM; g) with standard deviations (in parentheses) of the dams and sires from Lake Konnevesi (LK-Vendace (*C. albula*) and LK-Whitefish (*C. lavaretus*)), Lake Superior (­LS-Cisco (*C. artedi*)), and Lake Ontario (LO-Cisco).

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | LK-Vendace | |  | LK-Whitefish | |  | LS-Cisco | |  | LO-Cisco | |
| Sex | TL | FM |  | TL | FM |  | TL | FM |  | TL | FM |
| Female | 144.67 (16.51) | 18.36 (5.95) |  | 256.57 (11.63) | 117.00 (19.16) |  | 428.92 (44.40) | 676.02 (181.51) |  | 380.33 (24.18) | 567.59 (122.89) |
| Male | 140.83 (9.22) | 13.85 (2.27) |  | 285.75 (40.86) | 171.34 (87.22) |  | 400.25 (34.35) | 523.82 (134.65) |  | 366.56 (25.30) | 443.29 (103.16) |

Table 3. Embryo model selection

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Trait | Region | Model | Effect Tested | df | χ2 | p-value |
| Embryo Survival | Great Lakes | **t + pop + t:pop + family + dam** |  |  |  |  |
|  | pop + family + dam | t | 3 | 443.54 | < 0.001 |
|  | t + family + dam | pop | 1 | 600.61 | < 0.001 |
|  | t + pop + family + dam | t:pop | 3 | 198.56 | < 0.001 |
|  | t + pop + t:pop + dam | family | 1 | 181.47 | < 0.001 |
|  | t + pop + t:pop + family | dam | 1 | 23.36 | < 0.001 |
| Finland | **t + pop + t:pop + family + dam** |  |  |  |  |
|  | pop + family + dam | t | 3 | 223.54 | < 0.001 |
|  | t + family + dam | pop | 1 | 993.43 | < 0.001 |
|  | t + pop + family + dam | t:pop | 3 | 52.94 | < 0.001 |
|  | t + pop + t:pop + dam | family | 1 | 48.43 | < 0.001 |
|  | t + pop + t:pop + family | dam | 1 | 13.52 | < 0.001 |
| Incubation Period (DPF) | Great Lakes | **t + pop + t:pop + family + dam + sire** |  |  |  |  |
|  | pop + family + dam + sire | t | 3 | 27,176.01 | < 0.001 |
|  | t + family + dam + sire | pop | 1 | 3,173.76 | < 0.001 |
|  | t + pop + family + dam + sire | t:pop | 3 | 1,113.95 | < 0.001 |
|  | t + pop + t:pop + dam + sire | family | 1 | 64.82 | < 0.001 |
|  | t + pop + t:pop + family + sire | dam | 1 | 60.90 | < 0.001 |
|  | t + pop + t:pop + family + dam | sire | 1 | 8.59 | 0.003 |
| Finland | **t + pop + t:pop + family + dam + sire** |  |  |  |  |
|  | pop + family + dam + sire | t | 3 | 6,976.53 | < 0.001 |
|  | t + family + dam + sire | pop | 1 | 727.92 | < 0.001 |
|  | t + pop + family + dam + sire | t:pop | 3 | 157.91 | < 0.001 |
|  | t + pop + t:pop + dam + sire | family | 1 | 8.25 | 0.004 |
|  | t + pop + t:pop + family + sire | dam | 1 | 36.19 | < 0.001 |
|  | t + pop + t:pop + family + dam | sire | 1 | 6.03 | 0.014 |
| Incubation Period (ADD) | Great Lakes | **t + pop + t:pop + family + dam + sire** |  |  |  |  |
|  | pop + family + dam + sire | t | 3 | 14,370.19 | < 0.001 |
|  | t + family + dam + sire | pop | 1 | 3,495.26 | < 0.001 |
|  | t + pop + family + dam + sire | t:pop | 3 | 160.60 | < 0.001 |
|  | t + pop + t:pop + dam + sire | family | 1 | 61.35 | < 0.001 |
|  | t + pop + t:pop + family + sire | dam | 1 | 60.90 | < 0.001 |
|  | t + pop + t:pop + family + dam | sire | 1 | 14.08 | < 0.001 |
| Finland | **t + pop + t:pop + family + dam + sire** |  |  |  |  |
|  | pop + family + dam + sire | t | 3 | 2,811.03 | < 0.001 |
|  | t + family + dam + sire | pop | 1 | 706.17 | < 0.001 |
|  | t + pop + family + dam + sire | t:pop | 3 | 440.18 | < 0.001 |
|  | t + pop + t:pop + dam + sire | family | 1 | 10.58 | 0.001 |
|  | t + pop + t:pop + family + sire | dam | 1 | 36.87 | < 0.001 |
|  | t + pop + t:pop + family + dam | sire | 1 | 5.01 | 0.025 |

Table 4. Larval model selection

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Trait | Region | Model | Effect Tested | df | χ2 | p-value |
| Length-at-Hatch | Great Lakes | **t + pop + dam** |  |  |  |  |
|  | pop + dam | t | 3 | 592.28 | < 0.001 |
|  | t + dam | pop | 1 | 443.20 | < 0.001 |
|  | t + pop | dam | 1 | 87.81 | < 0.001 |
| Finland | **t + pop + t:pop + family + dam** |  |  |  |  |
|  | pop + family + dam | t | 3 | 308.13 | < 0.001 |
|  | t + family + dam | pop | 1 | 1846.10 | < 0.001 |
|  | t + pop + family + dam | t:pop | 3 | 8.85 | 0.031 |
|  | t + pop + t:pop + dam | family | 1 | 15.81 | < 0.001 |
|  | t + pop + t:pop + family | dam | 1 | 41.46 | < 0.001 |
| Yolk-sac Volume | Great Lakes | **t + pop + t:pop + dam** |  |  |  |  |
|  | pop+ dam | t | 3 | 731.20 | < 0.001 |
|  | t + dam | pop | 1 | 100.48 | < 0.001 |
|  | t + pop + dam | t:pop | 3 | 36.50 | < 0.001 |
|  | t + pop + t:pop | dam | 1 | 299.71 | < 0.001 |
| Finland | **t + pop + t:pop + dam + sire + block** |  |  |  |  |
|  | pop + dam + sire + block | t | 3 | 6,976.53 | < 0.001 |
|  | t + dam + sire + block | pop | 1 | 727.92 | < 0.001 |
|  | t + pop + dam + sire + block | t:pop | 3 | 157.91 | < 0.001 |
|  | t + pop + t:pop + sire + block | dam | 1 | 82.19 | < 0.001 |
|  | t + pop + t:pop + dam + block | sire | 1 | 5.35 | 0.021 |
|  | t + pop + t:pop + sire + dam | block | 1 | 14.80 | < 0.001 |

**FIGURES:**

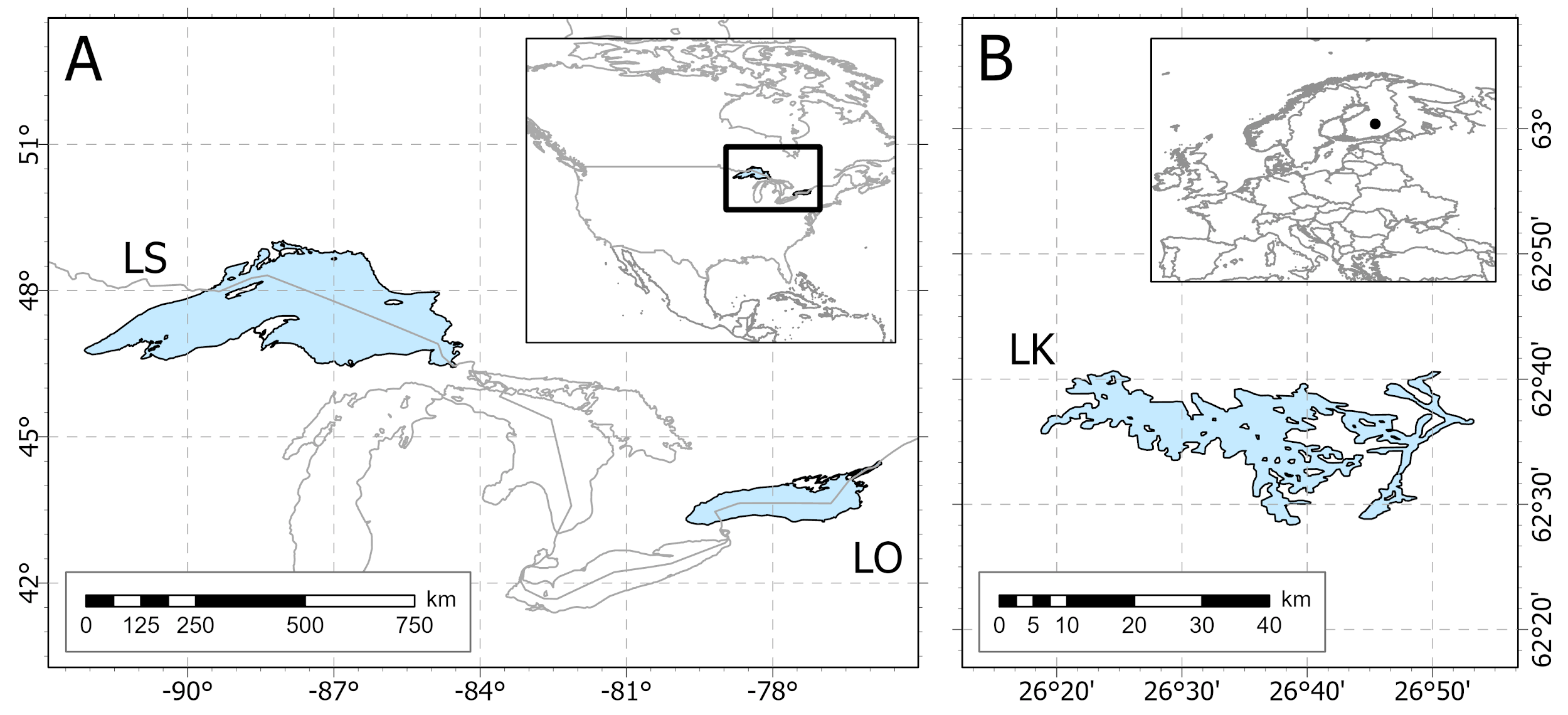


Figure X. Map showing the location of each lake (LS = Lake Superior; LO = Lake Ontario; LK = Lake Konnevesi) sampled in North America (A) and Europe (B).

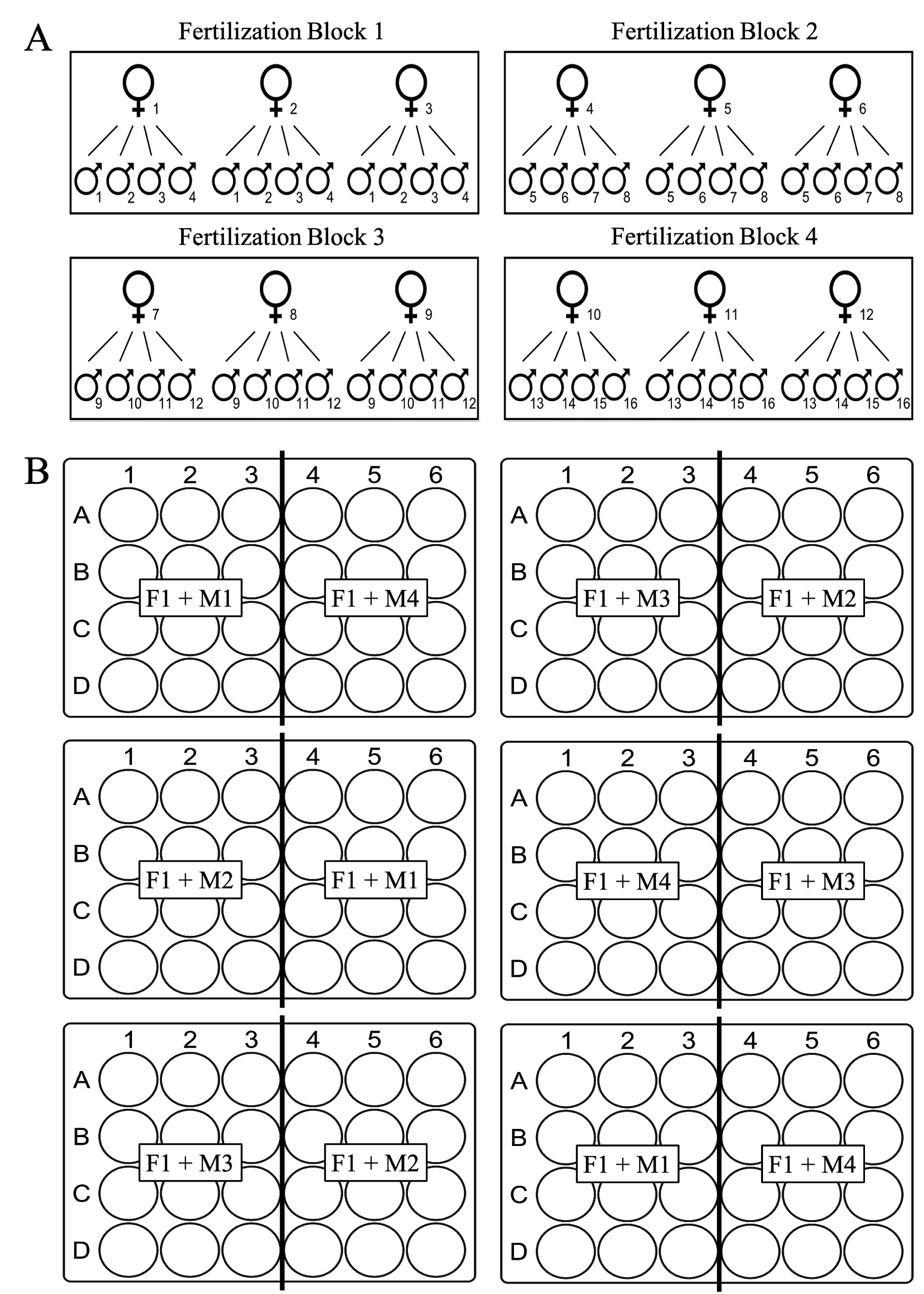


Figure X. Crossbreeding design (A) and a theoretical division of families from a single female into microplates (B) when the number of offspring equals 36.

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Figure X.

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Figure X.

Figure X. Heritability

**SUPPLEMENTAL INDEXS:**

SI X. Bootstrap bias-corrected mean additive genetic variation (VA), phenotypic variation (VP), and narrow-sense heritability (h2) estimates for embryo survival (%) from Lake Konnevesi (LK-Vendace (*C. albula*) and LK-Whitefish (*C. lavaretus*)), Lake Superior (­LS-Cisco (*C. artedi*)), and Lake Ontario (LO-Cisco) across each incubation temperature treatment (°C). Number of individuals (N) and standard error of estimates in parentheses below a value are presented.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Incubation Temperature | VA | VP | h2 | N |
| LK-Vendace | 2.2 | 0  () | 0  () | 0  () | 667 |
| 4.0 | 0  () | 0  () | 0  () | 985 |
| 6.9 | 0  () | 0  () | 0  () | 961 |
| 8.0 | 0  () | 0  () | 0  () | 994 |
| LK-Whitefish | 2.2 | 0  () | 0  () | 0  () | 351 |
| 4.0 | 0  () | 0  () | 0  () | 592 |
| 6.9 | 0  () | 0  () | 0  () | 539 |
| 8.0 | 0  () | 0  () | 0  () | 502 |
| LS-Cisco | 2.0 | 0  () | 0  () | 0  () | 916 |
| 4.4 | 0  () | 0  () | 0  () | 856 |
| 6.9 | 0  () | 0  () | 0  () | 892 |
| 8.9 | 0  () | 0  () | 0  () | 836 |
| LO-Cisco | 2.0 | 0  () | 0  () | 0  () | 2043 |
| 4.4 | 0  () | 0  () | 0  () | 2012 |
| 6.9 | 0  () | 0  () | 0  () | 2022 |
| 8.9 | 0  () | 0  () | 0  () | 1987 |

SI X. Bootstrap bias-corrected mean additive genetic variation (VA), phenotypic variation (VP), and narrow-sense heritability (h2) estimates for incubation period (number of days post-fertilization) from Lake Konnevesi (LK-Vendace (*C. albula*) and LK-Whitefish (*C. lavaretus*)), Lake Superior (­LS-Cisco (*C. artedi*)), and Lake Ontario (LO-Cisco) across each incubation temperature treatment (°C). Sample size (N) and standard error of estimates in parentheses below a value are presented.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Incubation Temperature | VA | VP | h2 | N |
| LK-Vendace | 2.2 | 0  () | 0  () | 0  () | 559 |
| 4.0 | 0  () | 0  () | 0  () | 745 |
| 6.9 | 0  () | 0  () | 0  () | 785 |
| 8.0 | 0  () | 0  () | 0  () | 680 |
| LK-Whitefish | 2.2 | 0  () | 0  () | 0  () | 192 |
| 4.0 | 0  () | 0  () | 0  () | 220 |
| 6.9 | 0  () | 0  () | 0  () | 171 |
| 8.0 | 0  () | 0  () | 0  () | 90 |
| LS-Cisco | 2.0 | 0  () | 0  () | 0  () | 771 |
| 4.4 | 0  () | 0  () | 0  () | 757 |
| 6.9 | 0  () | 0  () | 0  () | 798 |
| 8.9 | 0  () | 0  () | 0  () | 647 |
| LO-Cisco | 2.0 | 0  () | 0  () | 0  () | 2029 |
| 4.4 | 0  () | 0  () | 0  () | 1998 |
| 6.9 | 0  () | 0  () | 0  () | 1966 |
| 8.9 | 0  () | 0  () | 0  () | 1457 |

SI X. Bootstrap bias-corrected mean additive genetic variation (VA), phenotypic variation (VP), and narrow-sense heritability (h2) estimates for incubation period (accumulated degree-days) from Lake Konnevesi (LK-Vendace (*C. albula*) and LK-Whitefish (*C. lavaretus*)), Lake Superior (­LS-Cisco (*C. artedi*)), and Lake Ontario (LO-Cisco) across each incubation temperature treatment (°C). Sample size (N) and standard error of estimates in parentheses below a value are presented.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Incubation Temperature | VA | VP | h2 | N |
| LK-Vendace | 2.2 | 0  () | 0  () | 0  () | 559 |
| 4.0 | 0  () | 0  () | 0  () | 745 |
| 6.9 | 0  () | 0  () | 0  () | 785 |
| 8.0 | 0  () | 0  () | 0  () | 680 |
| LK-Whitefish | 2.2 | 0  () | 0  () | 0  () | 192 |
| 4.0 | 0  () | 0  () | 0  () | 220 |
| 6.9 | 0  () | 0  () | 0  () | 171 |
| 8.0 | 0  () | 0  () | 0  () | 90 |
| LS-Cisco | 2.0 | 0  () | 0  () | 0  () | 771 |
| 4.4 | 0  () | 0  () | 0  () | 757 |
| 6.9 | 0  () | 0  () | 0  () | 798 |
| 8.9 | 0  () | 0  () | 0  () | 647 |
| LO-Cisco | 2.0 | 0  () | 0  () | 0  () | 2029 |
| 4.4 | 0  () | 0  () | 0  () | 1998 |
| 6.9 | 0  () | 0  () | 0  () | 1966 |
| 8.9 | 0  () | 0  () | 0  () | 1457 |

SI X. Bootstrap bias-corrected mean additive genetic variation (VA), phenotypic variation (VP), and narrow-sense heritability (h2) estimates for length-at-hatch (mm) from Lake Konnevesi (LK-Vendace (*C. albula*) and LK-Whitefish (*C. lavaretus*)), Lake Superior (­LS-Cisco (*C. artedi*)), and Lake Ontario (LO-Cisco) across each incubation temperature treatment (°C). Sample size (N) and standard error of estimates in parentheses below a value are presented.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Incubation Temperature | VA | VP | h2 | N |
| LK-Vendace | 2.2 | 0  () | 0  () | 0  () | 176 |
| 4.0 | 0  () | 0  () | 0  () | 180 |
| 6.9 | 0  () | 0  () | 0  () | 180 |
| 8.0 | 0  () | 0  () | 0  () | 180 |
| LK-Whitefish | 2.2 | 0  () | 0  () | 0  () | 104 |
| 4.0 | 0  () | 0  () | 0  () | 96 |
| 6.9 | 0  () | 0  () | 0  () | 73 |
| 8.0 | 0  () | 0  () | 0  () | 36 |
| LS-Cisco | 2.0 | 0  () | 0  () | 0  () | 135 |
| 4.4 | 0  () | 0  () | 0  () | 125 |
| 6.9 | 0  () | 0  () | 0  () | 55 |
| 8.9 | 0  () | 0  () | 0  () | 54 |
| LO-Cisco | 2.0 | 0  () | 0  () | 0  () | 240 |
| 4.4 | 0  () | 0  () | 0  () | 235 |
| 6.9 | 0  () | 0  () | 0  () | 191 |
| 8.9 | 0  () | 0  () | 0  () | 164 |

SI X. Bootstrap bias-corrected mean additive genetic variation (VA), phenotypic variation (VP), and narrow-sense heritability (h2) estimates for yolk-sac volume (mm3) from Lake Konnevesi (LK-Vendace (*C. albula*) and LK-Whitefish (*C. lavaretus*)), Lake Superior (­LS-Cisco (*C. artedi*)), and Lake Ontario (LO-Cisco) across each incubation temperature treatment (°C). Sample size (N) and standard error of estimates in parentheses below a value are presented.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Population | Incubation Temperature | VA | VP | h2 | N |
| LK-Vendace | 2.2 | 0  () | 0  () | 0  () | 176 |
| 4.0 | 0  () | 0  () | 0  () | 180 |
| 6.9 | 0  () | 0  () | 0  () | 180 |
| 8.0 | 0  () | 0  () | 0  () | 180 |
| LK-Whitefish | 2.2 | 0  () | 0  () | 0  () | 104 |
| 4.0 | 0  () | 0  () | 0  () | 96 |
| 6.9 | 0  () | 0  () | 0  () | 73 |
| 8.0 | 0  () | 0  () | 0  () | 36 |
| LS-Cisco | 2.0 | 0  () | 0  () | 0  () | 135 |
| 4.4 | 0  () | 0  () | 0  () | 125 |
| 6.9 | 0  () | 0  () | 0  () | 55 |
| 8.9 | 0  () | 0  () | 0  () | 54 |
| LO-Cisco | 2.0 | 0  () | 0  () | 0  () | 240 |
| 4.4 | 0  () | 0  () | 0  () | 235 |
| 6.9 | 0  () | 0  () | 0  () | 191 |
| 8.9 | 0  () | 0  () | 0  () | 164 |