Table 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 |

Table 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; DPF) 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 |

Table X. Bootstrap bias-corrected mean additive genetic variation (VA), phenotypic variation (VP), and narrow-sense heritability (h2) estimates for incubation period (accumulated degree-days; ADD) 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 |