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Salmon in Hot Water Featured scientists: Wesley Larson, Meredith Everett, and Jim Seeb from the University of Washington

## Research Background:

Chinook salmon are important members of freshwater and ocean food webs. Salmon transport nutrients from the ocean to freshwater habitats. Traces of nutrients from salmon can be found in everything from trees to bears! Salmon also support sport and commercial fisheries, and are used for ceremonial purposes by Native Americans. Climate change poses a threat to salmon populations by warming the waters of streams and rivers where they reproduce. To maintain healthy populations, salmon rely on cold, freshwater habitats and may go extinct as temperatures rise in coming decades. Warm temperatures can cause large salmon die-offs. However, some salmon individuals have higher **thermal tolerance**, or the ability to withstand and live in warm temperatures. These individuals may be better able to survive when water temperatures rise.

Salmon individuals with certain gene variants that give them higher thermal tolerance may be better able to survive in warmer waters. Scientists want to know whether there is a genetic basis for the variation observed in salmon's thermal tolerance. If differences in certain genes control variation in thermal tolerance, scientists can identify the location on the genome responsible for this very important adaptation. Once identified, management agencies could then screen for these genes in populations of Chinook salmon in order to identify individuals that could better survive in a future warmer environment. Hatchery programs could also breed thermally tolerant fish in an attempt to preserve this important fish species.



Data Nuggets developed by Michigan State University fellows in the NSF BEACON and GK-12 programs

To identify the genes responsible for a particular trait, scientists look for Quantitative Trait Loci (QTL). A QTL is a genetic variant that influences the phenotype, or observable trait, determined by multiple genes. Examples of phenotypes are human height, eye or skin color. Many genes may also determine thermal tolerance in salmon. Scientists can find QTL by conducting experimental matings then examining the phenotypic (observable) and genetic (from DNA) characteristics of the offspring. In this study, parent fish from one population of salmon were mated. Some of these parents were tolerant to warm water and some were not. The offspring then had a mix of genetic backgrounds from their parents. In other words, some offspring inherited genetic variants that made them more tolerant to high temperatures and some did not. Each offspring was tested for their thermal tolerance, and had their genomes (DNA composition of all genes) sequenced, or identified. Differences in the genome between offspring that are tolerant and those that are not reveal areas of the genome that are linked with thermal tolerance and survival in warm water. If differences in certain genes control variation in thermal tolerance, the scientists predicted they could find regions in the salmon genome that are correlated with survival in warm water.

<u>Scientific Question</u>: Are there regions in the genome are significantly correlated with a salmon's ability to survive thermal stress? If so, how many?

<u>What is the hypothesis?</u> Find the hypothesis in the Research Background and underline it. A hypothesis is a proposed explanation for an observation, which can then be tested with experimentation or other types of studies.

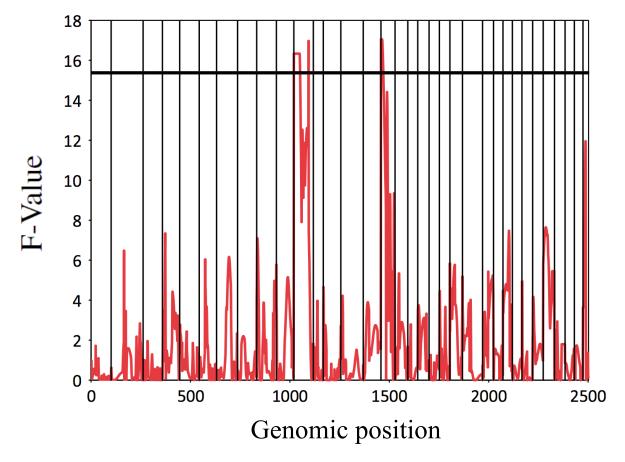


Salmon eggs used in the QTL experiment

Scientists working in the lab

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<u>Scientific Data</u>: The graph below shows data from a QTL study. Position within the genome is plotted on the x-axis, and each box is a different chromosome. The red line indicates the level that a particular genome region was correlated with thermal tolerance, measured by the F-Value. Areas of the genome with high F-Values are highly correlated with thermal tolerance. The black horizontal line with an F-Value close to 16 represents the significance threshold. In other words, it is extremely unlikely that an F-Value above the black line could have occurred by chance. If the red line goes above the horizontal black line we have significant evidence that a genomic location is correlated with thermal tolerance.



Use the data presented in this graph to answer the scientific question:

<u>Interpret the data</u>: Make a claim based on the evidence that helps answer the original research question. Connect the pattern in the data to a pattern in the natural world. Justify your reasoning using data.

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Interpret the data: continued

<u>Your next step as a scientist</u>: Science is an ongoing process. Did this study fully answer your original question? What new questions do you think should be investigated? What future data should be collected to answer them?