

Genome in rainbow trout and steelhead



**ASSIGN
BUSTER**

(lead author John Whitt)

Abstract

When being thrown into a different environment those new pressures can lead a population to have fast changes via natural selection. These evolutions can occur at a species level or can occur between two closely related species that have differentiated but share a common ancestor as long as the trait is beneficial for them. Population genetic and quantitative research methods have proven that certain linked areas of the genome in rainbow trout and steelhead are tied to the life history strategies of their species. Using genotype testing on 95 nucleotides it has been determined that the specific chromosome that is responsible for the life history strategies is Omy5.

1. Introduction

Being thrown into a new environment leads to quick changes in a population and the traits may even change in multiple species if they are being acted on by the same environmental forces. Different species who share a common ancestor that develop similar phenotype changes due to the habitat pressures acting on them are said to have parallel evolution. These physical changes may arise from the same genetic change in both species or can stem from different regions in both species that happen to cause the same phenotypic expression. While it is not impossible for parallel evolution to occur from a random new mutation it is much more likely to occur because of a sequence change in existing alleles. It is extremely important for researchers to determine the location of the genes they are testing for and

<https://assignbuster.com/genome-in-rainbow-trout-and-steelhead/>

without this, it is impossible to see how evolution is occurring at the genetic level. It turns out most of the important traits are not controlled by a single genetic or habitat factor. They are often complex and difficult to locate. The most difficult to genetically locate are traits that affect numerous physical changes, influence the behavior, or have a physiological effect on the species. The researchers are using advanced techniques like genomic mapping and screening along with sequencing the entire genome of the animals being tested to help locate the area of the genome that is being affected from these rapid evolutions caused by new environments.

There have been many genetic studies done on the migration of animals and it is commonly accepted that genetics play a major role in the phenotypic differences that accompany these migration characteristics. These threshold traits are determined not only by the physical traits but also by the animal's physiological traits. Though migration has all these complex traits that act on it, researchers have also found single genes that have an effect on the migration of animals as well, so it can also be quite simple at times. The single Clock gene in the Pacific salmonid is a large contributor on when the salmonid migrates. One of the world's most abundant and common fish is the *Oncorhynchus mykiss*. *O. mykiss* have one of the most comprehensive migratory variations. For example, the rainbow trout never leaves freshwater, whereas the steelhead are more located in the salt water. It has been determined that these varying migration tendencies are genetically passed down. Though the differences between the steelhead and the rainbow trout are great, they are the closest related *O. mykiss*. Steelheads have more of a complexity when it comes to factors affecting their migration. They have the

typical traits that usually affect migration, but also have smoltification which gives them the traits required to go from freshwater to saltwater and ability to travel far. The rainbow trout on the other hand only keeps the ability to swim in fresh water but gain the ability to sexually reproduce sooner.

Past studies have been completed on two populations of *O. mykiss* that happened to be separated by an environmental barricade. They were then tested for F_{st} value and found that the loci had the highest values displayed linkage disequilibrium which means that they were not independently assorted. The loci were also genetically located at the same position in both of the populations. When further tested it was determined that the two populations had 3 loci that had linkage disequilibrium as well as allelic frequency patterns that matched with gnomonic mapping tests that gave the same locations for characteristics growth rate and smoltification. These were all found on the *Omy5*. These determined that the *Omy5* location was responsible for all the traits across populations even if they were separated, meaning that there was no genetic flow going on between the two. Miller and colleague's goals are to find out how SNPs that coded for physical traits like maturation time, growth rate, and smolting from past experiments are linked to the *Omy5* gene.

2. Material and methods

(a) Population samples

Using locations from California and Oregon 21 samples of steelhead and rainbow trout were obtained from populations that were separated by natural or artificial barriers. They took the samples from above and below

<https://assignbuster.com/genome-in-rainbow-trout-and-steelhead/>

the barriers and also took samples from rainbow trout hatcheries, so that they could have samples from all the life stages. They believed that all of the fish samples that were obtained in the wild were of natural origin, but were not one hundred percent on the status of the hatchery samples.

(b) Marker development, genotyping and analysis

Miller and colleague discovered 344 single nucleotide polymorphisms that were linked to Omy5 with RAD sequencing from two of the hatchery strains. They created 55 unique SNPtype assays by adding 150bp from cloned BAC strains onto the flanking sequences of the SNP. They also utilized assays that were developed by other researchers. Miller Pearse et al also used three loci found by Abadia Cardoso and his colleagues. For the analysis part, they used EP1 systems and followed the recommended protocols. They used two control groups for every array. Linkage disequilibrium as well as, Hardy-Weinberg equilibrium were test for. Miller and colleagues only counted p-values that were under the Bonferroni-corrected value due to the large number of linked disequilibrium tests. They quantify the Omy5 in different ways. They ranked 55 loci of the Omy5 based on the r^2 values and then compared those to rest of the loci. R^2 value is calculated by checking to see if an allele is present at two different loci. For example, one could look for allele 1 at locus 1 and locus 2 and then one would check to see if allele 2 is present at locus 1 and locus 2. These result could then be used to calculate r^2 . Using statistical packages the researcher visualized linkage disequilibrium of the Omy5 in all of the population sampled. They also computed the amount of linkage association that was over the critical value that was

shared between locus and loci. For a reference population Miller Pearse et al used the Scoot Creek steelhead because it had the biggest sample size and have had the greatest polymorphic loci. To find if there was a link between Omy5 and life history Miller took allele frequencies from all the populations and compared them to one another still using the Scott Creek as a reference population he determined the frequency p for all the sample populations.

3. Results and analysis

(a) Genetic data

There was a total of 95 single nucleotide polymorphism tested eight of those failed due to not being amplified, did not show signs of polymorphism or weren't in line with Mendelian segregation. This left Miller with 87 loci which were comprised of 55 Omy5 loci and loci from the other 32 were on other linked groups. Of these 87 it was determined that 4 were not in Hardy-Weinberg equilibrium.

(b) Population structure

Based on the 32 loci from other linked groups it was determined that they followed a similar trend as that of past studies. Stating that the closer the populations were to each other the more related the populations would be. Miller found when looking at the Omy5 loci it was the opposite meaning the population displayed a high separation between the populations that were separated by the waterfalls or dams.

(C) Linkage disequilibrium

Miller performed a total of 495 linkage disequilibrium tests on the 32 other linked groups. After the tests were Bonferroni corrected for numerous attempts it was determined that none of those groups had a significant value. Miller now looked at the loci of the 55 Omy5 groups and the results were that out of 1430 there were a total of 602 that were significant, which gave them a total of 42% of the test samples having a significant p-value. These results conferred that the linkage on Omy5 was, in fact strong.

To visualize linkage disequilibrium in all of the populations Miller took the values for the r^2 which went from 0.008 – 0.53 (no units) and used these to order the populations. Miller found that there were 14 loci with r^2 values that exceeded the critical value which is 0.9. Once analyzed there obviously a cluster of loci that were in strong linkage disequilibrium.

(d) Allele frequency and haplotype variation among populations

The results for allelic frequency variations agreed with the linkage disequilibrium analysis performed on the 55 Omy5 loci. The results also gave groups of the loci whose frequencies were closely related and were linked to populations that were above and below the natural or artificial barriers. Miller took the loci with the greatest average r^2 values and labeled them as one linked haplotype. These 30 loci were linked to the steelhead and rainbow trouts life-history strategies. Miller Pearse et al then used the haplotype to determine the haplotype frequency for the steelhead and rainbow trout by using their average allele frequencies. Miller Pearse et al found that rainbow trout haplotype frequencies were higher in the areas that were above the barriers and had significantly decreased haplotype

frequencies in the below barrier populations. This was accurate with the collecting data of the rainbow trout as they were found in the four populations that were taken from above the natural and artificial barriers. Miller and colleagues then compared that new species versus the older species and found that the older species had a great number of Steelhead haplotypes.

4. Discussion

Miller concludes that the results prove that adaptation in natural populations can occur rapidly and are caused by the environments pressures that act upon those populations. Miller also states that artificial factors have a higher evolutionary influence on the populations than is seen with natural selection. What is still unclear to Miller is that how these pressures affect the genetic evolution of the populations. For example, if species are undergoing parallel evolution are they just developing similar traits that are better suited for their environment, or are these changes also occur similarly at the genetic level. Miller Pearse et al results imply that the parallel pressures of natural selection are also having parallel affects genetically. These effects are occurring specifically on the Omy5. Which they have concluded to be linked to the life-history patterns of that population and used the data collected from the frequency haplotyping to demonstrate that the population responds to environmental pressures that are acting on them. The Omy5 also acts as a command center of some sorts and controls actions like migration.

Looking to the past Millers et al experiment is in line with others performed. There have been experiments that have used different populations of

sticklebacks and moved them from their normal saltwater environment to a new freshwater environment which resulted in the loss of defensive traits like armor. There are also examples of Scott Creek population that went through a pigmentation change even though it resulted in a reduction in the fitness of the population. Miller hypothesizes that life-history strategies are linked to the genetic of the population, specifically at the Omy5 region is supported by his and these past experiments. There is also evidence from past experiments that suggest that Omy5 has resistance to recombination, and is likely due to chromosome inversion. This is interesting because the region that is responsible for the change in life-history patterns is resistant to change. Could look at this like the population of *O. mykiss* do not want to change those traits. It is also important to note that it is not hundred percent sure exactly what traits are being affected by the Omy5 section of the genome. It is known that the Clock gene is within the Omy5 region. The Clock gene has been linked to smolting and it is hypothesized that sense smolting is extremely complicated that there are multiple genes that are responsible for its coding.

(a) Conservation implication.

Miller also states that his results are showing a decrease in rainbow trout in older above barrier location and the hypothesis that if enough time passes there might be no rainbow trout in above barrier locations due to the migration history patterns of these fish, so far his hypothesis seems to accurate, because all of the rainbow trout they collected were below the barriers. He also states that because of the artificial barriers that do not allow the populations to make migration chooses of their own that it locks <https://assignbuster.com/genome-in-rainbow-trout-and-steelhead/>

them into this cycle even more. Meaning that if they were natural barriers the fish might be able to find a way past them, but since they are artificial barriers like dams that are meant to block passage that the above barrier and below barrier populations are going to stay separated. Miller Pearse et al discusses the effects of large closed bodies of waters or reservoirs and states that these could be the reason for the higher frequency of rainbow trout haplotype since these environments favor their population more so than the steelhead.

Miller and his colleagues experiment give many facts about the rapid evolution due to environmental pressures caused by a change in habitat, but they also provide some more subtle information that may be lost in the numbers. Miller's experiment shows declining number of rainbow trout in older areas and presents facts about how artificial barriers affect the different population of fishes. The article also discusses how only the fish that are below the barriers are protected. This is probably not the best way to try and keep these fish population from being endangered. The reason being that both species share such a close ancestor that they are both able to produce the same phenotypes, which should result in both of them being protected.