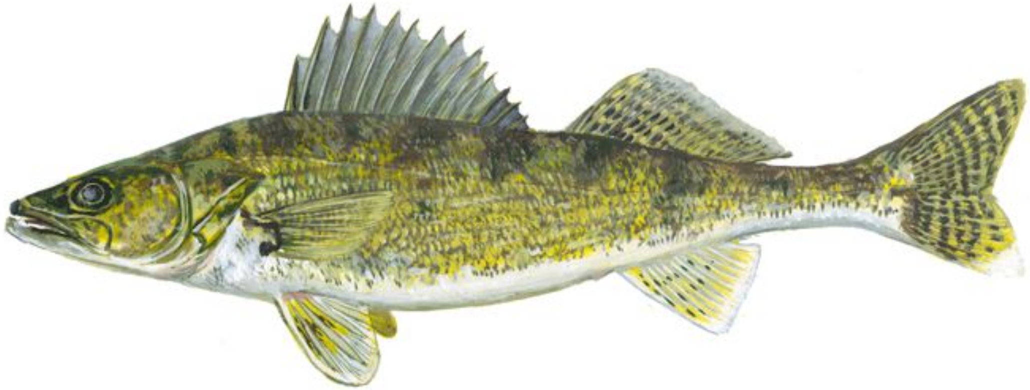
Great Sacandaga Lake Walleye

Review

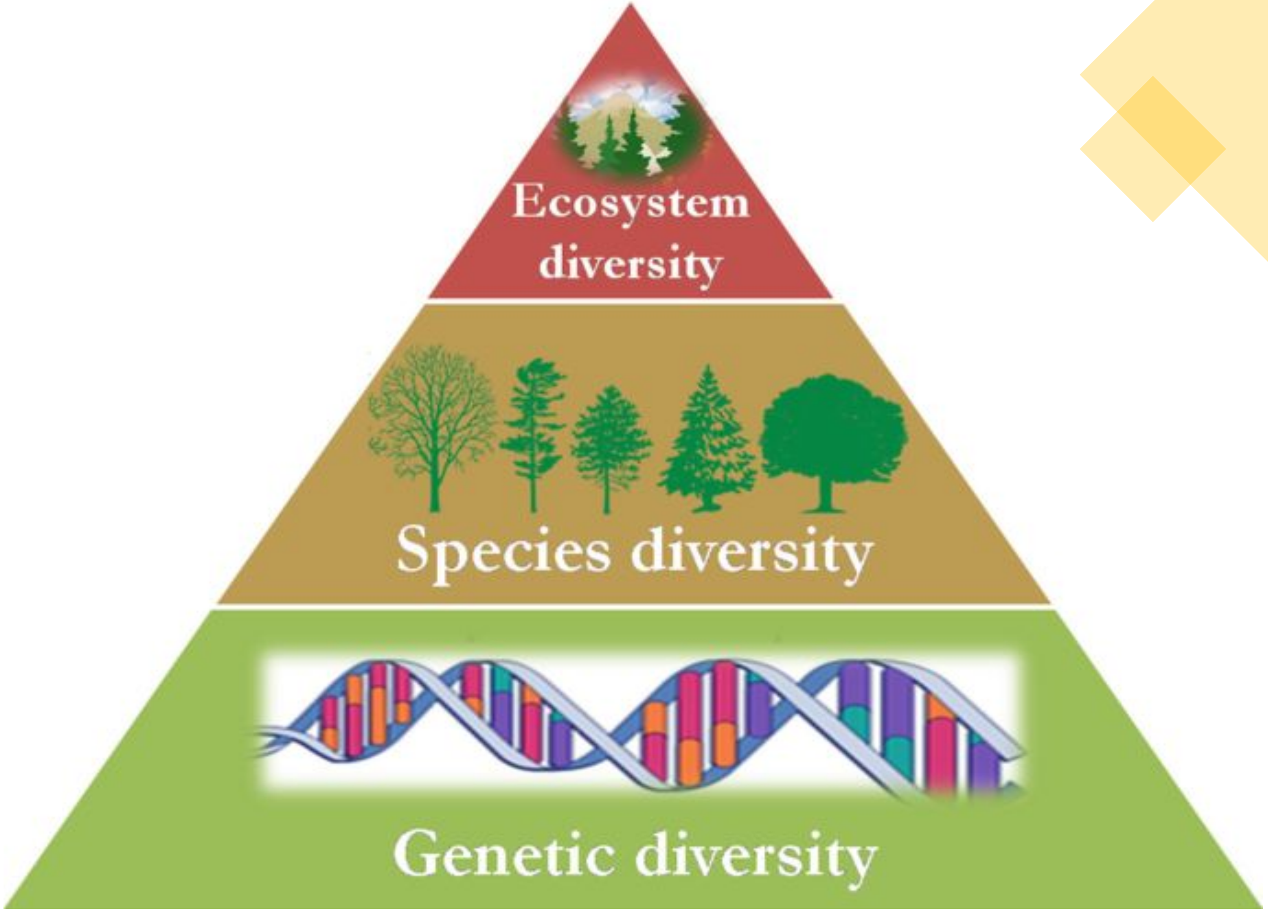
- Before we can look at our results, let's recall what we are researching
- Two populations of walleye
  - Hatchery population and a wild population
- We want to know:
  - Genetic diversity of each population
  - Impacts of Great Sacandaga Lake Fisheries Federation stocking
  - Contribution of stocked walleye in harvestable population



https://dnr.wisconsin.gov/topic/Fishing/species/walleye.html

Genetic Diversity

- We measured different genetic diversity metrics in each population
- But what exactly does that mean?
- Genetic diversity: differences in DNA of individuals in a population
- Why is genetic diversity important?
    - Low diversity = less variation
    - High diversity = more variation



Nonić, M. and Šijačić-Nikolić, M., 2021. Genetic diversity: sources, threats, and conservation. Life on land, pp.421-435.

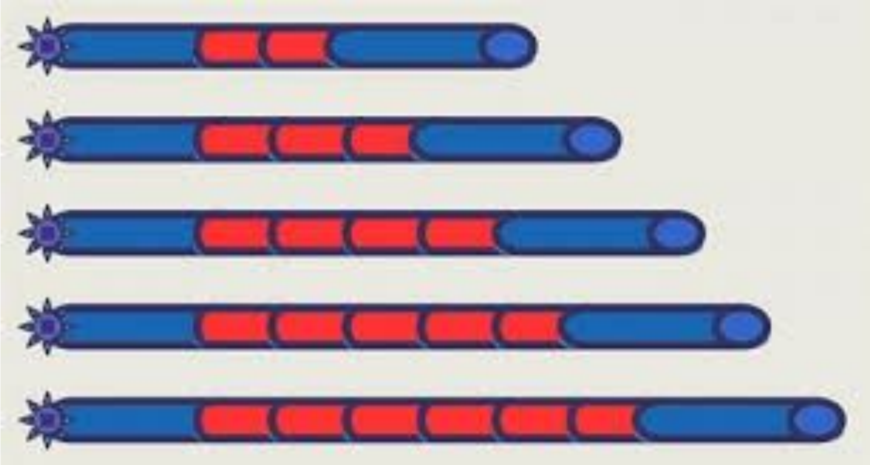
Genetic Diversity

- Think apples in a grocery store
- All apples, but very different in size, taste, etc.
  - Thank genetic diversity
- What if all apples were the same (low diversity), and a disease came along?
  - Higher diversity helps with population health

https://www.prevention.com/food-nutrition/g20481875/apple-varieties-and-recipes/

Genetic Diversity

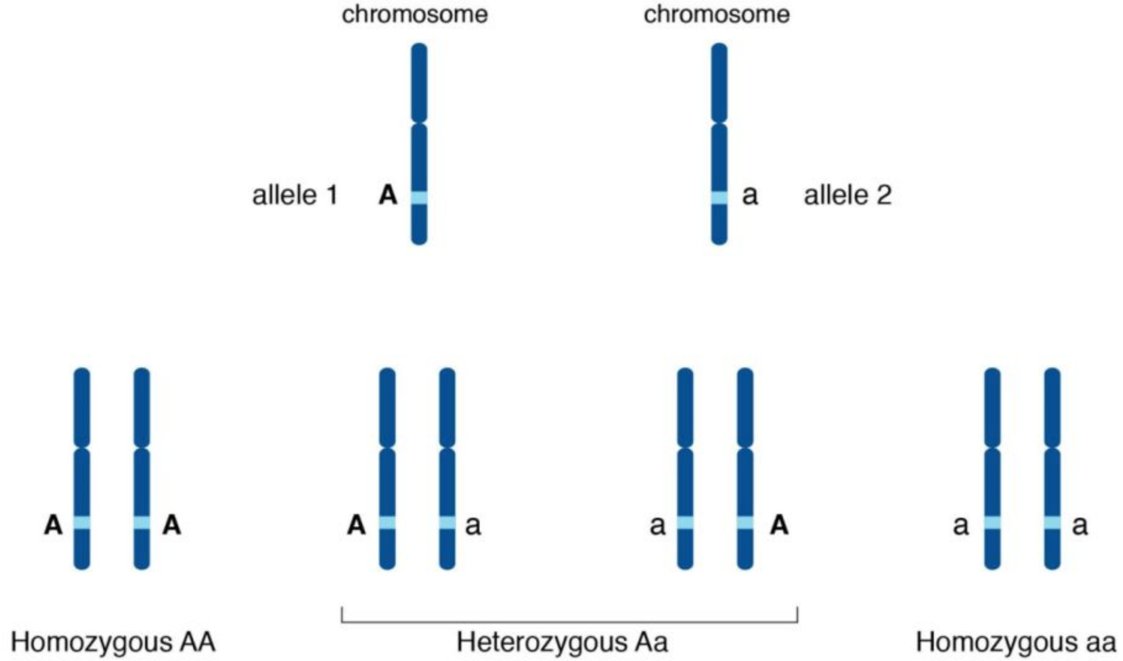
- Now you know about genetic diversity
- But how do we measure genetic diversity?
- Recall microsatellites
- Microsatellites found throughout the whole genome
- Measure microsatellites at different parts of the genome
- Representative sample of genetic diversity of the individual
- Sample enough individuals to represent the population



https://sourcebioscience.com/genomics/

Genetic Diversity

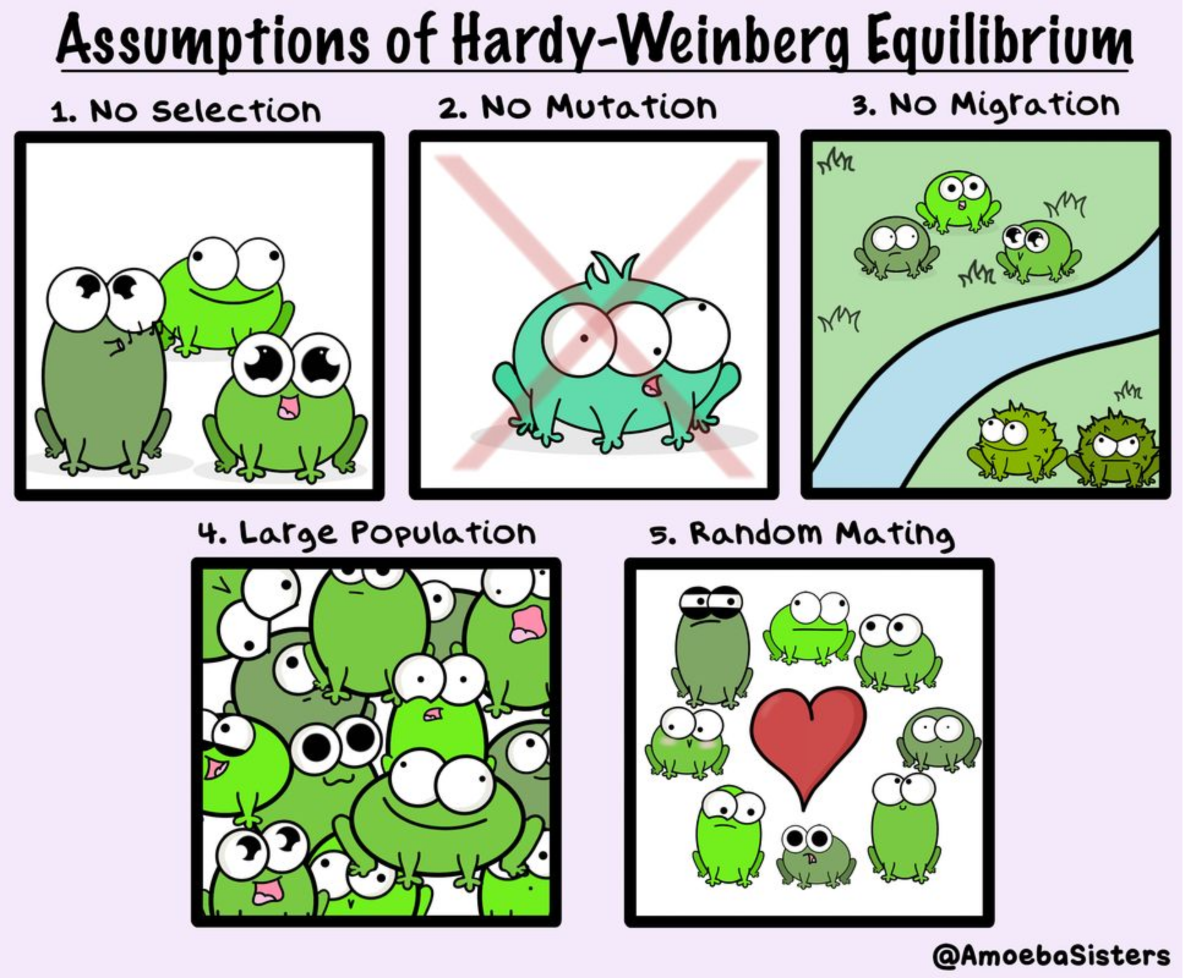
- To measure genetic diversity, we look at different metrics
- Let's define a few metrics below:
- Heterozygosity- two alleles at one locus
  - Allele: different forms of a gene
  - Locus: physical location in the genome



https://jackwestin.com/resources/mcat-content/mendelian-concepts/homozygosity-and-heterozygosity

Hardy-Weinburg Equilibrium

- Genetic variation (diversity) will remain the same from one generation to the next
- This is a key principle in our work
- This model assumes 5 principles
    - No migration
    - No mutation
    - Random mating
    - Very large population size
    - No selection
- If we find deviation from this equilibrium, it is due to one (or more) of the five reasons



https://www.amoebasisters.com/parameciumparlorcomics/hardy-weinberg-equilibrium-assumptions

Genetic Diversity

- F_{st}: genetic differences between two populations
- Scored on a 0-1 scale
- Low (0-0.05): different populations, but share some genetic material
- Medium (0.05-0.20): isolated populations, differentiating
- High (0.2+): very different populations, isolated for long period of time

Genetic Diversity

- Effective population size (N_e)
- Number of individuals that participates in producing the next generation
- Another way of thinking about it
- Number of individuals in a population who mate and pass on genes
- Low N_e = lose genetic diversity more quickly than large N_e
- Researchers generally use an N_e of 500 as a benchmark for a healthy population

Results

- We now know the terms that describe genetic diversity
- Let’s look at the results we found from Great Sacandaga Lake

Genetic Diversity: Results

- F_{st} value: 0.09
  - Significant finding. These populations are genetically distinct
- Hardy-Weinberg Equilibrium
  - Both populations deviate from HWE
- Heterozygosity
  - Both populations have less observed heterozygosity than expected
- N_e = Wild (123) Hatchery (140)
  95%: 61.4-654.7 42-∞

Genetic Diversity: Results

- The two populations did not have significantly different allelic richness
- The two populations did not significantly differ in observed heterozygosity
- The two populations did not significantly differ in expected heterozygosity
- The populations did not significantly differ in F_{IS} values
- Overall, do not differ in genetic diversity metrics

STRUCTURE Plots

- The following slides contain STRUCTURE plots
- This software analysis shows us ancestry of each individual
- It allows us to visualize ancestry of each population, and contribution of the ancestry to each individual
- K is the number of inferred populations
- We can test different K values to determine which is most likely to be correct

Differences between populations?

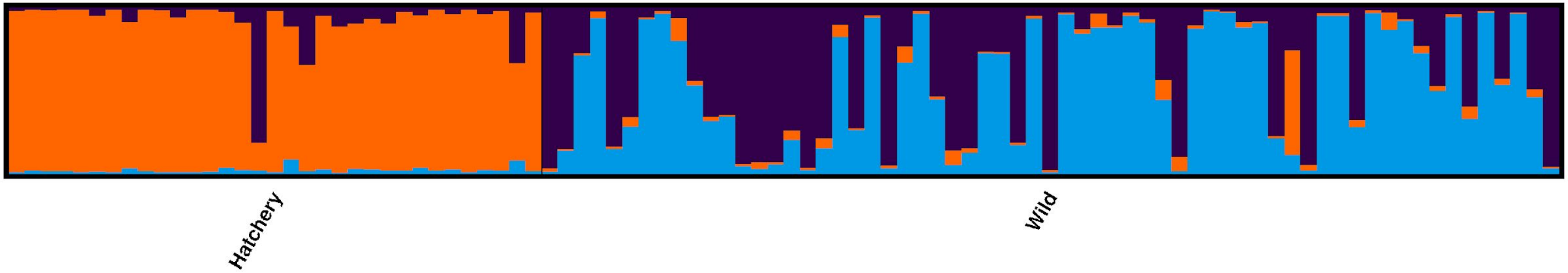
K = 2

Orange = Hatchery

Blue = Wild

Differences between populations?

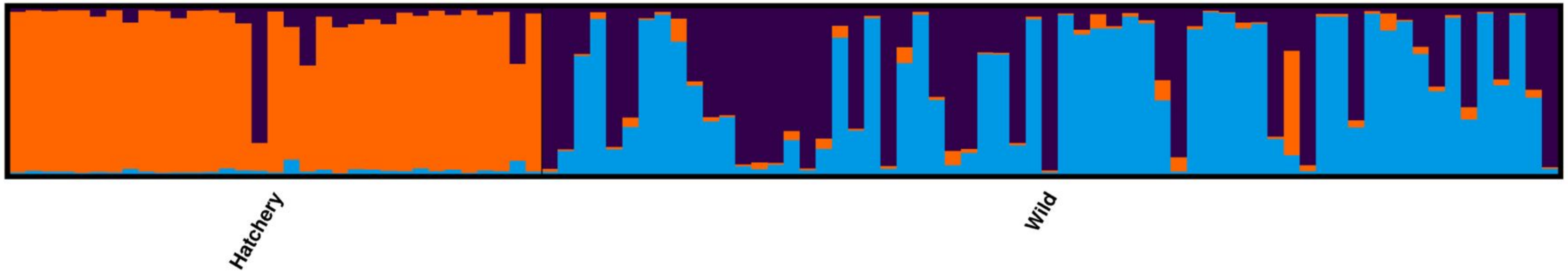
K = 3



Orange = Hatchery

Purple = Unknown population

Blue = Wild



STRUCTURE Results

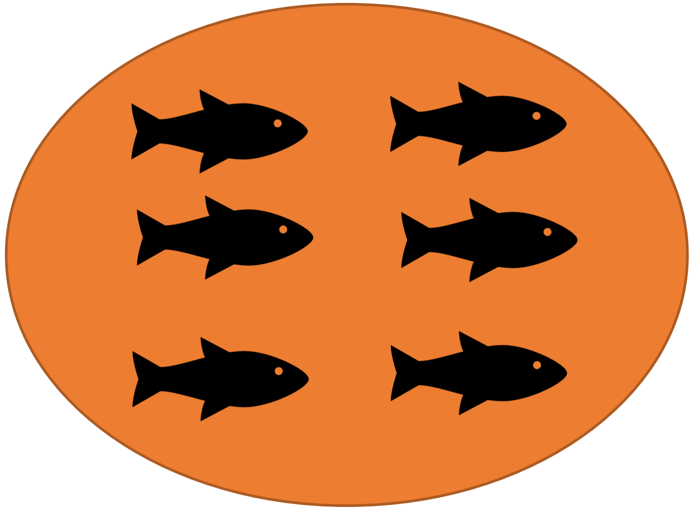
- Our work indicates the most likely K = 2
- However, K = 2 and K = 3 are close in probability of being true
- Purple indicates what could be a potential second population in the wild
- What does this mean??

Results

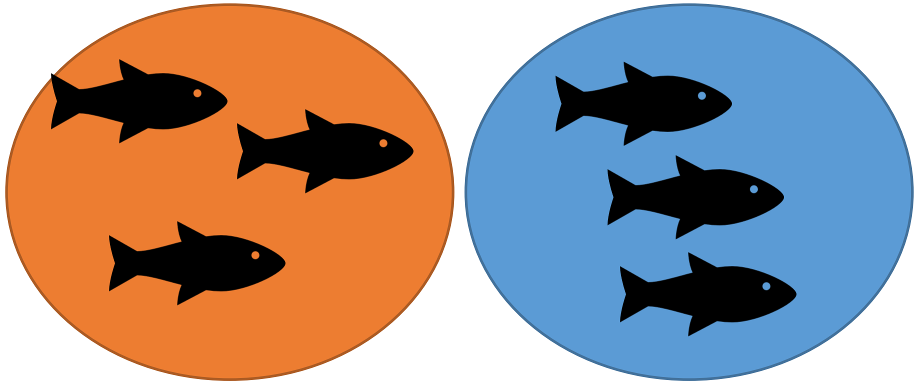
- Let's highlight and review what we have found so far
- Reduced heterozygosity in both populations
  - Compared to what was expected
- Both populations deviate from HWE
  - Remember the 5 assumptions
- Significant F_{st} value
  - The populations are genetically distinct
- The populations did not significantly differ in genetic diversity metrics
- Wild population N_e lower than the hatchery population
  - However, only 1 wild population?

Wahlund Effect

- Observed heterozygosity is lower than expected due to sup-population structure
- We assume there is one population
- Measure heterozygosity
- Low heterozygosity due to assuming there is one population
- Our most likely number of populations was 2 (Hatchery and Wild)
- However, 3 could potentially be true as well



Assume



Reality

Conclusions

- We averaged 7.6% ancestry of hatchery population in wild population
    - Ranges from 0.7% to 68% ancestry
- Populations did not significantly differ in genetic diversity metrics
- Both populations deviated from Hardy-Weinberg expectations
- The wild population has a smaller effective population size
    - Could impact genetic diversity in future generations
- This may need to be managed by NY agencies

Evaluation

- We now know the results of our genetic analysis
- But, how do we get to these results?

Microsatellites

- Microsatellites: short segment of DNA, repeated many times
- Below, we see a microsatellite “ACT” repeated 10 times
- We are able to measure the number of repeats in the lab

TAGCAGTATGCACTACTACTACTACTACTACTACTACTACTGCTATGCTGACTGG

Microsatellites

- Walleye and humans both have two sets of chromosomes
- If the sample is homozygote, ACT will be repeated 10x on both sets

TAGCAGTATGCACTACTACTACTACTACTACTACTACTACTGCTATGCTGACTGG

TAGCAGTATGCACTACTACTACTACTACTACTACTACTACTGCTATGCTGACTGG

Microsatellites

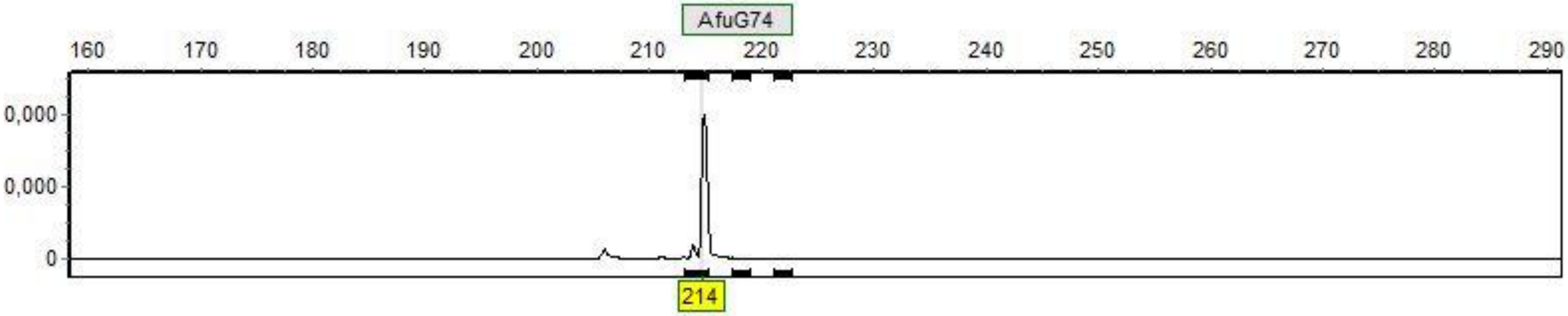
- There are two sets of chromosomes
- If the sample is heterozygote, ACT will be repeated 10x on both sets of chromosmes
- In this example, we see a 10x repeat on one set and a 5x on the second set

TAGCAGTATGCACTACTACTACTACTACTACTACTACTACTGCTATGCTGACTGG

TAGCAGTATGCACTACTACTACTACTGCTATGCTGACTGG

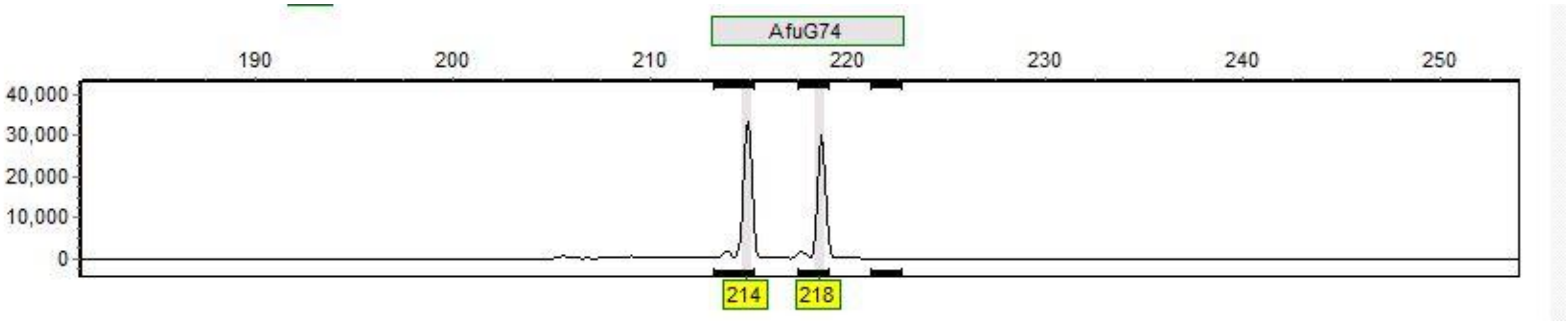
Microsatellites

Below is an example of what we observe in the lab. The example is homozygote with 214 basepairs



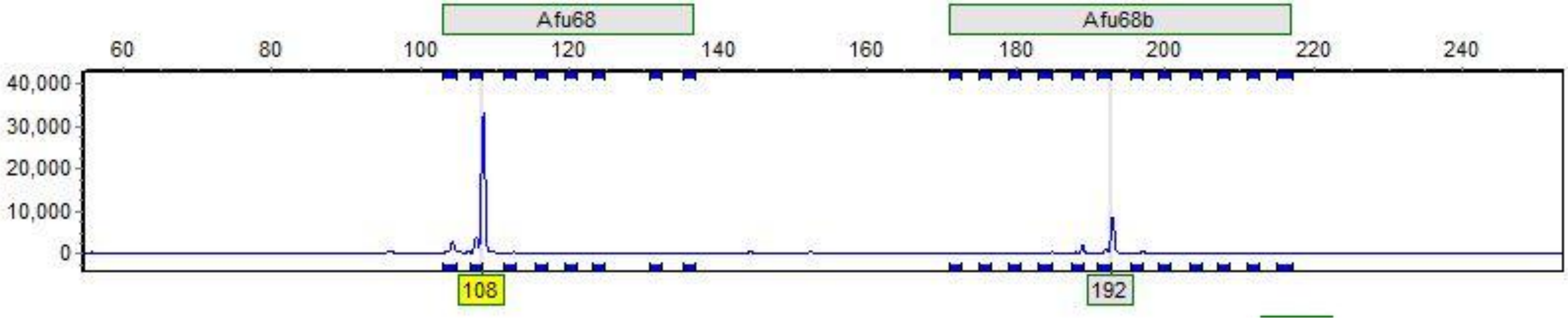
Microsatellites

Below is an example of what we observe in the lab. The example is heterozygote with 214 repeats and 218 basepairs



Microsatellites

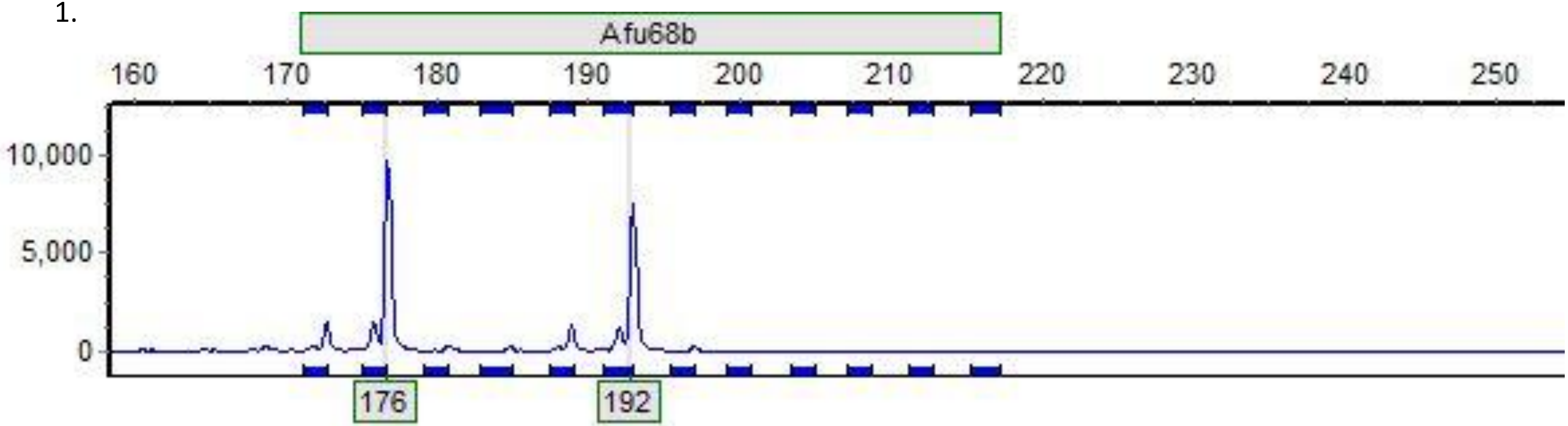
Below is an example of what we observe in the lab. This example shows two different genes in one picture, so be careful scoring



Try for yourself!

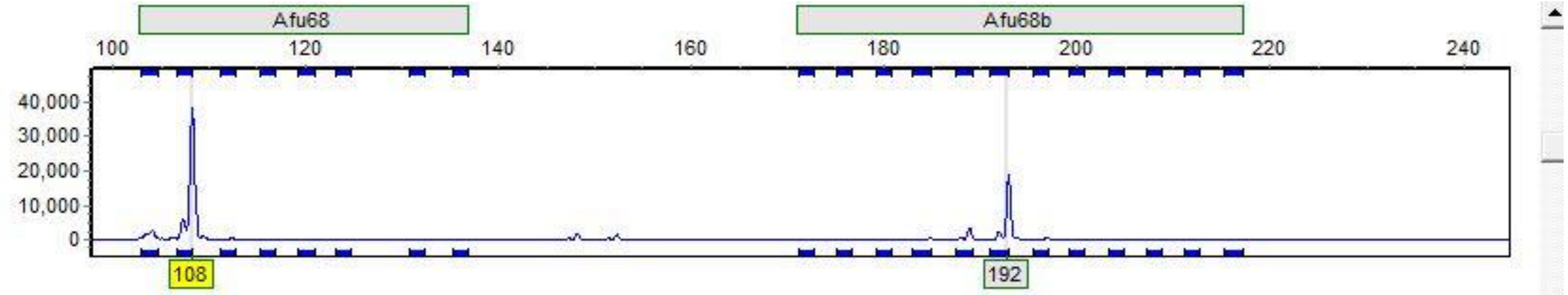
For scoring purposes, use even numbers only and round as necessary

1.



Try for yourself!

2.



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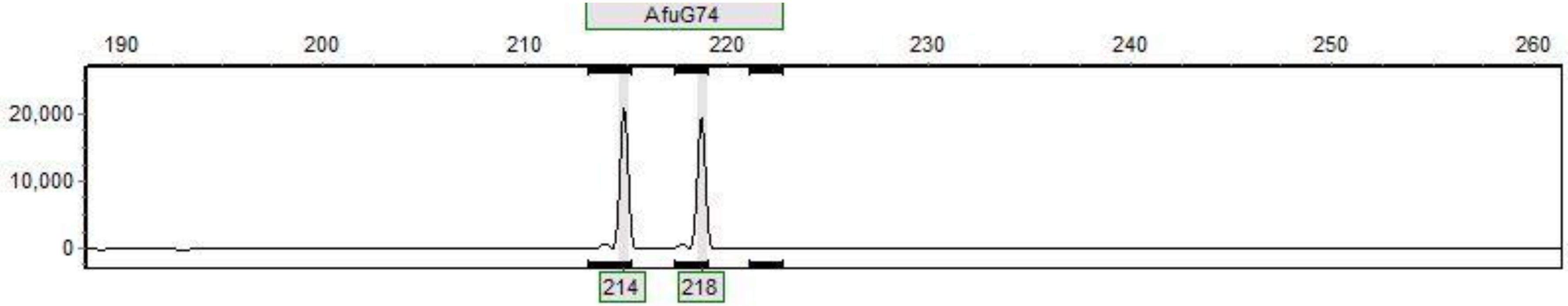

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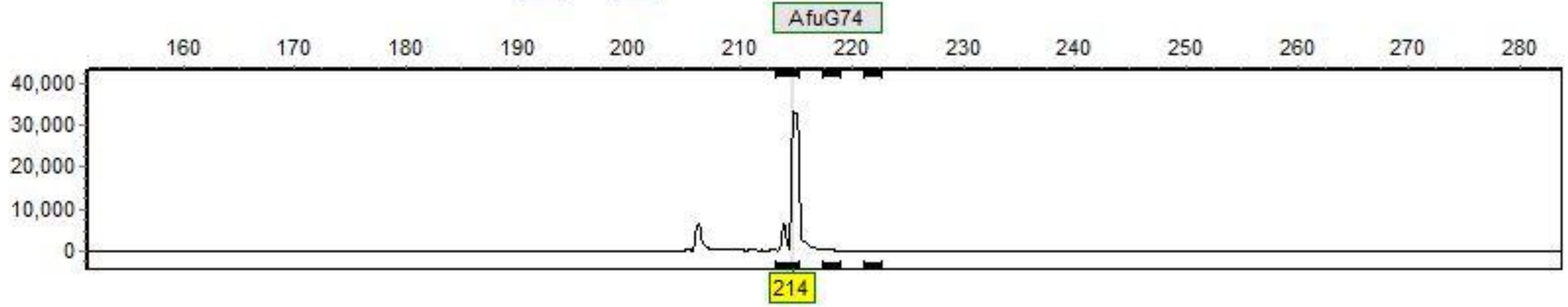
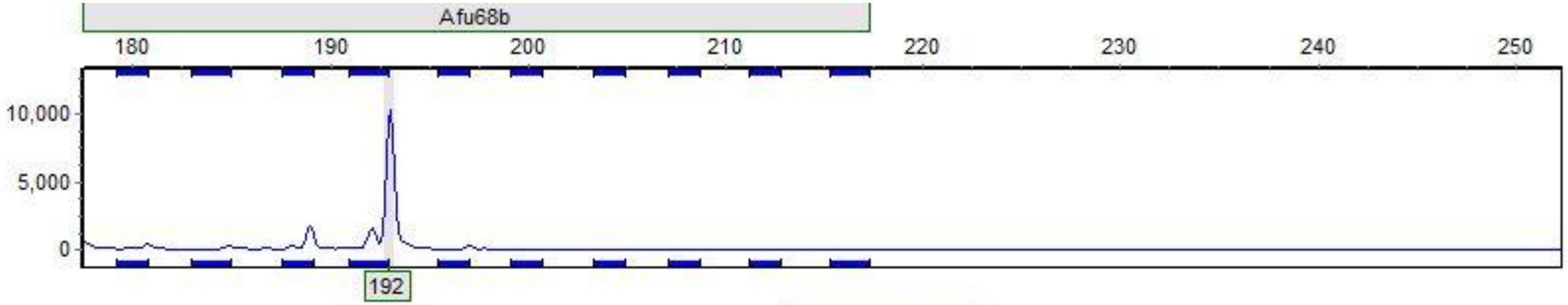

AfuG74
160
170
180
190
200
210
220
230
240
250
260
270
280
40,000
30,000
20,000
10,000
0
214

5.


Afu68
Afu68b
100
120
140
160
180
200
220
40,000
20,000
0
104
108
176
192

6.


Afu68b
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230
240
250
10,000
5,000
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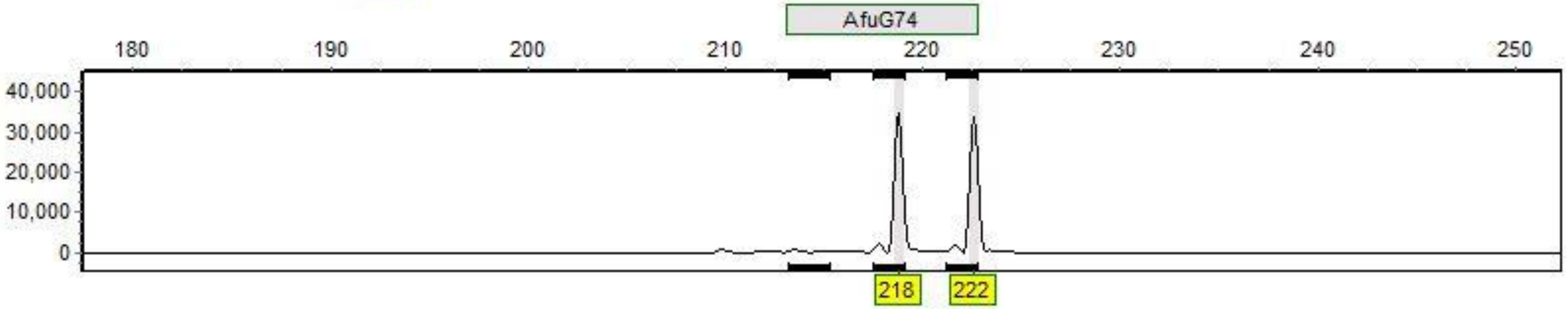
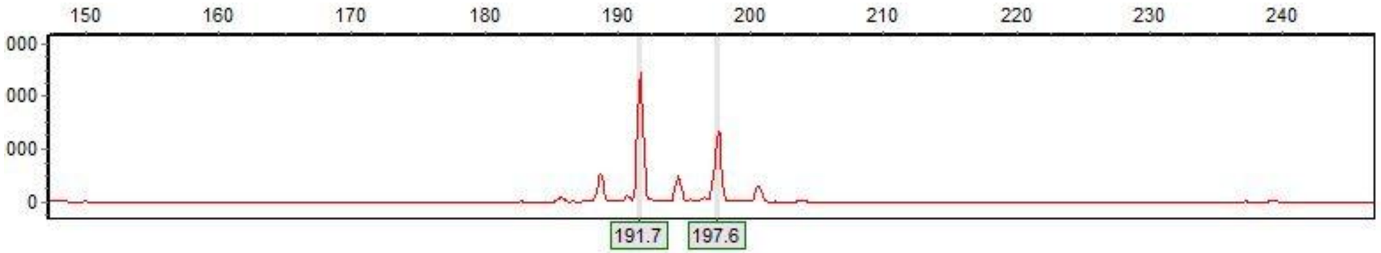
192

7.


AfuG74
180
190
200
210
220
230
240
250
40,000
30,000
20,000
10,000
0
218
222

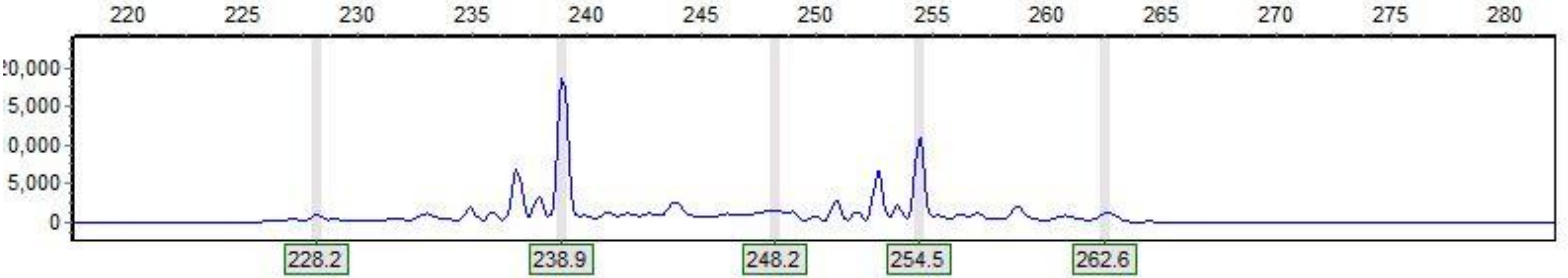
Microsatellites

- The previous slides were from a Lake Sturgeon project
- This project did the same protocol as we did, but the results look much cleaner
- Below is an example of the walleye results we obtained



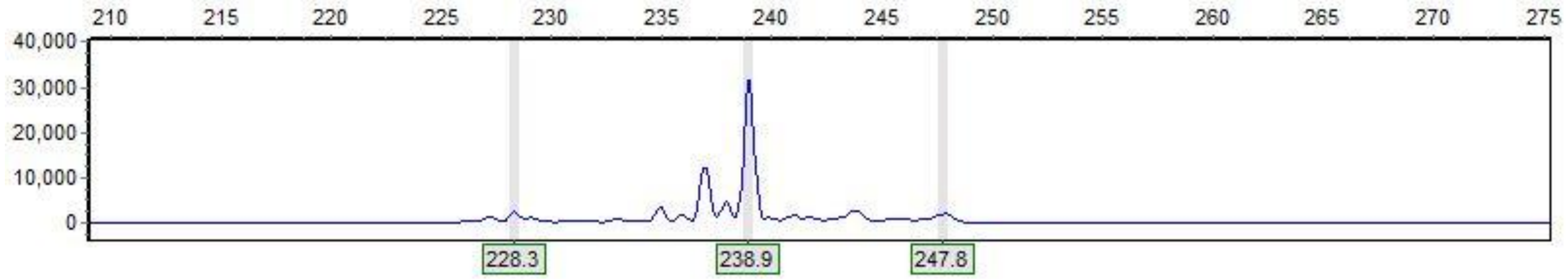
Try for yourself!

1.



Try for yourself!

2.



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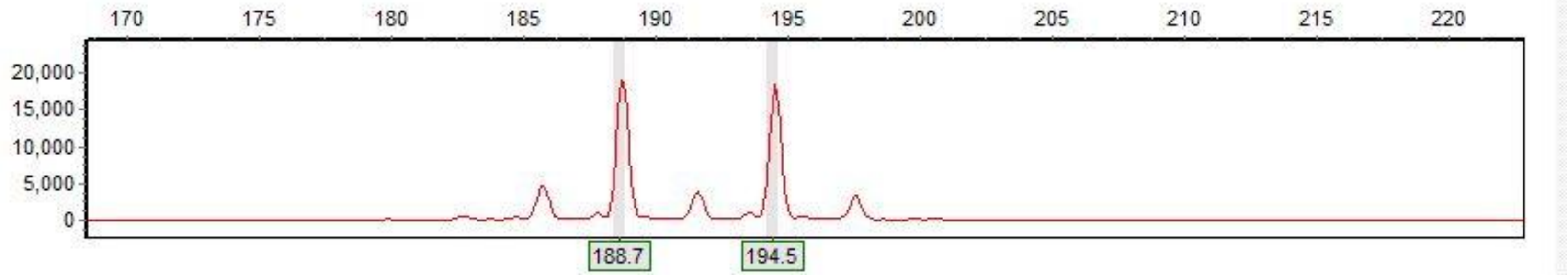
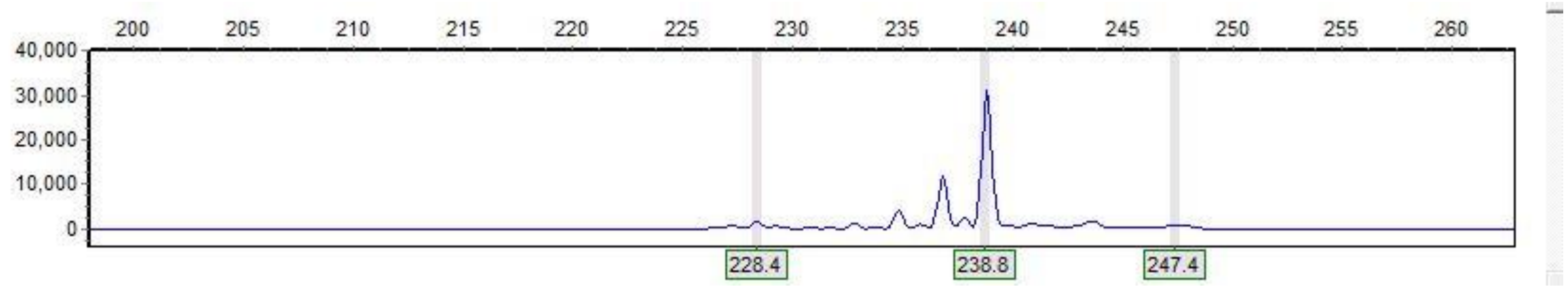


Try for yourself!

4.



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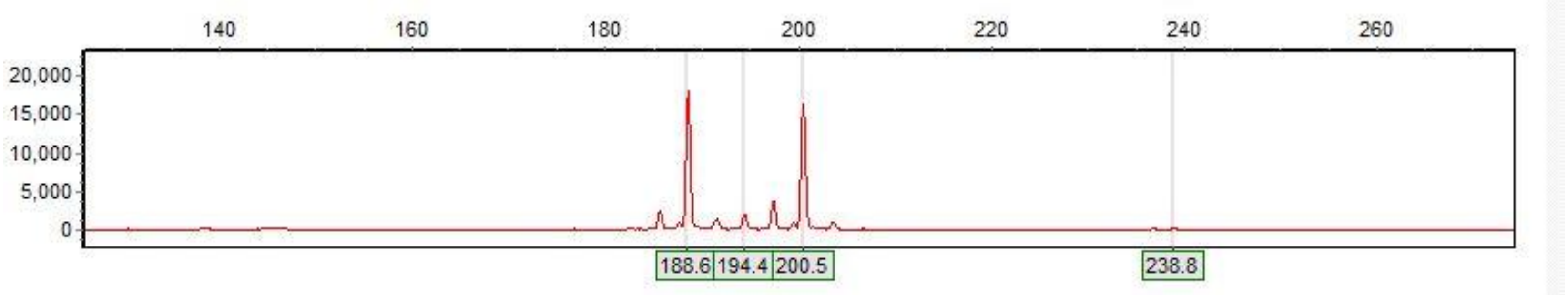

Try for yourself!

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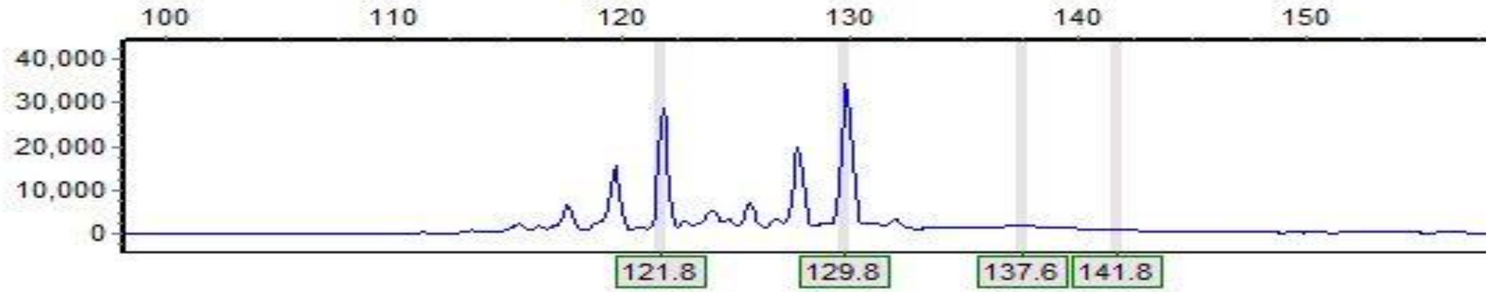

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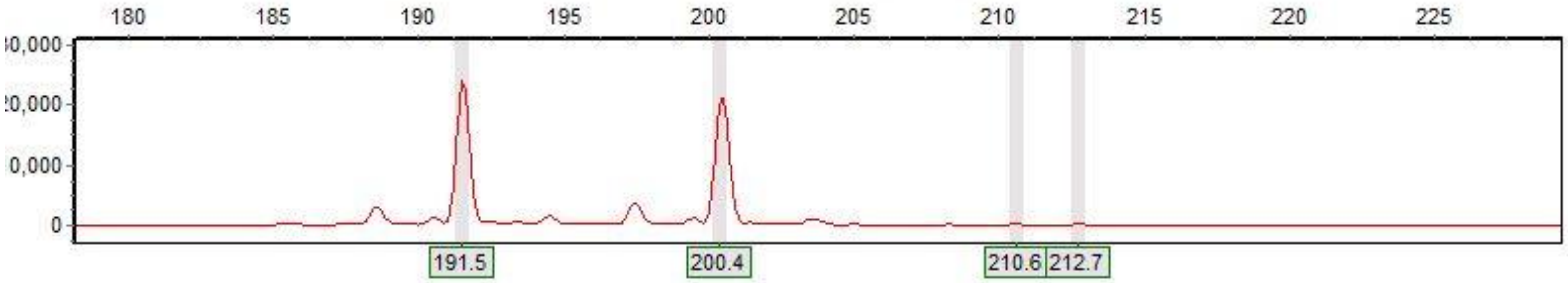

Walleye Results

- We can use the scores from the graphs to calculate heterozygosity
- This is done by the computer in different software programs
- Compiling all these results allows us to calculate genetic diversity to assess questions we may have about a natural population
- These results are used to inform local management agencies in best management practices