Ecological genetics of a trichome polymorphism in *Arabidopsis kamchatica*, and balancing selection on the GL1 gene.

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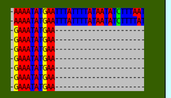
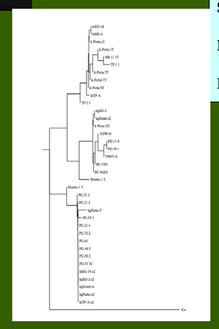
Intro:
Polyploid means having a chromosome number that is more than double the basic or haploid number (more then 2n). Both plants and animals can show polyploidy. Polyploid plants tend to be more successful reproductively
There is an explanation to why these creatures experience polyploidy, one of which could be from uneven splitting in meiosis, where more then one chromosome gets pulled to a pole. This would show a problem in gene expression, in which too many proteins could be produced. Another explanations could be from a mutation in the genome.
There are a few types of polyploidness. Autopolyploid, is having more than two haploid sets of chromosomes that are derived from the same ancestral species, some of which are apples, potatoes, and bananas. Allopolyploid, on the other hand, is having more than two haploid sets of chromosomes that are dissimilar and derived from different species, some of which being wheat, and rye.
Arabidopsis kamchatica is a polyploid with four copies of it's chromosomes. We believe this plant to be an allopolyploid because it is believed that it converged from 2 different species *A. petraea* and *A. gemmifera* by allotetraploid speciation (Wolf). This plant also unique for that in has the feature of creating trichomes, or leaf hairs. These leaf hairs are used when the conditions outside are dryer then usual. However, not all *A. kamchatica* have trichomes. This is evolutionarily beneficial because it takes a lot of effort to make them.





Results:
The petraea sequence is dominant over the gemmifera sequence. As seen in the sequence on the top right picture, there are sections missing on the bottom (gemmifera) while the top (petraea) still has them. When plotting the samples on a phylogenetic tree, the samples sequenced with the petraea primers (top half) show differences in trichome absence and non-absence while the samples sequenced with the gemmifera primers (bottom half) show no differences.

Methods and Materials:
-PCR Cleaner: Wizard

-DNA Extraction kit: % Prime

-PCR Beads: GE Healtcare

-Thermocycler: DNA Engine DYAD

We collected samples from the UAF greenhouse located on upper campus at the University of Alaska Fairbanks. We collected about 14 leaf samples from 14 different plants, 5 non-trichomed and 8 trichomed. We followed protocol for extracting DNA from the 14 samples using the 5 prime extraction kit. We diluted the samples to a 1/10 DNA solution. We used PCR beads made by GE healthcare, and made our cocktail with our first set of primers, (GL1-gem f1 and GL1-REV). The Reaction was run with an annealing temp of 50 C We repeated the procedure using a second primer set (GL1-f5 and GL1-gem r1). We verified that our PCR worked by visualizing them on am agarose gel. We added a molecular binder from Wizard to clean the solutions so we could vacuum out the impurities without losing the DNA. We cycle sequenced sequenced out gene using Big Dye Chemistry and the same primers used for amplification. To Clean the samples again we run them through sephadex and run them through a centrifuge. We send our samples off to the UAF DNA Core Lab to get them sequenced.

Discussion:
We believe that the petraea sequence is dominant over gemmifera because in the code sequence of the Glabra 1 gene, there are sections of the gem code that are missing that the pet gene still has. As you see in the sequence (Top Left), the sequences share similarities until the point where the bottom (gem) goes blank and the top (pet) continues. This isn't the only point where this happens, there are many different sections of gaps on the gem side that have missing sequence. Another thing is that if you plot the samples on a phylogenetic tree as seen on the bottom left photo, the ones on the top are were sequenced with the petraea primers show distinguishing characteristics between trichomed and non trichomed, and are plotted on there respected sides. The ones sequenced with the gemmifera primers show no distinguishing characteristics between trichomed and non-trichomed and are plotted in the same generation in random orders. This all shows that whatever the gemmifera code is missing, codes for trichome polymorphism and other distinguishing in which the petraea does code for. So we can conclude that the gemmifera sequence does not code for trichome polymorphism in *Arabidopsis kamchatica* as petraea does.

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