If an Organism is Adapted to Consume a Specific Sugar, is There a Gene in the Genome That Will be Consistent With Other Organisms With the Same Adaptation? by Andrew Krainer

INTRODUCTION: Through this experiment, I hope to locate a gene that leads to a specific adaptation in the organisms I am observing. The adaptation I am testing for is Antose consumption. I hypothesize that there is a gene that leads to Antose consumption in the organisms, and that I will be able to locate this gene by comparing genomes of organisms who have this adaptation to each other, and to organisms that do not have the adaptation. The purpose of my study is to determine whether or not there is a gene that leads to Antose consumption. If I can locate multiple mutations in the genome that lead to Antose consumption, I believe that one of these mutations will consistently lead to a higher fitness for the organism. There are many studies that have narrowed down specific traits in organisms to a specific gene. One such study is one that located a gene that leads to Lactose consumption. As children, most people are able to digest lactose with no problem, because of an enzyme they have called lactase. As people get older, however, only a minority of people continue to produce this enzyme. "In 2002 that ability was traced in Europeans to a mutation in regulatory DNA that controls the lactase gene" (Kingsley pg. 58). Recently, different mutations that caused the same effect were found. This adaptation of lactose consumption has risen independently around the world. Not every trait can be traced back to a specific gene, however. Scientists have located a gene that can on average add a centimeter to a person's height. However, tallness itself can not be traced back to any one specific gene, because "there are hundreds of genes associated with height" (Zimmer pg. 100).

METHODS: For the experiment, I always used the same ancestor organism as the starting point. I ran the populations at a 3% mutation rate, in a 60x60 petrie dish size, with every sugar available in the environment. I allowed the organisms to mutate until I observed multiple organisms in the petrie dish with an ability to consume Antose. If the organisms mutated for a long time, and none of them seemed to be developing this adaptation, I would discard the dish and start a new population. When I did see multiple organisms with an adaptation to consume Antose, I would select and freeze organisms that were relevant to my study. For my study, I selected and froze three types of Antose consuming organisms; organisms that consumed only Antose, organisms that consumed only Antose and Ornose, and organisms that consumed only Antose and Nanose. I ran multiple populations until I had three of each type of organism, and I froze 4 organisms that consumed only Antose for more of a comparison. I also froze organisms that consumed only Ornose, and only Nanose, to compare to organisms that consumed these sugars in addition to Antose. Then, using the Avida-Ed program, I looked at the genomes for each of these organisms, in addition to the genome of the ancestor organism (Appendix Section 1). Then I began to compare and contrast the genomes. First, I compared the genomes in groups (Appensdix Section 2). I compared the genomes of the organisms that only consumed Antose to the other organisms that only consumed Antose (Appendix 2.1), and I did this for the Antose and Nanose consuming organisms (Appendix 2.2), the Antose and Ornose consuming organisms (Appendix 2.3), and I also compared the ancestor organism, Nanose consuming organism, and Ornose consuming organism in their own group (Appendix 2.4). I then

located the genes which all Antose consuming organisms had in common (Appendix 2.5), and compared these to the ancestor organism, to determine if in fact these genes led to the adaptation.

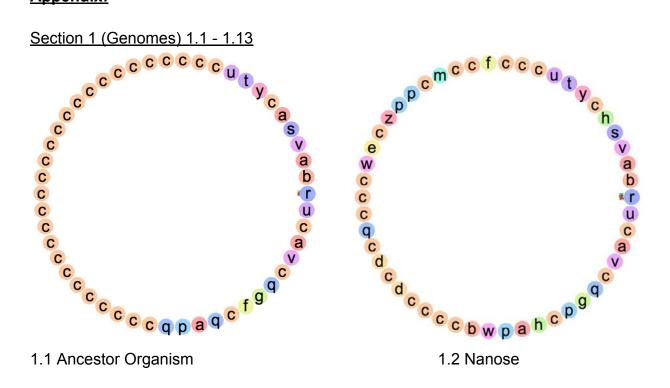
RESULTS: When looking over my data, I first compared the genomes in different groups (Antose, Antose&Nanose, Antose&Ornose, and a fourth group which compared the Ancestor organism, Nanose, and Ornose). I then compared the Antose groups, and determined which genes each Antose consuming organism had in common. After locating these genes, I compared those genomes to the genome of the Ancestor organism. When I did this, I discovered that the genes that all the Antose consuming organisms had in common, they also had in common with the Ancestor organism, which did not consume Antose. I also compared the genomes of the organisms had in common. After figuring out the genes that these organisms had in common, I compared these to every Antose consuming organism. I found that there were two genes that the three organisms that did not consume Antose had, which none of the organisms that did consume Antose did have (Appendix 2.6).

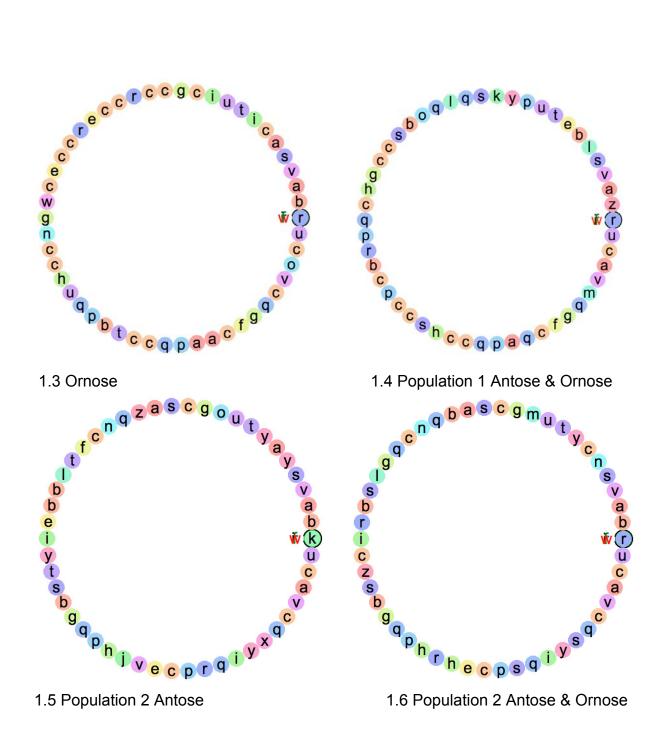
DISCUSSION: If there was a gene that caused Antose consumption in the organisms, every Antose consuming organism would have this gene in common. I did find a few genes that the Antose consuming organisms had in common. However, when I compared these genes to the genes of the ancestor organism, I realized that the ancestor organism had the same genes in common. This led me to conclude that these

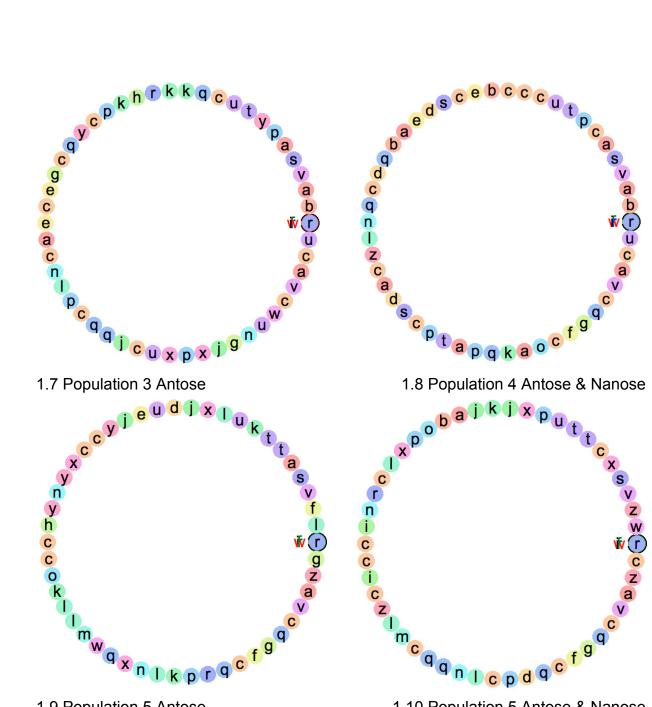
genes I found did not lead to Antose consumption. However, when I compared the genes of the organisms that did not consume Antose, I found similarities between the genes of these organisms. There were two genes these organisms all had in common, that none of the Antose consuming organisms had. Based on this observation, I believe I may have located an "anti-gene," or a gene that, when shut off, leads to Antose consumption. Although I found similarities between the groups of Antose consuming organisms, I did not compare enough organisms in each individual group to determine whether or not the genes they had in common were coincidental or in fact responsible for their similar adaptations. To determine whether or not it is a coincidence or not, I could replicate my experiment and look at the genomes of a larger number of organisms for each of my groups. After looking at a larger number of organisms, if they all were to continue to have the same similarities, it will point to a gene for their specific type of Antose mutation. Also, to look further into the "anti-gene," I could look at the genomes of many more Antose organisms. If they all continue to lack these genes, it would help strengthen the conclusion that it is in fact the lack of these genes that cause Antose consumption. However, if just one Antose consuming organism had one of these genes, it would rule out the lack of that gene as the cause of Antose consumption. Also concerning this "anti-gene," if I looked at more of the genomes of organisms that do not consume Antose, and they also have the "anti-gene," it would help strengthen the conclusion that this gene leads to Antose consumption when it is absent. However, I believe that it would be possible for an organism to not have the "anti-gene" and not be adapted to consume Antose, however, if my conclusion is correct, it would not be possible for an Antose consuming organism to have this gene. Finding an "anti-gene,"

or a gene, that when absent in the organism, leads to a certain adaptation, is a little bit more tricky than finding a gene that when present leads to an adaptation. If I were to find a gene that I believe caused an adaptation, I could breed an organism that has this gene and adaptation. I could then remove this gene from the genome, and if the offspring were to lose this adaptation, it would point to the conclusion that this gene did in fact lead to this particular adaptation.

Appendix:

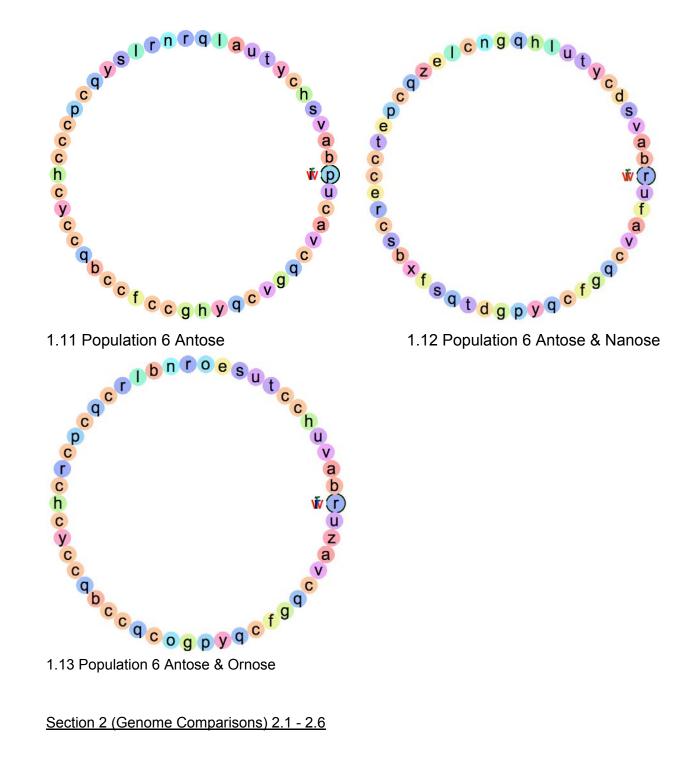




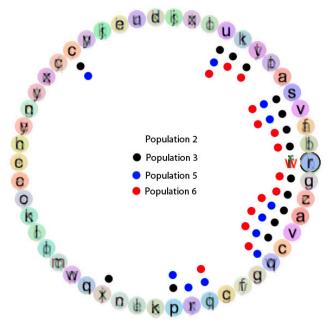




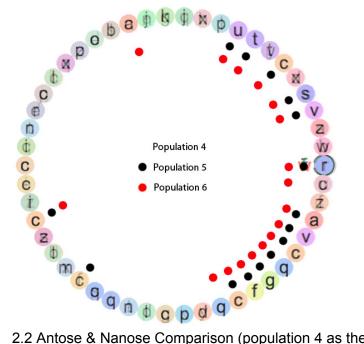
1.10 Population 5 Antose & Nanose



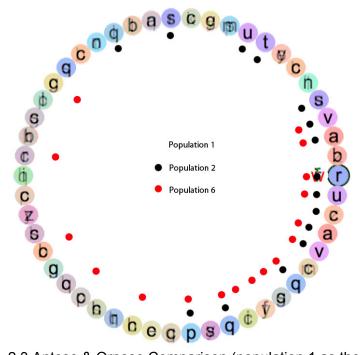
Section 2 (Genome Comparisons) 2.1 - 2.6



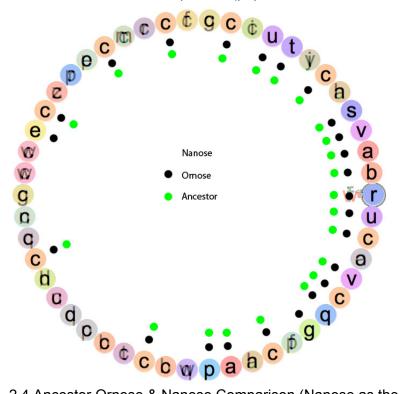
2.1 Antose Comparison (population 2 as the basis of comparison)



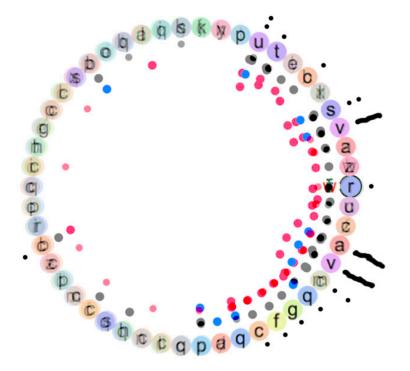
2.2 Antose & Nanose Comparison (population 4 as the basis of comparison)



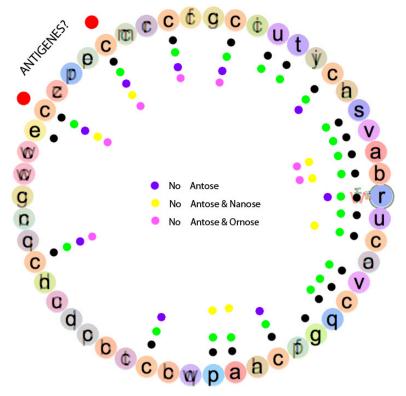
2.3 Antose & Ornose Comparison (population 1 as the basis of comparison)



2.4 Ancestor Ornose & Nanose Comparison (Nanose as the basis of comparison)



2.5 All Antose Comparison (Black lines are only genes all had in common)



2.6 Antose Organisms Compared to Non Antose Organisms. A mark is made for the Antose organisms in the genome on the genes that are present in all non Antose organisms, but not present in the Antose organisms.

<u>Bibliography</u>

Kingsley, David M. "From Atoms to Traits." Scientific American. January 2009.

Zimmer, Carl. The Tangled Bank. Colorado: Roberts and Company, 2010.