



All in on Strawberries: DNA, Taste, and Varieties



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ABSTRACT

Due to artificial selection and breeding of strawberry strains to make better looking, tasting, and sized strawberries, the evolutionary track of many strawberries has been confused and is, often, unknown. We hypothesized that the genetic material of the commercial strawberry varieties will differ from the genetic material of the wild strawberry varieties, but there will not be a 2% genetic diversity which must be present to assume that they are separate species.¹² The goal of this experiment was to identify genetic differences between different commercial strawberries and discuss whether they should be recognized as their own species. The experiment also aimed to investigate how the differences in the quantity of DNA affects the concentration of sugar. The results showed that all of the online sequences of the *Fragaria virginiana* strawberry were 100% similar. These results supported the hypothesis because it demonstrated how the differentiation is incredibly small even though these strawberries are from different regions. With more time, the project could have been carried out with ISSR which would show more differentiation.

INTRODUCTION

The *Fragaria* is a wild strawberry genus that contains about 22 living species within the Rosaceae family. Over the past hundreds of years, different wild strawberry species have been used to develop commercial strawberries around the world. There are now upwards of 500 different commercial strawberry varieties globally that are weakly differentiated.² This means that it is difficult to discern different traits and genetic backgrounds that would be useful in breeding and property rights cases.² New York City is home to *Fragaria virginiana*.³ This specific species is a modern domesticated garden strawberry native to North America.⁴ It is very common within communities and used in many studies. The amount of knowledge on *F. virginiana* and access to it within our community gives us the ability to use it to compare it using DNA barcoding to various commercial strawberries within our community. Based on differences within the rbcL+matK genome sequences⁵, the relatedness and diversity of the wild strawberry and commercial strawberries can be inferred.

MATERIALS AND METHOD

To conduct this experiment, we purchased a variety of commercial strawberries from local stores in New York (Figure 1), and we collected *Fragaria virginiana* leaves found locally in Central Park. Through analyzing the sequences, we determined whether or not certain strains and species have drifted. The project was conducted by following the guidelines established by the Urban Barcoding Project using both rbcL and matK primers for comparison; both primers should create sequences with about 1000-900 base pairs.¹¹ We used PCR in order to amplify the DNA. Subsequently, we used gel-electrophoresis to determine if our PCR was successful. After PCR, we sent our samples to Genewiz for sequencing. We worked with DNA Subway to compare our results and expand the knowledge of strawberries for the scientific community. All samples and extractions were stored on site in the Kingson Biology lab at The Browning School. The experiment also used ISSR primers to further study genetic variation (divergence and similarities) between the various samples.² They were compared using resolving power (Rp), which has been used in correlation with finding the differences between genotypes².

Use online samples of wild and commercial strawberries relating to the *Fragaria* family to study the differences.

Figure 1: This is taken from the sample tracker. It is an image of the *Fragaria virginiana* leaves. It was used to help identify the correct leaves in central parkj.



RESULTS

Figure 3 represents five different *Fragaria virginiana* rbcL codes taken from different strawberries across multiple states. There is also an out group that is a raspberry in order to demonstrate the genetic difference. Figure 3 clearly shows that all of the rbcL genomes are completely or 100% the same so there is no genetic diversity. It also shows that the raspberry is 98.19% similar to those strawberries so there are clear genetic differences.

Figure 2: This is the gel image dates for the rbcL and matK from the *Fragaria virginiana* sample.

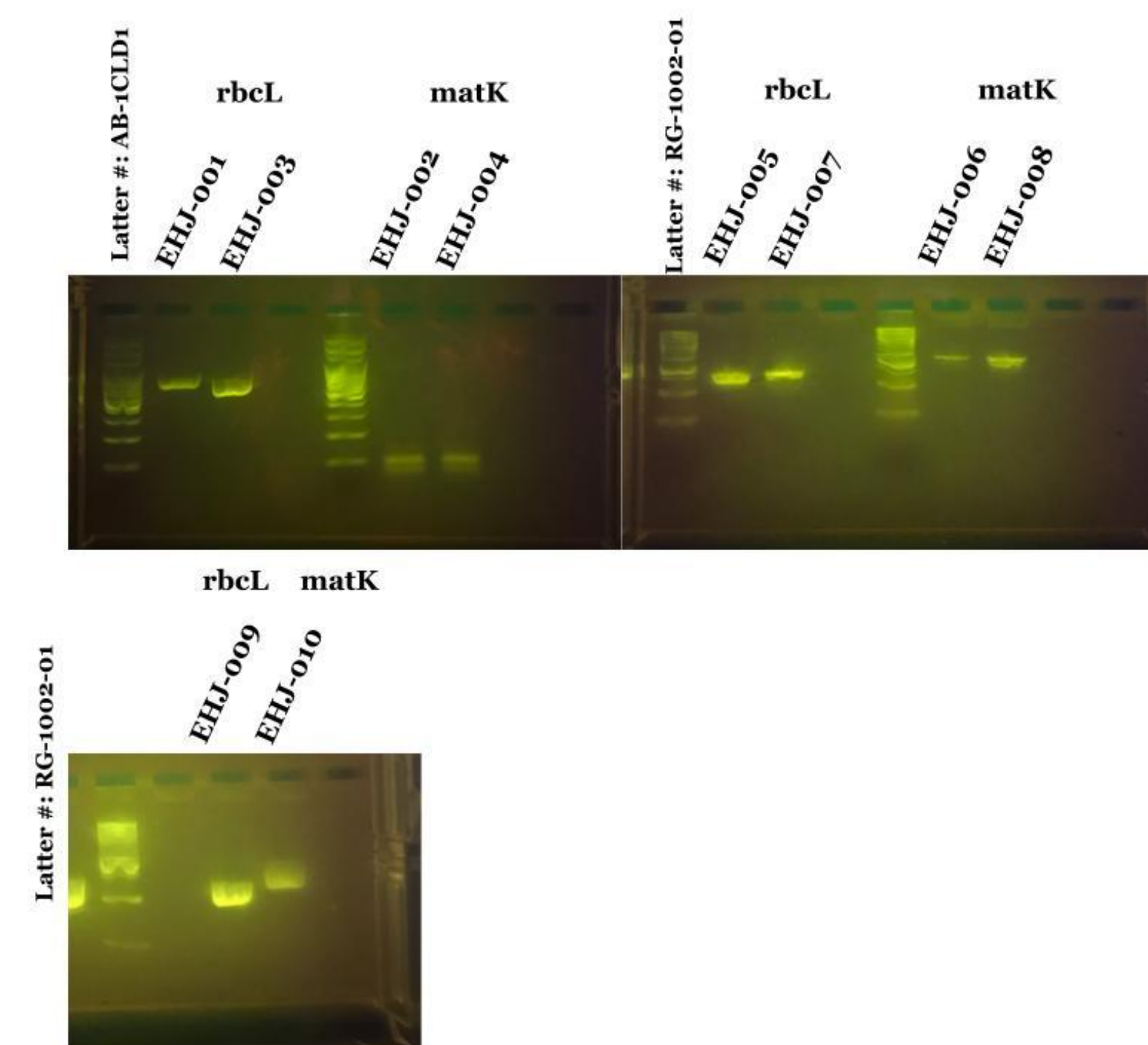
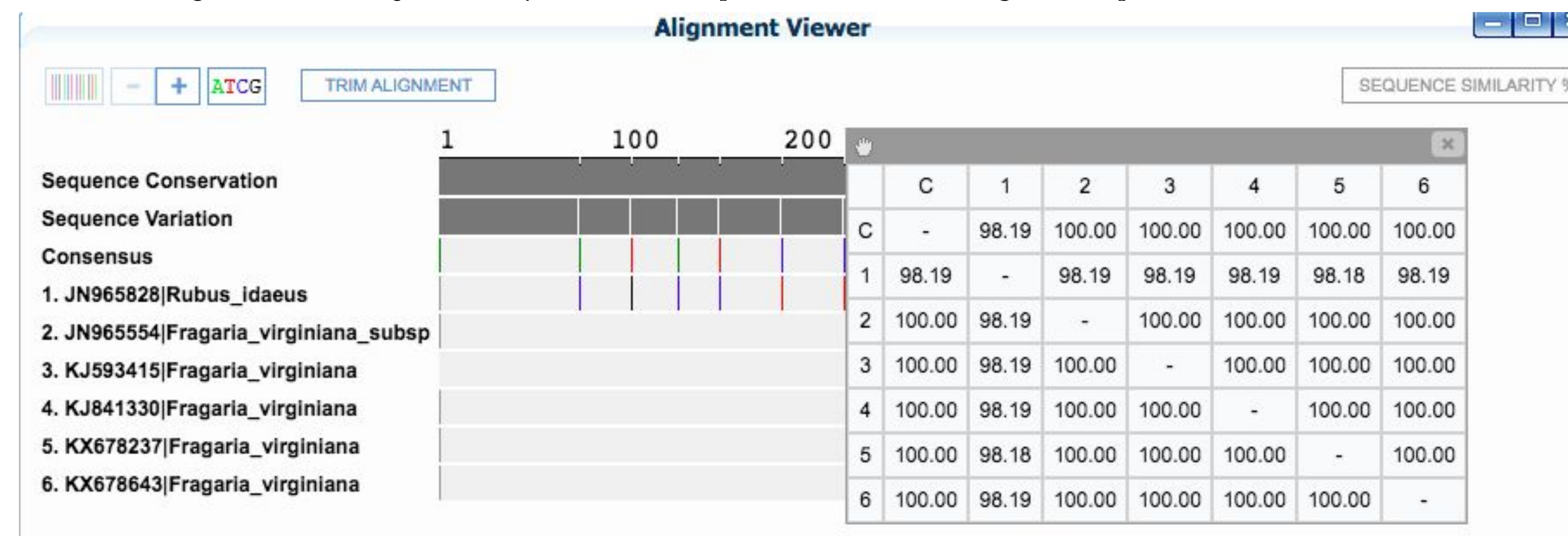


Figure 3: Percentage Similarity in the rbcL Sequences of Different *Fragaria* samples that were found online.



DISCUSSION

The hypothesis was confirmed by the online data that is represented in Figure 3. It clearly demonstrates that there is no genetic diversity across the rbcL genome. The strawberries are consistently similar even across states. As stated in the introduction, ISSR may have been a better tool in viewing the genetic diversity in the strawberries. It is a longer genome that highlights the evolutionary path of genomes, so it would have alluded to greater diversity. An error within the experiment was with time management and the inability to carry out all of the procedures. In future and similar experiments, the experiment should just focus on ISSR and look at differentiation through that because it is more detailed.

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