**Introduction**

Corn, also known as *Zea mays*, is economically and culturally important. Two aspects of corn’s biology that can influence its production are the abilities to reproduce and produce seed kernels. Both are affected by the plants ability to flower, inflorescence. In Midwest Maize: How Corn Shaped the U.S. Heartland, it states that the growth of urban markets, manufacturing, and developments in transportation relied on growth in farm countries (Anderson, 2016). There are two types of inflorescence architecture produced by *maize*, the female ear and the male tassel (Figure 1; Wei, 2019). These two architectures are controlled by quantitative trait loci and are related to crop yield (Manfri, 2018). Also, the size of males affects crop yield (Gage, 2017). The maize genome has been roughly estimated by looking at related plants and using processes to determine if they possess alike genes. Genome four, which is the focus in this experiment, is estimated and contains rough locations of genes. The problem with genome four is that there is no clear information on the location of the genes and where they are transcribed from. In the experiment, if the locations of inflorescence genes and their sources of transcription can be confirmed within the *Zea mays* genome, it could alter agriculture systems worldwide.

**Results**

Table 1: Gene List Comparison Table of all genes available in genome four that are estimated to be related to inflorescence genes in *Zea Mays*. The focus gene for this project is *MADS-box 1* (gene 13).

<table>
<thead>
<tr>
<th>Transcript</th>
<th>RT-PCR size (bp)</th>
<th>Provides evidence for revision to gene model</th>
<th>Expected or Observed</th>
<th>Domain likely missing?</th>
<th>Likely Functional?</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isoform 1</td>
<td>922</td>
<td>Yes</td>
<td>E</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Isoform 2</td>
<td>676</td>
<td>Yes</td>
<td>E</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Isoform 3</td>
<td>123</td>
<td>No</td>
<td>E</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Isoform 4</td>
<td>103</td>
<td>Yes</td>
<td>E</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Isoform 5</td>
<td>370</td>
<td>Yes</td>
<td>E</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Isoform 6</td>
<td>39</td>
<td>Yes</td>
<td>E</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Isoform 7</td>
<td>590</td>
<td>Yes</td>
<td>O</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
<tr>
<td>Isoform 8</td>
<td>259</td>
<td>Yes</td>
<td>O</td>
<td>Unknown</td>
<td>Unknown</td>
</tr>
</tbody>
</table>

Figure 7. Diagrammatic domain evidence for *MADS-box 1* Protein domains are indicated by colored bars and represent the domain location and approximate length. The algorithm in which the domain was identified is noted at the left of the image.

Figure 8. Reverse-Transcription PCR Test of RNA using Tubulin Primers. Agarose gel electrophoresis was used to separate RT-PCR products using corn RNA samples as noted above each sample. Marker OGeneRuler (ThermoFisher) sizes are noted at right while the observed fragment size is noted at left. Expected size 195 bp. This is Cassandra Perrone’s sample.

Figure 9. Marker OGeneRuler (ThermoFisher) sizes are noted at left while the observed fragment size is noted at right. Best annealing temperature 51.2 degrees Celsius.

Figure 10. Reverse-Transcription PCR Test of RNA at 51.2 degrees Celsius for annealing temperature. Agarose gel electrophoresis was used to separate RT-PCR products using corn RNA samples as noted above each sample. Marker OGeneRuler (ThermoFisher) sizes are noted at left while the observed fragment size is noted at right. Observed sizes fall between 1000 and 100 bp.

**Conclusions & Future Directions**

Over the years it has been a topic on many news channels whether genetically modified organisms are harmful to the environment and humans. In Midwest Maize: the author mentions a scientific consensus proving the process of genetically modifying to be more beneficial than harmful (Anderson, 2016). The results of this experiment can be used to further the benefits of genetic engineering. The leaf RNA extraction was successful. The reverse transcription process was also successful, but RT-PCR should be repeated in future experiments to produce clearer results. The best annealing temperature for gene 13 was determined to be 51.2°C. Based on the results from the final RT-PCR, the gene structure should be revised due to unexpected isoforms and unobserved isoforms that were predicted. The region of interest is in a protein domain and the brown and blue bars towards the middle of the diagram (Figure 7) lie in the middle of the domain and their function may be compromised. Their functions relate to the K-box and this will affect folding of alpha-helices in the proteins. It is likely that these bars will be compromised and will affect the genes expression if more proteins are made with the region compromised the functionality of the proteins produced is unknown because you cannot know if the domains are missing or not as shown in the comparison table (Table 2).

**Methods**

Gene data collected using RNA evidence from Apollo was used to construct gene models which were used to determine the conserved splice isoforms, identify family, and create primers to focus on in future tests.

The first test was a Reverse-Transcription PCR test of RNA using a Tubulin marker, in order to highlight the presence isoforms in base pairs (bp) length at the corn leaf samples.

The second test was putting the primers designed through the thermocycler to determine the best temperature for annealing and to make sure that throughout the experiment there is always a value.

These test results lead to the final experiment of using the RT-PCR and using the best annealing temperature shown to be 52°C for efficiencies and base pair numbers that would show on Reverse-Transcription PCR results.

**Figure 4. Gene structure for *MADS-box 1* region of maize (A) possible splicing organisation (different isoforms possible from the estimated location of primers) with the expected base pair amount for each exon that is represented by a change in block appearance.

**Figure 5. Expected efficiency for gene structure splicing variants with the calculated base pair numbers that would show on Reverse-Transcription PCR results.

**Figure 6. Gene List Comparison Table for all genes available in genome four that are estimated to be related to inflorescence genes in *Zea Mays*. The focus gene for this project is *MADS-box 1* (gene 13).

**Figure 7. Diagrammatic domain evidence for *MADS-box 1*. Protein domains are indicated by colored bars and represent the domain location and approximate length. The algorithm in which the domain was identified is noted at the left of the image.

**Figure 8. Reverse-Transcription PCR Test of RNA using Tubulin Primers. Agarose gel electrophoresis was used to separate RT-PCR products using corn RNA samples as noted above each sample. Marker OGeneRuler (ThermoFisher) sizes are noted at right while the observed fragment size is noted at left. Expected size 195 bp. This is Cassandra Perrone’s sample.

**Figure 9. Marker OGeneRuler (ThermoFisher) sizes are noted at left while the observed fragment size is noted at right. Best annealing temperature 51.2 degrees Celsius.

**Figure 10. Reverse-Transcription PCR Test of RNA at 51.2 degrees Celsius for annealing temperature. Agarose gel electrophoresis was used to separate RT-PCR products using corn RNA samples as noted above each sample. Marker OGeneRuler (ThermoFisher) sizes are noted at left while the observed fragment size is noted at right. Observed sizes fall between 1000 and 1000 bp.

**Figure 11. Gene Structure for *MADS-box 1* using Apollo annotation of genome 5. The lines represent exons and the blue, red, and white blocks represent introns.

**Figure 12. Reference Sequences for *MADS-box 1* from Apollo annotation of genome 5. The lines represent exons and the blue, red, and white blocks represent introns.

**Figure 13. Gene Structure for *MADS-box 1* from Apollo annotation of genome 5. The lines represent exons and the blue, red, and white blocks represent introns.

**Figure 14. Gene Data Collection Using RNA Evidence from Apollo was Used to Construct Gene Models Which were Used to Determine the Conserved Splice Isoforms, Identify Family, and Create Primers to Focus on in Future Tests.

**Table 1. Gene List Comparison Table of all genes available in genome four that are estimated to be related to inflorescence genes in *Zea Mays*. The focus gene for this project is *MADS-box 1* (gene 13).

**Table 2. Comparison Table. This table summarizes the results of each anticipated isoform in comparison to what was expected and how the results effect the future experiments and results for genome free. If the results provide evidence for the revision of the gene model it signifies that the results prove the location of certain exons in the genome and can be used for future testing.

**Reference**


This reference text does not provide any additional information.