## Experimental Validation of Helitrons

The different lines of maize have been isolated and inbred over many generations, resulting in differing evolutionary development, with different mutations passed down through the various inbred lines. Helitrons have transposed after the differentiation between lines, so they rarely appear in every inbred line. Instead, they are found in lines that are related by hereditary linkages after the Helitron inserted into the maize genome. Though computational methods indicated Helitrons of interest, experimental methods using plus/minus polymorphism (showing that the Helitron is present in some inbred lines and not in others) confirms the presence of these Helitrons.

To determine plus/minus polymorphism of the Helitron, we attempted two different approaches. The first was to look for the Helitron insertion sequence in every inbred line. The second was to look for the empty insertion site (paralogous sequence) in the same ten lines. By looking for both the presence and the absence of the Helitron, we can come to a conclusive result. To look for these sites, we designed several primers to amplify different segments of the Helitron and insertion site.

### Computational and Molecular Investigation of Helitrons in the Maize Genome

### Experimental findings have led to a putative understanding of the structure of Helitron insertions. The current accepted understanding indicates that Helitrons transposable elements insert in the maize genome between genes and conserved sequences. The termini of the Helitron insertions contain a generally well conserved sequence alignment and order. These conserved termini flank a sequence of between 200 to 25,000 base pairs consisting of a variety of genomic DNA fragments. Our work will provide a basis for further discussion of Helitron captures, and future analysis of additional Helitrons.

## Conclusions and Future Prospects

Our evidence suggests support for the efficacy of our computational methods. However, further molecular analysis can be done on other Helitrons which may contain full, active genes. As of yet, it is uncertain whether this gene capture plays an active role within the genome. Additional future analysis of additional Helitrons may contain full, active genes. Our work will contribute to the understanding of Helitron capture mechanisms.