**Introduction and Aims**

- Decreasing prices and technology improvements have allowed scientists to sequence hundreds of genomes across all kingdoms.
- Knowing the genome sequence is only the first step, and then the functional aspects of the genome.

**Materials & Methods**

**Zea mays project**
- Corn transcriptome data was visualized in the Apollo genome viewer/annotation platform with current gene models for genes related to plant immunity in corn.
- Gene models and data for 12 genes were evaluated for areas of incongruence such as untranslated regions (UTR), intron retention, differing exon borders, or alternative splice sites.
- Areas of incongruence were recorded, and a new gene model was then generated in the annotation space.

**Cryptococcus neoformans project**
- Transcriptome data, genome sequence, and the current genome annotation were uploaded to a genome annotation platform, GenSAS.
- Informed computational gene models using a new algorithm (PASA) were generated.
- Gene models for six genes in the *C. neoformans* HOG pathway were also evaluated for areas of incongruence.
- Areas of incongruence were recorded, and revised gene models were generated.

**Results**

- The next steps in genomic science will be to annotate the structural components, and then the functional aspects of the genome.

**Conclusions**

- Out of the 12 *Zea mays* immunity related genes evaluated for the first portion of the project, only one gene (Zm00001d016237) showed adequate RNA evidence for manual annotation and curation. This gene contained 3 areas of incongruence: UTR, 3' alternative splice site, and the addition of an intron.
- A total of six *Cryptococcus neoformans* HOG pathway genes were annotated: AQP1, ENAI, NHAI, HKKI, SRX1, and ATF1. A total of thirteen areas of incongruence were found and edited within the *C. neoformans* project: one 5' UTR, five 3' UTR, two retained introns, one differing exon border, one alternative 5' splice site, one addition of an exon, one addition of an intron, and one gene model being split.
- The new revised gene models and transcripts for the *Zea mays* immunity-related gene as well as the six *C. neoformans* virulence-related HOG pathway genes provide not only more accurate information to plan and execute experiments but may also aid in better understanding each gene’s regulation and expression, as well as the encoded protein’s function.
- In turn, more accurate experimental results may lead to a clearer understanding of each protein’s role in the *Zea mays* genome as well as the virulence of *Cryptococcus neoformans*.
- Future steps would include a BLAST search to confirm and identify structure of each gene and the encoded protein’s function.

**Literature Cited**