# **Final Project for EEOB 563 (2021)**

Phylogenetic Analysis of a Novel gene related to leaf angle in Maize

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Leaf angle is one of the most important yield related traits, which is as the key component in forming the smart-canopy cereal species, particularly maize, rice, wheat and sorghum. Leaf angle can affect the light interception efficiency and then promote different photosynthetic rates. It is important to figure out the genetic architecture of the leaf angle control and identify the novel genes regulating the leaf angle patterns of the canopy.

To date, few genes related leaf angles have been identified and their physiological functions have been well characterized. Here, I want to analysis the function of the novel genes and see whether it can facilitate understanding the mechanism of leaf angle pattern across canopy.

The B73 Maize reference genome has been sequenced and assembled accurately ([Schnable et al., 2009](https://www.frontiersin.org/articles/10.3389/fpls.2015.01013/full" \l "B27)).The genomic sequence of the novel gene can be found in the B73 reference genome ([Schnable et al., 2009](https://www.frontiersin.org/articles/10.3389/fpls.2015.01013/full" \l "B27)). I will align the genomic DNA sequences with full-length cDNA and reveal that genetic structure of these genes.

There are several phylogenetic questions need to be solved by this study.

What is the characteristic of expression and phylogeny for these novel genes?

Whether the isoforms of these novel genes are present in all green plants (from algae to monocots)?

To investigate the relationship between SSV and other SSs, we collected SSs from more than several plant species (including monocots and eudicots). Compare the topologies of phylogenetic trees, constructed by multiple methods, whether the results from these models agree with one another. How many groups and clades are contained in the built phylogenetic tree.

After sequences were aligned and configured for highest accuracy, phylogenetic trees were constructed by multiple methods, including the neighbor-joining, maximum likelihood and maximum parsimony methods, implemented in MEGA, PHYML and PHYLIP on protein sequences of the GT5 domain. Reliability of internal branches was assessed using the bootstrapping method (1000 bootstrap replicates). high bootstrap values, perhaps reflecting the rapid evolution of these genes in lower plants.