DNA sequence variation in the *Arabidopsis WUSCHEL* gene

Shoot meristems contain a population of cells with characteristics of stem cells. Cell division serves to constantly renew the meristem and to provide cells that will differentiate into plant organs and tissues. In *Arabidopsis thaliana*, a negative feedback loop involving the *CLAVATA (CLV)* transmembrane receptor complex and the *WUSCHEL (WUS)* transcription factor is thought to play a crucial role in maintaining the meristem's integrity. In *wus* mutants, the stem cells appear to undergo differentiation. However, in *clv* mutants, there is an overproliferation of the meristem.

In this project, we evaluated nucleotide variation in the *WUS* gene. We sequenced the 5' flanking region, exon 1 and intron 1 from nine accessions of *A. thaliana*. When we aligned these sequences, we saw that there are 22 polymorphic sites. There are only two polymorphisms in the coding region: a synonymous substitution in Wei-0 that has no effect on the amino acid sequence, and a replacement in Wei-0 that results in serine instead of alanine. Two accessions (Ler and Wei-0) show many of the same nucleotide differences. We found that both Ler and Wei-0 differ from the other accessions by 15 nucleotides, located mainly in the 5' flanking region. These 5' polymorphisms are intriguing; if they affect the transcription of *WUS*, then they could alter the signal transduction that occurs between *WUS* and *CLV*. 