Identification and Characterization of a Gene Controlling Tomato Growth and Branching

Mahfuz, Ayesha (School: Vista del Lago High School)

This project is the beginning of a gene identification and characterization project with implications in potential genetically engineerable traits for bush crops. We have found a candidate gene for shoot apical meristem (SAM) regulation and subsequently branch development in tomato plants. To establish this candidate gene, we used a combination of modern and classical genetic techniques. These included bioinformatics and statistical analysis, biomolecular analysis and microscopy, and mendelian genetic analysis. We found that some of our mutant plants produced more compact and shorter branching, which could be a useful trait to engineer into tomato crops and other bush crops. Since the candidate gene was isolated in the second generation, we concluded that the mutant branching phenotype and the SAM abortion phenotype were genetically related, and found that a missense mutation on the S gene could be the genetic basis of these phenotypes. We propose that the SAM abortion mutation is the result of a semi-penitrant, dominant allele of the S gene. Our bioinformatic analysis bolsters this idea, as the S gene was found to be homologous to the WOX9 gene in Arabidopsis that has been proven to regulate SAM growth. Taken together, our findings suggest a new pathway necessary for SAM development and branching in tomato plants, which has potential for tremendous utility in translational agricultural research. As global food demand skyrockets and land availability dwindles, this phenotype could help sustainably feed the world’s growing population by fighting agriculturally driven aspects of climate change.

Awards Won:
Fourth Award of $500