**The Identification of Genes Involved in Plant Cell Adhesion**

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The Kohorn Laboratory is currently investigating the involvement of various genes and their associated proteins in the process of cellular adhesion in the plant *Arabidopsis thaliana*. Recently, the laboratory found a new gene that is currently thought to be involved in this cellular adhesion process. It has been named ELMO1 because its mutant phenotype produces curled and partially broken cells that stain red when the plant is treated with dye, allowing it to look like Elmo from Sesame Street.

Given that my fellowship this summer was remote, the work I did mainly consisted of bioinformatics. Using the sequence of the ELMO protein, I first searched for similar genes in *A. thaliana* using a variety of databases. I found that there was one protein of a high degree of similarity in  *A. thaliana*. Following this search, I investigated the presence of a protein like ELMO in other plants and found some striking results. Of the major plant genuses I searched, I found that ELMO was highly conserved. I found a homologue of this gene in 30 different plant species including corn, tomatoes, rice, apple trees, oak trees, wild cabbage, and many others. Not only is the gene itself conserved across at least 30 different species, it is highly similar in most cases aside from two notable exceptions.

When looking at an alignment of the protein sequences of all of the ELMO homologues, I found two major mutations occurring at the 39th and 70th amino acid in the sequence. Given that we do not know what this particular protein does, I also used the Swiss tool ExPASy to see if I could get an idea of its structure. This tool aligned the ELMO protein with proteins of known structure, in order to produce a rough idea of the structure of ELMO. Doing this, I found that the structure changes depending on the mutations present in the ELMO gene, which could indicate some function changes. My next steps will be utilizing PyRosetta, a Python based version of the Rosetta molecular modeling program, in order to generate a more accurate model of ELMO both with and without its various mutations, as well as performing laboratory assays in order to determine the function of the ELMO protein.

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