Predicting and assessing SAUR gene function through phylogenetics and CRISPR-Cas9 genome editing

Small-Auxin-Up RNAs (SAURs) are a family of auxin-responsive genes found in nearly every plant species. Though we have a general idea of their involvement with auxin, the specific functions of each SAUR have not been exhaustively studied due to their unusual abundance. This research had two goals; the first was to knock out four saur genes in order to investigate their role in light response. Arabidopsis was the focus of the wet lab research, where four saur genes were targeted for deletion via CRISPR-Cas9-mediated genome editing in a line already missing nineteen saurs. After many rounds of screening, the deletion of saur9 and saur16 have been confirmed to create the highest-order saur mutant ever studied. The second goal was to identify SAURs through mining available sequence data and to explore their evolution and potential functions. Ten plant species ranging from algae to angiosperms representing a variety of morphologies were studied. Sequences from all ten species were included in phylogenies, and tomato, Arabidopsis, and rice sequences were correlated with N-terminal analysis data. In the process, thirty-six never-before studied SAUR proteins were discovered. From these analyses, we were able to identify which SAUR N-terminal domains exhibited conserved features such as strongly predicted basic hydrophobic domains, histidine-rich N-termini, and alpha helices. These findings can inform future decision-making regarding more genes to target with CRISPR-Cas9 and provide useful hypotheses regarding how unstudied SAURs function in the plant.