Simulate To Innovate: Cell Signaling Simulations of Stem Cell Mutants With Enhanced Transcription Factor Binding To Optimize Crop Productivity

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Stem cells are critical for the development of all tissue types. The stem cells located within the Shoot Apical Meristem (SAM) of plants produce all above-ground plant parts that account for nearly 80% of the biomass that sustains life on earth. The SAM of the model system - Arabidopsis thaliana - is divided into the Central zone (CZ), which contains stem cells, the peripheral zone (PZ), located on the sides of the SAM, and the Rib meristem (RM), situated beneath the CZ where the stem cell descendants differentiate. Understanding how these interconnected functional domains are maintained in dynamically developing SAMs requires computational modeling. The WUSCHEL (WUS) gene, expressed in the RM, encodes the transcription factor WUSCHEL (WUS) that promotes stem cells and SAM development. On the other hand, CLAVATA3 (CLV3), a signaling molecule produced in the CZ, represses WUS expression. To add, WUS activates the transcription of the CLV3 to regulate itself, making a balanced meristem. This study quantified the dynamics between WUS and CLV3 through computational simulations implemented on meristem anatomy to quantitatively understand the WUS-mediated CLV3 transcription, where WUS binding rules were used to develop the model. The model was then used to test the hypothesis that increasing WUS binding affinity to the CLV3 gene will increase CLV3 transcription. Surprisingly, the simulations revealed a decrease in CLV3 transcription, refuting the hypothesis. The possible mechanisms of transcription and the power of computer simulations as a cost-effective way of optimizing meristem regulators in improving crop productivity are discussed.

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