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INVESTIGATING THE ROLE OF METABOLITES IN MAINTAINING STEMNESS IN HUMAN ADULT STEM CELLS

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A major goal of regenerative medicine is to understand the unique characteristics of adult stem cells that result in their flexible and adaptive functions. Adult stem cells divide indefinitely and can differentiate into organ-specific cell lines to replace aging or damaged cells. Previous studies on the optimization of adult stem cell therapy have focused on the use of specific activator genes to turn on relevant stem cell genes, which may be inconvenient when considering costs and its resulting effect on the accessibility of stem cell therapy. The purpose of this project is to study the activation of key genes relevant to adult stem cells and develop natural metabolite treatments to maintain stemness in adult stem cells. To determine a set of relevant adult stem cell genes, we use a Python script to compile a ranked list of terms associated with “stem cell metabolism” and narrow down highly characterized genes, including the well-known Yamanaka factors. For initial screenings of these genes, we use a luciferase reporter assay to analyze the activation pathways across several human cell lines. Different reporter genes are activated with specific activator genes via transfection experiments, and the resulting readout is quantified using a luminescence plate reader. Reporter activation is optimized by varying the dosage ratios of reporter and activator and cross-referencing with data in current scientific literature. Metabolite screenings of these optimized reporters are then conducted to find a minimal combination of metabolites that can be used to produce similar activation patterns. This study finds that while combinations of natural metabolites have the ability to activate stem cell genes of interest, the activation level is not as prominent as that of specific activator genes, suggesting further research on the effect of metabolites on stem cell gene biochemical pathways.