An Exploration of the Epigenome: Establishing Naegleria gruberi as a Model Organism for Ten Eleven Translocation Enzyme Studies

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Methylation marks are a type of epigenetic mark established during cellular differentiation that change with time and are often associated with aging and degenerative diseases. Thus, manipulation of methylation marks would be a promising avenue for new therapies for countless degenerative diseases. However, until the mechanisms of the enzymes involved in methylation are fully understood, epigenetic based therapies that are specific and directable are unfeasible. This study aims to find out more about Ten Eleven Translocation Enzymes (TET), which demethylate DNA. Naegleria gruberi is an amoeba that transforms into a flagellate under stress when suspended in a non-nutrient TK buffer, a transformation with unknown mechanisms. Since N. gruberi has a homolog of TET enzymes, it is possible that their transformation to a flagellate is directed by methylation changes and Naegleria TET-like enzymes. Through Nanopore Sequencing, this study aimed to assess TET homolog involvement in this transformation to evaluate N. gruberi as a model organism for TET studies and to better understand how TET enzymes react to different environmental conditions. The study concluded that DNA demethylation and the Naegleria TET homologs were likely involved in this transformation. N. gruberi was also found to exhibit a similar paradigm of aging to human cells, showing global hypomethylation with age. Overall, N. gruberi is a promising model for both aging and TET studies.

Awards Won: