Genetics Day Poster Submission

Presenter: Shan Hua

Category: Graduate Student

Authors: SHAN HUA, Kristin Murphy, Fanju Meng, Patrick Murphy

Title: H2A.Z REGULATION OF CTCF BINDING AND HIGHER-ORDER CHROMATIN STRUCTURE

Abstract: Maintaining proper higher-order chromatin structure is critical for regulating gene expression in cells. CTCF acts as an architectural protein in the genome, helping to maintain this structure by forming loop domains within the chromatin. These loop domains create insulated spatial neighborhoods that separate heterochromatic and euchromatic regions of the genome. In addition, CTCF can form boundaries that control the expression of imprinted genes and Hox genes, which are critical for organismal growth, and establishing the body plan of organisms, respectively. Dysregulation of CTCF can lead to improper gene expression or genome instability, which can cause various diseases, including cancer. However, the epigenetic regulation of CTCF binding is still poorly understood. Prior studies suggest that H2A.Z, a histone variant, might influence CTCF but it remains unknown whether it functions to promote or inhibit binding. Our research has found that H2A.Z enrichment is highly correlated with CTCF enrichment, and changes in CTCF binding occur at H2A.Z marked locations in the absence of ANP32E, the H2A.Z removal chaperone. These changes are also associated with imprinted genes and Hox genes dysregulation. Based on these findings, we hypothesize that H2A.Z antagonizes CTCF binding in the regulation of chromatin looping. To test this hypothesis, I will manipulate H2A.Z installation in mouse embryonic fibroblasts using CRISPR genome editing techniques and examine the genome-wide impacts on H2A.Z, CTCF, and chromatin conformation. By studying the fundamental mechanisms of the role of H2A.Z in higher-order chromatin maintenance, our project may provide insights into the development of various diseases, including cancer.