Histone Modification Patterns Across the X Centromere Reflect Genomic Environment

Kristen Kopf, '08
Illinois Wesleyan University

Beth A. Sullivan, Faculty Advisor
Illinois Wesleyan University

Follow this and additional works at: https://digitalcommons.iwu.edu/jwprc

Kopf, '08, Kristen and Sullivan, Faculty Advisor, Beth A., "Histone Modification Patterns Across the X Centromere Reflect Genomic Environment" (2007). John Wesley Powell Student Research Conference. 31.
https://digitalcommons.iwu.edu/jwprc/2007/posters/31

This is protected by copyright and/or related rights. It has been brought to you by Digital Commons @ IWU with permission from the rights-holder(s). You are free to use this material in any way that is permitted by the copyright and related rights legislation that applies to your use. For other uses you need to obtain permission from the rights-holder(s) directly, unless additional rights are indicated by a Creative Commons license in the record and/ or on the work itself. This material has been accepted for inclusion by faculty at Illinois Wesleyan University. For more information, please contact digitalcommons@iwu.edu.
©Copyright is owned by the author of this document.
HISTONE MODIFICATION PATTERNS ACROSS THE X CENTROMERE REFLECT GENOMIC ENVIRONMENT

Kristen Kopf and Beth A. Sullivan*
Biology Department, Illinois Wesleyan University
and Duke University

Centromeres, the primary point of constriction on chromosomes, are essential for proper chromosome segregation during meiosis and mitosis. Due to their large sizes and repetitive DNA content, centromere regions have been excluded from genome projects. However, being such fundamental functional elements that are epigenetically regulated, we want to understand their genomic organization and the relationship between underlying DNA sequence and chromatin and protein organization. In collaboration with a colleague at NHGRI, we are using chromatin immunoprecipitation-PCR (ChIP-PCR) to generate epigenomic profiles that overlay histone modifications onto the centromeric-pericentromeric genomic assemblies from human-mouse hybrid chromosomes. Our findings indicate that centromeric chromatin organization is regulated via epigenetic factors rather than wholly DNA sequence. This information is being used to identify genomic features that structurally, and potentially functionally, separate the centromere from the rest of the genome.