Volume 13

Washington University
Undergraduate Research Digest

Spring 2018

A P-element Mobilization Screen in Drosophila melanogaster Using a Transgene Containing GAA Repetitious Sequence

Frank Chen
Washington University in St. Louis

Mitchell Grinwald
Washington University in St. Louis

Mikayla Johnson
Washington University in St. Louis

Kendra Woodruff
Washington University in St. Louis

A P-element Mobilization Screen in *Drosophila melanogaster* Using a Transgene Containing GAA Repetitious Sequence

Frank Chen, Mitchell Grinwald, Mikayla Johnson, and Kendra Woodruff

Mentor: Sarah C. R. Elgin

Eukaryotic genomes are packaged in euchromatin and heterochromatin. Heterochromatin is mainly located around centromeric and telomeric regions of the chromosomes, and plays a crucial role in maintaining genome stability. While euchromatin is enriched with genes, heterochromatin consists primarily of repetitious sequences and has relatively few genes. Heterochromatic regions have compact nucleosomal arrays, rendering DNA inaccessible to the transcriptional machinery. Placement of euchromatic genes into heterochromatin results in sporadic gene silencing (Position Effect Variegation). Expansion of a GAA triplet repeat results in local heterochromatin formation in humans, causing Friedrich's Ataxia. Our research employed the model organism *Drosophila melanogaster* and utilized a *P*-element transgenic construct containing 310 copies of GAA located upstream of the reporter gene *hsp70-white*, which is required for fly eye pigmentation. The presence of the GAA repeats results in PEV of *hsp70-white* when the transgene is located at the base of the second chromosome. Insertion of GAA_{310}*hsp70-white* into several other locations did not produce a PEV phenotype. We conducted a large-scale genetic mobilization screen aimed at identifying new genomic locations of the transgene which give a PEV phenotype. Using stable fly lines containing either the functional P-element transposase or our reporter, we performed genetic crosses to mobilize the construct and observe its transposition pattern. We determined chromosomal locations of new insertion sites using genetic tools, and then mapped the sites on the molecular level. Our results show that most insertion sites resulting in variegation occur in hot spots in telomeric and pericentric regions of the second and third chromosomes; three sites were found on the heterochromatic Y chromosome, but none were observed in the heterochromatic fourth chromosome. Variegating transposition sites account for 4.3% of the total number of mobilizations detected. Our next goals are to confirm GAA dependence and investigate which factors affect GAA-mediated heterochromatin formation.