Using Reporter Transgenes to Verify Polymorphic Enhancers in Drosophila

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Mutation is the fundamental precursor to evolution, without which species could not adapt to the selective pressures of a given environment. Genetic mutations (base substitutions, deletions, insertions) produce either structural or regulatory variation, both of which facilitate a specg L. ‘ eit ב M l’

a tightly regulated process that controls what genes are transcribed and then translated inat ns at

variation in the usage of cis-regulatory elements between and within Drosophila species is a major contributing factor to phenotypic variation between and within species.Palopoli lab has assessed the extent of enhancer function similarity within and between species of *Drosophila*.

The work the Palopoli lab has previously done supports the hypothesis. The Principal Component Graph above groups together populations based on similarity in chromatin conformation genome-wide. As shown, The

The project goals for summer 2023 was to (1) Verify presence of enhancer titled E1 in constructed plasmid created in Summer 2022 (2) Identify additional enhancers present in melanogaster genome (3) Amplify selected sequences and insert into pJFC28-UAS-GFP plasmid (4) Verify inserts by sequencing (5) Send constructed plasmids for insertion into Drosophila genome.

Tracks were browsed using position ranges generated by statistical analysis that identified the locations of significant polymorphic peaks. These peaks were then compared to NCBI RefSeq gene transcripts to ensure either intronic or intergenic location. If peaks were determined to be significantly polymorphic and intergenic or intronic, they were flagged as a potential cis-