Title: Gene Annotation and Evolution of the PolyQ Regions in Fmr1 in Drosophila Species

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Abstract:

Up to 700,000 individuals worldwide are affected by PolyQ Fmr1 related disorders, which include Fragile X syndrome, Fragile X Tremor/Ataxia Syndrome, and Premature Ovarian Failure. Fragile X Mental Retardation 1 (Fmr1) is critical for normal brain development and acts as a synaptic functional regulator. PolyQ tracts are regions within genes that have several CAG (glutamine) repeats, as the length increases these tracts become increasingly unstable. The length of these tracts directly corresponds to the severity of the impact on Fmr1 orthologs. One of the main objectives was to determine if the PolyQ tracts are hypervariable between species. This study aims to investigate the evolution of Polyglutamine (PolyQ) tracts within the orthologs of the Fmr 1 gene within *D. sechellia*, *D. rhopaloa,* and *D. willistoni.* through comparison and annotation. These three species were chosen because they are in different branches of the *Drosophila* species, at varying degrees of separation in their evolutionary tree providing adequate information on the evolution of polyQ tracts in relation to the model organism *D. melanogaster*. Through annotation and comparative analysis using sequence alignments of the Fmr 1 orthologs in *D. sechellia*, *D. rhopaloa*, and *D. willistoni*. it is expected that most of the length polymorphisms to be most variable in the area that encodes for the PolyQ tracts compared to the rest of the protein-coding sequence. I successfully annotated the Fmr1 gene orthologs within these three species using the Genomics Education Partnership (GEP) pathways annotation walkthrough. Using sequences from the orthologs of the target species' Fmr1 gene, I performed a comparative analysis using the Molecular Evolutionary Genetics Analysis (MEGA) program. The comparative analysis showed that the last third of the sequence in all isoforms is the most variable and that PolyQ tracts are hypervariable between all species, especially *D. willistoni*. These results support the implications of PolyQ impacts on Fmr1 and suggest there is more research to be done surrounding PolyQ tract length polymorphisms within *D. willistoni.*