The hunt in FMR-1

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The FMR-1 gene encodes for the protein FMRP and is responsible for brain development. Mutations in this gene can lead to a genetic disorder known as Fragile X syndrome, affecting both men and women. The genus of fruit fly *Drosophila* produces a homolog of this protein that is useful for researchers to study as mutations in the *Drosophila* FMR-1 gene (d-FMR-1) shows similar phenotypes to those found in mammals. The dFMR-1 gene has several interesting features including isoforms that contain a non-canonical (or non-AUG) start site. In a previous analysis of an ortholog of this gene in the species *D. erecta*, evidence of a non-canonical start site start was identified in two of the same isoforms. In this project, we wanted to see if there was evidence for the conservation of this non-canonical feature in the different isoforms of FMR-1. Here we looked at four additional species of *Drosophila*, *D. ficusphila, D. obscura, D. buskii,* and *D. arizonae* chosen based on their divergence from the species *D. melanogaster*. Using computer analysis, the annotations of the FMR-1 gene were carried out in all four species of *Drosophila.* The GEP UCSC genome browser was used to obtain the proposed location of the gene with confirmation of the location done through GENBANK. The gene record finder was then used to narrow down the individual start and stop sites for each coding exon. Evidence of the non-canonical start site was confirmed by analyzing the reading frames for the specific amino acids encoded by the exons, using *Drosophila melanogaster* as a starting point. As the non-canonical start site for *D. melanogaster* was located on the G and H isoforms, we focused on those isoforms for the species in this project. Of the four species annotated, only one species, *D. ficusphila*, presented the non-canonical start site on the same two isoforms.