

# Evolution of the *FOXO* Gene in the *Drosophila* Genus

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## Background Information

- Foxo is responsible for mediating the inhibitory action of insulin or insulin like growth factors of specific key functions.
- Alterations to this gene can change an organism's lifespan through the insulin like receptor dInR
- InR occurs earlier on within the insulin signaling pathway and interacts with several genes before indirectly interacting with the *FOXO* gene.

## Hypothesis

There are many proteins involved in the insulin signaling pathway. We hypothesized that the evolution of proteins acting earlier in the pathway will be more evolvable than those presented later in the pathway. More specifically we hypothesized that the gene *PTEN* will have more evolutionary changes than *FOXO* when comparing within the same species (Figure 1).

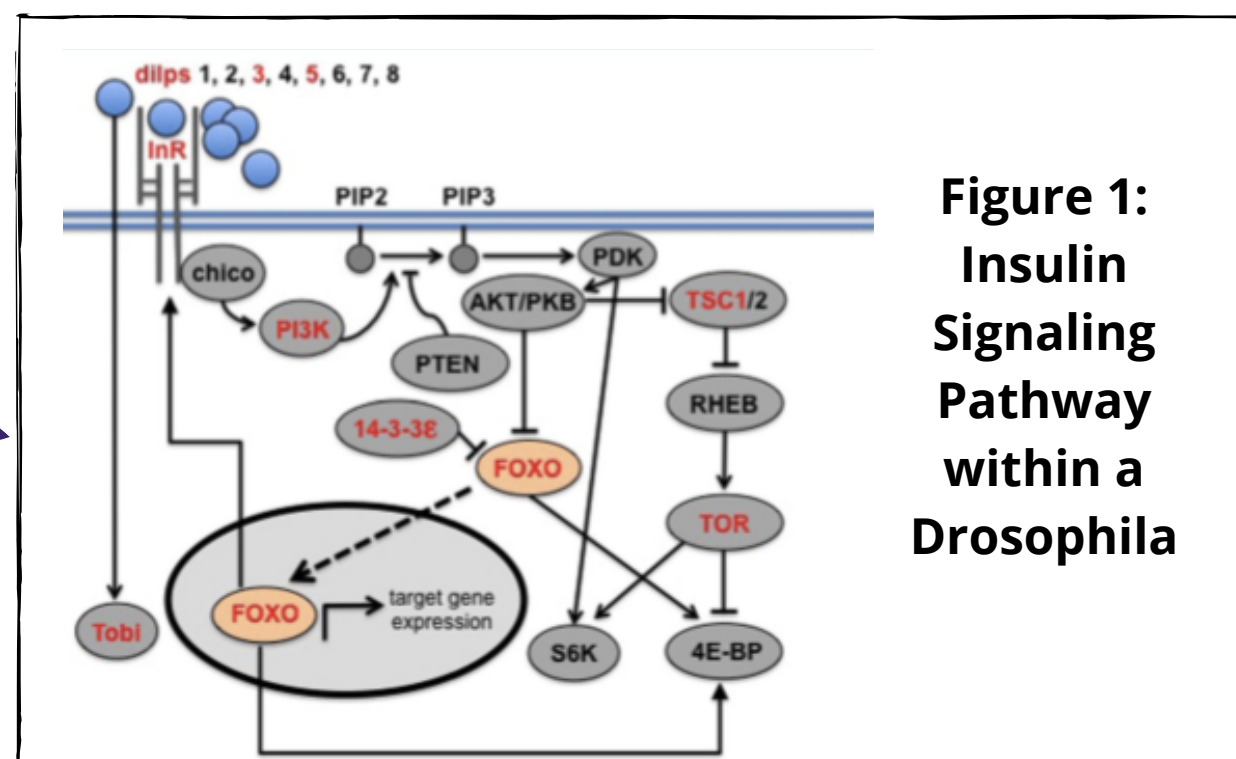


Figure 1: Insulin Signaling Pathway within a *Drosophila*

## Research Objective 1

Annotate the orthologs of the *FOXO* gene on *D. suzukii* and *D. navajoa* using *D. melanogaster* as reference species (Figures 2-3).

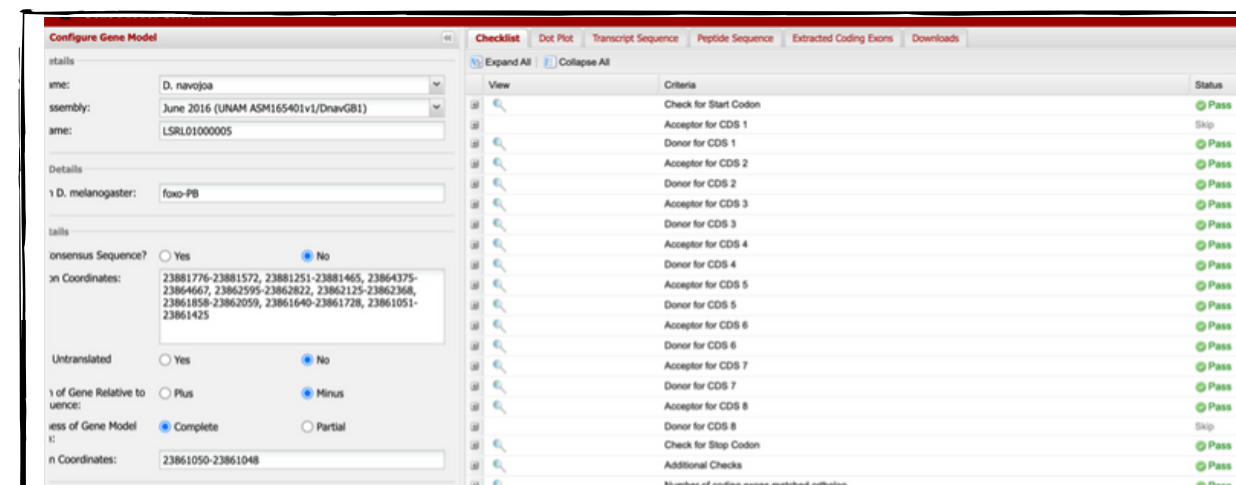


Figure 2: Results of Gene Checker for PB FOXO isoform on *D. navajoa* and genomic neighborhood shows that we accurately annotated the FOXO ortholog in this species

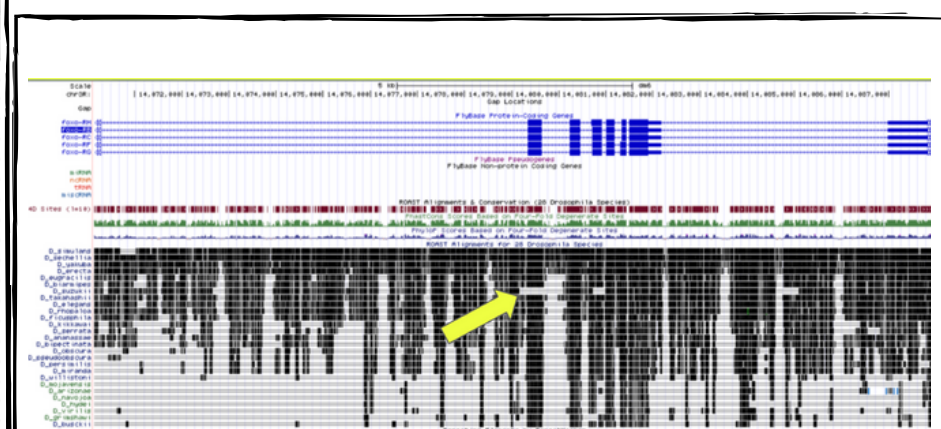


Figure 3: Genome Browser of *D. Melanogaster* for *FOXO* gene. *D. suzukii* still in progress because it seems like it is in a different genomic location or a different version of *FOXO*

## Research Objective 2

Proteins encoded by the FOXO gene for *Drosophila navajoa* and *Drosophila melanogaster* were sequenced using the Molecular Evolutionary Genetic Analysis (MEGA) software Compute the genetic distance of amino acid sequences

## Research Objective 3

Compare the Amino Acid substitution rates of three different proteins (CHICO, PTEN, and FOXO) as they exist in our *Drosophila* species compare to *D. melanogaster* to see if there are differing evolutionary rates of the coding sequences for each protein

## Summary of our Progress

Per amino acid substitution rates (compared to *D. melanogaster* orthologs)

	<i>chico</i> (early)	<i>pten</i> (middle)	<i>foxo</i> (late)
<i>D. navajoa</i>	No seq available	No seq available	0.189
<i>D. miranda</i>	0.363	0.380	TBD
<i>D. suzukii</i>	TBD	0.100	TBD
<i>D. rhopalaoa</i>	0.156	TBD	TBD

We were able to successfully determine the amino acid substitution rates for the *miranda* and *rhopalaoa* version of *CHICO* to *melanogaster* as well as *miranda* and *suzukii* versions of *PTEN* to *melanogaster* and finally *navajoa* to *melanogaster*. This is our progress so far and future work will help us determine amino acid substitution rates of other comparisons here so that we may further test our hypothesis.



Figure 5: Portion of the aligned Amino Acid Sequences showing good conservation of Amino Acid Order using the ClustalW Algorithm When We Computed the per amino acid substitution rate we got 0.189

## Special Thanks to

Kobey and Nikki for their contribution of the *D. rhopalaoa* research as well as Marjie for her contribution with *D. miranda* research