

Drosophila guanche - S6k

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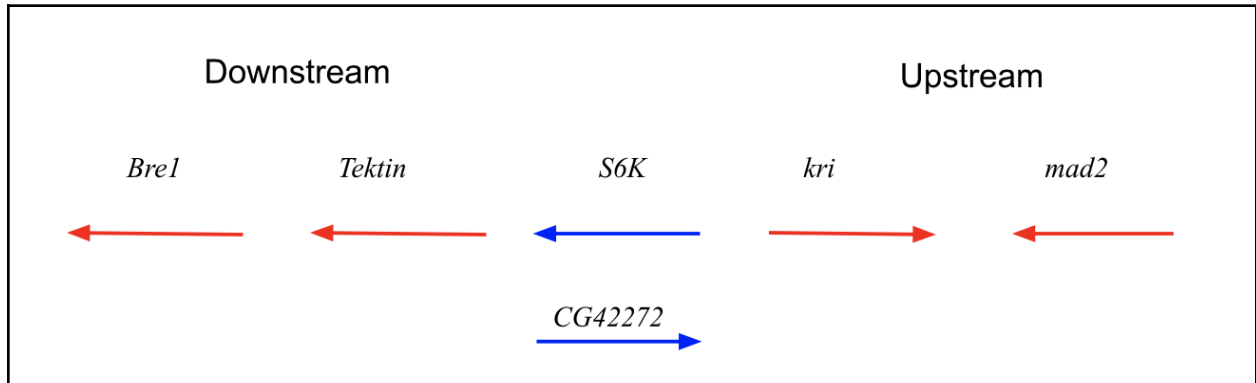
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Abstract

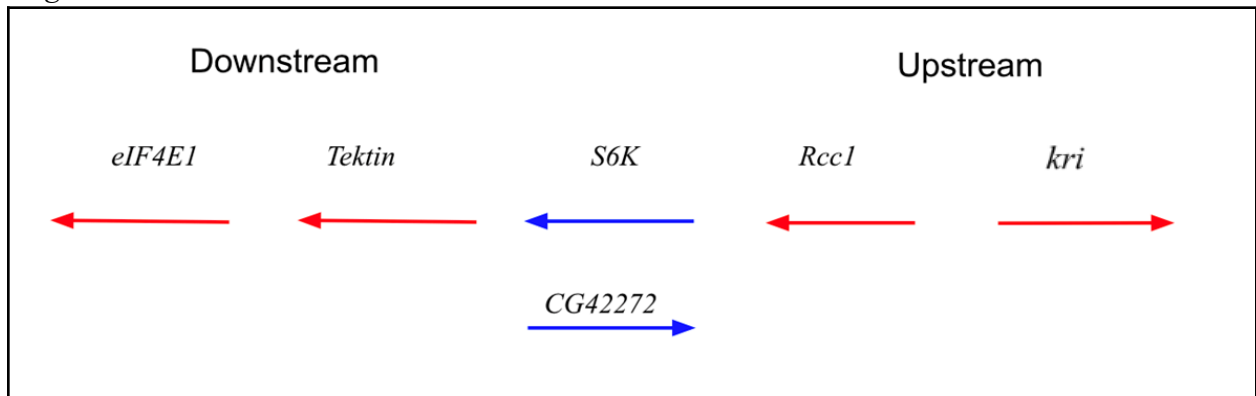
Gene Model for *S6k* in *D. guanche* assembly(dgua_S6k) assembly(GCA_000001215.4)

A

D. melanogaster



D. guanche



- A. Synteny of genomic neighborhood of *S6K* in both *D. melanogaster* and *D. guanche*. Gene arrows pointing in the same direction as *S6K* in both *D. melanogaster* and *D. guanche* are on the same strand as *S6K*, and genes pointing in the opposite direction are on opposite strand. The thin blue arrow under *S6K* *D. melanogaster* pointing to the left indicates that *S6K* is located on the - strand, and the blue arrow under *S6K* in *D. guanche* indicates that *S6K* is on the + strand.

Description

Introduction

The dTOR pathway (*Drosophila* target of rapamycin) is a highly conserved pathway, found in *Drosophila* and is central to cell proliferation and growth- especially during larval development. Activated by growth factors, the dTOR pathway, is homologous to the mammalian target of rapamycin (mTOR), and is activated by growth factors, insulin, and PI3K signaling (Pubmed,2004). S6K also known as (dS6K, S6 kinase, p70S6K, fs(3)07084, RPS6-p70-protein kinase, FBgn0283472) is phosphorylated downstream of the mTOR pathway, and in its activated form, phosphorylates rpS6 (ribosomal protein S6) (FlyBase, 2023). In the mTOR pathway rpS6 is part of the 40S small ribosomal subunit. Phosphorylation of rpS6 by S6K drives translation of specific classes of mRNA (ScienceDirect, 2008). The gene model reported (Dgua_S6K) was determined in the May 2020 (DGUA_6/DguaRefSeq1; GCF_900245975.1) of *D.guanche* and compared to the ortholog dmel_S6K (GCA_000001215.4,) FB2023_02;FlyBase). *D.guanche* is part of the Sophophora subgenus of *Drosophila*, and is part of the *D.subobscura* subgroup along with *D. madeirensis* and *D.subobscura*. *D.guanche* was discovered in the canary islands (Wikipedia).The Genomics Education Partnership maintains the UCSC Genome Browser available at <http://gander.wustl.edu>. The predicted gene model in *D.guanche* for S6K was found in NCBI RefSeq Accession XM_034266925.

Synteny

In *D. melanogaster*, ribosomal protein S6 kinase (*S6k*) is located on the negative strand of chr3L. On the positive strand, there is the nested gene *CG42272*. The closest upstream gene, *kri*, is on the positive strand. The 2nd closest upstream gene, *mad2*, is on the negative strand. The closest downstream gene, *Tektin*, is on the negative strand. The 2nd closest downstream gene, *Bre1*, is on the negative strand.

In *D. guanche*, the ortholog to *S6k* (XM_034266925/XP_034122816/NP_001261450) is located on the negative strand of the scaffold DGUA_6. According to a *tblastn* search, this genomic location of the ortholog in the *D. guanche* genome has an e-value of 1e-76, a percent identity of 59.05%, and a query cover of 89% for the *S6k* protein. A *blastp* search produced an e-value of 0.00 and a percent identity of 94.93%. All *blastp* searches were performed using the predicted protein sequence from each gene *D. guanche* as the query sequence and the protein sequence from *D. melanogaster* as the subject sequence.

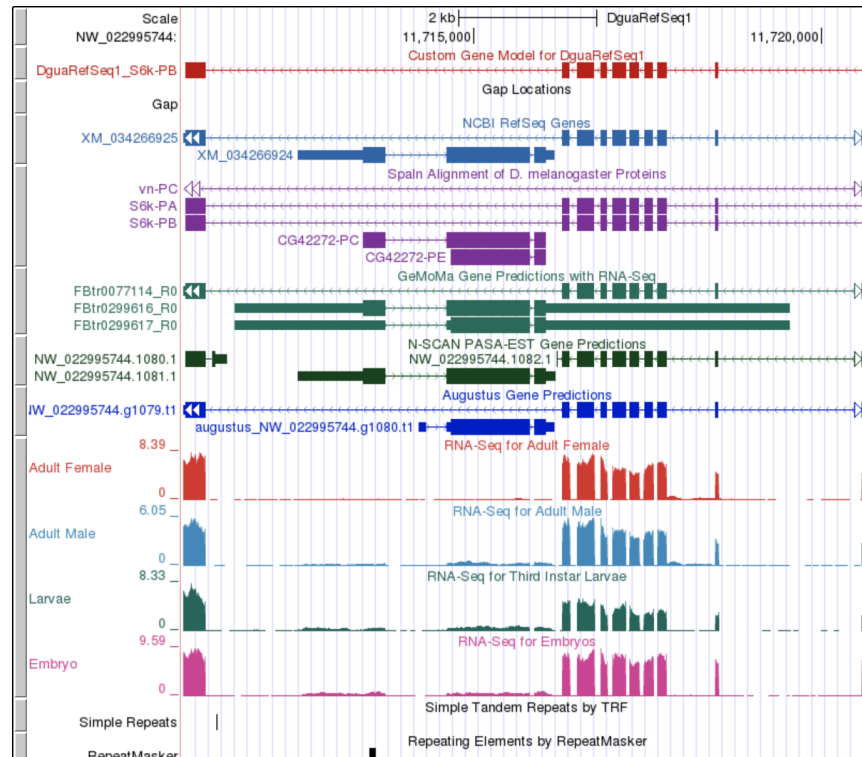
The nested gene in *D. guanche* (XM_034266924/XP_034122815/NP_729102) and the closest downstream gene (XM_034265179/XP_034121070/NP_001097520) are the orthologs to *CG42272* and *Tektin*, respectively, in *D. melanogaster*. A *blastp* search produced an e-value of 0.00 and a percent identity of 83.41% for the nested gene and an e-value of 0.00 and a percent identity of 96.91% for the closest downstream gene.

The 2nd closest downstream gene in *D. guanche* (XM_034265185/XP_034121076), the closest upstream gene in *D. guanche* (XM_034266927/XP_034122818), and the 2nd closest upstream gene in *D. guanche* (XM_034266929/XP_034122820) are not the orthologs to *Bre1*, *kri*, and *mad2*, respectively, in *D. melanogaster*. The 2nd closest downstream gene in *D. guache* correlates to the gene *elF4E1* in *D. melanogaster* producing an e-value of 1e-148 and a percent identity of 80.08% from a *blastp* search. The

closest upstream gene in *D. guanche* correlates to the gene *Rcc1* in *D. melanogaster* producing an e-value of 0.0 and a percent identity of 65.47% from a *blastp* search. The 2nd closest upstream gene in *D. guanche* correlates to the gene *kri* in *D. melanogaster* producing an e-value of 3e-158 and a percent identity of 94.25% from a *blastp* search.

Despite some lack of synteny, the target gene and nested gene are consistent across both species. Additionally, *Tektin* is in the same position and orientation in both genomes. Although there are some differences between the genomic neighborhoods of *D. guanche* and *D. melanogaster* the same genes are present in each genome. A genetic event likely resulted in the shifting of these genes so they are now simply in a different order.

Figure B



(B) The Custom Gene model for Gene Model *D. guanche*, “DguaRefSeq_S6k-PB” (red), NCBI RefSeq Genes (lighter blue alignment) Spaln Alignments of *D. melanogaster* Proteins (purple alignment), GeMoMa Gene Prediction with RNA Seq (light green alignment), N-SCAN PASA-EST Gene Predictions (darker green alignment), Augustus Gene Prediction (darker blue alignment), and the RNA-Seq for Adult Female, Adult Male, Third Instar Larvae, and Embryos is depicted in this image. Custom Gene Model was acquired from the Gene Model Checker using the coordinates for *S6k-PB*.

Protein Model

There are 2 RNA isoforms of *S6k*: *S6k-PA* and *S6k-PB*. The *S6k-PA* and *S6k-PB* isoforms have identical protein coding sequences, represented by the *S6k-PB* protein isoform we have annotated. In *D. melanogaster*, both the *S6k-PA* and *S6k-PB* protein models are encoded by 10 coding exons. In *D. guanche*, the *S6k-PA* and *S6k-PB* isoforms are also encoded by 10 coding exons (shown in Figure B). The 10 coding exons of the *S6k* isoforms are found in chr3L in *D. melanogaster* while the 10 coding exons in *D. guanche* are located in scaffold DGUA_6 within scaffold accession number NW_022995744.

Special characteristics of the gene model

Inserted gene: *S6k* in *D. guanche* has one inserted gene present *CG42272*. This inserted gene is consisted of two isoforms (*CG42272-PC* and *CG42272-PE*). Isoform *CG42272-PC* contains total of 3 exons while isoform *CG42272-PE* contains only 2 exons. Both isoforms correlate to one NCBI RefSeq Transcript (mRNA) Accession XM_034266924 and one NCBI Ref Seq Protein Accession XP_034122815. The *CG42272-PC* and *CG42272-PE* isoforms are both oriented on the negative strand and are found in Scaffold Accession Number NW_022995744 in the *D. guanche* genome.

Extended Data

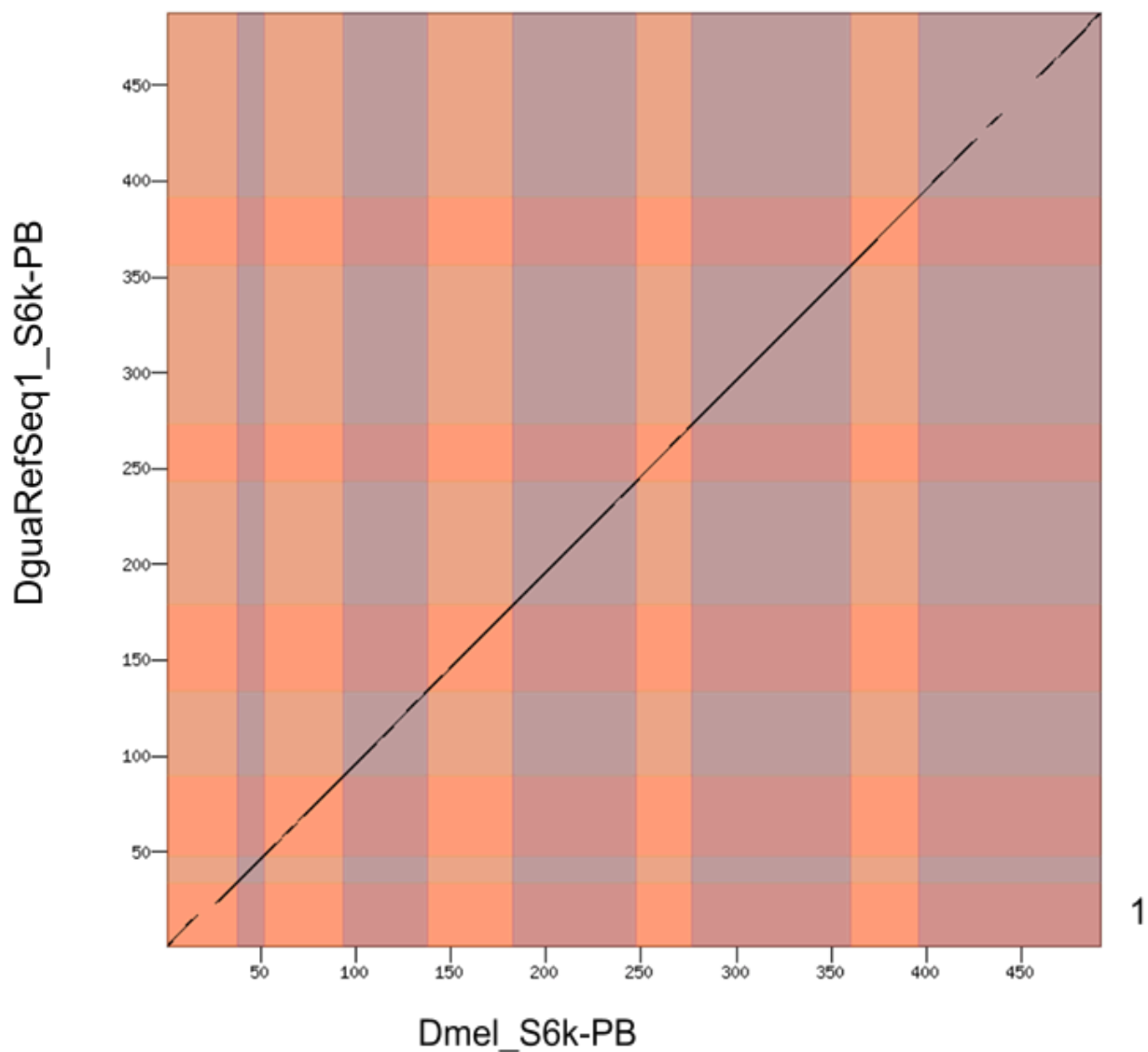
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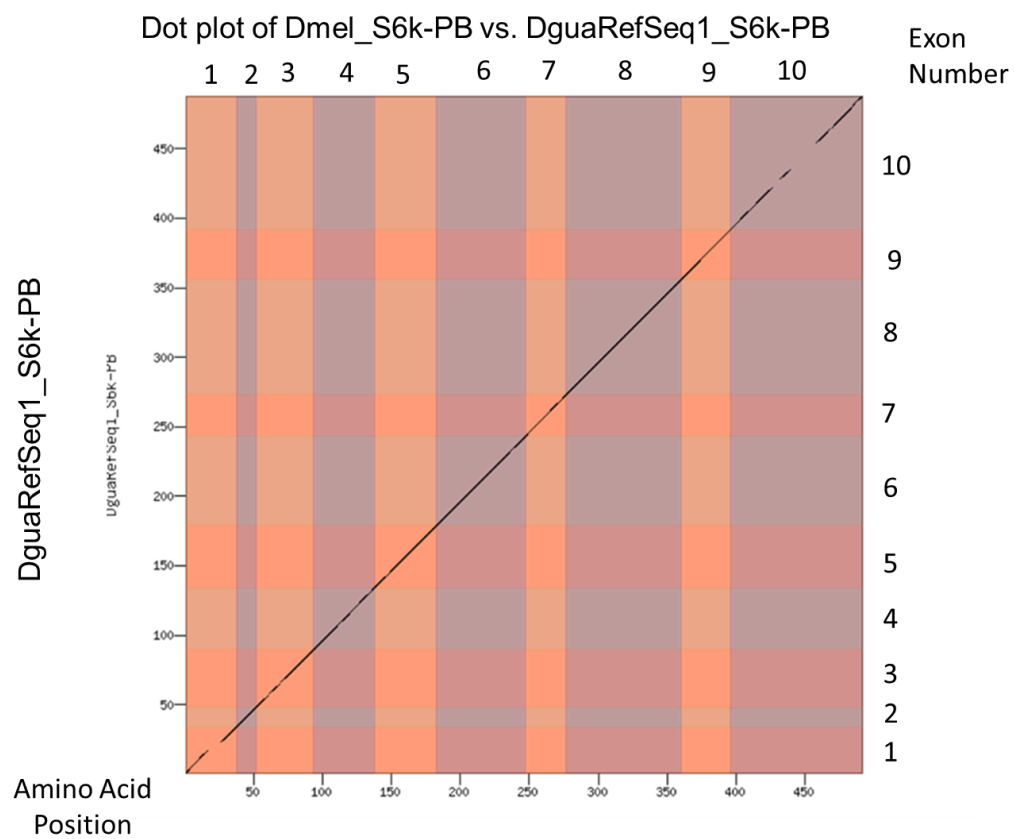
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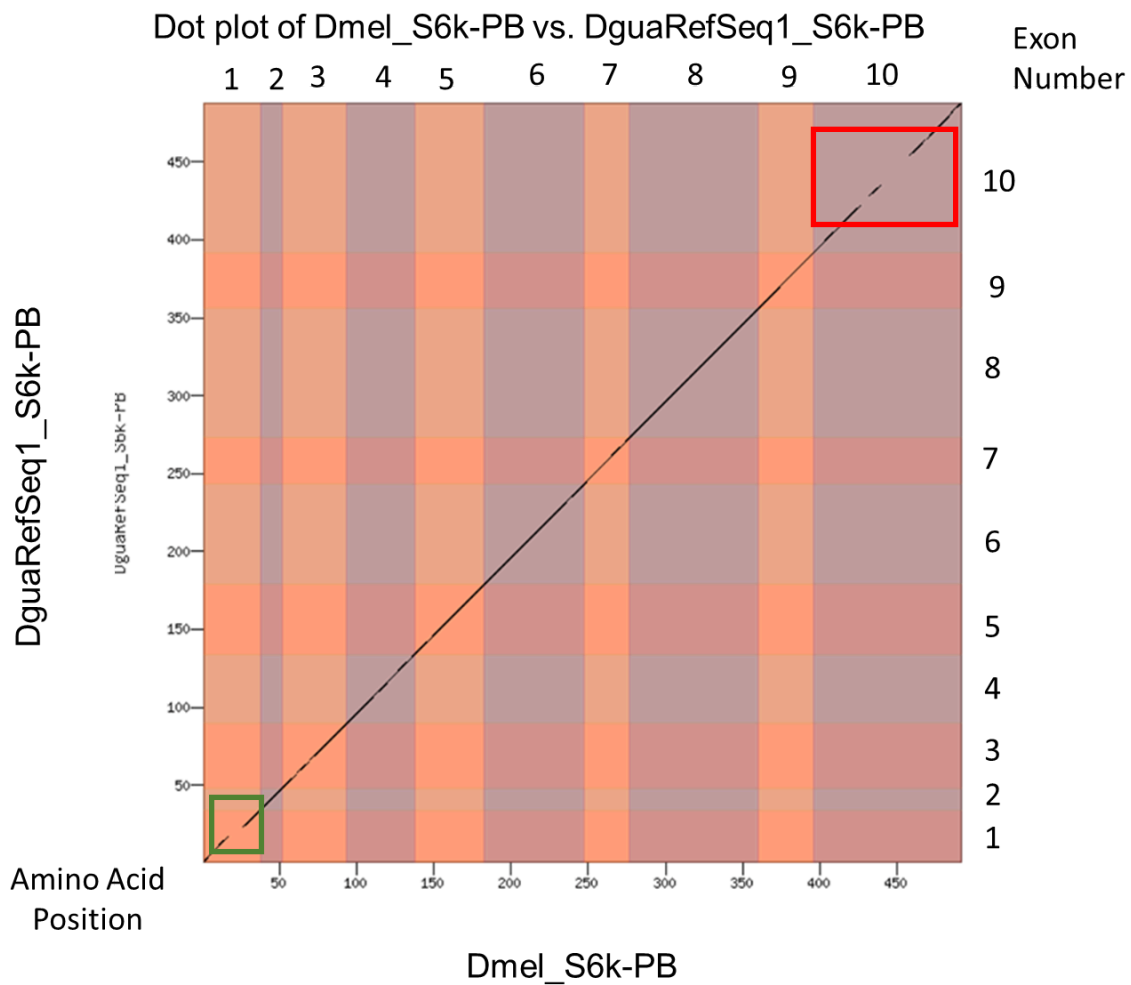
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C

Dot plot of Dmel_S6k-PB vs. DguaRefSeq1_S6k-PB







C) Dot plot of amino acid identified for S6K-PB in *D.melanogater* (x-axis) vs S6K-PB in *D.guanche* (y- axis). Amino acid number is found along the bottom. Exon number is found along the top and right hand side. Each colored rectangle represents an exon. We see that there is a lack of synteny found in regions 1 and 10.

References

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