Drosophila grimshawi – Rheb

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## Figure 1: (A) Synteny of genomic neighborhood of Rheb in both D. melanogaster and D. grimshawi; (B) Curated Gene Model in Apollo: A screenshot of the Apollo instance housing the gene model, containing student annotations, D. mel proteins, NCBI RefSeq Genes, transdecoder transcripts, RNA-Seq tracks, and splice junctions; (C) Dot Plot of the gene model in D. melanogaster (x-axis) vs. the curated gene model in D. grimshawi (y-axis); (D) The multiple sequence alignment of 28 Drosophila species shows that the region near the beginning of the third coding exon in D. melanogaster (part a) has lower levels of sequence similarity compared to the group of species from D. kikkawai to D. miranda (part b) and compared to D. grimshawi (part c).

## Introduction

The Ras homolog enriched in brain (*Rheb*) encodes a Ras homolog (Karassek et al., 2010; Aspuria et al., 2004). Ras is a family of genes that make proteins involved in cell signaling pathways that control cell growth and cell death (Banerjee and Resat, 2016).The gene model reported here (*dgri\_Rheb*) was developed for the May 2011 assembly of *D. grimshawi* Agencourt dgri\_caf1/DgriCAF1 (GCA\_000005155.1). In *D. grimshawi*, the feature was previously annotated as a protein-coding gene with the gene symbol *LOC6564413* (locus\_tag *Dgri\_GH18989*), and it has a single transcript with the RefSeq accession number XM\_001989756.1.

## Synteny and Orthology

The *Rheb* gene on chromosome 3R in *D. melanogaster* is surrounded by the genes *CG12746*, *CG2931*, *CRMP*, and *CG2926*. The best candidate for the *Rheb* ortholog gene in *D. grimshawi* based on a *tblastn* search is found on scaffold\_14906, and is surrounded by the genes *LOC6564411*, *LOC6564412*, *LOC6564414*, and *LOC6564415* (likely orthologous to *Cenp-C, CLS, Nup93-2*, and *CG2519* in *D. melanogaster* respectively, Figure 1A). Although none of these the genes flanking *Rheb* appear to be orthologous between the two species, we determined this region contains the ortholog for *Rheb* in *D. grimshawi* because this location had a substantially better *blastp* hit to the *Rheb* protein sequence than to the second-best hit. We specifically performed a *blastp* search of the *D. grimshawi* protein sequence for XP\_001989792.1 (derived from the NCBI RefSeq transcript record XM\_001989756.1) against the *D. melanogaster* protein sequences in the **refseq\_protein** database.

## Gene Model

The D. melanogaster Rheb gene has two isoforms (A and B) (Figure 1B). Both isoforms have identical coding sequences and only differ in their 5' UTRs. Consequently, this article focuses on the coding region annotation for the A isoform of the Rheb ortholog in D. grimshawi. The major differences between the D. melanogaster Rheb-PA protein and its D. grimshawi ortholog are located within the first and third coding exons (which correspond to the gaps along the diagonal line in the dot plot in Figure 1C). The whole genome multiple sequence alignment of 28 Drosophila species shows lower sequence conservation near the beginning of the third coding exon of Rheb-PA (Figure 1D). Since this study only focuses on the annotation of the coding regions, further investigation of the untranslated regions would be needed to ascertain if the B isoform of Rheb exists in D. grimshawi.

## Special characteristics of the gene model

Changes in the splice donor site for coding exon four**:** Rheb-PA in D. grimshawi has a canonical GT splice donor site at the end of coding exon four. In contrast, the end of coding exon four of Rheb-PA in D. melanogaster, and in most of the other Drosophila species across the genus Sophophora, use a non-canonical GC splice donor site.

# References

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**Supporting Materials:** Gene model and sequence files - dgri\_Rheb-PA.gff, dgri\_Rheb-PA.fna, dgri\_Rheb-PA.faa;

Supplemental results - FigShare link

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