**Drosophila yakuba – Tsc1**

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**Abstract**

Gene Model for *Tsc1* in the *Drosophila yakuba*’s DyakCAF1 assembly (GCA_000005975.1).

**Figure 1.**

(A) Synteny of genomic neighborhood of *Tsc1* in both *D. melanogaster* as well as *D. yakuba* around our focal gene: the thin arrows at the back indicate the strand in each species, whereas the thick arrows with the gene names in them indicate direction relative to *Tsc1*; (B) 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 (Yang et al., 2018; SRP006203) and splice junctions, exon reading frames are indicated in blue, green, and red as in legend; (C) Dot Plot of gene in *D. melanogaster* (x-axis) vs. the gene in *D. yakuba* (y-axis), the numbers on the bottom and left correspond to amino acid position, and the numbers on the top and right correspond to exon number, the vertical and horizontal stripes of color highlight the exon corresponding to each number, the purple boxes represent a lack of
sequence similarity in the protein sequences within coding exons three and six; (D) An image of exon three in the gene model from the GEP mirror of the UCSC Genome Browser for D. yakuba. The Conservation Track of 28 Drosophila species compared to exon three in D. melanogaster Tsc1-RA contains regions lacking sequence similarity (vertical red box; D. yakuba is highlighted in the horizontal red box). The gray scale at the top of the image represents the three reading frames, where Tsc1-RA is in reading frame +2 of Drosophila melanogaster. In the grayscale, the red boxes are stop codons and the green represent start codons. The maroon, green, and purple/pink tracks above the species alignments represent the ROAST alignments and conservation (28 Drosophila species), PhastCons Scores Based on Four-fold Degenerate Sites, and PhyloP Scores Based on Four-fold Degenerate Sites, respectively. For the Drosophila conservation track for 28 Drosophila species at the bottom of the figure, darker values to indicate higher levels of overall conservation as scored by phastCons.

**Description**

**Introduction**

Tsc1 (LOC6538776) in D. yakuba is an ortholog to the Tsc1 gene in D. melanogaster. We used the D. yakuba CAF1 assembly (GCA_000005975.1, Drosophila 12 Genomes Consortium et al., 2007) and the D. melanogaster dm6 assembly (GCA_000001215.4, Release 6.32 FB2021_01). Mutations in either the Tsc1 or Tsc2 gene can cause the hamartoma syndrome tuberous sclerosis complex (TSC) (Dabora et al., 2000). These two genes operate together in the insulin signaling pathway as tumor suppressors because of their ability to control cell growth (Gao, 1970). A mutation in the Tsc1 gene can also cause benign tumors to form in multiple organs (Potter, Huang, Xu, 2001). The NCBI RefSeq predicted model in D. yakuba, with a RefSeq accession number of XM_002099254.2 (RefSeq Release 204), has the same number of exons as the Tsc1 gene (LOC6538776) in D. melanogaster indicating they have an orthologous relationship. The methods and dataset versions used to establish the gene model are described in Rele et al. (2021). The GEP maintains a mirror of the UCSC Genome Browser (Kent WJ et al., 2002; Gonzalez et al., 2020), which is available at https://gander.wustl.edu and contains additional information about data sources and versions.

**Synteny**

The Tsc1 gene, located on chromosome 3R in D. melanogaster, is neighboring the genes Root, GatB, Sec10, and Ncp2f. The best candidate for the Tsc1 ortholog gene in D. yakuba based on the tblastn search is found on chromosome 3R. The candidate is also surrounded by the genes LOC6538778, LOC6538777, LOC6538775, and LOC6538774 (which are likely orthologous to Root, GatB, Sec10, and Ncp2f in D. melanogaster respectively, Figure 1A). We performed a blastp search of protein sequence XP_002099290.1 in D. yakuba against the protein sequences found in the refseq_protein database for D. melanogaster and it showed a high percent identity to Tsc1 in comparison to the second-best hit. After confirming that the genes surrounding Tsc1 are orthologous between the two species and the blastp results indicated a high percent identity for the Tsc1 gene between the two species, we determined that this region contains the ortholog for Tsc1 in D. yakuba.

**Gene Model**

Tsc1 has one isoform in D. yakuba, Tsc1-PA, with six exons. There are also six exons in the Tsc1 gene located in D. melanogaster. A blastp search of the protein sequence of Tsc1 in D. yakuba against D. melanogaster yields a 97.00% identity with only 33 amino acids differing out of 770. There was a small lack of sequence similarity between the protein sequences of the two species in coding exon three and six as is displayed by the purple boxes in the dot plot (Figure 1C). The large lack of sequence similarity in exon six, shown by the red vertical box in Figure 1D, can also be seen in the conservation tracks of 28 different Drosophila species in the UCSC Genome Browser. The coordinates of the curated gene model can be found in NCBI at GenBank/BankIt using the accession BK014573. These data are also available in Extended Data files below, which are archived in CaltechData.

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**Extended Data**


**References**


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