

**Manual gene annotation of the longevity-regulation pathway in *Diaphorina citri*, the vector for citrus greening disease**

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**Abstract**

The genome of *Diaphorina citri*, the vector of citrus greening disease (Huanglongbing), has been the focus of a community annotation program to provide high quality gene models for development of molecular therapeutics. Here we present the annotation of the longevity regulating pathway (Kegg dme04213). The pathway is associated with lifespan and stress responses during dietary restriction. Binding of the insulin-like peptide (DILP) to the receptor (InR) initiates the pathway. Upon activation, TOR plays a key role in regulating nutrient signaling, reproduction and other important cellular processes. Additional genes in the pathway, including Akt and FoxO, have been shown to be associated with longevity. Annotation began with collecting orthologous sequences from NCBI which were then used to locate longevity pathway genes in the *D. citri* genome by using the Citrusgreening.org WebApollo genome browser and editor. Reciprocal BLASTp analysis was performed to confirm the identified genes. Manual annotation was based on short read RNA-seq and PacBio Iso-seq transcript evidence to correct gene structure, intron/exons borders and untranslated regions. Manually annotated genes will be available as a part of the version 3.0 Official Gene Set. Annotation of the longevity regulating pathway provides insights into the genes that regulate lifespan, stress response and nutrient signaling in *D. citri*. Identification of these genes in *D. citri* provides the molecular data required to develop tools for vector control.