Annotation and Comparison of Parasitoid Wasp GAPDH Gene

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Abstract

Endoparasitoid wasps are members of the hymenoptera superfamily that are dependent on other arthropod species for reproduction, consisting of the host's exploitation after the first sting for the preparation of egg insertion. The element that allows the manipulation of host biology is the introduction of venom gland derived proteins into their host. This venom has the ability to alter the host's gene expression and paralyze the arthropod to allow the wasp's eggs to develop inside the host without a fight. Once the eggs begin to develop, they become completely dependent on the host for their nourishment and development, meaning that the host will lack its nourishment and what is needed to continue living. A painful and quiet death awaits the host while it is being eaten alive from the inside out for the benefit of the parasitoid wasp. This research project focuses on the evolutionary relationships between venom proteins from three different endoparasitoid wasps: Leptolina. heterotoma, L. boulardi, and Ganaspis. The genes aligning to the venom transcriptome of the following species were identified with the help of the University of California Santa Cruz Genome Browser, allowing easy identification of precise and accurate coding regions through comparison with other insect orthologs. The goal of this research project is the annotation of glyceraldehyde-3-phosphate dehydrogenase (GAPDH) in the three parasitoid species. GAPDH is a glycolytic enzyme that has significant cellular functions in glycolysis and gluconeogenesis, responsible for the interconversion of 1,3-diphosphoglycerate and glyceraldehyde-3-phosphate. This enzyme catalyzes the conversion of glyceraldehyde 3-phosphate to 1,3-diphosphoglycerate, producing ATP and pyruvate in the Cytoplasm of the cell through anaerobic glycolysis. RNA-seq data from the venom transcriptome suggests that the three GAPDH orthologs have a similar gene structure and are highly homologous to the *Nasonia vitripennis* predicted GAPDH peptide sequence. The GAPDH peptide from *Ganapsis* species has shares 93% identity and 97% similarity to *N.*

vitripennis ortholog, whereas the *L. boulardi* ortholog is more divergent with 88.4% identity and 93.1% identity. These gene models will be used in a comparative genomics study to investigate parasitoid wasp venom evolution.