

Bioinformatic Analysis of the Evolution and Function of Parasitoid Wasp Venom

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Hymenopteran parasitoid wasps are a diverse collection of species that infect a range of arthropod hosts. These wasps often use factors found in their venoms to manipulate host immune responses, physiology, and behaviour to allow for successful parasitization. Individual venom components have been identified from multiple parasitoid species, and more recently, whole venoms have been profiled using proteomic approaches. Here, we present a bioinformatic characterization of the venom protein content from one of these parasitoids, *Ganaspis sp. 1*, a species that parasitizes fruit flies of the genus *Drosophila*. We previously demonstrated that *Ganaspis sp. 1* venom antagonizes intracellular calcium signaling in infected *Drosophila melanogaster* hosts, and we have uncovered venom proteins with multiple shared predicted functions, including calcium ion binding. Additionally, we have explored two potential mechanisms of the origin of the venom encoding genes: evolution by gene duplication and horizontal gene transfer. Overall, this analysis represents an important step towards understanding the composition and activity of parasitoid wasp venoms.