

TOPIC: Chagas

APPROACH: Vector biology and eco-epidemiology

Chemosensory proteins in *Triatoma infestans*: gene annotation and comparative analysis across hemipterans

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Triatoma infestans is the main vector of *Trypanosoma cruzi*, the causative agent of Chagas disease in the southern cone. Resistance to pyrethroid insecticides reported in *T. infestans* populations could be one of the main causes of the persistence of vectorial transmission in the Argentinean Gran Chaco ecoregion. Chemosensory proteins (CSPs) are small soluble proteins from arthropods, with a studied role in olfaction. Recent evidence points to a role of these proteins in insecticide susceptibility and resistance. Accordingly, previous results from our group showed that some members of *T. infestans* CSP family are modulated four hours after an intoxication with deltamethrin. The main goal of this work was to annotate CSPs encoding-genes in an available genome on *T. infestans*, and to perform comparisons of CSP gene family across hemipteran species. The genomic regions where CSPs are encoded were identified through BLAST searches, and the gene models were predicted using Fgenesh+ tool. The genomic position of the identified models was used to identify CSP gene clusters in the species, which could indicate a common gene regulation. A maximum-likelihood phylogenetic analysis was performed including these proteins along with the previously identified CSP sequences from other hemipteran insects such as the triatomines *Triatoma dimidiata*, *Triatoma pallidipennis* and *Rhodnius prolixus* and the pentatomid *Nezara viridula*. Moreover, the genomes of the cimicid insect *Cimex lectularius*, the pentatomid *Halyomorpha halys*, the delphacidae *Nilaparvata lugens*, and the anthocoridae *Orius laevigatus* were analyzed. The phylogenetic analysis revealed a conservation of some CSP genes throughout the Hemiptera evolution, while others seem to be specific for some families or genus. The results presented here provide valuable information on the evolution of this gene family. The comparison among species with different feeding habits and/or environmental niches could be useful to hypothesize about CSP genes involved in detoxification and/or insecticide resistance in harmful insect species.