

A Transcriptome Analysis of *Parawixia bistriata* Venom Gland.

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Venom animals have developed, throughout their evolutionary processes, chemical compounds capable of stunning, paralyzing or even kill predators and prey. Many of the venom compounds act as potent neurotoxins and neuroprotectors, with specificities and affinities directed at receptors, transporters and neural-glia ion channels, as well as painkilling, anti-depressive and anti-convulsive properties in mammals or even insecticidal in invertebrates. Furthermore, some compounds present other properties such as anti-bacterial, anti-fungicide, and anti-tumoral, and studying these compounds further broadens the research perspectives and the offer of materials of biotechnological interest. From a cDNA library prepared from the *Parawixia bistriata* spider's venom glands, 1.344 sequences averaging 450 bp in size, grouped in 780 clusters with 124 contigs, composed of more than one EST and 656 unique sequences were analyzed. Approximately 48% of sequences showed homology to genes in databases with use of BlastX tool, and could be associated with security to gene products previously described. Categorization of sequences with aid of the Gene Ontology revealed important cellular processes for the production of venom, which include high protein synthesis, post-transduction modifications and transport, activities demonstrably important in venom production. Group sequences that included ESTs similar to toxins described in other organisms were also identified. The contig consensus sequences were also submitted, with the BlastX tool, to the exclusive Araneae database, and 22% (7 of 77 contigs) found homologous genes previously described in other spiders, with e-value <10⁻⁵, of which 47% (8 contigs) are homologous to toxin codifying genes. Among the most frequently found spiders in the search are *Diguitia canites*, *Lycosa singoriensis*, *Ornithoctonus huwena* e *Aliatypus plutonis*.

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