

Comparative proteomics and transcriptomics of *Nephilingis cruentata* spider venom and glands

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Introduction: The Nephilidae family comprises 61 spiders, including the highly synantropic genre *Nephilingis*, commonly characterized by large webs and remarkable sexual size dimorphism. Despite some few studies about characterization of acylpolyamines in venom, there is a lack of studies of *Nephilingis cruentata* venom proteome and transcriptome. **Objectives:** Investigate the *N. cruentata* venom and gland proteome by data dependent LC-MS/MS acquisition and transcriptomics comparing protein matches among biological samples. **Material and Methods:** Venom extracted by a low voltage electrical stimulator and gland supernatant pools were separated, centrifuged and stored at -80°C until digestion. Disulfide bonds were reduced and alkylated with dithiothreitol and iodoacetamide, respectively and pools were digested with trypsin at 37°C overnight. Peptides were separated in 75 µm x 100 mm capillary columns by a linear gradient of 5-35% of acetonitrile and 0.1% of formic acid, ionized by ESI and analyzed in data dependent acquisition mode in a LTQ Orbitrap Velos. Proteins were identified in PEAKS Studio against the compiled transcriptome database. **Results and Discussion:** A total of 33.108 predicted proteins were translated from the venom gland transcriptome and 406 proteins were found in *N. cruentata* venom and gland proteomes. 276 proteins were unique for glands, as arginine kinase, while 105 proteins were exclusively found in venoms, such as astacin-like metalloprotease toxin. Only 25 out of 406 proteins were common to both groups, showing a wide diversity of proteins in pools of venom and glands of *N. cruentata*. **Conclusions:** The findings in *N. cruentata* venom show a great diversity of proteins in gland and venom. That diversity may be related to proteins with metabolism functions in glands but also with roles in the maturation of venom toxins.