IPD Project Details

Project ID: IPD6128

Project Title: Stings on wings: venom proteomics and tissue transcriptomics of the lesser banded hornet, Vespa affinis

Description: The project aims at unraveling the venom repertoire of the lesser banded hornet (Vespa affinis) and investigate the regimes of natural selection underpinning their venom evolution. The study also sheds light on the clinical repercussions of the V. affinis venom.

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Sample Preparation: The proteomic composition of V. affinis venom was determined using tandem mass spectrometry wherein, following SDS-PAGE separation, the excised protein bands were treated with dithiothreitol (DTT, Sigma-Aldrich, USA), alkylated with iodoacetamide (Sigma-Aldrich, USA).

Peptide Separation: The process followed by trypsin digestion (2 µg/µl; Promega Corporation, USA) and subsequently, the analytes were subjected to tandem mass spectrometry analysis in Thermo Orbitrap Fusion Mass Spectrometer (Thermo Fisher Scientific, MA, USA).

Protein Characterization: PEAKS Studio X (Bioinformatics Solutions Inc.) was used to identify protein families by searching the raw MS/MS spectra against NCBI's 'non-redundant' (www.ncbi.nlm.nih.gov) protein database, as well as V. affinis venom gland tissue transcriptome generated in this study. A monoisotopic mass search was performed with 'semispecific' trypsin digestion and a maximum of three missed cleavages, and the parent and fragment mass error tolerance of 10 ppm and 0.06 Da, respectively. Carbamidomethylation was set as a fixed modification, while oxidation (M) was set as a variable modification. Quality filtering parameters were set to a False Discovery Rate (FDR) of 0.1%, detection of ?1 unique peptide and a -10lgP protein score of ?50. The Common Repository of Adventitious Proteins (CRAP; www.thegpm.org/crap/) database was included during the spectral searches to effectively eliminate common contaminants.

Experiment Type: Shotgun proteomics

Species: Vespa affinis-882735

Tissue: Venom (bto:0001439)

Cell Type:

Disease: Unknown

Instrument Details: Orbitrap Fusion (MS:1002416) Data in instrument_details

Protein Modifications: monohydroxylated residue, iodoacetamide derivatized residue

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