

PROFILING THE VENOMICS OF THE AFRICANIZED HONEYBEES (*Apis mellifera*)

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The knowledge about Arthropod venoms composition is important to improve the treatments against envenomations and provides good tools to investigate the nervous system, the immunological defense, blood coagulation and inflammatory responses. Up to now the knowledge about honeybee venom (HBV) is of limited impact due to the apparent paucity of the venom. The number of reports involving honeybees in Brazil is increasing, reaching approximately 15.000 stinging accidents in the last five years. Despite of this, there is no specific treatment and there is only a partial identification of antigenic proteins from HBV. The proteomic profile that is known up to now is limited to only 50 proteins. The aim of this work is to identify the complete protein complement from HBV by using a proteomic approach through 2D-SDS-PAGE, MALDI TOF/TOF and nanoESI-LC/MS-MS. 2D gels revealed up to 90 distinct protein spots; almost all of them were identified. It could be found 16 PLA₂ isoforms, the major allergen from this venom, involved in inflammatory signaling cascades and in platelet aggregation; also, hyaluronidase, mellitin-precursor, alpha-glucosidase, zinc finger protein and transferrins were identified. Some proteins were identified for the first time in HBV such as: MRJP-2 and -9, PDGF- and VEGF-related factors, which need to be studied to elucidate their function in venom.

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