Proteome analysis of *Potamotrygon falkneri* stingray sting

Oliveira-Júnior, N.G., Cardoso, M.H.S. and Franco, O.L.

1Programa de Pós-Graduação em Ciências Genômicas e Biotecnologia, Universidade Católica de Brasília, Brasília-DF, Brazil; 2Centro de Análises Proteômicas e Bioquímicas, Pós-Graduação em Ciências Genômicas e Biotecnologia, Universidade Católica de Brasília, Brasília-DF, Brazil; 3Programa de Pós-Graduação em Biologia Animal, Universidade de Brasília, Brasília-DF, Brazil.

**INTRODUCTION.** *Potamotrygon falkneri* consists in a stingray species which belongs to Potamotrygonidae family. This stingray is a benthic species showing a long tail with a knurled sting covered by a glandular epithelium with the ability of produce venom. The clinical manifestations observed in accidents by freshwater stingrays may cause painful injuries causing necrosis and ulcers of affected area. Only few are known about venomous secretion total protein constituent were elucidated until now. In this study in-gel proteomic tools were utilized for protein content elucidation of *P. falkneri* venom. **MATERIAL AND METHODS:** The protein extraction was performed by sting shaving n a 50mM of sodium phosphate buffer in the presence of proteases inhibitor cocktail (PIC). Unidimensional gel electrophoresis was carried out to analyze the range of protein mass and sample integrity. Two dimensional gel electrophoreses were utilized for initial proteomical analyses. Gels produced were subjected to in silico analysis through the ImageMaster Platinum software (GE Life Sciences healthcare) and only the gels with $R^2$ higher than 0.90 where considered. The tripsinization was performed with the IGD kit (Sigma) and further sequenced by MALDI-ToF technology. **RESULTS AND DISCUSSION:** Protein spots with a range of pH of 3-11 and molecular masses about 10-220 kDa were observed in gels. Approximately 119 spots were identified by gel and the $R^2$ obtained was greater than 0.95. The sequencing analysis indicated the presence of proteins commonly related to pain and necrosis previously described in literature. **CONCLUSION:** In summary, global venomic analyses here presented suggest that *P. falkneri* venom showed a wide range of proteins and proteolytic enzymes shedding some light over the complex envenomation mechanisms. Nevertheless more studies must be done in order to improve the understanding of such toxins actions in order to minimize the damage caused.

Keywords: Proteome, Stingray, *Potamotrygon falkneri*.
Acknowledgments: UCB, UnB, CNPq and CAPES