A New Inflammatory Peptide from the Venom of the Freshwater Stingray *Potamotrygon gr. orbignyi*.

Conceição K.[1]; Melo R.L.[1]; Klitzke C.F.[1]; Bruni F.M.[1]; Borges M.H.[2]; Fernandez J.H.[3]; Lopes-Ferreira M. [1].

[1]Laboratório Especial de Toxinologia Aplicada (CAT/CEPID), Instituto Butantan, SP; [2]FUNED, Belo Horizonte MG, [3]LQFPP, Universidade Federal Norte Fluminense – Campos, RJ.

Fish venoms are rich resources of bioactive molecules with extreme variability in structure and function. They become new targets of Proteomics and Genomics studies and some bioactive proteins and peptides have been identified. *P. gr orbingyi* stingray is one of fish species of medical importance in Brazil and their venom was screened for bioactive peptides search based on toxicity to microcirculation. An inflammatory peptide, named Porflan, was isolated and subsequently characterized by proteomic techniques (RP-HPLC separation; MALDI-ToF/MS and Q-ToF-MS/MS). It contains 18 linear amino acids and its sequence presented no similarity with any other known protein or peptide. This peptide was shown to be effective "*in vivo*" in mice microcirculatory environment, causing an intense increase in the leukocyte rolling. We also describe and compare the activity of three Porflan analogues detecting high differences in activity between them. The possible mechanism of interaction of Porflan with biological membranes is under investigation "in silico", using molecular simulations systems with DPPC membranes and circular dichroism analysis. We observe the immediate electrostatic interaction of the carboxylic groups of Glu residues of the peptide with the hydrophilic layer of the membrane followed by the total interaction with the DPPC membrane at the fifth ns, adopting an stable conformation in the last 5 ns of simulation. These results show, for the first time, that this peptide could play a role in triggering proinflammatory events observed by the whole venom.

KEYWORDS: Porflan, Potamotrygon stingrays; bioactive peptide.

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