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Resumo	The Cnidaria phylum comprises animals presenting a great diversity of toxins and more than 250 molecules from this taxon have been identified. The Anthozoa class is one major contributor of isolated cnidarian toxins. However, some animals of this class remain poorly studied, in spite of the biotechnological potential already described. Here, we describe the study of the proteome of the crude extract of Z. sociatus, a species widely present in the Brazilian shores. The aqueous extract was separated by centrifugation in two fractions (precipitate and supernatant). The supernatant was submitted to a Reversed phase C18 solid phase extraction (SPE), and the analytes were eluted using methanol. The fractions (F1 to F3) obtained from SPE, the extract as well as the precipitate had their molecular mass profile assessed by SDS-PAGE, MALDI-TOF/MS and ESI-IT-TOF/MS-MS. The SDS-PAGE analysis showed that the majority of the protein content of the extract of Z. sociatus remains in the precipitate, showing proteins with MM ranging from 97 to 14 kDa. On the other hand, the supernatant and SPE fractions, showed absence of proteins at this MM. When evaluated by MALDI-TOF/MS, the supernatant and F3 displayed mainly peptides ranging from 2 e 6 kDa. The trypsin/pepsin-based proteomic analysis revealed that the precipitate is mainly composed of NBD_sugar-kinase_HSP70_actin, Histone (H4/H2B), SMC and DNA2 superfamilies. These molecules have already been found in other Anthozoans. Additionally, the supernatant an F3 showed the presence of molecules from Ion_transport superfamily, resistin-like molecule (RELM) hormone family, and Trypsin-like serine proteases. The different content of proteins and peptides found between these fractions shows that is possible to further explore the biotechnologicalproperties of these molecules, once that the extract presents both proteins with antimicrobial potential (lysine-rich and arginine-rich histones) and RELM, potentially used for studies of modulation of insulin secretion.
Fomento	