Proteomic analysis to elucidate experiments with RcAlb-PepII, a small synthetic peptide bioinspired in the albumin 2S of the seed cake of Ricinus communis, against Klebsiella pneumoniae and Candida parapsilosis

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Antimicrobial peptides (AMPs), by participating in the front line of pathogen attacks, are of great relevance to the immune system. For this reason, in 2019, a group of researchers from the Federal University of Ceará made the design of a small peptide, RcAlb-PepII from the 2S albumin of Ricinus communis seed cake and performed tests against Klebsiella pneumoniae and Candida Parapsilosis. The experiments demonstrated that there was inhibition of growth, morphological changes in the cell surface and degradation of the cells of the biofilm formed by both organisms. However, it was not possible to know which proteins act in this treatment. For this reason, the present study is necessary.

From the files of the mass spectrometry results, MASCOT MS/MS ions search tool of MATRIX SCIENCE was used with the UP2311_S_cerevisiae and UP219602_F_oxysporum databases and using as fixed modification parameter: carbamidomethyl, variable modification: oxidation, load from +2 to +4 and as instrument the ESI-QUAD-TOF. For each protein found, the data generated were put into a spreadsheet, especially the name and intensity. With the organized data, it was possible to carry out the screening of which compounds were exclusive of the control group or the treaty and which were common to both, and their intensity variation. If this value was between 0.5 and 1.5 it was considered without change in the abundance of proteins, if below it there was a decrease, otherwise an increase. To know the possible sites of interference in the cell by the peptide, the gene ontology was performed based on the data available in UniProt.

536 proteins were identified. Of these, 252 were exclusive to the control group, 235 to the treaty and 49 belonged to both. Of these, 16 had decreased abundance, 19 were stable and 14 suffered increase. Of this group, two proteins stand out: \"C2H2-type domain-containing protein\" and \"Dynein heavy chain, cytoplasmic\". For they had, respectively, a relative abundance of 3514% and 1545.63%. The first is present in the nucleolus and acts as co-regulator of transcription activity, the second acts on nuclear organization, mainly of cytoplasmic microtubules, where it is found. On the other hand, the \"pre-mRNA-splicing factor ATP-dependent RNA helicase\" had 1% abundance, being the one with the largest reduction. This protein plays a key role in mRNA processing

With the data generated from proteomics, it is possible to reaffirm what was exposed by the experimental in 2019. Because, the cell of the microorganism when coming into contact with the treatment, begins the process of trying to repair the damage caused by the peptide, for this reason it exorbitantly increases proteins linked to transcription and cell repair. However, it is possible that with the decrease in the synthesis of helicase, this attempt at repair is not efficient, so that it was possible to observe the damage in the microscopes

Agradecimentos: Agradecimentos especiais aos professores Dr. Pedro Noronha e Dr^{a}. Rossana Cordeiro, aos doutorandos Me. Francisco Eilton Lopes e Me. Maria Laína Silva e a todos os colegas pesquisados do BIOs . Aos familiares, em especial Angelique Abreu e Terezinha Rosa Silva por serem meus exemplos de estudiosas e mulheres. Ao Matheus Henrique Mariano por todo apoio e companheirismos nessa jornada.