Antibacterial potential of two peptides derived of a ribosomal protein from *Pyrobaculum aerophilum*

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INTRODUCTION: Increasing efforts have been deposited in the discovery of novel compounds with broad-spectrum activities against pathogenic bacteria. In this scenario, the antimicrobial peptides (AMPs) have emerged as promising alternative molecules, being prospected by several methods such as purification, proteomics, transcriptomic, as well as by screening for potential antimicrobial sequences within proteins already described. **OBJECTIVE:** Thus, this work focused on the functional/structural characterization of two novel AMPs derived of a ribosomal protein from *P. aerophilum*. **MATERIAL AND METHODS:** Initially, protein sequences from the non-redundant database were submitted to antimicrobial predictor algorithms including Pratt 2.1, random forest, support vector machine and discriminant analysis. Data revealed a fragment with 19 amino acids in length, named PaAMP1R3 from *P. aerophilum*. A slide window of 10 amino acid residues was also applied to PaAMP1R3, generating ten candidate sequences. Among them PaAMP1R3F10 was selected for further analysis due to probable higher antibacterial potential. The two peptides were synthetized by Fmoc and analyzed on MALDI-ToF. The antibacterial activities were determined against susceptible/resistant *Escherichia coli* and *Klebsiella pneumoniae* and susceptible *Pseudomonas aeruginosa, Enterococcus faecalis* and *Staphylococcus aureus.* Molecular modeling and dynamics during 200ns in water were also performed. **RESULTS AND DISCUSSION**: MALDI-ToF analyses presented ions of 2296.4 Da for PaAMP1R3 and 1244.9 Da for PaAMP1R3F10. PaAMP1R3 was more active than its ten residues analogue, presenting minimum inhibitory concentration values from 4 to 32 μg.mL^{-1} and 8 to 64 μg.mL^{-1}, respectively, against susceptible and resistant *E. coli* and susceptible *K. pneumoniae*, *E. faecalis* and *P. aeruginosa*. *In silico* simulations predicted that PaAMP1R3 maintained a well-define α-helical structure during 200ns in water, while a random coil was observed for PaAMP1R3F10. **CONCLUSION:** In summary, PaAMP1R3 and PaAMP1R3F10 revealed to be very active peptides toward pathogenic bacteria, with some advantage for PaAMP1R3, which might be explained by its high structural stability, even in hydrophilic environments.

Keywords: antimicrobial peptide, bacteria, biophysics, bioinformatics.