Identification of Novel Cathelicidins with Potent Antimicrobial Effect from the Genome Analysis of Python bivittatus

Lee, Ju Yeon

Antimicrobial peptides (AMPs) are small peptides that function as a part of innate immunity in first-line nonspecific defense. AMPs could be alternatives of existing antibiotics, especially for resistance bacteria because of their potency in activity and difference in acting mechanisms. Recent increase in the availability of analyzed genome information in the public database allows genome analysis with computational tools. Therefore, this research focuses on identifying novel AMP family molecule, Cathelicidin using bioinformatics analysis on available reptile genome information. As the target organism, Python bivittatus was selected because more detailed genome information was available than other reptiles. Six potential Cathelicidins were discovered from Python bivittatus genome with bioinformatics. Analysis tools such as “AMPA” and “PSIPRED workbench” analyzed the sequence information in silico and determined sequences that are likely to have antimicrobial activity, named GBP01, GBP04, and GBP05. Using APD3 database, these three peptides were verified to have a-helix structure, amphipathicity, and positive charge. On the basis of these results, GBP01, GBP04, and GBP05 were chemically synthesized, and minimal inhibitory concentration (MIC) assay was conducted on Escherichia coli, Staphylococcus aureus and Pseudomonas aeruginosa to verify antimicrobial effects. Interestingly, all three peptides consistently showed strong antimicrobial effect on gram-negative bacteria E. coli and P. aeruginosa but not on gram-positive bacteria S. aureus. The novel peptides found in this study are likely to be either new Cathelicidins or undescribed Cathelicidin family genes of reptiles. These new AMPs may serve as interesting candidates in antimicrobial drug development.

Awards Won: