Bioprospecting of marine biofilms for novel antimicrobial peptides

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Abstract

Antimicrobial peptides (AMPs) have become a viable source of novel antibiotics that are effective against human pathogenic bacteria. In this study, we construct a bank of culturable marine biofilm bacteria constituting 713 strains and their nearly complete genomes and predict AMPs using ribosome profiling and deep learning. Compared with previous approaches, ribosome profiling has improved the identification and validation of small open reading frames (sORFs) for AMP prediction. Among the 80,430 expressed sORFs, 341 are identified as candidate AMPs with high probability. Most potential AMPs have less than 40% similarity in their amino acid sequence compared to those listed in public databases. Furthermore, these AMPs are associated with bacterial groups that are not previously known to produce AMPs. Therefore, our deep learning model has acquired characteristics of unfamiliar AMPs. Chemical synthesis of 60 potential AMP sequences yields 54 compounds with antimicrobial activity, including potent inhibitory effects on various drug-resistant human pathogens. This study extends the range of AMP compounds by investigating marine biofilm microbiomes using a novel approach, accelerating AMP discovery.

Keywords: Marine biofilm, Antimicrobial peptide

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