Development of Antimicrobial Peptide Prediction Tool using Support Vector Machine based Approach

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ABSTRACT

With the advent of machine learning techniques, a large number of biological problems have been given a solution. The interpretation of massive genomic data is a big challenge to the researchers but literature shows many computational approaches to counter such problems. Out of many biological issues, one is regarding the Antimicrobial peptides (AMPs) which are the hosts' defence molecules gaining extensive research attention worldwide. Today, resistance to chemical antibiotics is an unsolved and growing problem. AMPs may be a natural alternative to chemical antibiotics and a potential area of research under applied biotechnology. The present work shows application of machine learning algorithms i.e. Support Vector Machine (SVM) for *in silico* prediction/identification of AMPs of cattle. Total of 99 AMPs related to cattle collected from various databases and published literature were taken into study. N-terminus residues, C-terminus residues and full sequences were used for model development and identification/ prediction. With SVM, the best models identified for C-terminus residues, N-terminus residues and full sequence were with kernels RBF, Sigmoid and RBF with accuracy as 95%, 99% and 97%, respectively. Hence, SVM models were implemented on web server and made available to users at http://cabin.iasri.res.in/amp/. This computational server can accelerate novel AMP discovery from whole genome proteins of a given species for bulk discovery with very high accuracy. This is the first successful report with species specific approach which may be used further as a model in other species as well.

Keywords: Antimicrobial peptides, Cattle, Artificial Neural Network, Support vector machine, accuracy.