ABSTRACT

A large number of diseases became treatable since the discovery and advancement in the field of antibiotics. In the present scenario due to the emergence of drug resistant bacteria, the diseases that were treatable earlier have now become difficult to treat. The advent of these drug resistant bacteria has become a challenge for the medical practitioners and the scientists. The bacteria adapt various mechanisms to become resistant towards the existing conventional antibiotics. Thus a need arises for the development of alternative drugs which could be effective against these drug resistant bacteria. The essential characteristic required for these alternative drugs is that the bacteria should not be able to develop resistance against these easily. The antimicrobial peptides have come in the light as the most potential candidates to be developed as the alternative drug.

Three toxins from *Staphylococcus aureus* Enterotoxin A (ETA), Enterotoxin B and Panton-Valentine leukocidin (PVL) were docked against four antimicrobial peptides JCpep7, Sesquin, Snakin-2 and Ib-AMP1. After analysing the global energies and docking interactions of all the sets of dockings it was predicted that Ib-AMP1 is the potential antimicrobial peptide that showed significant interactions and global energies with the toxins.

The four antimicrobial peptides of length 20 amino acids from *Impatiens balsamina* Ib-AMP1, Ib-AMP2, Ib-AMP3 and Ib-AMP4 were studied for their interactions against the Transcription activator ToxT of *Vibrio cholerae*. The docking and comparative molecular dynamics study predicted Ib-AMP1 as the potential antimicrobial peptide. Further the *In silico* characterization and toxicity prediction of Ib-AMP1 predicted Ib-AMP1 to be toxic. Thus, Ib-AMP1 was discarded from further studies to be developed as an alternate drug compound.

Further five antimicrobial peptides each from plant and microorganism origin of length less than or equal to 10 amino acids was considered for interaction studies against catalytic

domain of diphtheria toxin. Microcin C7 was predicted to be the best among the five microorganism antimicrobial peptides, i.e., Anionic peptide SAAP, Microcin C7, Bacteriocin, Curvalicin 28-c and NRWC. Alliumin was predicted to be the best among the five plant antimicrobial peptides, i.e., JCpep7, Antimicrobial peptide 1, Cr-ACP1, Sesquin and Alliumin. Comparative molecular dynamics studies predicted Alliumin to be potential antimicrobial peptide. It was taken for further studies.

The selected peptide Alliumin was studied for its interaction with the Transcription activator ToxT of *Vibrio cholerae.* The docking and molecular dynamics studies predict that the confirmation of ToxT becomes more stable after binding to the antimicrobial peptide Alliumin. This predicts that Alliumin interacts quite effectively with the transcription activator ToxT to inhibit it.

The selected peptide Alliumin was studied for its interaction with the superbug protein New Delhi Metallo-β-lactamase (NDM-1). The molecular dynamics and docking studies predicted a significant interaction between protein and peptide. Binding with Alliumin provides more stability to the confirmation of NDM-1 and makes it more compact. This predicts that Alliumin interacts quite effectively with NDM-1 to inhibit it.

Alliumin was predicted to be non-toxic and non-hemolytic in *In silico* prediction. The mass of synthesized Alliumin and the *in silico* predicted molecular weight of the sequence of Alliumin were equal. Further, the antibacterial assay carried out against *S. aurues* and *E.coli*, showed Alliumin to be effective against these bacteria. Thus, Alliumin showed antibacterial activity. Therefore, Alliumin was predicted as potential antimicrobial peptide to be developed as alternate drug.