**In Silico Screening for Antimicrobial Peptides Using the Arum Lily (Zantedeschia aethiopica) Transcriptome Data Set**


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**INTRODUCTION.** In silico prediction methods are very useful for antimicrobial peptides (AMP) identification using specific data sets. In this concern, this work reports the AMP screening from *Zantedeschia aethiopica* transcriptome, an African plant with traditional medicine properties, which represents a potential source of antimicrobial molecules. **MATERIAL AND METHODS:** Cysteine-rich AMPs (lipid transfer protein, defensin, hevein, thionin and snakin) patterns were used to search AMPs transcripts into *Z. aethiopica* RNA-Seq data transcriptome, containing 29,506 sequences. Sequences were selected by the maximum 350 residues size, and were further submitted to Phobius for signal peptide prediction. Sequences with signal peptide and without transmembrane domains were selected and then submitted to InterPro Scan for domain identification. Sequences without AMP domain were discarded. Therefore the sequences with tails larger than 30 amino acid residues were removed. Therefore, remaining sequences were submitted to CS-AMPPred for antimicrobial activity prediction. Molecular modeling was performed through Modeller 9.10 using the templates provided by LOMETS server. **RESULTS AND DISCUSSION:** According the established parameters it was possible to recognize 34 sequences through the AMP patterns. From these, 15 show a signal peptide and no transmembrane domains were selected and then submitted to InterPro Scan for domain identification. Sequences without AMP domain were discarded. Therefore the sequences with tails larger than 30 amino acid residues were removed. Therefore, remaining sequences were submitted to CS-AMPPred for antimicrobial activity prediction. Molecular modeling was performed through Modeller 9.10 using the templates provided by LOMETS server. **CONCLUSION:** Through the data mining method here applied, three reliable AMP candidates were found in the *Z. aethiopica* transcriptome. In the next steps, the molecular models will be evaluated by molecular dynamics simulations to validate the structural predictions. In the future, these LTPs could have their activities evaluate in vitro against phytopathogens and further utilized for genetic modified crop plants construction.

Keywords: Antimicrobial peptides, data mining, molecular modeling, Transcriptome
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