INSIGHT INTO SEQUENCE-STRUCTURE-FUNCTION RELATIONSHIP OF CATHARANTHUS ROSEUS RNA BINDING PROTEIN USING INSILICO APPROACH

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Abstract: RNA binding protein regulates numerous aspects of RNA metabolism such as pre-mRNA processing, transport and translation. This study describes sequence-structure-function relationship between the Catharanthus roseus and their homologs plant species through computational approach. After using sequence analysis techniques, it was observed that only 11 plant species showed higher similarity with RNA binding protein of C. roseus. Also, multiple sequence alignment illustrate only two conserve regions between C. roseus and their respective homologs plant species. Hence, the structural molecular model of the RNA binding protein was developed through homology modeling using the software MODELLER (9v5). Using PROCHECK and VERIFY-3D, the energy of constructed models was minimized and qualities of each models were evaluated. The corresponding Ramachandran plot specify 93.70% amino acid residues were in the most favoured regions. Final predicted model structure was submitted to Protein Model Database having deposition number PM0080432.

Keywords: RNA binding protein; Catharanthus roseus, Homology modeling, RNA recognition motif

REFERENCES


