World Academy of Science, Engineering and Technology
International Journal of Biological and Ecological Engineering
Vol:12, No:06, 2018

Cellular RNA-Binding Domains with Distant Homology in Viral Proteomes

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Abstract : Until today, viruses remain controversial and poorly understood; about their origin, this problem represents an enigma and one of the great challenges for the contemporary biology. Three main theories have tried to explain the origin of viruses: regressive evolution, escaped host gene, and pre-cellular origin. Under the perspective of the escaped host gene theory, it can be assumed a cellular origin of viral components, like protein RNA-binding domains. These universal distributed RNA-binding domains are related to the RNA metabolism processes, including transcription, processing, and modification of transcripts, translation, RNA degradation and its regulation. In the case of viruses, these domains are present in important viral proteins like helicases, nucleases, polymerases, capsid proteins or regulation factors. Therefore, they are implicated in the replicative cycle and parasitic processes of viruses. That is why it is possible to think that those domains present low levels of divergence due to selective pressures. For these reasons, the main goal for this project is to create a catalogue of the RNA-binding domains found in all the available viral proteomes, using bioinformatics tools in order to analyze its evolutionary process, and thus shed light on the general virus evolution. ProDom database was used to obtain larger than six thousand RNA-binding domain families that belong to the three cellular domains of life and some viral groups. From the sequences of these families, protein profiles were created using HMMER 3.1 tools in order to find distant homologous within greater than four thousand viral proteomes available in GenBank. Once accomplished the analysis, almost three thousand hits were obtained in the viral proteomes. The homologous sequences were found in proteomes of the principal Baltimore viral groups, showing interesting distribution patterns that can contribute to understand the evolution of viruses and their host-virus interactions. Presence of cellular RNA-binding domains within virus proteomes seem to be explained by closed interactions between viruses and their hosts. Recruitment of these domains is advantageous for the viral fitness, allowing viruses to be adapted to the host cellular environment.

Keywords : bioinformatics tools, distant homology, RNA-binding domains, viral evolution
Conference Title : ICEBEP 2018 : International Conference on Evolutionary Biology and Evolutionary Processes
Conference Location : New York, United States
Conference Dates : June 03-04, 2018