World Academy of Science, Engineering and Technology
International Journal of Medical and Health Sciences
Vol:13, No:01, 2019

Evolutionary Prediction of the Viral RNA-Dependent RNA Polymerase of Chandipura vesiculovirus and Related Viral Species

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Abstract : Chandipura vesiculovirus is an emerging (-) ssRNA viral entity belonging to the genus Vesiculovirus of the family Rhabdoviridae, associated with fatal encephalitis in tropical regions. The multi-functionally active viral RNA-dependent RNA polymerase (vRdRp) that has been incorporated with conserved amino acid residues in the pathogens, assigned to synthesize distinct viral polypeptides. The lack of proofreading ability of the vRdRp produces many mutated variants. Here, we have performed the evolutionary analysis of 20 viral protein sequences of vRdRp of different strains of Chandipura vesiculovirus along with other viral species from genus Vesiculovirus inferred in MEGA6.06, employing the Neighbour-Joining method. The p-distance algorithmic method has been used to calculate the optimum tree which showed the sum of branch length of about 1.436. The percentage of replicate trees in which the associated taxa are clustered together in the bootstrap test (1000 replicates), is shown next to the branches. No mutation was observed in the Indian strains of Chandipura vesiculovirus. In vRdRp, 1230(His) and 1231(Arg) are actively participated in catalysis and, are found conserved in different strains of Chandipura vesiculovirus. Both amino acid residues were also conserved in the other viral species from genus Vesiculovirus. Many isolates exhibited maximum number of mutations in catalytic regions in strains of Chandipura vesiculovirus at position 26(Ser→Ala), 47 (Ser→Ala), 90(Ser→Tyr), 172(Gly→Ile, Val), 172(Ser→Tyr), 387(Asn→Ser), 1301(Thr→Ala), 1330(Ala→Glu), 2015(Phe→Ser) and 2065(Thr→Val) which make them variants under different tropical conditions from where they evolved. The result clarifies the actual concept of RNA evolution using vRdRp to develop as an evolutionary marker. Although, a limited number of vRdRp protein sequence similarities for Chandipura vesiculovirus and other species. This might endow with possibilities to identify the virulence level during viral multiplication in a host.

Keywords : Chandipura, (-) ssRNA, viral RNA-dependent RNA polymerase, neighbour-joining method, p-distance algorithmic, evolutionary marker

Conference Title : ICID 2019 : International Conference on Infectious Diseases
Conference Location : Sydney, Australia
Conference Dates : January 30-31, 2019

Open Science Index, Medical and Health Sciences Vol:13, No:01, 2019 publications.waset.org/abstracts/99638.pdf