World Academy of Science, Engineering and Technology
International Journal of Bioengineering and Life Sciences
Vol:16, No:10, 2022

Genome Characterization and Phylogeny Analysis of Viruses Infected Invertebrates, Parvoviridae Family

Authors : Niloofar Fariborzi, Hamzeh Alipour, Kourosh Azizi, Neda Eskandarzade, Abozar Ghorbani

Abstract : The family Parvoviridae consists of a large diversity of single-stranded DNA viruses, which cause mild to severe diseases in both vertebrates and invertebrates. The Parvoviridae are classified into three subfamilies: Parvovirinae infect vertebrates, Densovirinae infects invertebrates, while Hamaparovirinae infects both vertebrates and invertebrates. Except for the NS1 region, which is the prime criterion for phylogeny analysis, other parts of the parvoviruses genome, such as UTRs, are diverse even among closely related viruses or within the same genus. It is believed that host switching in parvoviruses may be related to genetic changes in regions other than NS1; therefore, whole-genome screening is valuable for studying parvoviruses' host-virus interactions. The aim of this study was to analyze genome organization and phylogeny of the complete genome sequence of the 132 Paroviridae family members, focusing on viruses that infect invertebrates. The maximum and minimum divergence within each subfamily belonged to Densovirinae and Parvovirinae, respectively. The greatest evolutionary divergence was between Hamaparovirinae and Parvovirinae. Unclassified viruses were mostly from Parovirinae and had the highest divergence to densoviruses and the lowest divergence to Parovirinae viruses. In a phylogenetic tree, all hamparoviruses were found in the center of densoviruses, with the exception of Syngnathid Ichthamaparvovirus 1 (NC_055527), which was positioned between two Parvovirinae members (NC _022089 and NC_038544). The proximity of hamparoviruses members to some densoviruses strengthens the possibility that densoviruses may be the ancestors of hamaparoviruses or vice versa. Therefore, examination and phylogeny analysis of the whole genome is necessary to understand Parvoviridae family host selection.

Keywords : densoviruses, parvoviridae, bioinformatics, phylogeny
Conference Title : ICE 2022 : International Conference on Entomology
Conference Location : Paris, France
Conference Dates : October 27-28, 2022