Letter to the editor

Exploring the novel Yaravirus genome can enhance the broad understanding of viruses

Dear Editor,

Yaravirus (*Yaravirus brasiliensis*) was named after a mythological water goddess in Brazilian culture. It is the first virus isolated from Acanthamoeba spp. The virus is neither a part of the complex group of nucleocytoplasmic large DNA viruses (NCLDV) nor the representative of a novel evolutionary branch of viruses. At 80 nm, Yaravirus is smaller than other amoebal viruses and does not have a complex genome.

Until the discovery of Yaravirus, 90% of its genes have not been described previously, characterizing ORFans are defined as ORFs (Open Reading Frames). In fact, genetic analysis has not revealed any identifiable sequences for the capsid gene or other viral genes (1). Thus, according to the current metagenomic protocols for viral detection, Yaravirus is not considered a viral agent (2). This new type of virus was extracted from *Acanthamoeba castellanii* cells. Previously described amoebal viruses, such as giant virions, have approximately 20 vertically inherited genes, indicating a monophyletic origin (3) whereas, Yaravirus genome comprises six types of transfer RNAs that do not resemble any of the previously described codons. Only three of its genes show homology with known sequences such as a packaging-ATPase gene, a bifunctional DNA polymerase gene, and a recombinase gene. Thus, Yaravirus may be the first example of a novel bona fide group of amoebal viruses. However, we cannot ignore the possibility that the Yaravirus might constitute a small NCLDV that lacks the hallmark proteins of NCLDVs.

If Yaravirus is considered to be an NCLDV, then it would thus far be the smallest of the NCLDVs, in the context of both particle as well as genome size. It has a punctilious infectious cycle in Acanthamoeba and there is a possibility that other organisms in the environment can act as its hosts. All the known amoebal giant viruses have a capsid composed of a major capsid protein (MCP) associated to the D13L protein of the vaccinia virus (4). The amoeba species that are hosts to these viruses carry copies of the MCP genes, indicating the horizontal transfer of genes from the virus to the protist host (5). Yaravirus capsid genes are not homologous to NCLDV MCP genes, but gene 41 had structural convergence with double-jelly roll domain of MCP of the Paramecium bursaria Chlorella virus type 1 (1).

As Yaravirus cannot infect humans, it is not a potential threat to human health (1). However, there is a strong possibility that the insights gained from studying this virus will be useful to understand other viruses, including those affecting humans. Because the Yaravirus genome does not resemble to other viruses, it could be used to help identify novel viral genomes. Indeed, the evolutionary distance between Yaravirus and other viruses indicates that we are still at the initial stages of understanding viral genomic diversity. The number of unknown proteins that have been identified in the Yaravirus genome demonstrates the incredible variability among viruses and suggests that we might see a dramatic increase in the new viral genomes described in the future.

CONFLICT OF INTEREST

The authors declare that there is no conflict of interest regarding the publication of this paper.

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