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2024 SEA Faculty Meeting Abstract

Maryville University of Saint Louis

St. Louis MO

Corresponding Faculty Member: Olga Lubman (olubman@maryville.edu)



Olga Lubman

Bioinformatic Analysis of Pandoravirus dulcis Secreted Proteome​

Kavali Tanuvasa-Lole, Rosa Barakat, Brittany Rogers, Olga Lubman

Herein, we analyzed protein-encoding sequences of Pandoravirus dulcis, a virus belonging to the newly discovered family of Pandoraviridae, known to have double-stranded DNA genomes reaching up to 2.5 million bases and a viral particle  of  one micrometer in length.  What makes Pandoravirus truly mind-boggling is that a mere 7% of its 2,556 encoded genes match any known genes (6). In essence, 93% of its genome remains an enigmatic frontier, a treasure trove of genetic secrets yet to be unveiled. The host of Pandoravirus dulcis is a  free-living amoeba, Acanthamoeba castellanii, known to harbor endosymbionts such as obligate intracellular bacteria that use amoeba as “training grounds” to facilitate bacterial pathogenesis in eukaryotic cells.  The origins of  Pandoraviruses are a subject of intense scientific inquiry. Based on genomic analyses, some researchers propose that Pandoraviruses  may have evolved from a cellular ancestor, such as bacteria. This hypothesis suggests that viruses might have undergone significant genome reduction and adaptation to a parasitic lifestyle over time. The acquisition of cellular-like genes could have facilitated their survival and replication within host organisms. However, the exact nature of symbiosis and the benefit it represents for the amoeba host are unknown. Using various bioinformatics tools, we selected 28 putative secreted proteins and 66 putative membrane-bound proteins encoded by the Pandoravirus dulcis strain of the virus. Through an extensive literature search, sequence alignments, and fold prediction algorithms, we identified open reading frames (ORFs) with structural homology to bacterial and host  Acanthamoeba proteins that play important roles in metabolism, DNA replication, cell signaling, and cytoskeletal motility. Specifically,  P. Duclis encodes a putative chorismate synthase, polyketide synthase, mitochondrial translocase, DNA clamp loader, structural components of extracellular matrix, carbohydrate, and actin-binding proteins, and several serine/ threonine kinases. Our computational analysis favors the defensive symbiosis hypothesis, where competition with intracellular bacteria inside the host itself creates the need for the Pandoravirus  to adapt to interact not only with amoeba but also with bacteria present in the same intracellular niche