**[Horizontal Gene Transfer Between Eukaryotes and Viruses]**

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**Abstract**

Gene exchange that occurs between hosts and viral cells function as a key factor for horizontal gene transfer. Before this point in time, most of our understanding of the process came from bacterial and viral organisms and their co-evolution. However, the importance of this interaction remains merely up to theory and anecdote at this current date and time. In this study, the focus was on systematically characterized viral–eukaryotic gene exchange across eukaryotic and viral diversity through the thorough study of thousands of transfers and taking further note on their frequency and predicted/intended function in Nucleocytoviricota. In the case of viral-derived eukaryotic genes, similar interaction was studied and recorded.

**Introduction**

Horizontal gene transfer has been happening since the dawn of time, though it usually occurs between organisms and cells of the same genera, it has recently been studied to occur between eukaryotic cells and Viruses, having previously only been observed between RNA-Viruses and eukaryotic cells. This exchange becomes the basis of many evolutionary properties that are acquired by the virus or cell over time. Even in the case of humans, since 8% of our DNA is derived from ancient viruses. (The Non-Human Living Inside You). A study like such, has been important to understand the possible evolutionary factors, which have led many eukaryotic cells to their current stage, and will possibly give us insight into where they may go next.

**Recent Progress**

Recent progress on this endeavor has led to the discovery of the importance of the genetic transfer between eukaryotes and viral organisms, and how they have influenced each other's evolution. Emerging new viruses may also be influenced by horizontal gene transfer. In the case of gene transfers from viral to eukaryotic we are beginning to see results which suggest the of viral manipulation of certain cellar pathways to obtain more genetic material. “, horizontally acquired glycosyltransferases have recurrently impacted transitions as fundamental as the evolution of tissues and divergence of mitochondria, reminiscent of how retroviral genes, such as fusogens, have repeatedly driven placental evolution in animals” (Irwin)

**Discussion**

“The exchange of genes between viruses and eukaryotes through horizontal gene transfer (HGT) is a key evolutionary driver capable of facilitating host manipulation and viral resistance host-derived genes are known to be employed by viruses for replication and cellular control.” (Irwin). The results beckon some form of attention regarding their importance while the main idea of the study was of how it became intertwined with general taxonomy and other concepts.

In other investigations of the eukaryotic-derived viral genes, through the use of the heterologous expression, we may also come to find insights on how viruses actually manipulate the cellular pathway, and even bypass the need for a tractable host-viral model system. From a eukaryotic focus, the analysis works to provide further evidence, that in some cases viruses take part in eukaryotic transduction, or viral- eukaryotic gene exchange, in karyokinesis and evolution of eukaryotic morphology. In this case it is important to note that particular horizontally acquired glycosyltransferases often impact the transitions which as extremely fundamental and important to eukaryotic evolution, such as the “evolution of tissues and divergence of mitochondria, reminiscent of how retroviral genes, such as fusogens, have repeatedly driven placental evolution in animals” (Irwin) Overall the general importance of issues such as these could easily have a great impact in the medical and microbiological worlds as they help us to further understand what has and possibly will happen with infectious and living factors.

“Results found in the study also “highlight the key cellular systems associated with eukaryote-derived viral genes which, given their known roles in host manipulation, may provide insights into common viral infection strategies.” (Irwin). Better understanding of the processes used by viral infectious agents could easily be used in the medical field, especially if you take into consideration the occurrence of horizontal gene transfer. As mentioned before it could help us to predict what is coming and what is yet to come.

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         Another thing that begs to be discussed is the uncertainty that has been unearthed by this research project. As stated in the report itself, “Along with these transfers to eukaryotes, we identified a number of genes seemingly exchanged before the eukaryotic radiation. These transfers are inherently challenging to interpret given their antiquity, potential rooting uncertainty and ambiguity resulting from intra-eukaryotic HGT” (Irwin). It begs to question whether there are ways to track down common eukaryotic ancestors through the discovery and understanding of the genes that have been involved in horizontal gene transfer.

         The exchanged genetic material also follows the typical rules it would in the original chain often producing the same responses and reactions, as said within the report, “This indicates that eukaryote-derived gene products tend to function in the same subcellular context as the original host-encoded proteins.” (Irwin). The indication that they perform in a similar manner suggests the fact that there may be some form of a common ancestor, or the usability of the universal code that is genetics.

         We are also far away from fully being able to understand the data in front of us, “Accordingly, these transfers have important evolutionary, ecological and health implications; nonetheless, we lack a general understanding of the mode, tempo and functional importance of viral–eukaryotic gene exchange, largely due to the absence of standardized analyses across diverse taxa.” (Irwin). Due to a lack of knowledge in the general function of multiple genes across several taxa, we are unable to truly begin to understand the potential importance of a study like this. While some genetic material may be shared in a lot of cases, we do not know with what else it is shared with, learning something like this could help us better understand the general taxonomy and the function of certain sections of the genome.

**References**

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