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Impact of Totiviridae L-A dsRNA Virus on Saccharomyces Cerevisiae Host: Transcriptomic and Proteomic Approach

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Abstract : Totiviridae L-A virus is a persistent Saccharomyces cerevisiae dsRNA virus. It encodes the major structural capsid protein Gag and Gag-Pol fusion protein, responsible for virus replication and encapsulation. These features also enable the copying of satellite dsRNAs (called M dsRNAs) encoding a secreted toxin and immunity to it (known as killer toxin). Viral capsid pore presumably functions in nucleotide uptake and viral mRNA release. During cell division, sporogenesis, and cell fusion, the virions remain intracellular and are transferred to daughter cells. By employing high throughput RNA sequencing data analysis, we describe the influence of solely L-A virus on the expression of genes in three different S. cerevisiae hosts. We provide a new perception into Totiviridae L-A virus-related transcriptional regulation, encompassing multiple bioinformatics analyses. Transcriptional responses to L-A infection were similar to those induced upon stress or availability of nutrients. It also delves into the connection between the cell metabolism and L-A virus-conferred demands to the host transcriptome by uncovering host proteins that may be associated with intact virions. To better understand the virus-host interaction, we applied differential proteomic analysis of virus particle-enriched fractions of yeast strains that harboreither complete killer system (L-A-lus and M-2 virus), M-2 depleted orvirus-free. Our analysis resulted in the identification of host proteins, associated with structural proteins of the virus (Gag and Gag-Pol). This research was funded by the European Social Fund under the No.09.3.3-LMT-K-712-19-0157“Development of Competences of Scientists, other Researchers, and Students through Practical Research Activities” measure.

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