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Re-analysis of RNA-Sequencing Data on Apple Stem Grooving Virus infected Apple reveals more significant differentially expressed genes

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Abstract

RNA sequencing (RNA-Seq) technology has enabled the researchers to investigate the host global gene expression changes in plant-virus interactions which helped to understand the molecular basis of virus diseases. The re-analysis of RNA-Seq studies using most updated genome version and the available best analysis pipeline will produce most accurate results. In this study, we re-analysed the Apple stem grooving virus (ASGV) infected apple shoots in comparison with that of virus-free in vitro shoots [1] using the most updated Malus x domestica genome downloaded from Phytozome database. The re-analysis was done by using HISAT2 software and Cufflinks program was used to mine the differentially expressed genes. We found that ~20\% more reads was mapped to the latest genome using the updated pipeline, which proved the significance of such re-analysis. The comparison of the updated results with that of previous was done. In addition, we performed protein-protein interaction (PPI) to investigate the proteins affected by ASGV infection.

References

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