



Category: Plant Genomics

# 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

[1] Chen, S., Ye, T., Hao, L., Chen, H., Wang, S., Fan, Z., et al. (2014) Infection of apple by *apple stem grooving virus* leads to extensive alterations in gene expression patterns but no disease symptoms. *PLoS ONE* 9: e95239-e95239. <https://doi.org/10.1371/journal.pone.0095239>

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