# Article information:

Sweet potato viromes in eight different geographical regions in Korea and two different cultivars | Scientific Reports  
<https://www.nature.com/articles/s41598-020-59518-x>

# Article summary:

1. Sweet potato viromes were studied in eight different regions in Korea and two cultivars using RNA-Seq technology.

2. The most frequently identified viruses infecting sweet potato in Korea were SPFMV and SPVC, but two novel viruses, SPVE and SPVF, were also identified.

3. Phylogenetic analyses showed that SPVE is a newly discovered species in the genus Potyvirus, while SPVF is a newly discovered species in the genus Carlavirus.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article "Sweet potato viromes in eight different geographical regions in Korea and two different cultivars" provides a comprehensive study of sweet potato viromes using RNA-Seq technology. The study identified 10 different viruses infecting sweet potato, with SPFMV being the most frequently identified virus. The article also reports the identification of two novel viruses, SPVE and SPVF, which were tentatively named based on their genome sequences.

Overall, the article provides valuable insights into the diversity of sweet potato viruses in Korea. However, there are some potential biases and limitations to consider. Firstly, the study only focused on sweet potato samples collected from Korea, which may not be representative of sweet potato viromes in other regions or countries. Therefore, caution should be exercised when generalizing the findings to other regions.

Secondly, the article does not provide information on how the samples were selected for analysis. It is unclear whether all samples showing disease symptoms were included or if a random sampling approach was used. This lack of information could potentially bias the results if certain samples were overrepresented or underrepresented in the analysis.

Thirdly, while the identification of two novel viruses is an important finding, more information is needed to confirm their classification as new species within their respective genera. The article only provides limited evidence for this claim based on sequence identity thresholds for species demarcation criteria.

Finally, while the article notes that multiple viruses can coinfect sweet potato plants and reduce yield, it does not explore potential strategies for managing these infections or mitigating their impact on crop production. This missing point of consideration could limit the practical applications of this research for farmers and agricultural policymakers.

In conclusion, while this study provides valuable insights into sweet potato viromes in Korea using RNA-Seq technology, there are some potential biases and limitations to consider. Further research is needed to confirm the classification of novel viruses and explore strategies for managing multiple viral infections in sweet potato crops.

# Topics for further research:

* Strategies for managing viral infections in sweet potato crops
* Sweet potato viromes in other regions or countries
* Sampling methods for sweet potato virome analysis
* Confirmation of novel virus classification
* Impact of viral infections on sweet potato crop yield
* RNA-Seq technology for virome analysis in other crops

# Report location:

<https://www.fullpicture.app/item/07cf5d7786710c4e34ec5862af3e48ba>