Deep Sequencing Reveals the Complete Genome Sequence of *Sweet potato virus G* from East Timor

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We present the first complete *Sweet potato virus G* (SPVG) genome from sweet potato in East Timor and compare it with seven complete SPVG genomes from South Korea (three), Taiwan (two), Argentina (one), and the United States (one). It most resembles the genomes from the United States and South Korea.

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**REFERENCES**

1. Clark CA, Davis JA, Abad JA, Cuellar WJ, Fuentes S, Kreuze JF, Gibson RW, Mukasa SB, Tugume AK, Tairo FD, Valkonen JPT. 2012. *Sweet potato viruses*: 15 years of progress on understanding and managing complex diseases. Plant Dis 96:168–185. http://dx.doi.org/10.1094/PDIS-07-11-0550.

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2. Kwak HR, Kim J, Kim MK, Seo JK, Jung MN, Kim JS, Lee S, Choi HS. 2015. Molecular characterization of five potyviruses infecting Korean sweet potatoes based on analyses of complete genome sequences. Plant Pathol J 31:388–401. http://dx.doi.org/10.5423/PPJ.OA.04.2015.0072.

3. Li F, Xu D, Abad J, Li R. 2012. Phylogenetic relationships of closely related potyviruses infecting sweet potato determined by genomic characterization of Sweet potato virus G and Sweet potato virus 2. Virus Genes 45:118–125. http://dx.doi.org/10.1007/s11262-012-0749-2.

4. Ndunguru J, Taylor NJ, Yadav J, Aly H, Legg JP, Aveling T, Thompson G, Fauquet CM. 2005. Application of FTA technology for sampling, recovery and molecular characterization of viral pathogens and virus-derived transgenes from plant tissues. Virol J 2:45. http://dx.doi.org/10.1186/1743-422X-2-45.

5. Kehoe MA, Coutts BA, Buirchell BJ, Jones RAC. 2014. Plant virology and next generation sequencing: experiences with a Potyvirus. PloS One 9:e104580. http://dx.doi.org/10.1371/journal.pone.0104580.

6. Katoh K, Misawa K, Kuma K, Miyata T. 2002. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res 30:3059–3066. http://dx.doi.org/10.1093/nar/gkf436.

7. Revers F, Garcia JA, Karl M, Thomas CM. 2015. Molecular biology of potyviruses. Adv Virus Res 92:101–199. http://dx.doi.org/10.1016/bs.aivir.2014.11.006.

8. Bao Y, Chetvernin V, Tatusova T. 2014. Improvements to pairwise sequence comparison (PASC): a genome-based web tool for virus classification. Arch Virol 159:3293–3304. http://dx.doi.org/10.1007/s00705-014-2197-x.

9. Adams MJ, Antoniw JF, Fauquet CM. 2005. Molecular criteria for genus and species discrimination within the family Potyviridae. Arch Virol 150:459–479. http://dx.doi.org/10.1007/s00705-004-0440-6.

10. King AMQ, Adams MJ, Lefkowitz EJ. 2011. Virus taxonomy: classification and nomenclature of viruses: ninth report of the International Committee on Taxonomy of Viruses, vol 9. Elsevier Academic, San Diego, CA.