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Identification of Viruses Infecting Sweet Potato in Yeosu, Korea by Next-generation Sequencing

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[Introduction]

Sweet potato [*Ipomoea batatas* (L.) Lam] is a dicotyledonous perennial plant belonging to the family Convolvulaceae. Sweet potato is one of important crops in tropical and temperate regions. Sweet potato contains a high amount of nutrients including carbohydrates, dietary fiber, beta carotene. In Korea, sweet potato is the third important crops and is consumed as diverse food materials. Due to clonal propagation, most sweet potato plants are infected by different viruses. In order to identify viruses infecting sweet potato, we conducted next-generation sequencing.

[Materials and methods]

Leaf samples were collected from sweet potato showing viral disease symptoms including leaf curling and yellowing in Yeosu, Korea. In addition, we collected leaf samples from two different sweet potato cultivars “Beni Haruka” and “Hogammi”. We prepared three different libraries for RNA-Sequencing which were further paired-end sequenced using HiSeq2000 system. Raw sequences from each library were *de novo* assembled using Trinity program. Assembled contigs were subjected to BLAST search against the plant viral database.

[Results and discussion]

From three different libraries, we identified a total of 319 virus-associated contigs assigned to seven viruses infecting sweet potato. They are five RNA viruses including Sweet potato feathery mottle virus (SPFMV), Sweet potato latent virus (SPLV), Sweet potato virus 2 (SPV2), Sweet potato virus C (SPVC), and Sweet potato virus G (SPVG) as well as two DNA viruses including Sweet potato leaf curl virus (SPLCV) and Sweet potato symptomless mastrevirus 1 (SPSMV). Based on viral reads, SPFMV was the dominant virus followed by SPVC, SPLCV, and SPVG. The proportion of virus-associated reads in each library ranged from 0.13% to 0.29%. We also confirmed the identified viruses infecting sweet potato by RT-PCR with newly designed primers. Taken together, the next-generation sequencing based approach revealed comprehensive overview of viruses infecting sweet potato in Yeosu, in which is one of major sweet potato producing region in Korea.

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