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Soybean Viromes in Four Single Soybean Plants Revealed by RNA-sequencing

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[Introduction]

Soybean (*Glycine max* (L.) Merrill) belonging to the subfamily Fabaceae is one of important crops in Korea. In Korea, soybean is widely consumed as a plant oil and food materials. Soybean is known to be susceptible to various viruses. Several viruses infecting soybean in Korea have been reported. Of them, soybean mosaic virus (SMV), soybean yellow mottle mosaic virus (SYMMV), and soybean yellow common mosaic virus (SYCMV) are the most common viruses infecting soybean in Korea. Although soybean is frequently co-infected by different viruses, virome in a single soybean plant has not been reported.

[Materials and methods]

In this study, we carried out RNA sequencing (RNA-seq) to reveal virome in a single soybean plant. For that, we collected four different leaf samples from soybean plants displaying viral disease symptoms. Four soybean samples were grown in different regions. Collected leaf samples were used for total RNA extraction followed by library preparation for RNA-seq. The four different libraries were paired-end sequenced using HiSeq2000 system. We *de novo* assembled raw sequences from individual library using Trinity program. Several bioinformatics analyses revealed four different viromes in four single soybean plants.

[Results and discussion]

We identified five viruses including Peanut mottle virus (PeMoV), Peanut stunt virus (PSV), Soybean mosaic virus (SMV), Soybean yellow common mosaic virus (SYCMV), and Soybean yellow mottle mosaic virus (SYMMV) from 109 virus-associated contigs. Except GAWO-62 infected by four viruses, other three samples were infected by five viruses. Although several viruses were co-infected viruses, there was a dominant virus in each sample. For example, GYGI-106 was dominantly infected by SYMMV while GAWO-62 was dominantly infected by SMV. Similarly, PSV was the dominant virus in CHBU-139 while PeMoV was the dominant virus in GYBU-92. The proportion of virus-associated reads in each library ranged from 0.88% (GYGI-106) to 31.66% (GAWO-62). In summary, this is the first study showing virome in a single soybean plant by RNA-seq.

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