



First report of brassica yellows virus infecting cowpea in China

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In 2017 and 2018, we found that about 21% to 35% of cowpea (*Vigna unguiculata* (L.) Walp.; family Leguminosae) samples from the surveyed field in Chongqing showed symptoms of viral diseases, including mottle chlorosis, wrinkle, and leaves with down-curling. Total RNA was extracted from 35 cowpea leaves to construct the small RNA libraries following the instruction of TruSeq@Small RNA Library Prep Kit. After high throughput Illumina sequencing, a total of 1.2810⁷ clean reads had been collected and 1104 contigs were yielded after *de novo* assembly. Contigs blast results revealed four known viruses in these samples: cucumber mosaic virus (CMV; Query Cover: 100%; Per. Ident: 97.6%); bean common mosaic virus (BCMV; Query Cover: 94.0%; Per. Ident: 83.7%); grapevine rootstock stem lesion-associated virus (GLRaV-2-PN; Query Cover: 100%; Per. Ident: 74.4%) and brassica yellows virus (BrYV; Query Cover: 97.0%; Per. Ident: 93.4%). Also, The RT-PCR results suggested that a total of 6 species of

plant virus were detected in all the cowpea samples, including CMV, potato virus X (PVX), potato virus Y (PVY), BCMV, turnip mosaic virus (TuMV), and BrYV. Only 3 of 35 cowpea samples were mixed infected with BrYV, and BCMV, PVX, and CMV were also detected in these samples. Then the CP sequence of BrYV Chongqing isolates (BrYV-JD) was submitted to the GenBank database (Accession No. MN164463). BLAST analysis showed that BrYV-JD had the highest nucleotide sequence identity (99.2%) to the BrYV Beijing leaf mustard isolate pXHY1031-9 (EF126150). As we know, Solanaceae and Cruciferae are common hosts of BrYV (Lim et al. 2015; Wang et al. 2015), and there is no previous report showing that BrYV can infect leguminous plants. Therefore, this is the first report of cowpea as the natural host of BrYV in China, which has important implications for the production of Leguminosae sp.

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