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Next generation sequence data of partial *NIa-VPg* protein in Kenyan BCMV isolate reveal close resemblance to BCMV-NKY022 strain from China

Bonphace Collins Mangeni[1], **Sue Jones**[2], **Lesley Torrance**[2], **Benard Mukoye**[1] and **Hassan K Were**[1]
[1]Masinde Muliro University of Science and Technology, Kenya
[2]The James Hutton Institute, UK

Bean common mosaic virus (BCMV) is a highly variable and severe pathogen infecting beans in Kenya. To determine the variations within BCMV strains in Kenya, 45 bean leaf samples showing mosaics under field conditions were collected in western Kenya. Total RNA was extracted from samples positive for BCMV by ELISA using All Prep RNA Mini Kit (Qiagen RNeasy) according to the manufacturers' instructions. 11 mRNA-seq libraries were constructed using the Illumina TruSeq stranded mRNA library prep Kit following the manufacturer's instructions. Libraries were pooled for multiplexed sequencing using an illumina HiSeq 2500 to generate single end reads of 50 nt. Reads were analyzed using the Galaxy project platform. Read quality was assessed using Fast QC. Trimming was done and only reads greater than 30 nt with 4 bases to average across average quality of 20 were retained. Reads were mapped onto RefSeq plant genome and then to P. vulgaris v1.0 reference genome using Bowtie2 version 2.2.3. The unmapped reads were then aligned to BCMV RefSeq complete genome (NC_003397.1) maintaining the Bowtie2 parameters. From the extracted SAM file, reads were viewed using Tablet version1.0 referenced against BCMV genome (NC_003397.1). The contig was later probed in Blast (blastx) to identify the specific sections of BCMV genome and proteins coded for by the sections. The contig aligned at between 6092-6158 bp, a section that partially codes for *NIa-VPg* protein in BCMV with close resemblance (100%) to NKY 022 strain from China. Further analysis revealed limited nucleotide variation within *NIa-VPg* genes with 0% of reads mapped at the region being different. The sequences obtained show limited variation frequencies indicating limited evolution within the region. This multifunctional region of BCMV genome can be explored taking advantage of the limited evolution to provide useful evolutionary history in addition to the conventional coat protein region.

mangeniboniface@gmail.com