

First Full Length Genome Sequence of Bean Common Mosaic Necrosis Virus (BCMNV) Isolated from Common Bean in Western Kenya

Abstract

Bean common mosaic necrosis virus (BCMNV) is one of the most common and most destructive viruses of common bean and can cause a yield loss as high as 100%. The common bean (*Phaseolus vulgaris* L) is an important legume crop for food and cash in Kenya. In Kenya, there is inadequate documentation on the strains of the virus infecting common bean. This information is crucial in devising control measures. This study therefore, sought to characterize BCMNV isolates from western Kenya. Leafy samples showing virus-like symptoms were collected and analysed by Enzyme linked immunosorbent Assay (ELISA) and or next generation sequencing (NGS). Extraction of total RNA from ELISA positive samples was done using RNeasy Plant Mini Kit and NGS carried out following Illumina protocol to determine diversity of the virus. NGS data was trimmed and the sequence reads assembled into contigs, which were analyzed against virus sequence database. Phylogenetic analyses and comparisons were performed using MEGA7 program. The first complete genome sequence of Bean common mosaic virus (BCMNV) is reported from a Kenyan isolate. NGS technology revealed full-length sequence of BCMNV from an isolate BG 12 from Bungoma County with a genome of 9584 nt in length. Phylogenetic analysis of full-length sequences available through the Genbank clustered the isolate with the Tanzanian isolate strain TN-1 and two USA isolates, TN1a and NL-3K.

Authors.

[Mangeni Bonphace Collins](#), [Were Hassan Karakacha](#), [Mukoye Benard](#), [Ndong'a Milicent](#),