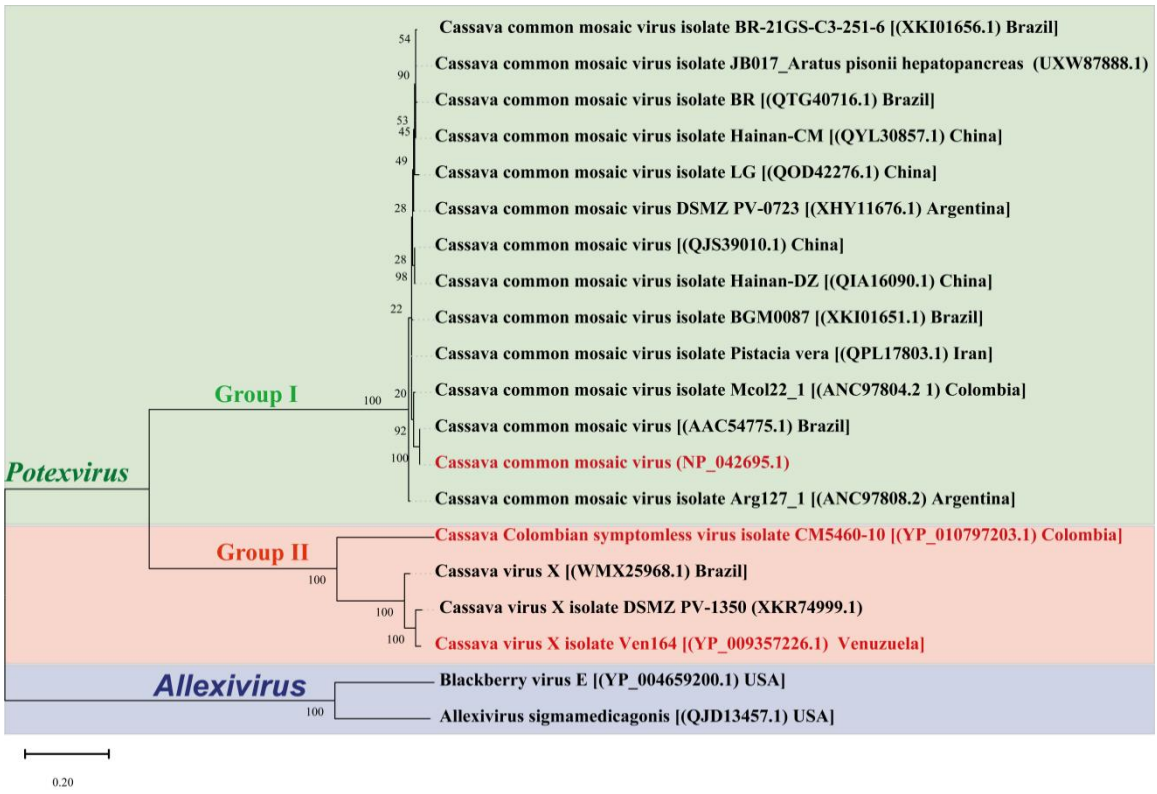

Supplementary Figure 1: Phylogenetic analysis of Cassava Common Mosaic Virus (CsCMV) RNA-dependent RNA polymerase (RdRp). MEGA12 was utilized to infer the phylogenetic tree by constructing maximum likelihood phylogenetic trees, using best-fit substitution models LG + G + I, with 1,000 bootstrap replicates. Virus sequences were downloaded from the National Center for Biotechnology Information (NCBI) database. Allexiviruses were used as an outgroup. Viruses names highlighted in red are officially recognized by International Committee on Taxonomy of Viruses (ICTV, 2023).