First Report of the Occurrence of African cassava mosaic virus in a Mosaic Disease of Soybean in Nigeria

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First Report of the Occurrence of African cassava mosaic virus in a Mosaic Disease of Soybean in Nigeria

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African cassava mosaic virus (ACMV; genus Begomovirus, family Geminiviridae) is one of six viruses documented in cassava (Manihot esculenta Crantz.) plants showing cassava mosaic disease in sub-Saharan Africa (SSA). In addition to cassava, the natural host range of ACMV includes a few wild Manihot species, Jatropha multifida, and Ricinus communis L. in Euphorbiaceae, and Hewittia sublobata in Convolvulaceae. The experimental host range of ACMV includes Nicotiana sp. and Datura sp. in the Solanaceae (2). Recently, natural occurrence of ACMV was reported in Combretum confertum (Benth.), Leucana leucocephala (Lam.) De Witt, and Senna occidentalis (L.) Link belonging to Leguminasae from Nigeria (1,3). During reconnaissance studies conducted on soybean (Glycine max L. Merr.) in September and October of 2007 in the Ibadan (N = 19) and Benue (N = 23) regions and in February of 2008 in Ibadan (N = 16), we observed soybean showing yellow mosaic and mottling symptoms. Samples from these plants (N = 58) were tested by indirect ELISA and symptomatic leaves tested negative to Cucumber mosaic virus, Cowpea mottle virus, Southern bean mosaic virus, Tobacco ringspot virus, Soybean dwarf virus, Cowpea aphid-borne mosaic virus, Blackeye cowpea mosaic virus, Peanut mottle virus, and Broad bean mosaic virus, which have been documented in soybean in SSA. However, 8.6% of these samples (5 of 58) (one each from Ibadan and Benue in the 2007 survey and three from Ibadan in the 2008 survey) tested positive in triple-antibody sandwich-ELISA with a monoclonal antibody (SCR33) to ACMV. ELISA results were further confirmed by PCR with ACMV specific primers AL1/F and AR0/R that amplified a 987-bp DNA fragment corresponding to the intergenic region, AC-4 and AC-1 genes of DNA-A segment (4). The PCR product was cloned into pCR2.1 (Invitrogen, Carlsbad, CA) and three independent clones were sequenced in both orientations. Pairwise comparison of the derived consensus sequence (GenBank Accession No. EU367500) with corresponding ACMV sequence of ACMV isolate from Nigeria (GenBank Accession No. X17095) showed 98% identity at the nucleotide level. To further confirm the virus identity, complete nucleotide sequence of the DNA-A segment was determined by PCR amplification of viral DNA with four primers, cloning of overlapping products into pCR2.1 vector and sequencing. The derived sequence (2,781 nucleotides; GenBank Accession No. EU685385) was compared with the DNA sequences available at NCBI database using BLAST. This revealed 97% nucleotide sequence identity with ACMV-[NG:Ogo:90] (Accession No. AJ427910) and ACMV-[NG] (Accession No. X17095) from Nigeria. These results confirm the presence of ACMV in symptomatic soybean leaves. To our knowledge, this is the first report of soybean as a natural host of ACMV in SSA. On the basis of previous reports (1) and the results currently presented it seems that ACMV has a wide host range.


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