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# plant disease

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## DISEASE NOTES

# First Report of *Maize chlorotic mottle virus* and Maize Lethal Necrosis on Maize in Ethiopia

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Maize lethal necrosis is a disease of maize caused by the combination of *Maize chlorotic mottle virus* (MCMV) and any of the viruses belonging to the *Potyviridae* family. Maize lethal necrosis was first identified on the African continent in Kenya in 2012 ([Wangai et al. 2012](#)), and subsequently in Rwanda ([Adams et al. 2014](#)), and the Democratic Republic of Congo ([Lukanda et al. 2014](#)). In Africa, maize lethal necrosis symptoms have been associated with MCMV and *Sugarcane mosaic virus* (SCMV). In July 2014, maize plants exhibiting severe yellowing and chlorotic mottle symptoms were observed in the Upper Awash Valley of Ethiopia. From a survey of 12 farms in the Central Rift Valley, 126 samples were collected from maize (100 samples) and other grass species (26 samples, including Johnsongrass, couch grass, unidentified grass sp., *Digitaria* sp., sedge, sorghum,

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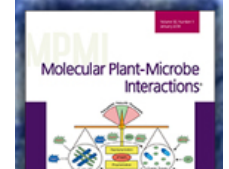
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Activation,  
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*Setaria* spp., and sugarcane), and either with symptoms or without virus symptoms. Samples were analyzed for the presence of SCMV and MCMV using enzyme-linked immunosorbent assay (ELISA) with polyclonal antibodies produced against the East African strains of MCMV and SCMV. Of the nonmaize samples, MCMV was detected in Johnsongrass, *Digitaria* sp., sedge, *Setaria* sp., sugarcane, and an unidentified grass species, whereas SCMV was detected only in *Setaria* sp. To confirm ELISA results, greenhouse-grown maize plants were mechanically inoculated with sap extracted from eight MCMV-positive maize samples. Chlorotic mottle symptoms were observed, and the presence of MCMV confirmed by ELISA. Maize plants inoculated with sap extracted from MCMV-positive *Digitaria* sp. developed typical MCMV symptoms, and the presence of MCMV confirmed by ELISA. Plants inoculated with sap extracted from SCMV-positive samples developed mild to severe mosaic symptoms and tested positive for SCMV. None of the plants inoculated with sap extracted from Johnsongrass, sedge, or sugarcane samples tested positive for MCMV. To establish the genetic affinity of the Ethiopian strains to those previously described in Kenya and Rwanda, whole virus genomes were sequenced from six samples using IlluminaMiSeq (2 samples) and IlluminaHiSeq (4 samples) as described by Adams et al. (2014). All the six samples contained MCMV and three samples had SCMV. Phylogenetic tree constructed based on the complete genomes of MCMV showed that the isolates found in Ethiopia were highly similar (>99% identity) to those found previously in East Africa (Adams et al. 2013, 2014). In contrast, phylogenetic tree constructed using coat proteins of the sequenced SCMV isolates from Ethiopia were found to be similar to each other and to those found in Rwanda (Adams et al. 2014) with 96% identity, but relatively distant from those originally found in Kenya (Adams et al. 2013). To our knowledge, this is the first report of MCMV and maize lethal necrosis on maize in Ethiopia, as well as MCMV in some alternate Poaceae family hosts. The results illustrate the need for further studies to identify alternate hosts for maize lethal necrosis-causing viruses, investigate the role of seed transmission of SCMV and MCMV, create awareness among the stakeholders about maize lethal necrosis, and strengthen diagnostic and surveillance capacity in sub-Saharan Africa to minimize further spread of the disease.

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