New Disease Reports

First report of *Papaya ringspot virus* in pumpkin in Sudan

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Papaya ringspot virus (PRSV) has great economic importance for papaya (*Carica papaya*) cultivation worldwide, and for cucurbits depending on the region. PRSV is divided into two biotypes: PRSV-P that infects papaya and cucurbits and PRSV-W that infects only cucurbits. In Africa, the virus has been reported on papaya in Nigeria and later in Kenya, Sierra Leone, South Africa, Tanzania, Togo, Uganda and Zambia (CABI/EPPO, 2003; Taylor, 2001); and on cucurbits in Tunisia (Cherif & Ezzaier, 1987) and more recently in Egypt (Omar *et al*., 2011).

In February 2012, a field survey of viral diseases of pumpkin (*Cucurbita maxima*) was done in three locations in Sudan (Shambat and Wad-Ramly in Khartoum State, and Elnuba in Gezira State). Symptoms of leaf mosaic, malformation and blistering were observed on young plants (Fig. 1). In total, 20 plant samples with symptoms (nine from Shambat, eight from Wad-Ramly and three from Elnuba) were analysed by molecular assays for potyviruses commonly infecting cucurbits: *Moroccan watermelon mosaic virus*, PRSV, *Watermelon mosaic virus* and *Zucchini yellow mosaic virus* (ZYMV). Total RNA was extracted from 100 mg leaf tissue using the RNeasy Plant Mini Kit (Qiagen, Hilden, Germany) and one step RT-PCR was performed using specific primers for the four potyviruses (Tomassoli & Mohammed, unpublished data).

ZYMV was found in 11 samples and in all surveyed locations. None of the other viruses were detected except in Wad-Ramly, one of the most important areas of pumpkin production in Sudan, where PRSV was also detected in seven samples. Five of these seven samples were co-infected with ZYMV. Primers, designed in a conserved region of the nuclear inclusion protein (NIb) and coat protein (CP) genes following alignment of PRSV sequences retrieved from GenBank, amplified expected fragments of approximately 650 bp (PRSV-1298: 5´-TCACAGCGGCAATGATAGAG-3´; PRSV-1942: 5´-ATTGTGAATGAGTGGCACGA-3´) and 475 bp (PRSV-326: 5´-TCGTGCCACTCAATCACAAT-3´; PRSV-800: 5´-GTTACTGACACTGCCGTCCA-3´). The PCR products were purified, bi-directionally sequenced and contigs assembled. The Sudanese isolates showed high sequence identity to each other (99%). The sequence of one isolate was deposited in GenBank (Accession No. JX430436). When compared with other PRSV sequences using BLASTn, Sudanese PRSV isolates were most closely related to a Taiwanese isolate from papaya (DQ340771) with 91.5% identity at the nucleotide level and 93.2 % at the amino acid level. Further phylogenetic analysis revealed that Sudanese PRSV isolates grouped with the Asian population of the virus (Olarte Castillo *et al*., 2011) and were distant from Egyptian isolates, the only other sequences available from Africa (Fig. 2). To our knowledge, this is the first report of the natural occurrence of PRSV in Sudan. Epidemiological studies are underway to determine the distribution of PRSV in Sudan and its economic impact on cucurbit crops.

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Figure 1

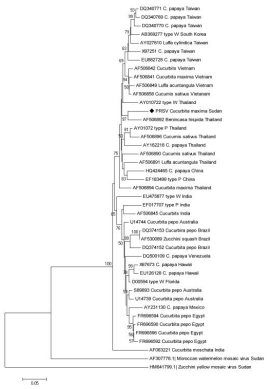

Figure 2

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