



First report of Maize yellow mosaic virus infecting maize in Burkina Faso

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Maize yellow mosaic virus (MaYMV) is a new polerovirus discovered recently in China in maize (*Zea mays*) displaying foliar yellowing and mosaic (Chen *et al.*, 2016). Interestingly, a few months later, MaYMV was reported from Ecuador in maize (A. Bernreiter, pers. comm) and Nigeria in sugarcane and itch grass (Yahaya *et al.*, 2017), suggesting that this new polerovirus is broadly distributed and is potentially emerging worldwide.

In August-September 2016, during a sampling survey carried out by the Agricultural Research Centre of Kamboinsé (ARCK, Burkina Faso), maize leaves showing yellow stripes, yellowing and yellow mosaic symptoms (Figs. 1-3) were collected from five fields surrounding ARCK, from which 15 to 20% of the plants appeared diseased. Leaves of fourteen diseased plants were tested by RT-PCR for the presence of poleroviruses using generic detection primers (PoleroNB3897F/PoleroNB4160R) as described by Palanga *et al.* (2016) and five MaYMV-specific detection primer pairs (vsi-F2/vsi-R2, vsi-F1/R1, MaYMV-F/MaYMV-R, F1/R1 and F1/vsi-R3) as described by Chen *et al.* (2016). Seven of the fourteen samples (MaYMV-BF6, MaYMV-BF7, MaYMV-BF8, MaYMV-BF9, MaYMV-BF11, MaYMV-BF14 and MaYMV-BF16) tested positive using all six primer pairs. Amplicons of 263 to 2700 bp generated using these six primer pairs were sequenced using the Sanger method (Genewiz, USA). The sequences were assembled, aligned and trimmed using DNA Baser V4 (Heraclio BioSoft S.R.L., Romania) to give consensus sequences of 1763 nt. These sequences covered the open reading frames coding the coat protein (CP), the movement protein, the P3a protein and part of the RdRp. Pairwise identities between the consensus sequences obtained from the seven samples (GenBank Accession Nos. KY711382-KY711388) and polerovirus sequences from GenBank were determined using SDT v1.2 (Muhire *et al.*, 2014). The seven consensus sequences from Burkina Faso shared 98-98.7% identity with the Chinese MaYMV isolates. Moreover, nucleotide identities between the Burkina Faso isolates were 99-100%. A neighbour-joining phylogenetic tree was inferred (MEGA6; Tamura *et al.*, 2013) from the CP amino acid sequences of the seven Burkina Faso isolates, the MaYMV CP sequences from China and Ecuador and eight

other representative polerovirus and luteovirus CP sequences (Fig. 4). Sequences from the Burkina Faso isolates clearly cluster with MaYMV CP sequences from China and Ecuador.

Altogether, these results support the conclusion that MaYMV is present in Burkina Faso, indicating a global distribution of this recently discovered virus including Africa, Asia and South America.

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Figure 1



Figure 2



Figure 3

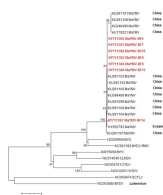


Figure 4

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