



## First report of Maize yellow mosaic virus infecting maize in Ecuador

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Maize yellow mosaic virus (MaYMV) was first described in maize (*Zea mays*) from China and proposed as a new virus in the genus *Pterovirus* (Chen *et al.*, 2016). Recently, MaYMV was also detected in symptomatic maize plants in Burkina Faso (Palanga *et al.*, 2017) indicating a global distribution for the virus. In May 2016 maize plants showing leaf chlorosis and downward curling of leaf tips were collected from a large production area (c. 125,000 hectares in maize cultivation) in the Los Rios Province in Ecuador. It has been estimated that the disease causes yield losses of 10-30%.

Total RNA from symptomatic leaf samples was extracted using the RNeasy Plant Mini Kit (Qiagen, USA) and subjected to deep sequencing analysis using the Illumina platform. Quality filtered paired end reads (8,777,028) were aligned with reference genomes of known plant viruses using standard bioinformatic tools. The transcriptome was highly enriched with viral RNA reads (>5%) showing significant similarity with *Sugarcane mosaic virus* (SCMV) and other MaYMV sequences. These short reads were assembled into contigs and full-length and nearly full-length genome sequences of SCMV (9632 nt; Genbank Accession No. K006657) and MaYMV (5488 nt; KY052793) were identified. Alignments and phylogenetic trees were performed using SeaView software (Gouy *et al.*, 2010).

The Ecuadorian MaYMV isolate had the highest nucleotide identity (96%) with a Chinese isolate (KU291103). MaYMV has a typical *Pterovirus* organisation with six open reading frames (ORFs; 0-5) including ORF3a. ORF3a is translated from a non-standard start codon (in this case AUA) and encodes a protein responsible for long distance movement of the virus in plants (Smirnova *et al.*, 2015). ORF3a (nt 3389-3523) shows a single amino acid substitution compared with the Chinese isolate (KU291103). ORF0 (nt 42-836) shows 97% amino acid identity with MaYMV isolate KU291100 (Table 1) and harbours an essential F-box like element (Pazhouhandeh *et al.*, 2006). The phylogenetic tree (Fig. 1) constructed from ORF0 amino acid sequences indicates significant similarity to the Chinese MaYMV isolate and high variability between different species of the genus *Pterovirus*. Phylogenetic analysis of ORF3 from selected species of the genera *Enamovirus*, *Luteovirus* and *Pterovirus* places the Ecuadorian isolate within a group of pteroviruses that infect a wide range of host

plants (Fig. 2).

MaYMV has been reported to be generally present in mixed infections with other viruses, including *Maize chlorotic mottle virus*, *Southern rice black-streaked dwarf virus* or *SCMV*, but has also been found in single infections in China (Chen *et al.*, 2016) displaying characteristic disease symptoms. The significance of mixed infections with *SCMV* in disease pathology in Ecuador is unclear and requires further investigation.

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### References

- Chen S, Jiang G, Wu J, Liu Y, Qian Y, Zhou X, 2016. Characterization of a novel pterovirus infecting maize in China. *Viruses* **8**, 120. <http://dx.doi.org/10.3390/v8050120>
- Gouy M, Guindon S, Gascuel O, 2010. SeaView version 4: a multiplatform graphical user interface for sequence alignment and phylogenetic tree building. *Molecular Biology and Evolution* **27**, 221-224. <http://dx.doi.org/10.1093/molbev/msp259>
- Palanga E, Longué RDS, Koala M, Néya JB, Traoré O, Martin DP, Peterschmitt M, Filloux D, Roumagnac P, 2017. First report of Maize yellow mosaic virus infecting maize in Burkina Faso. *New Disease Reports* **35**, 26. <http://dx.doi.org/10.5197/j.2044-0588.2017.035.026>
- Pazhouhandeh M, Dieterle M, Marrocco K, Lechner E, Berry B, Brault V, Hemmer O, Kretsch T, Richards KE, Genschik P, Ziegler-Graff V, 2006. F-box-like domain in the pterovirus protein P0 is required for silencing suppressor function. *Proceedings of the National Academy of Sciences, USA* **103**, 1994-1999. <http://dx.doi.org/10.1073/pnas.0510784103>
- Smirnova E, Firth AE, Miller WA, Scheidecker D, Brault V, Reinbold C, Rakotondrafara AM, Chung BY, Ziegler-Graff V, 2015. Discovery of a small non-AUG-initiated ORF in pteroviruses and luteoviruses that is required for long-distance movement. *PLoS Pathogens* **11**, e1004868. <http://dx.doi.org/10.1371/journal.ppat.1004868>

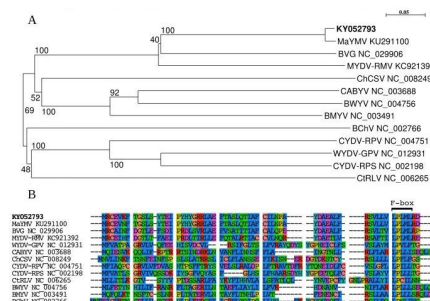


Figure 1

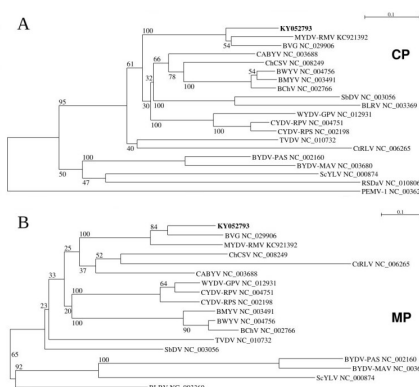


Figure 2

Table 1. Amino acid sequence identities of open reading frames of Maize yellow mosaic virus (KY052793) with other members of the genus *Pterovirus*.

Virus	Genbank Accession No.	Country	Amino acid identity (%)		
			ORF0	ORF3	ORF4
Maize yellow mosaic virus	KU291100	China	97.0	99.5	97.9
Maize yellow mosaic virus	KY684356	Nigeria	96.9	99.5	99.0
Barley virus G	NC_029906	South Korea	26.1	80.2	70.8
Maize yellow dwarf virus	KC921392	USA	23.4	77.4	63.7
Beet western yellows virus	NC_004756	USA	10.5	58.6	41.7
Cereal yellow dwarf virus-RPV	NC_004751	USA	8.6	59.2	38.3
Wheat yellow dwarf virus-GPV	NC_012931	China	8.1	54.4	39.6
Chickpea chlorotic stunt virus	NC_008249	Ethiopia	7.8	61.7	38.9
Beet chlorosis virus	NC_002766	UK	6.9	60.6	39.4

Figure 3

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