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DIVERSITY OF VIRUSES INFECTING OPEN-FIELD PEPPER CROPS IN COTE D'IVOIRE

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BACKGROUND and OBJECTIVES

Pepper (*Capsicum* spp.) is a major vegetable crop, grown in all regions of Côte d'Ivoire, throughout the year. It is usually grown in open fields and, given the diversity of agro-ecological conditions in Côte d'Ivoire, is exposed to a large panel of pathogens, including viruses.

MATERIAL and METHODS

To get an exhaustive and accurate view of the major viral constraints to pepper production, we performed a survey of pepper fields in several agro-ecological zones (AEZ) of Côte d'Ivoire in 2014 and 2015. Leaf samples were collected, kept desiccated on calcium chloride and tested by enzyme-linked immunosorbent assay (ELISA) for infection by *Pepper vein mottle virus* (PepVMV), *Cucumber mosaic virus* (CMV), *Potato virus Y* (PVY), *Tobacco mosaic virus* (TMV) and *Pepper mild mottle virus* (PMMoV) with polyclonal antisera. Pteroviruses were looked for by ELISA on a sample subset, using *Cucurbit aphid-borne yellows virus* (CABYV) polyclonal antiserum. Then, the most prevalent viruses and pteroviruses were characterized molecularly by RT-PCR and sequencing.

RESULTS

Among 525 plant samples corresponding to 110 farms and 43 localities, 142 (27.0%) presented virus infections. PepVMV was the most frequent virus and was detected in 92 samples (21.2%). It was followed by CMV (11%), PMMoV (2.5%) and TMV (1.3%). No PVY-infected sample was observed and some of the samples reacted positively with CABYV antibodies. Virus prevalence varied greatly between AEZ. Among AEZ where at least 29 samples were analysed, virus prevalence varied from 11.8% (AEZ VI, Sudanese savannah in North and North-West Côte d'Ivoire) to 52.2% (AEZ II, humid forest in South-West Côte d'Ivoire). PepVMV and CMV were most frequently detected in all AEZ, except in AEZ VI, where no PepVMV was detected. RT-PCR products corresponding to parts of the VPg and coat protein (CP) coding sequences of PepVMV isolates were sequenced directly. After withdrawal of sequences corresponding to mixed infections, phylogenetic trees were obtained with 43 VPg and 26 CP-coding sequences and allowed identifying four and three major clades, respectively. A high amino acid diversity was observed in the central region (positions 115 to 128) of the VPg, shown to be critical for adaptation to resistance genes in the case of PVY. Indeed 10 different haplotypes, could be distinguished using the amino acid sequence in this region. Concerning the detected pteroviruses, partial sequencing revealed that they belonged to the species *Pepper vein yellows virus* (PeVYV), and clustered with PeVYV isolates from Mali in the phylogenetic tree. This is the first report of PeVYV in Côte d'Ivoire.

CONCLUSIONS

The most frequent virus in open-field pepper crops throughout Côte d'Ivoire is PepVMV, except in the northern part of the country (AEZ VI). Pepper cultivars carrying a resistance to PepVMV are being released in Africa. Resistance is based on the combination of two recessive genes encoding eukaryotic translation initiation factors 4E that interact with the virus VPg. The high amino acid diversity in the central part of the VPg of PepVMV isolates from Côte d'Ivoire raises concerns about the efficiency and durability of this resistance.



Building bridges between disciplines for sustainable management of plant virus diseases



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Programme and Abstracts