First report of Dioscorea bacilliform virus, a badnavirus infecting yam in Burkina Faso

ABSTRACT

In Burkina Faso, yam plays an important role in food security and improving people's incomes. However, the sector is struggling to develop due to a number of constraints, including significant viral pressure. The Dioscorea bacilliform virus (DBV), prevalent in yam-growing areas of the West African region, is causing huge production losses. A survey followed by sample collection was carried out in yam fields in the Centre-Ouest and Cascades regions. A total of 32 samples were collected, of which 26 were symptomatic and 6 asymptomatic. The samples collected were subjected to biological, serological and molecular diagnosis. The study revealed the presence of DBV in all symptomatic samples tested. No asymptomatic samples were positive. Comparison of the sequences of the RT/RNase region of the samples collected with those in the GenBank database confirmed the presence of DBV, with similarity rates ranging from 97.73% to 99.02%. Our work has thus made it possible to describe for the first time a new virus infecting yam in Burkina Faso. Studies are now required to generate epidemiological data on the virus and to search for resistance genes through varietal screening.

Key words :**Dioscorea bacilliform virus, Dioscorea spp, Survey, Symptomatic, Asymptomatic**

INTRODUCTION

Yam (*Dioscorea* spp.) is an important vegetatively-propagated staple crop of people globally, particularly those in the developing countries of West Africa and the Pacific Islands (FAOSTAT, 2020). In Burkina Faso, yam is the second most important tuber and root crop after potato in terms of production. This national production, which was 43 295 tonnes in 2008, rose to 46735 tonnes in 2017 tonnes, which points to growth in its production in the country (MAAHM, 2019). Despite its economic and food importance, yam production in Burkina Faso, as in the rest of the world, are seriously affected by numerous abiotic and biotic factors that considerably reduce its yield.(Source)

More than fourteen yam-infecting viruses have been identified worldwide (Luo *et al*., 2022). Plant viruses are among the most detrimental of plant pathogens and have caused great losses of crop yield and quality, including those of yam. Dioscorea bacilliform virus (DBV), which belong to the genus Badnavirus, family *Caulimoviridae*, are an important DNA virus complex that infects yam. Of all these viruses, DBV is the most prevalent in areas of high production,

with an impact resulting in high yield losses ranging from 10% to 90% (Eni *et al*., 2008; Seal *et al*., 2014). DBV infection have the potential to impede yam germplasm movement and thus hinder international exchange of selected improved varieties (Bousalem *et al*., 2009).

The virus is present in various bordering countries such as Ghana, Togo, Benin and Côte d'Ivoire (Eni *et al*., 2008; Bakayoko *et al*., 2021), thereby posing a threat to Burkina Faso. Unfortunately, there is little information about the virus in Burkina Faso. Though, floliar virus-like symptoms, including chlorotic mosaic, puckering, crinkling and stunting were observed on yam in Centre-Ouest and Cascades regions of Burkina Faso. DBV, which is not known in Burkina Faso, was the subject of this study in order to identify this virus in the country's yam production areas.

MATERIALS AND METHODS

Experimental Site

In august 2023, leaf samples were collected from 26 symptomatic and 6 asymptomatic yam plants. After a symptom diagnosis, all samples were assayed by Double Antibody Sandwich - Enzyme Linked Immuno Sorbent Assay (DAS-ELISA) using DBV polyclonal antisera (developed in-house at IRD). To confirm DBV identity, total DNA was extracted from leaves samples using the CTAB method (Permengeat *et al*., 1998). PCR was performed using primers Badna FP (5'-ATGCCITTYGGIAARAAYGCICC-3') and Badna RP (5'-CCAYTTRCAIACISCICCCCAICC-3') (Bömer *et al.*, 2018), which were designed to amplify a fragment 579 bp of the RT/RNase H region. The amplification products from four samples were sequenced by Macrogen (Amsterdam, Netherlands) and the sequences were compared with other viral sequences in the NCBI database using BLAST (BLAST, http://www.ncbi.nlm.nih.gov/blast). Nucleotide identities between among Burkina Faso sequences were determined using SDTv1.2 software.

RESULTS AND DISCUSSION

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Initial identification on the basis of the symptoms observed led to the suspicion that DBV was present in the samples collected. Indeed, similar symptoms due to DBV have been reported by certain authors (Borah *et al.,* 2013; Toualy *et al.,* 2014; Bömer *et al.,* 2016). Results of serological diagnosis revealed that all symptomatic samples were positives for DBV. However, sample from the healthy plant were negatives. PCR reaction for all symptomatic samples produced the expected sizes of the fragments for DBV (Fig. 2). BLAST analysis revealed

nucleotides sequences shared 97.73% and 99.02% identity with DBV Genbank sequences. Using SDTv1.2, the nucleotides identities of the all Burkina Faso sequences among them ranged from 79.2 to 94.5%. The results of this study highlighted the presence of BSV in the Hauts Bassins and Boucle du Mouhoun regions. DBV is present in all yam-growing areas, including Côte d'Ivoire (Bakayoko *et al*., 2021), Ghana, Togo, Benin and Nigeria (Eni *et al*., 2008). Exchanges of plant material between countries could help to explain the spread of the virus in yam-growing areas in the sub-region.

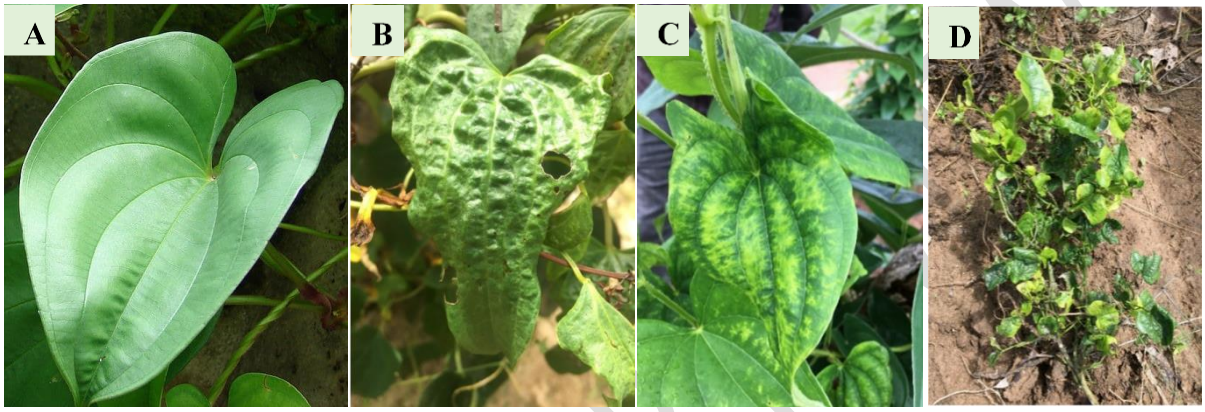

Fig 1. Symptoms observed in the surveyed yam plantations. (A) Healthy leave, (B) puckering and crinkling, (C) chlorotic mosaic, (D) stunting

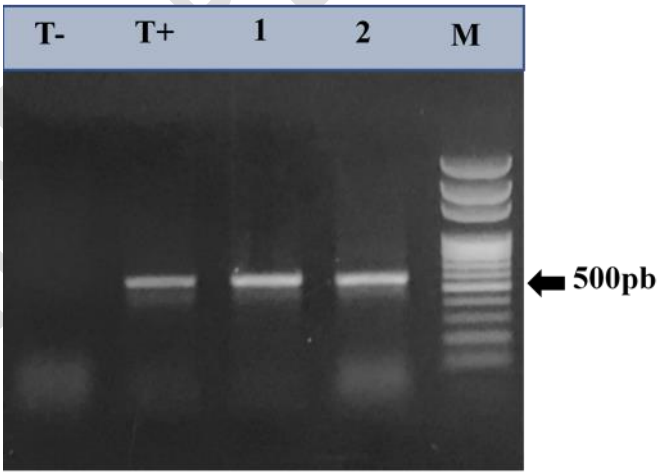

Fig 2. Agarose gel electrophoresis (1%) showing PCR amplified products obtained from yam samples: lane M = 100pb DNA ladder (Solis Biodyne); lanes 1, 2 = DBV infected samples, lane T- = negative control; lane T+ = positive control

CONCLUSION

Our study identified DBV in yam production fields in the Centre-Est and Cascades regions. To our knowledge, this is the first report of DBV in yam in Burkina Faso. This virus could pose an imminent threat to the growing yam if it allowed to spread in yam fields under conditions in Burkina Faso. This report is the primary step to initiate research epidemiology and crop losses due to DBV in Burkina Faso.Incorporate a bit of recommendation

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