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First Report of Banana Streak Virus Infecting Banana in Burkina Faso

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

Banana plants (*Musa* spp), both food and economic crops, are potential hosts for a various range of badnavirus species considered a major constraint to banana improvement and a threat to *Musa* production worldwide. A survey and sample collection were carried out in two main banana-growing

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regions of Burkina Faso. The samples collected were subjected to biological, serological and molecular diagnosis of the reverse transcriptase/ribonuclease H (RT/RNase H) region using Badna FP/RP primers, followed by sequence comparison with the Genbank database. Analyses confirmed the presence of Banana streak virus (BSV) in all symptomatic samples tested in both regions. Amplification bands of the expected size were obtained for the symptomatic samples tested positive in the serological test. These partial RT/RNase H gene sequences shared highest nucleotide identity ranging from 85.80% to 99.05% with BSV isolates in GenBank. These results are proof of the existence of BSV in Burkina Faso. It is therefore important to undertake studies that will provide basic information on the virus for the development of effective control strategies.

Keywords: Banana; banana streak virus; diagnosis; symptomatic; reverse transcriptase/ribonuclease.

1. INTRODUCTION

"Banana (*Musa spp*) is herbaceous plant belonging to the family *Musaceae* of the genus *Musa* and is native to the tropical region of South East Asia. Viruses are important constraints to the movement and propagation of plant germplasm, especially for vegetatively propagated crops such as banana and plantain. Banana production is threatened by the Banana streak disease (BSD), and its pathogen belongs to the genus Badnavirus*,* family *Caulimoviridae* (Chabannes et al., 2020; Geering et al., 2021). Banana streak virus (BSV) is widely distributed in the main planting areas of banana industry in Southeast Asia and Africa, and it had seriously affected the yield and quality of bananas resulted in huge economic losses" (Kumar et al., 2015). BSD can manifest with wide-ranging symptoms, from complete lack of visible impacts to plant death, depending on BSV isolates, host cultivars, and environmental conditions" (Dahal et al., 2000). However, the major symptoms of BSD are chlorotic and necrotic streaks.

In Burkina Faso, banana is produced in all agro-ecological zones and help combat food and nutritional insecurity and unemployment. From 2012 to 2014, production rose from 50.571 tonnes to 79.561 tonnes (TFB, 2015). In spite of this increase, production is struggling to cover national consumption needs. This is due to abiotic and biotic constraints including viral diseases causing drastic yield loses. Unfortunately, the viruses infecting bananas are not well documented in Burkina Faso's banana-growing areas (Muturi et al., 2016). BSV has never been reported in banana growing areas in Burkina Faso. Although, viral diseases symptoms similar to badnavirus symptoms was observed on banana plant in many regions. The present study firstly reports about Banana streak virus infecting banana in Burkina Faso.

2. MATERIALS AND METHODS

Twenty-five leaf samples were collected from symptomatic banana plants in two main production regions, Boucle du Mouhoun and Hauts-Bassins. Among those, 22 showed disease symptoms and 3 were symptomless. All samples were assayed to confirm BSV infection by Indirect Antigen Coated Plate Assay-ELISA with BSV polyclonal antisera (developed in-house at CIRAD, provided by Serge GALZI). BSV was detected in all samples tested. Total DNA was extracted by the CTAB protocol (Permingeat et al., 1998) from 25 samples. The fragment of RT/RNase H region was amplified by Polymerase chain reaction (PCR) using primers Badna FP (5'-ATGCCITTYGGIAARAAYGCICC-3') and Badna RP (5'-CCAYTTRCAIACISCICCCCAICC-3') (Yang et al., 2003). Amplification products were sent for sequencing to Macrogen (Amsterdam, Netherlands). Sequences were compared with other viral sequences in the NCBI database using BLAST (BLAST, http://www.ncbi.nlm.nih.gov/blast).

3. RESULTS AND DISCUSSION

During the survey, plants showing symptoms of discontinuous and continuous streaks, chlorotic streaks and necrotic streaks were observed in the plantations (Fig. 1). Based on the nature of the symptoms observed, infection by BSV was suspected. These symptoms are similar to the usual BSV symptoms reported by many authors (Umber et al., 2022; Ishwara Bhat et al., 2023).

(A) **(B)** **(C)**

Fig. 1. Symptoms observed in the surveyed banana plantations. (A) Healthy leaf, (B) Discontinuous and discontinuous chlorotic streaks, (C) Chlorotic and necrotic streaks

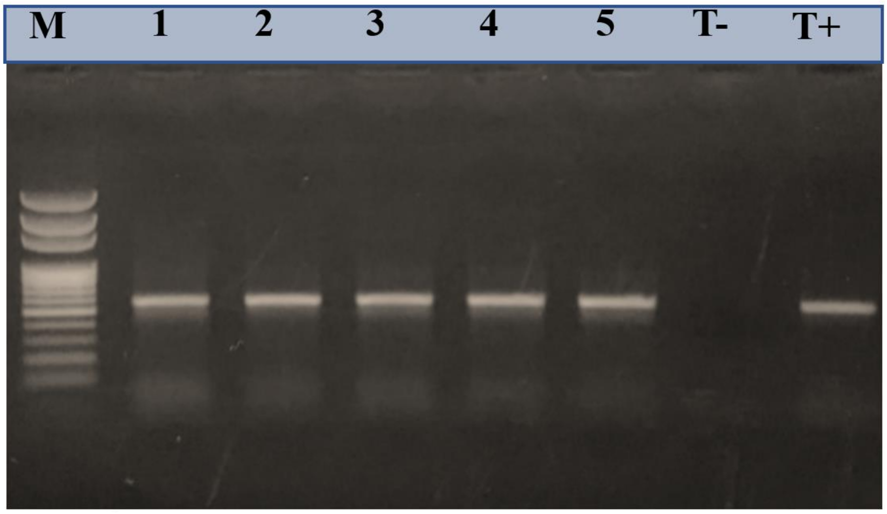

Fig. 2. Agarose gel electrophoresis (1%) showing PCR amplified products: lane M = 100pb DNA ladder (Solis Biodyne); lanes 1, 2 = BSV infected samples, lane T- = negative control; lane T+ = positive control

All symptomatic samples were positives for serological assay but any symptomless samples were positives. An amplification product of the expected size was obtained for all 22 symptomatic samples tested positive (Fig. 2). Five PCR products were directly sequenced. These five sequences showed identity ranging from 85.80% to 99.05% with each other BSV isolates. All these facts are evidence of the existence of BSV in the banana-growing areas surveyed in Burkina Faso. The presence of BSV in bordering countries such as Côte d'Ivoire (Kouadio et al., 2016), Benin (Pasberg-Gauhl et al., 1996), Togo (Lockhart, 1995) and Ghana, Nigeria (Agindotan et al., 2006) has already been reported. Exchanges of plant material between these countries could be cause of the spread of the virus in the sub-region.

4. CONCLUSION

To the best of our knowledge, this is the first report of BSV infecting banana in Burkina Faso. Based on the GenBank repository, the sequenced virus revealed the similarity of greater than 80% which is enough to confirmed the virus as BSV. Therefore, the obtained identity of 85.80% to 99.05% validated the virus is 85.80% to 99.05%. This report is the primary step to initiate research on the impact of the virus in banana production and germplasm exchange. Further research is needed to elucidate epidemiology and impact of the virus in banana production and germplasm exchange.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of this manuscript.

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COMPETING INTERESTS

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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