Abstract

Cassava brown leaf spot (BLS) is among the most damaging diseases that significantly reduce cassava root yields and quality. In this study, drought-resistant cassava varieties were screened on an experimental farm in Kitui County, Kenya. One variety, Kasukari, exhibited abnormal morphological aberrations suggesting BLS and necessitated systematic studies to establish the causal agents. Fungi were isolated from symptomatic leaves and purified on Potato Dextrose Agar (PDA) with antibiotics. Fungal pathogens were identified using morpho-cultural characteristics and molecular characterization through polymerase chain reaction (PCR) amplification and sequencing of the internal transcribed spacer (ITS). 162 Kasukari samples were used to determine the prevalence and severity of the disease, while 15 samples were used to determine the effects of the disease. Pathogenicity tests of ten isolates were conducted in vitro using detached leaves of the healthy Kasukari variety. The results indicated that the prevalence within the plots had no significant difference ($\chi2 = 6$, p-value = 0.1991). However, there was a significant difference in severity ($\chi2 = 53.013$, p-value = 1.166e-09). PCR with the ITS marker identified the fungal pathogens from the genera Alternaria, Epicoccum, Preussia, and Cladosporium. Epicoccum spp. had colonies of white clusters that formed concentric rings, while the reverse had grey-brown colonies and a regular margin. Conidia produced on PDA were oval, hyaline, unicellular, and aseptate, consistent with Epicoccum morphology. Based on ITS identification and pathogenicity assays, this study provides a preliminary report of an Epicoccum sp. associated with brown leaf spot (BLS) disease in cassava in Kenya. However, due to the absence of multi-locus sequence data and the limited number of isolates tested, the causal role of Epicoccum remains suggestive. These findings form the basis for future studies to confirm the causal role of Epicoccum spp. and clarify its epidemiology. The study will also help inform prevention and management strategies, including breeding programs and targeted control measures.