

# General Abstract

Banana *Xanthomonas* wilt (BXW), gray leaf spot (GLS) of Maize and Cassava brown streak disease (CBSD) are very destructive crop plant bacterial, fungal and viral diseases, respectively. Conventional methods currently being used for detection of these pathogens are inadequate. To address this, specific and rapid diagnostic tools have been developed for the detection of these pathogens. A combination of sequencing and bioinformatics approaches were used to design diagnostic PCR primers for the pathogens. The variability of intergenic regions and unique sequences were utilized in an attempt to design specific primers for PCR detection of BXW and GLS of Maize. Sequencing was done for the whole genome of *Xanthomonas campestris* p.v *musacrerium* (Xcm) for banana *xanthomonas* wilt and coat protein region for cassava brown streak virus for CBSD. This was the first genome sequence for Kenyan Xcm. A bioinformatics approach was utilised to design PCR diagnostic primers from intergenic regions and unique sequences for the pathogens. For more effective diagnosis of GLS of Maize, unique EST sequences and Malazy gene, a gypsy-like transposable element that is differentially expressed in the two *Cercospora* groups of *Cercospora zea-maydis* group I and *C. zeina* group II were utilized. Species specific primers developed were characterised and validated to be specific for the diagnosis of BXW, GLS of Maize and CBSD. These molecular diagnostic tools can be used to detect these diseases before symptoms are visualized or spread and to identify new emerging pathogen varieties. These tools can also be used in detecting pathogens in seeds, other plant material used for propagation and in marker assisted selection for disease resistant lines.