

## Abstract

Banana bacterial wilt caused by *Xanthomonas campestris* sp. *musacearum* has caused significant decline in banana dependent livelihoods of the African great lakes region. First line control using cultural packages are not sustainable for long term application. Use of resistant materials is most effective, however no resistant material is yet out for deployment. The need to understand the origins and host pathogen interaction at the molecular level is key for development of novel management approaches. Affordable genome sequencing has eased the application of genomic, post-genomic, and functional genomic approaches to problems of direct relevance to parasitic diseases in plants, humans and animals. The genetic diversity of *Xanthomonas campestris* sp. *musacearum* (Xcm) and *vasculorum* (Xvv) was used to mine for predicted pathogenicity determinants. Unique Type four (Tfp) pilus assembly protein PilF a fimbrial biogenesis protein, Type III effector protein RipT and YopJ type III secretion system effector protein hybridised in all Xcm strains tested but not in Xsp1131 nor Xsp1132. Type III effector HopAF1 was present in Xcm but not Xvv206. Genome-wide sequencing was used to determine the origin, distribution and variation of Xcm isolates from the great lakes region. This study also revealed two major sub-lineages with isolates of Xcm from Burundi, Kenya, Tanzania and Uganda comprising a separate sub-lineage that is distinct from isolates from and D. R. Congo, Ethiopia and Rwanda. In addition genome-wide sequence data from multiple isolates of Xcm and Xvv, identified genes specific to Xcm that could be used to specifically detect Xcm by PCR based methods. Next generation sequencing was deployed to identify virulence factors in a range of *Xanthomonas vasicolapv. vasulorum* isolates from maize and sugarcane. The sequence analyses revealed large differences in gene content among isolates of Xvv, both among isolates from sugarcane and also between isolates from sugarcane and a single isolate from maize. In addition it also identified two distinct types of lipopolysaccharide synthesis gene clusters among Xvv isolates. Two additional *Xanthomonas* strains (NCPB1131 and NCPB1132) that had been isolated from banana plants in Eastern and Western Samoa were sequenced to identify virulence factors related to Xcm. This is geared towards understanding the host-driven pathogen adaptation and potential to develop practical applications for crop protection.