Genomic Survey of Pathogenicity Determinants and VNTR Markers in the Cassava Bacterial Pathogen Xanthomonas axonopodis pv. Manihotis Strain CIO151

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Résumé en anglais	Xanthomonas axonopodis pv. manihotis (Xam) is the causal agent of bacterial blight of cassava, which is among the main components of human diet in Africa and South America. Current information about the molecular pathogenicity factors involved in the infection process of this organism is limited. Previous studies in other bacteria in this genus suggest that advanced draft genome sequences are valuable resources for molecular studies on their interaction with plants and could provide valuable tools for diagnostics and detection. Here we have generated the first manually annotated high-quality draft genome sequence of Xam strain CIO151. Its genomic structure is similar to that of other xanthomonads, especially Xanthomonas euvesicatoria and Xanthomonas citri pv. citri species. Several putative pathogenicity factors were identified, including type III effectors, cell wall-degrading enzymes and clusters encoding protein secretion systems. Specific characteristics in this genome include changes in the xanthomonadin cluster that could explain the lack of typical yellow color in all strains of this pathovar and the presence of 50 regions in the genome with atypical nucleotide composition. The genome sequence was used to predict and evaluate 22 variable number of tandem repeat (VNTR) loci that were subsequently demonstrated as polymorphic in representative Xam strains. Our results demonstrate that Xanthomonas axonopodis pv. manihotis strain CIO151 possesses ten clusters of pathogenicity factors conserved within the genus Xanthomonas. We report 126 genes that are potentially unique to Xam, as well as potential horizontal transfer events in the history of the genome. The relation of these regions with virulence and pathogenicity could explain several aspects of the biology of this pathogen, including its ability to colonize both vascular and non-vascular tissues of cassava plants. A set of 16 robust, polymorphic VNTR loci will be useful to develop a multi-locus VNTR analysis scheme for epidemiological surveillance of this disease.
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