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Diversity analysis of *Xanthomonas axonopodis* pv. *manihotis* (*Xam*) in Mali

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Understanding the diversity of pathogen populations in a regional scale is crucial in order to develop strategies for sustainable control of plant diseases. Our work deals with the study of the plant pathogenic bacterium *Xanthomonas axonopodis* pv. *manihotis* (*Xam*), which is the causal agent of cassava bacterial blight (CBB). CBB occurs in the tropics including in West-Africa where it has recently been reported in Burkina Faso and Ivory Coast, sometimes imposing severe yield losses to cassava producers. The status of CBB in Mali still remains unstudied.
To fill this gap, preliminary surveys were conducted in Dec. 2015 in two cassava production regions. Nearly 80 leaf samples were processed, leading to the isolation of about 50 *Xam* candidate isolates. Of these, 40 strains of *Xanthomonas axonopodis* pv. *manihotis* were validated through molecular diagnostic tests and pathogenicity assays. This study represents the first demonstration for the presence of CBB in Mali and enabled to initiate the establishment of a first collection of national *Xam* strains. Secondly, a MLVA strategy (Multiple-Locus Variable number tandem repeat Analysis) was developed based on the analysis of 14 microsatellites (VNTR) in order to assess the genetic diversity of the 40 strains isolated from our two regions under study, Bamako and Segou, which are 250km distant.
Our results demonstrate a greater diversity in populations of the Bamako region relative to that of Segou, with reference to the values of diversity indices. Also, comparison of all strains of Mali with a collection of 215 strains from border regions in Burkina Faso suggested that the Malian strains are less diversified. Further surveys covering most areas of cassava production in Mali are in progress to better understand *Xam* invasion routes in this country.

Keywords: Cassava, *Xanthomonas*, cassava bacterial blight, Mali, molecular diagnostic, MLVA-14