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The emergence of *Xanthomonas citri* pv. *citri* in Mali results from at least two independent introductions

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Citrus is threatened by various diseases including Asiatic Citrus Canker, caused by the bacterium *Xanthomonas citri* pv. *Citri* (Xcc). This pathogen is listed as a quarantine organism in Europe and is re-emerging in many countries in Africa, including Mali in 2008. Pathogenicity tests showed that Malian strains were related to pathotype A which is pathogenic on a wide range of *Citrus* species. A Multilocus Sequence Analysis (MLSA) based on six housekeeping genes indicated the presence in Mali of two Sequence Types (ST): ST2 in 4 provinces and ST3, only present in Bamako. A strain collection (n=714) was genotyped with two molecular typing systems using Variable Number of Tandem Repeats (VNTRs). The first system, called MLVA-31, has 31 minisatellite markers and aims to analyze the genetic diversity of a worldwide collection of Xcc. The MLVA-14 called second system has 14 microsatellite markers and is useful for outbreak investigation and epidemics understanding. Both systems data suggested a hypothetical epidemiological link between Malian population and a collection of 46 strains recently sampled in Burkina Faso. Furthermore, analysis of the Malian collection using MLVA-1 revealed a relatively low global genetic diversity ($H_t = 0.37$). In addition, presence of major clonal complexes supports the hypothesis of a recent emergence. Characterization and structuration of genotyping data defined two independent introductions of the pathogen in Mali. Our results provide additional information on the epidemiology of Xcc and its re-emergence in Africa and point out the importance of MLVA-based genotyping tools in molecular epidemiology analyses and global surveillance.