

Genetic and pathological diversity among *Xanthomonas* strains responsible for bacterial spot on tomato and pepper in the South West Indian Ocean region

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Bacterial spot of tomato and pepper (BSTP), a major problem in tropical and subtropical climates, can be caused by several *Xanthomonas* genospecies, *X. euvesicatoria*, *X. vesicatoria*, *X. perforans*, and *X. gardneri*. *X. campestris* pv. *raphani* strains primarily pathogenic to Brassicaceae have also been associated with outbreaks of BSTP on tomato. BSTP has been observed in the South West Indian Ocean (SWIO) region but no data is available about the status of *Xanthomonas* species associated with BSTP in this region. A total of 72 strains collected from Comoros, Madagascar, Mauritius, Réunion and the Seychelles were characterized using AFLP (Amplified Fragment Length Polymorphism) and MLSA (MultiLocus Sequence Analysis) based on four housekeeping genes. AFLP and MLSA consistently assigned strains at the species level. All strains were unambiguously classified in one species, namely: *X. euvesicatoria*, *X. vesicatoria*, *X. perforans* and *X. gardneri*. MLSA identified two to three sequence types per genospecies. No *X. campestris* pv. *raphani* strains were identified in the collection. Most of the strains were identified as *X. euvesicatoria* (65 %). MLSA data suggested that sequence variations primarily consisted of synonymous mutations, although a recombination event spanning several hundreds nucleotides was detected for some strains of *X. euvesicatoria* on the *atpD* gene coding for the F1-F0-ATPase β subunit. Pathogenicity tests were also performed with pathogenicity profiles of strains consistent with the classification in genospecies. Some pathological variations were primarily observed among strains identified as *X. euvesicatoria*. This study provides for the first time a comprehensive description of the status in the SWIO region of *Xanthomonas* species causing BSTP.