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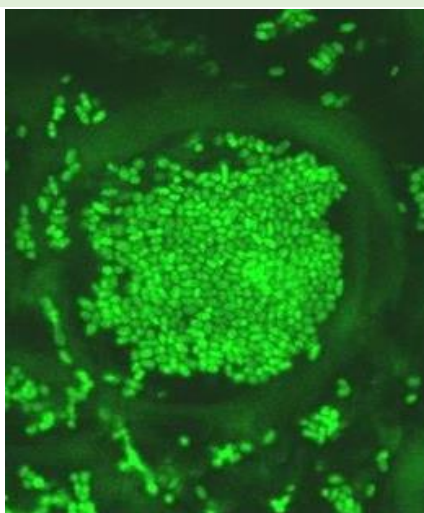
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ABSTRACT BOOK



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Genetic diversity of the type III effector RipAX2 in the *Ralstonia solanacearum* species complex and its impact on the deployment of eggplants carrying the *EBWR9* resistance locus in the South-West Indian Ocean

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The *Ralstonia solanacearum* species complex is responsible for the bacterial wilt disease on many food crops with high economic and food potential. This disease represents one of the major constraints to the sustainable production of Solanaceae crops, with heavy socio-economic consequences for small farmers in the South-West Indian Ocean islands (Comoros, Madagascar, Mauritius, Mayotte, Reunion, Rodrigues and Seychelles). The measures commonly used to limit losses are the implementation of regulations on the circulation of plant material, crop rotation and use of healthy seeds. These prophylactic methods are not totally effective and the use of resistant varieties remains the most promising strategies to control this disease.

We evaluated the effectiveness of bacterial wilt resistance of the eggplant AG91-25 carrying the *EBWR9* locus (Salgon et al., 2017). This resistance is conferred by the recognition of the type III effector RipAX2 (Morel et al., 2018). A study of RipAX2 diversity was performed by *in silico* analysis based on 550 genomes assemblies from public databases and by targeted gene sequencing of a collection of 807 global strains. We identified different alleles of RipAX2 and selected a subset of strains representative of this diversity that were inoculated on AG91-25 and MM738 used as a susceptible control. Strains displaying minor polymorphisms of RipAX2 (e.g. amino acid substitutions) were controlled by AG91-25 while those with major variations (e.g. insertion sequence event, frameshift, premature stop codon) were virulent and triggered bacterial wilt symptoms. The phenotyping of these strains complemented with the reference sequence of *RipAX2* confirmed the involvement of this effector in the interaction with AG91-25.

Finally, we performed a geographical mapping of the virulence profiles of all the strains analyzed in this study, to define a rational deployment plan of the *EBWR9* resistance limiting the risks of resistance breakdown in the agroecosystems of the different South-West Indian Ocean islands.