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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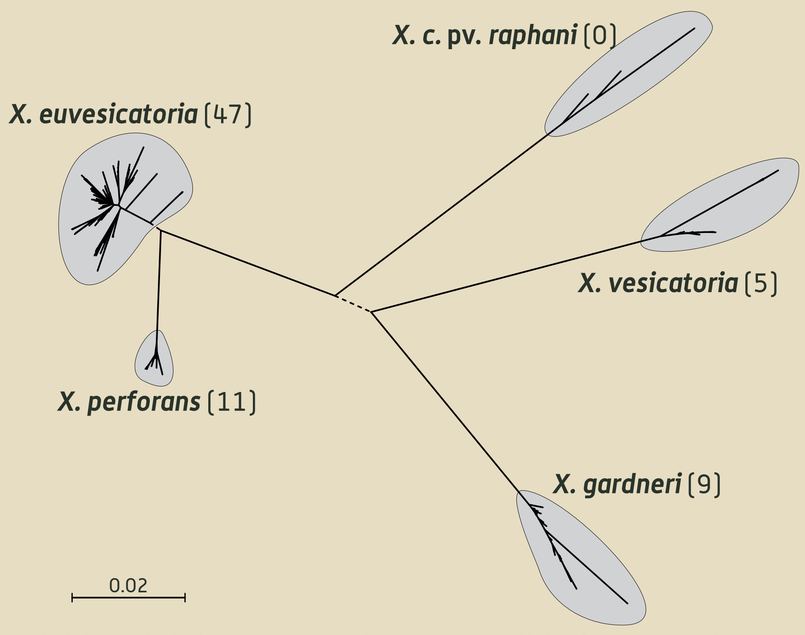
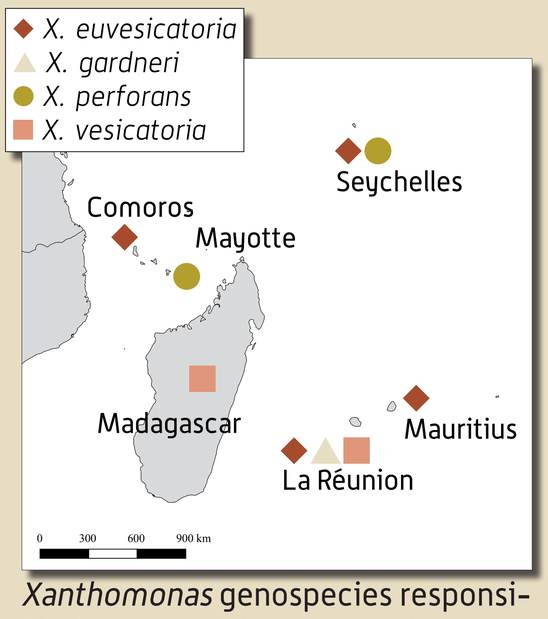
- Bacterial Spot of Tomato and Pepper (BSTP) can be caused by *Xanthomonas euvesicatoria*, *X. gardneri*, *X. perforans*, *X. vesicatoria* or *X. campestris* pv. *raphani*
- pathogens listed on the A2 list of the European and Mediterranean Plant Protection Organization (EPPO)
- prevalence of BSTP in the South West Indian Ocean (SWIO) territories (regional program for plant protection, http://www.prpv.org)
- accurate identification of strains causing BSTP is of particular importance for surveillance and pest management

Objectives

- a global survey of strains causing BSTP in the SWIO region
- identification at the species level using AFLP and MLSA
- pathological characterization



Neighbor-joining tree strains responsible for BSTP derived from EGD based on 485 AFLP markers. In brackets are the numbers of strains isolated in the SWIO region



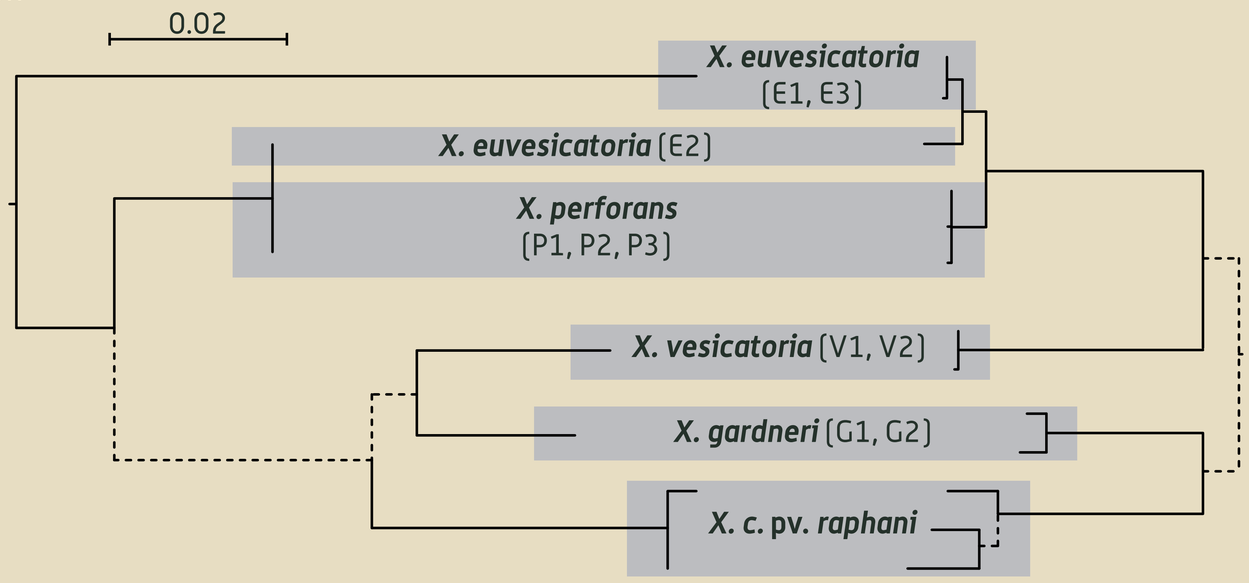
Xanthomonas genospecies responsible for BSTP in the SWIO region

Amplified Fragment Length Polymorphism

- 133 strains including 72 strains isolated in the SWIO
- all strains easily identified at the species level (EGD values < 0.030 nsps with one of the type strain of the genospecies associated with BSTP)
- all species except *X. campestris* pv. *raphani* are present in the SWIO region
- prevalence of *X. euvesicatoria* in the SWIO (65% of strains)
- *X. perforans* closely related to *X. euvesicatoria*

Multi-Locus Sequence Analysis

- based on the sequencing of 4 housekeeping genes : *atpD*, *dnaK*, *efp* and *gyrB* for 95 strains including all SWIO strains
- two to three sequence types per genospecies
- recombination event detected on the *atpD* gene for *X. euvesicatoria* strains (45/51)
- MLSA data consistent with AFLP data when analyzing concatenated dataset but the recombinant region



tree based on recombinant region from *atpD* only

tree based on concatenated sequences minus recombinant regions

maximum likelihood trees of *Xanthomonas* genospecies associated with BSTP based on *atpD*, *dnaK*, *efp* and *gyrB* partial sequences

Pathological characterization

- pathogenicity tests on tomato (*Solanum lycopersicum*) cv. Marmande and pepper (*Capsicum annuum*) cvs. Yolo wonder and Aiguille
- inoculation of all strains of the SWIO region (n=72) and 4 type strains (2 repetitions)
- pathological characteristics of SWIO strains causing BSTP agree with data available in the literature
- pathological variations observed among *X. euvesicatoria*

Inoculated host species and cultivar

Xanthomonas species	Tomato cv. Marmande	Pepper cv. Yolo wonder	Pepper cv. Aiguille
X. euvesicatoria (63)	+	+	+
X. euvesicatoria (9)	+	+	-
X. perforans	+	-	-
X. gardneri	+	+	+
X. vesicatoria	+	-	-

Pathogenicity profiles based on leaf infiltrations of 72 xanthomonad strains associated with bacterial spot of tomato and pepper in the South West Indian Ocean region

Conclusions

- first comprehensive description of the status of *Xanthomonas* species that cause BSTP in the SWIO region
- AFLP and MLSA consistently assigned strains at the species level : reliable tools for regional and international sanitary surveillance and pest management
- possible synonymy of *X. euvesicatoria* and *X. perforans* consistent with other recent data