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Biological and epidemiological studies of *P. s.* pv. *actinidiae* and *P. s.* pv. *actinidifoliorum* pathogenic on kiwifruit to improve their detection



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Global overview





Kiwifruit production areas



Kiwifruit producing countries

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1984: Japan





1992: Italy





1994: South Korea





2008: Italy





2009: Turkey





2010: France, Portugal, New Zealand, Chile, China





2011: Spain, Switzerland, Australia





2013: Germany, Slovenia





2014: Greece







Angular necrotic spots on leaves surrounded or not by a yellow chlorotic halo



Blossom necrosis





Red or white ooze exudating from leads or buds



Browning and discoloration below the bark



Dieback







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Photo: SRAL Rhones Alpes

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- I. What is the **diversity** of *Psa* in France?
- II. What is the origin of the epidemic of *Psa* in France?

III. How to improve the **detection** of *Psa*?

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I. What is the diversity of *Psa* in France?





• Detection of *Psa* in France in **2010**



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• The French Ministry of Agriculture established a **national monitoring plan** in 2011 to report the infected French orchards

• Since 2010 **280 strains** were isolated from symptomatic kiwifruit samples (LSV, Anses, Angers)



• P. s. pv actinidiae (Psa)

• P. s. pv actinidifoliorum (Psaf) (Cunty et al., 2014)

→ Psa LV (Low Virulent) (Chapman et al., 2012)

→ Psa biovar 4 (Vanneste et al., 2013)

 \rightarrow *PsHa* and *PsD* (Butler *et al., 2013*)

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Two kiwifruit pathogens isolated in France

- P. s. pv actinidiae (Psa)
 - \rightarrow necrotic spot on leaves
 - \rightarrow canker on wood
- \rightarrow severe yield losses



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- P. s. pv actinidifoliorum (Psaf)
 → necrotic spot on leaves
- \rightarrow No yield loss





• P. s. pv actinidiae (Psa)



(Vanneste et al., 2013)





• P. s. pv actinidiae (Psa)



- Among the 280 strains isolated in France:
 - 248 strains \rightarrow *Psa* b3
 - 32 strains \rightarrow *Psaf*

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Phylogeny of Psa and Psaf





Phylogeny of Psa and Psaf



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Psaf differs from Psa





✓ Phenotypic level:

 \rightarrow *Psaf* : esculine hydrolysis and fluorescent pigment

✓ Phylogenetic level:

- \rightarrow Psa b1, b2 and b3 clustered together
- → Psaf distant from Psa

✓ Pathogenic level:

- \rightarrow *Psa*: leaf symptoms + canker on wood; severe yield losses
- → *Psaf*: leaf symptoms; no yield loss







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✓ Pathogenic level:

- \rightarrow *Psa*: leaf symptoms + canker on wood; severe yield losses
- → *Psaf*: leaf symptoms; no yield loss



- \rightarrow Identification of *actinidifoliorum* pathovar was relevant to:
 - assign to the pathovar actinidiae only the strains responsible of the bacterial canker of kiwifruit



improve legislative management options in order to be only applied to the bacteria responsible for kiwifruit canker

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II. What is the origin of the *Psa* b3 epidemic in France?





 \rightarrow First *Psa* b3 detection in Europe:

- in Italy: 2008
- in France: 2010

→Plant material exchange, at the end of 2013:

- Psa registered on the A2 list of EPPO

- The Commission of the European Union: phytosanitary passport requiered for plant material exchange





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Hypothesis: Psa b3 introduced in France from Italy through infected plants

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 \rightarrow Study of the genetic structuring of the *Psa* b3 strains isolated in France and in Italy



→ Multilocus Variable-number tandem repeats Analysis (MLVA)

→ MLVA: powerfull technique used in epidemiological monitoring to study bacterial genetic structure at infraspecies and infrapathovar levels





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 \rightarrow Aim of MLVA: target variable number of tandem repeats (VNTRs)

 \rightarrow Detection of the TRs by PCR with primers designed on the flanking regions of each TR





- → 340 strains of *Psa* b3 :
 - Psa b3 France:264
 - Psa b3 Italy:53
 - *Psa* b3 **NZ**:12
 - *Psa* b3 **China**:8
 - *Psa* b3 **Chile**:3

\rightarrow MLVA scheme:

- Identification of 11 polymorphic VNTR loci
- Development of primers in the VNTR loci flanking regions





MLVA: Psa b3 MST



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MLVA: Psa b3 MST





The origin of the epidemic of *Psa* b3 in France



 \rightarrow MLVA revealed that strains isolated in France and in Italy were genetically close related



→ Multivariate method (DAPC), which allow identifying and describing clusters of genetically related individuals









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→ Results of MLVA and DAPC supported the hypothesis of a common origin (Cunty *et al.*, 2015 AEM)



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III. How to improve the detection of *Psa*?





GENE SEQUENCE ANALYSIS FOR THE MOLECULAR DETECTION OF *PSEUDOMONAS SYRINGAE* pv. *ACTINIDIAE*: DEVELOPING DIAGNOSTIC PROTOCOLS

A. Gallelli, A. L'Aurora and S. Loreti

A Multiplex PCR Assay for Detection of *Pseudomonas syringae* pv. *actinidiae* and Differentiation of Populations with Different Geographic Origin

G. M. Balestra, Department of Science and Technologies for Agriculture, Forestry, Nature and Energy, and M. C. Taratufolo, Department of Science and Technologies for Agriculture, Forestry, Nature and Energy, University of Tuscia, Viterbo, Italy; B. A. Vinatzer, Department of Plant Pathology, Physiology, and Weed Science, Virginia Tech, Blacksburg; and A. Mazzaglia, Department of Science and Technologies for Agriculture, Forestry, Nature and Energy, University of Tuscia, Viterbo, Italy

472 Plant Disease / Vol. 97 No. 4



Plant Pathology (2013)

Doi: 10.1111/ppa.12082

Real-time and qualitative PCR for detecting *Pseudomonas* syringae pv. actinidiae isolates causing recent outbreaks of kiwifruit bacterial canker

A. Gallelli, S. Talocci, M. Pilotti† and S. Loreti†*











 \rightarrow Objective develop simplex TaqMan real-time PCRs to detect:

- *Psa* b1
- *P*sa b2
- *Psa* b3
- pathovar actinidiae as a whole
- pathovar actinidifoliorum as a whole



- \rightarrow Validation of the method:
 - analytical sensitivity (limit of detection)
 - analytical specificity (inclusivity and exclusivity)
 - specificity









- → Genomic comparison of 49 Psa and Psaf genomes (44 available on NCBI and 5 Psaf genomes sequenced in this study (genome announcement submitted)):
 - Psa: effector gene
 - Psa b1: effector gene
 - Psa b2: gene encoding hypothetical protein
 - Psa b3: effector gene
 - Psaf: gene encoding hypothetical protein



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Development of specific primers and probes

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Specificity validated by in silico nucleic BLAST on NCBI

Development of specific primers and probes

Validation on a small strain collection

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Analytical sensitivity

→ asymptomatic wood samples artificially contaminated with 10-fold bacterial series (from 10^7 to 10^3 CFU/mL)



Target organism	CFU/mL	CFU/PCR reaction
Psa	10 ³	2
Psa b1	10 ³	2
Psa b2	10 ³	2
Psa b3	10 ³	2
Psaf	104	20

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→ Inclusivity: 15 target strains and exclusivity: 15 non-target strains





→ Inclusivity: 15 target strains and exclusivity: 15 non-target strains

→ Specificity on a large strain collection (416)

Pseudomonas			Other genera			
Psa b1	Psa b2	Psa b3	Psaf	P.syringae	Erwinia	Xanthomonas
7	3	342	39	22	1	1

→PCRs performed on the high-throughput plateform IdentyPath of Anses





Target organism	Inclusivity	Exclusivity	Specificity on 416 strains
Psa	100 %	100 %	100 %
Psa b1	100 %	100 %	100 %
Psa b2	100 %	100 %	98 %*
Psa b3	100 %	100 %	100 %
Psaf	100 %	100 %	100 %

- \rightarrow * false positives:
 - 3 Psa b3 strains isolated in France
 - 3 Pss strains isolated from kiwifruit in France (Gaignard, 1984)

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Specificity (naturally contaminated samples)

	12 wood <i>Psa</i> b3	12 leaves <i>Psa</i> b3	1 leave Psaf
Target organism			
Psa	12/12	12/12	0/1
Psa b1	0/12	0/12	0/1
Psa b2	0/12	0/12	0/1
<i>Psa</i> b3	12/12	12/12	0/1
Psaf	0/12	0/12	1/1





General conclusion



✓ The identification of *actinidifoliorum* pathovar was relevant to → include in the pathovar *actinidiae* only strains responsible of bacterial canker of kiwifruit

→ improve legislative management options



- ✓ MLVA scheme:
 - \rightarrow origin of *Psa* b3 epidemic in France is Italy

→ trace the epidemic routes of *Psa* b3 in **other countries** (New Zealand, Chile, Spain, ...)



- ✓ New TaqMan real-time PCRs:
 - \rightarrow good **sensitivity** and high **specificity**
 - → useful for Psa and Psaf detection
 - \rightarrow perspective: multiplex the real-time PCRs





Investigate, evaluate, protect

Charles Manceau Françoise Poliakoff Corinne Audusseau Sandrine Paillard Christelle François Carène Rivoal Valérie Olivier





EMERSYS Sophie Cesbron Marie-Agnès Jacques Marion Fisher-Le Saux Perrine Portier Martial Briand



Joël Vanneste









IdentyPath



→Statistic method determining **population structures**, which are **genetically different** by plotting them in a two-dimensional plan

55 anses 😳





→Statistic method determining population structures, which are genetically different by plotting them in a two-dimensional plan

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DAPC



→The horizontal axis allows the identification of **2 groups**:

- group 1: France and Italy (clusters 1 and 4)
- group 2: China, New Zealand and Chile (clusters 2 and 3) anses





 \rightarrow Structuring of strains at the pathovar and biovar levels

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