Corso di Dottorato in Scienze e Tecnologie Agrarie
XXXII Ciclo

COMPLEMENTARY RESEARCHES and BIOTECHNOLOGICAL INNOVATIVE APPROACHES TOWARDS ENVIRONMENTALLY-FRIENDLY CONTROL OF BACTERIAL DISEASES of PLANTS

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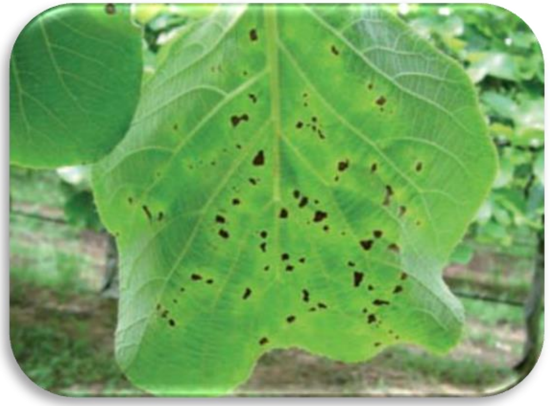
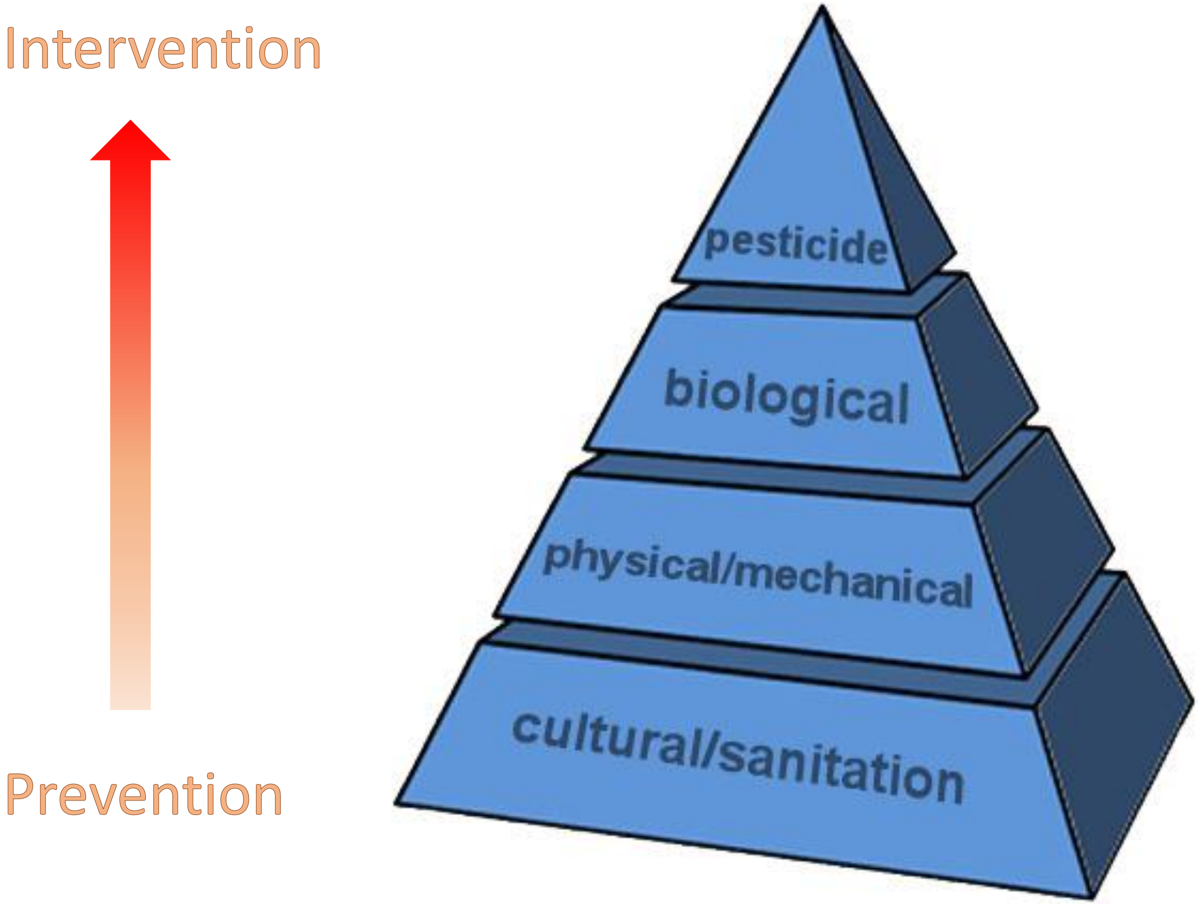
TUTOR: Prof.ssa Stefania Tegli
CO-TUTOR: Prof. Stefano Biricolti

Erwinia amylovora



Pseudomonas syringae pv. actinidiae

Xylella fastidiosa



"It doesn't seem to be covered in our invasive species management plan."

Control of Bacterial Plant Disease

Nasty side effects of copper treatments:

- ✓ accumulation into the topsoil
- ✓ negative impact on soil biology
- ✓ negative impact on transformation/dynamic of nutrients
- ✓ secondary pollution in watercourses
- ✓ serious negative ecotoxicological effects

…last but not least

- ✓ increase of copper- and antibiotic-resistant bacteria

Restriction of Copper Use

- Council Directive **91/414/EEC** of 15 July 1991 concerning the placing of plant protection products on the market.
- Commission Directive **2009/37/EC** of 23 April 2009 amending Council Directive 91/414/EEC to include chlormequat, copper compounds, propaquizafop, quizalofop-P, teflubenzuron and zeta-cypermethrin as active substances.
- Regulation (EC) No **1107/2009** of the European Parliament and of the Council of 21 October 2009 concerning the placing of plant protection products on the market and repealing Council Directives 79/117/EEC and 91/414/EEC.
- Commission Implementing Regulation (EU) No **540/2011** of 25 May 2011 implementing Regulation (EC) No 1107/2009 of the European Parliament and of the Council as regards the list of approved active substances.
- Commission Implementing Regulation (EU) No **541/2011** of 1 June 2011 amending Implementing Regulation (EU) No 540/2011 implementing Regulation (EC) No 1107/2009 of the European Parliament and of the Council as regards the list of approved active substances.
- Commission Implementing Regulation (EU) **2015/232** of 13 February 2015 amending and correcting Implementing Regulation (EU) No 540/2011 as regards the conditions of approval of the active substance copper compounds.

EFSA Journal

REASONED OPINION

ADOPTED: 1 March 2018

doi: 10.2903/j.efsa.2018.5212

Review of the existing maximum residue level[…] compounds according to Article 12 of Regul[…] No 396/2005

efsa European Food Safety Authority Supporting Publications

TECHNICAL REPORT

APPROVED: 30 August 2018

doi:10.2903/sp.efsa.2018.EN-1486

Outcome of the consultation with Member States, the applicant and EFSA on the pesticide risk assessment for copper compounds copper(I), copper(II) variants namely copper hydroxide, copper oxychloride, tribasic copper sulfate, copper(I) oxide, Bordeaux mixture in light of confirmatory data

CONCLUSION ON PESTICIDES PEER REVIEW

APPROVED: 20 December 2017

doi: 10.2903/j.efsa.2018.5152

Peer review of the pesticide risk assessment of the active substance copper compounds copper(I), copper(II) variants namely copper hydroxide, copper oxychloride, tribasic copper sulfate, copper(I) oxide, Bordeaux mixture

efsa

European Food Safety Authority

L 317/16 EN Official Journal of the European Union 14.12.2018

COMMISSION IMPLEMENTING REGULATION (EU) 2018/1981

of 13 December 2018

renewing the approval of the active substances copper compounds, as candidates for substitution, in accordance with Regulation (EC) No 1107/2009 of the European Parliament and of the Council concerning the placing of plant protection products on the market, and amending the Annex to Commission Implementing Regulation (EU) No 540/2011

(Text with EEA relevance)

Aim

COMPLEMENTARY RESEARCHES AND INNOVATIVE APPROACHES FOR THE SAFE AND ENVIRONMENTALLY-FRIENDLY CONTROL OF BACTERIA PLANT DISEASES

Gram-negative bacteria

Pseudomonas savastanoi pv. *nerii Psn23*

Approach

Genomic

Physiological

Studies

- ✓ MATE pumps
- ✓ IAA Homeostasis

Gram-positive bacteria

Curtobacterium flaccumfaciens pv. flaccumfaciens (Cff)

Approach

Genomic

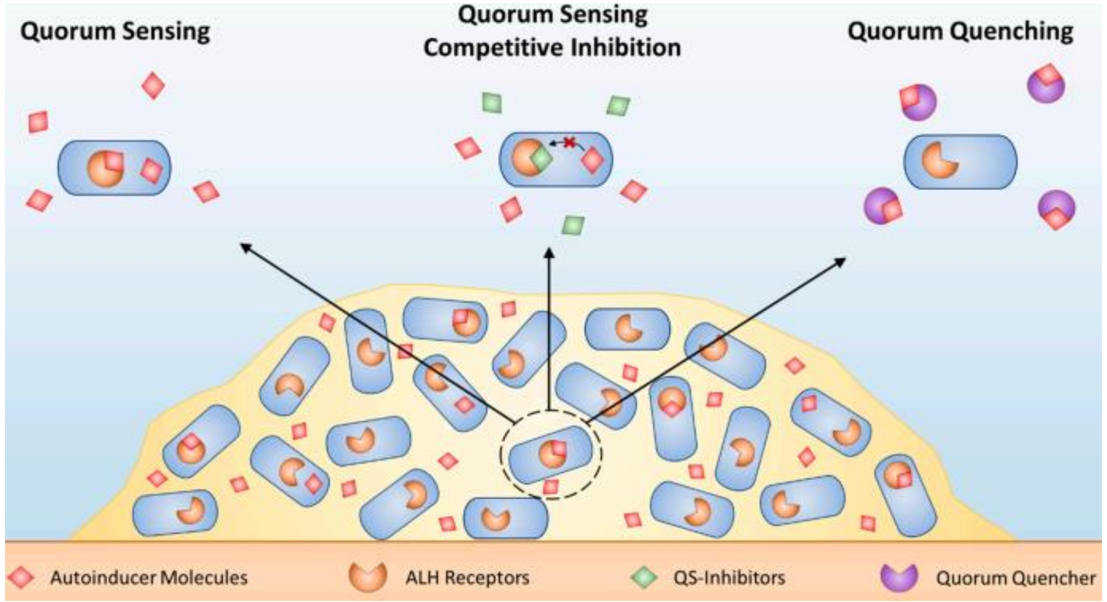
Epidemiological

Studies

- ✓ Population Analysis
- ✓ Genomic Studies

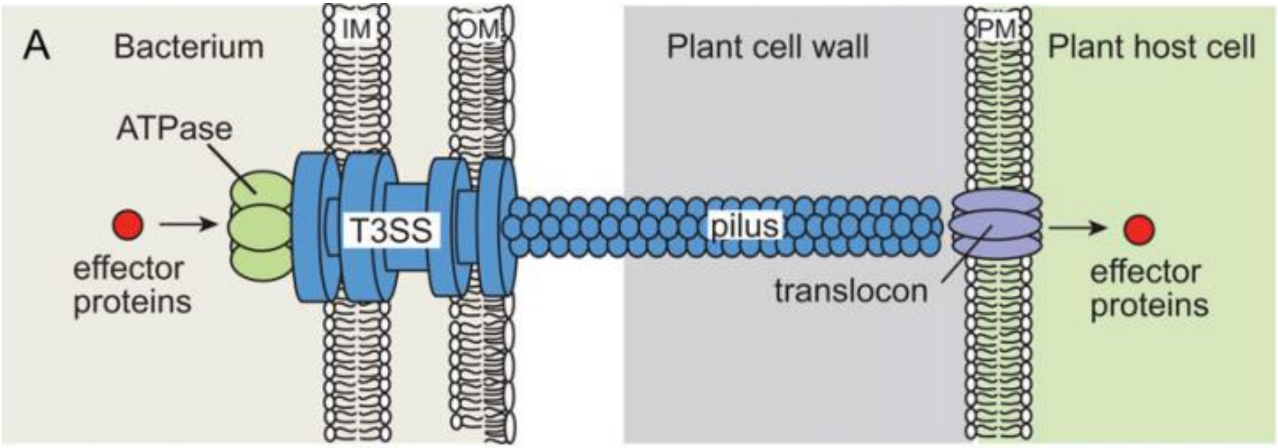
Pseudomonas savastanoi pv. nerii *Psn23*

Quorum Sensing



(Beitelshees *et al.*, 2018, *Materials)*

Type Three Secretion System (TTSS)



(Buttner and He, 2009, *Plant Physiology)*

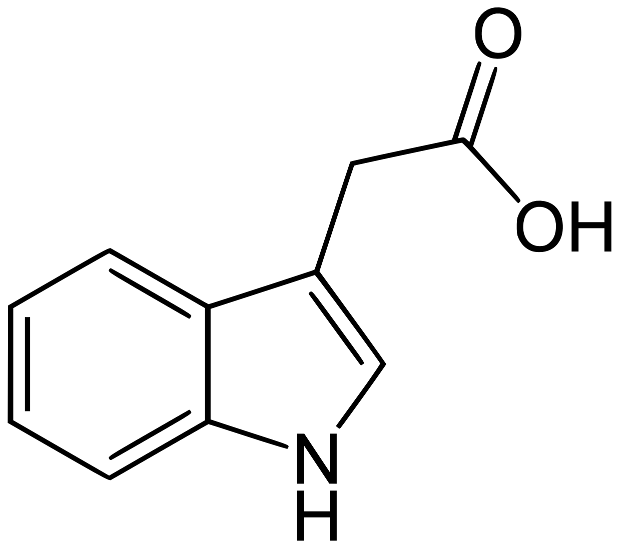
PLoS One. 2016; 11(9): e0163357. PMCID: PMC5036890
Published online 2016 Sep 26. doi: 10.1371/journal.pone.0163357 PMID: 27668874

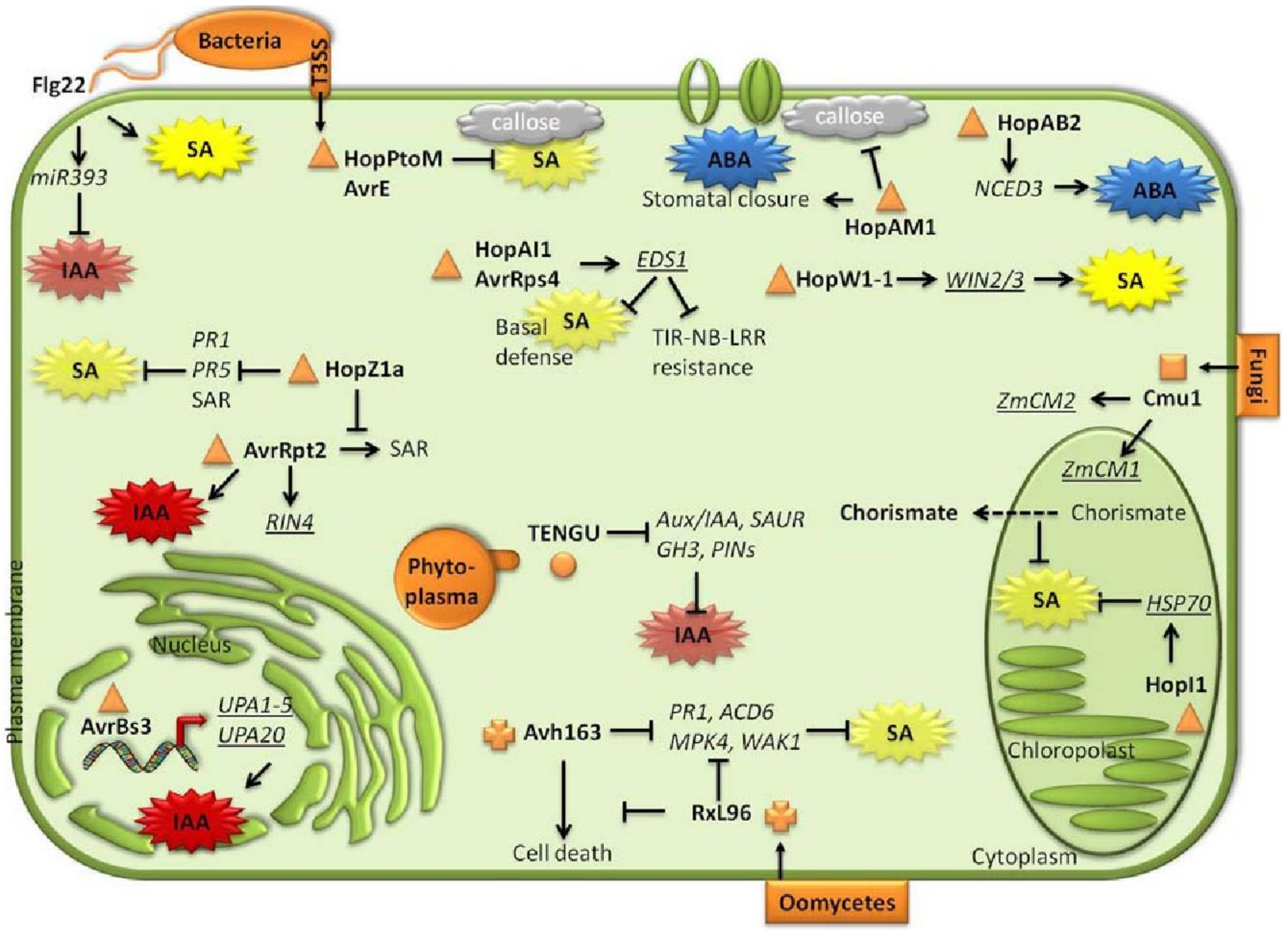
Global Analysis of Type Three Secretion System and Quorum Sensing Inhibition of *Pseudomonas savastanoi* by Polyphenols Extracts from Vegetable Residues

Carola Biancalani,[#1] Matteo Cerboneschi,[#1] Francesco Tadini-Buoninsegni,[#2] Margherita Campo,[3,‡] Arianna Scardigli,[4,‡] Annalisa Romani,[4,‡] and Stefania Tegli[#1,*]

Detecting alternative target

Indol-3-acetic acid





MPMI Vol. 11, No. 2, 1998, pp. 156–162. Publication no. M-1997-1126-01N.

Research Note

Auxin Production Is a Common Feature of Most Pathovars of *Pseudomonas syringae*

Eric Glickmann,[1] Louis Gardan,[2] Sylvie Jacquet,[2] Shafik Hussain,[2] Miena Elasri,[1] Annik Petit,[1] and Yves Dessaux[1]

[1]Institut des Sciences Végétales, Centre National de la Recherche Scientifique, Avenue de la Terrasse, F-91198 Gif sur Yvette Cedex; [2]Station de Pathologie Végétale, Institut National de la Recherche Agronomique, 42, rue Georges Morel, B.P. 57, F-49071 Beaucouzé Cedex, France

Accepted 3 November 1997.

ELSEVIER

Research in Microbiology

Volume 167, Issues 9–10, November–December 2016, Pages 774-787

Indole-3-acetic acid in plant–pathogen interactions: a key molecule for in planta bacterial virulence and fitness

Matteo Cerboneschi [a], Francesca Decorosi [b], Carola Biancalani [a], Maria Vittoria Ortenzi [a], Sofia Macconi [a], Luciana Giovannetti [b], Carlo Viti [b], Beatrice Campanella [c], Massimo Onor [c], Emilia Bramanti [c], Stefania Tegli [a]

PLOS | PATHOGENS

RESEARCH ARTICLE

Indole-3-acetaldehyde dehydrogenase-dependent auxin synthesis contributes to virulence of *Pseudomonas syringae* strain DC3000

Sheri A. McClerklin[☯], Soon Goo Lee[☯], Christopher P. Harper, Ron Nwumeh, Joseph M. Jez, Barbara N. Kunkel*

Department of Biology, Washington University, St. Louis, Missouri, United States of America

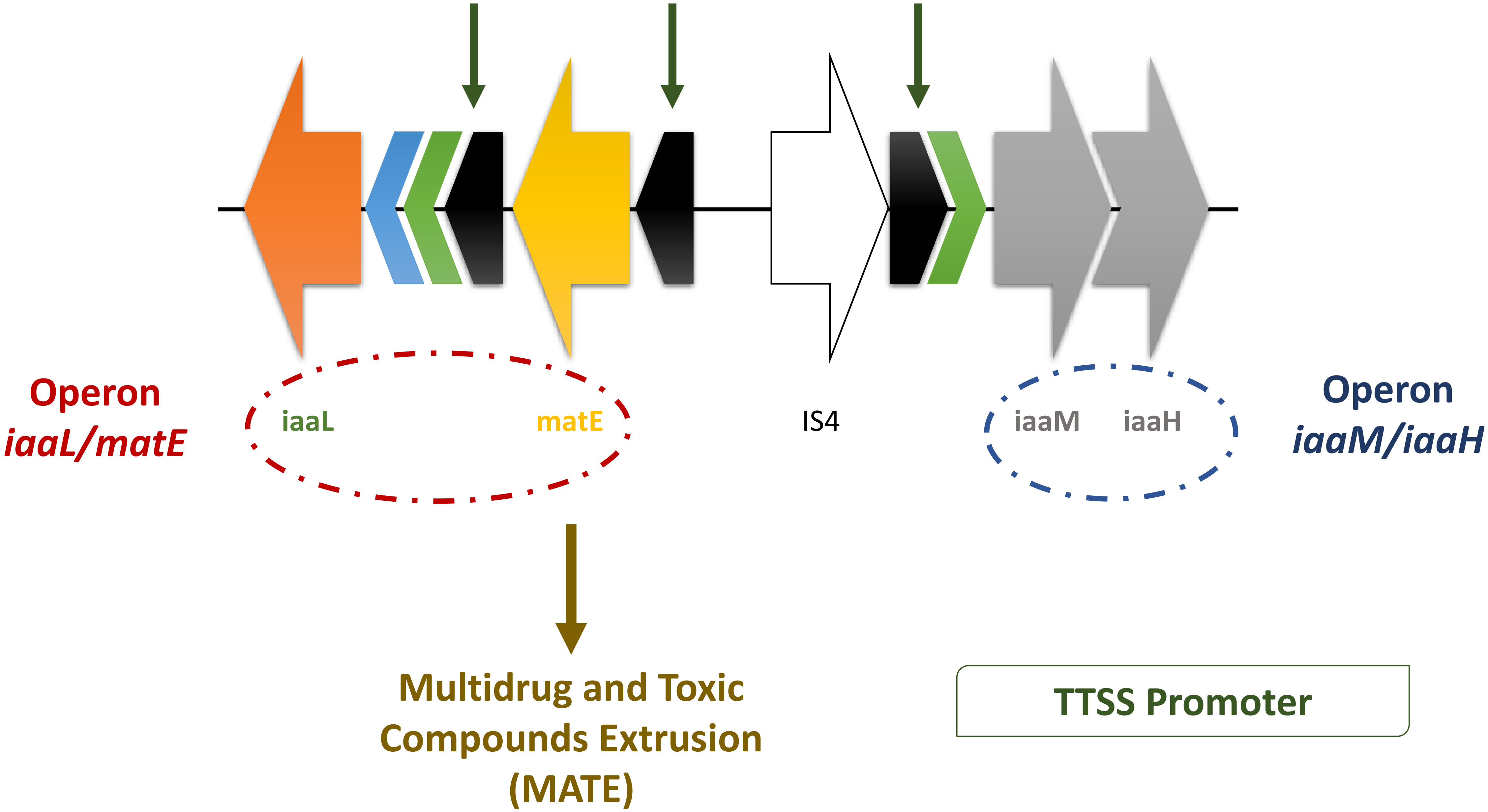
☯ These authors contributed equally to this work.

* kunkel@wustl.edu

Citation: McClerklin SA, Lee SG, Harper CP, Nwumeh R, Jez JM, Kunkel BN (2018) Indole-3-acetaldehyde dehydrogenase-dependent auxin synthesis contributes to virulence of *Pseudomonas syringae* strain DC3000. PLoS Pathog 14(1): e1006811. https://doi.org/10.1371/journal.ppat.1006811

Abstract

The bacterial pathogen *Pseudomonas syringae* modulates plant hormone signaling to promote infection and disease development. *P. syringae* uses several strategies to manipulate auxin physiology in *Arabidopsis thaliana* to promote pathogenesis, including its synthesis of indole-3-acetic acid (IAA), the predominant form of auxin in plants, and production of virulence factors that alter auxin responses in the host; however, the role of pathogen-derived auxin in *P. syringae* pathogenesis is not well understood. Here we demonstrate that *P. syringae* strain DC3000 produces IAA via a previously uncharacterized pathway and identify a novel indole-3-acetaldehyde dehydrogenase, AldA, that functions in IAA biosynthesis by


Operon
iaaL/matE
iaaL
matE
IS4
iaaM
iaaH
Operon
iaaM/iaaH
Multidrug and Toxic
Compounds Extrusion
(MATE)
TTSS Promoter

microorganisms

MDPI

Article

A MATE Transporter is Involved in Pathogenicity and IAA Homeostasis in the Hyperplastic Plant Pathogen *Pseudomonas savastanoi* pv. *nerii*

Stefania Tegli [1,*], Lorenzo Bini [1], Silvia Calamai [1], Matteo Cerboneschi [2] and Carola Biancalani [1]

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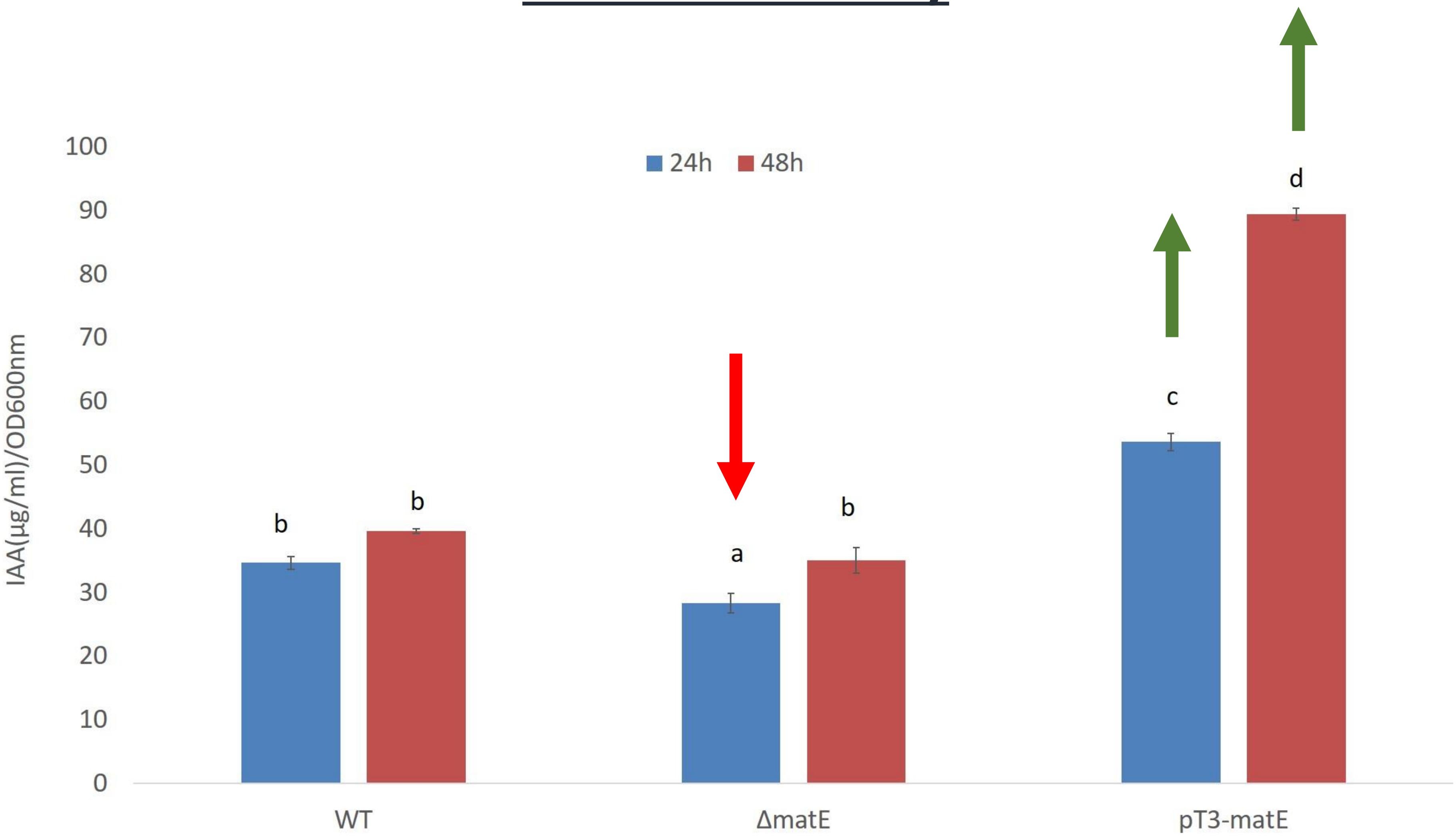
Received: 17 December 2019; Accepted: 18 January 2020; Published: 22 January 2020

Salkowski's assay

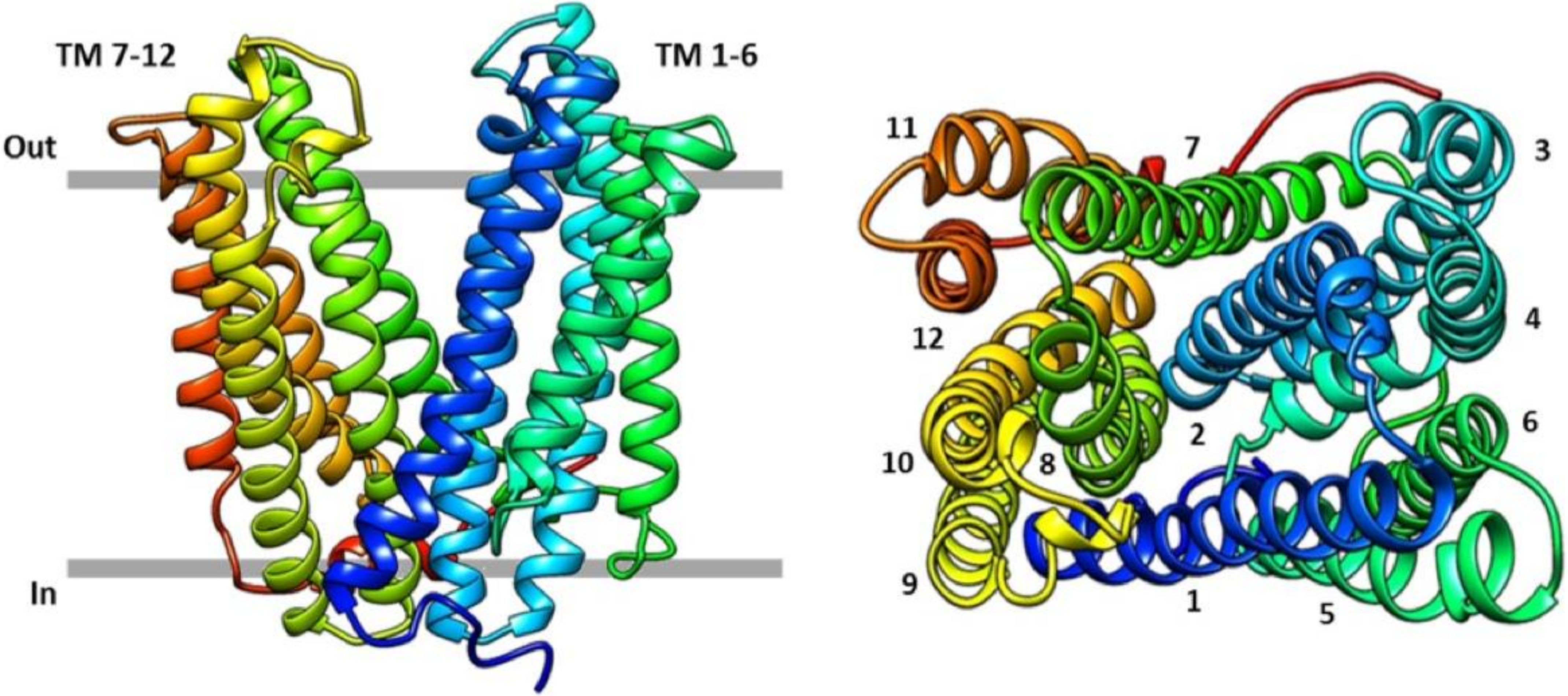
Mutants

ΔmatE

pT3_matE



Predicted structure of *Psn23* MatE



Molecular Docking

Ligand	Energy	H T175	H Y200	V T170	V T173	V T175	V Y200
IAA-free	-102.5	0	0	0	0	-1.5	-28.5
IAA-lysine	-95.1	-5.9	0	-2.1	-3.5	-3.9	-16.8

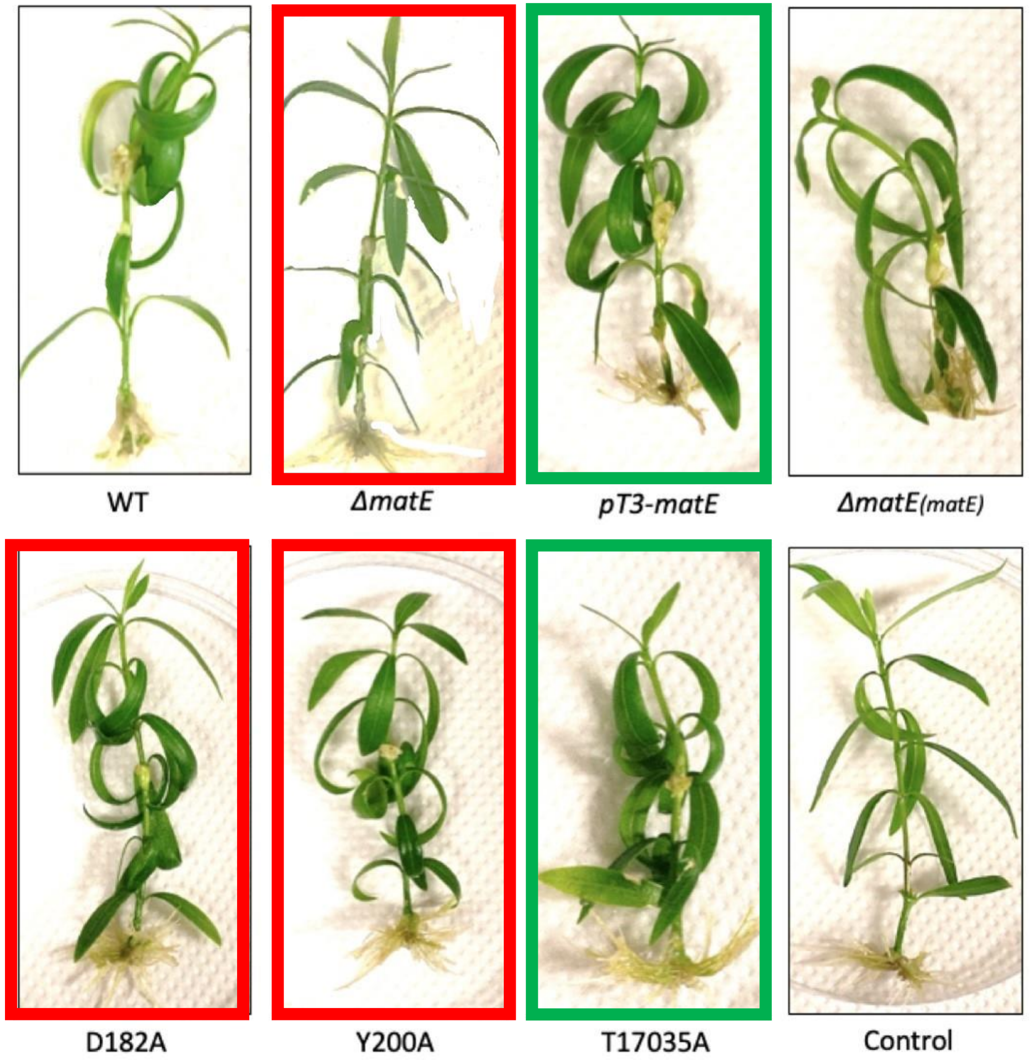
Mutants

D182A

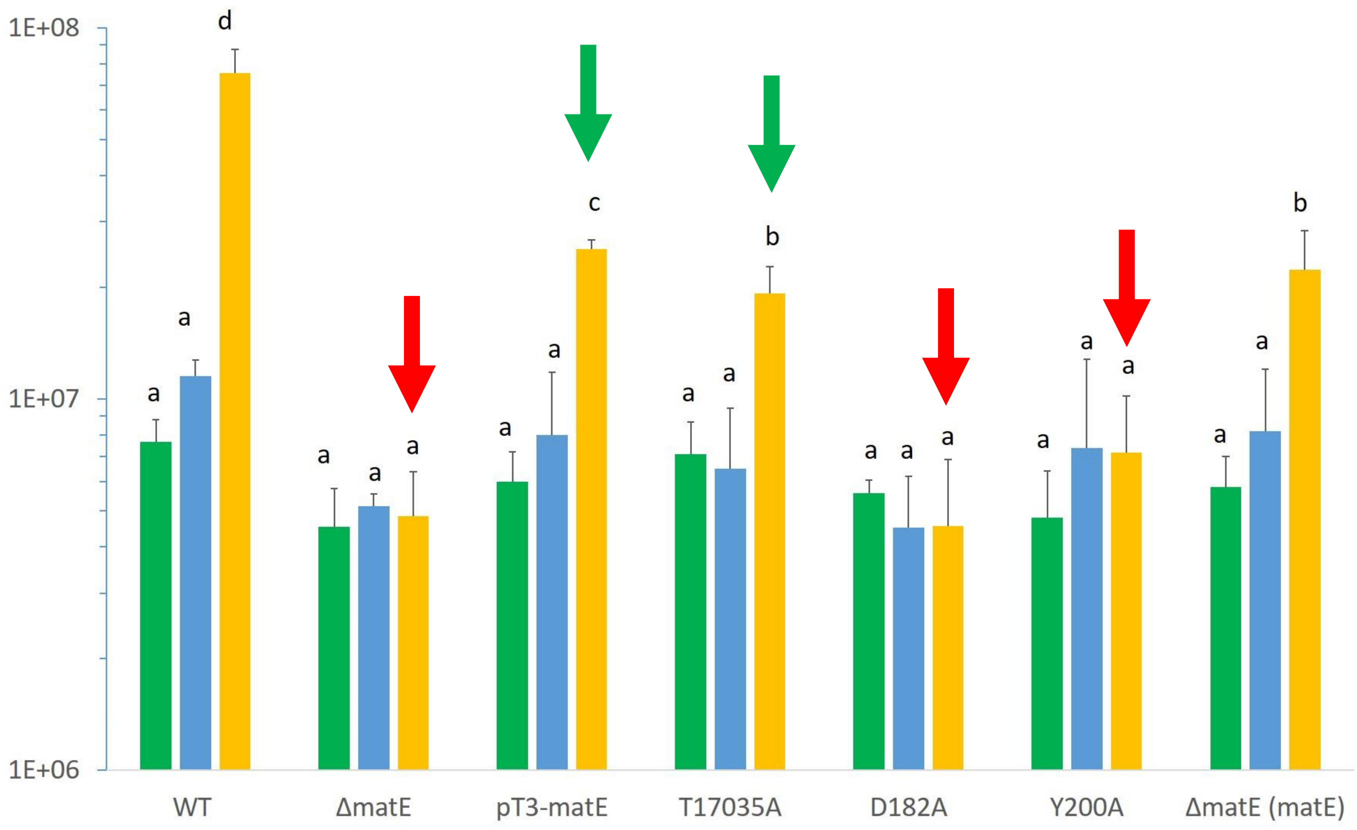
Y200A

T17035A

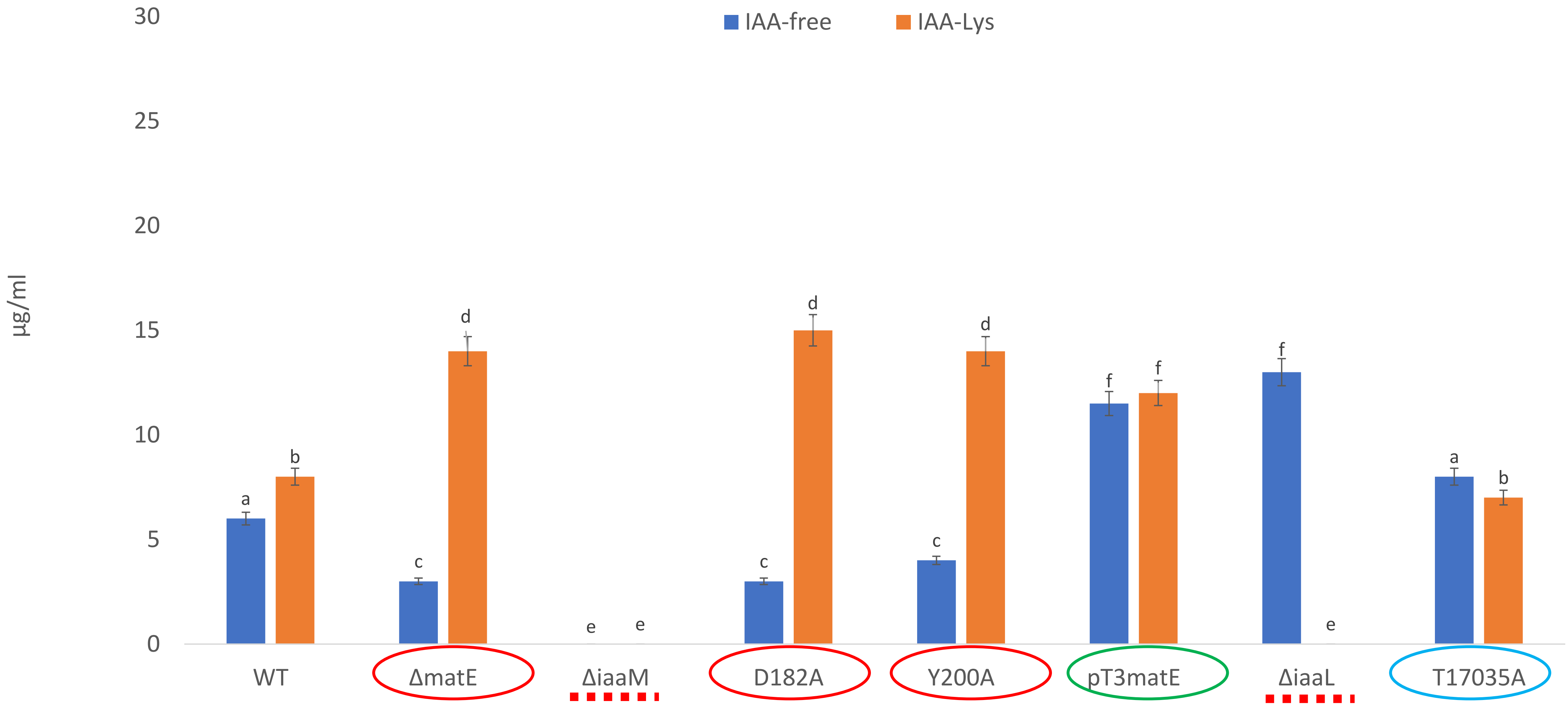
Pathogenicity Trials



Bacterial Growth *in planta*

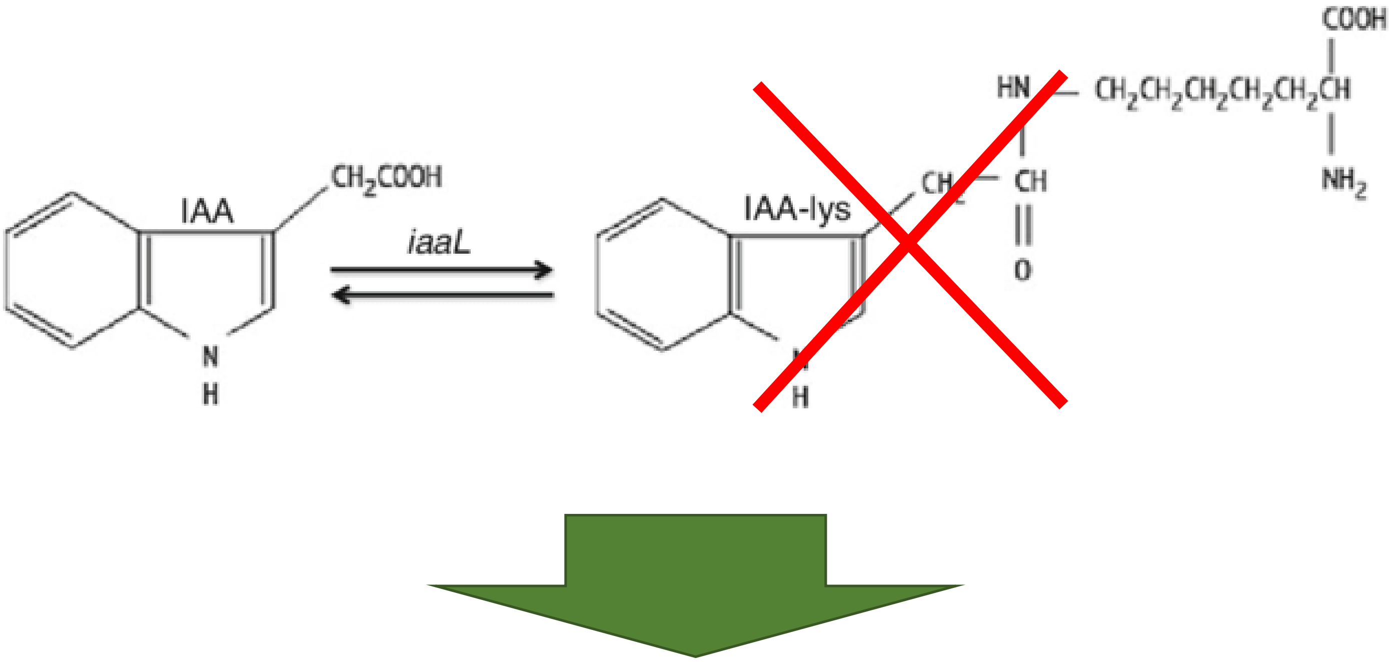


IAA and IAA-Lys Quantification by HPLC-FLD



Conclusion

✓ Psn23 MatE mediates IAA efflux and homeostasis



Alternative Target for Bacterial Plant Disease Control

Gram-negative bacteria

Pseudomonas savastanoi pv. *nerii Psn23*

Approach

Genomic

Physiological

Studies

- ✓ MATE pumps
- ✓ IAA Homeostasis

Gram-positive bacteria

Curtobacterium flaccumfaciens pv. flaccumfaciens (Cff)

Approach

Genomic

Epidemiological

Studies

- ✓ Population Analysis
- ✓ Genomic Studies

Curtobacterium flaccumfaciens pv. *flaccumfaciens* (*Cff*)

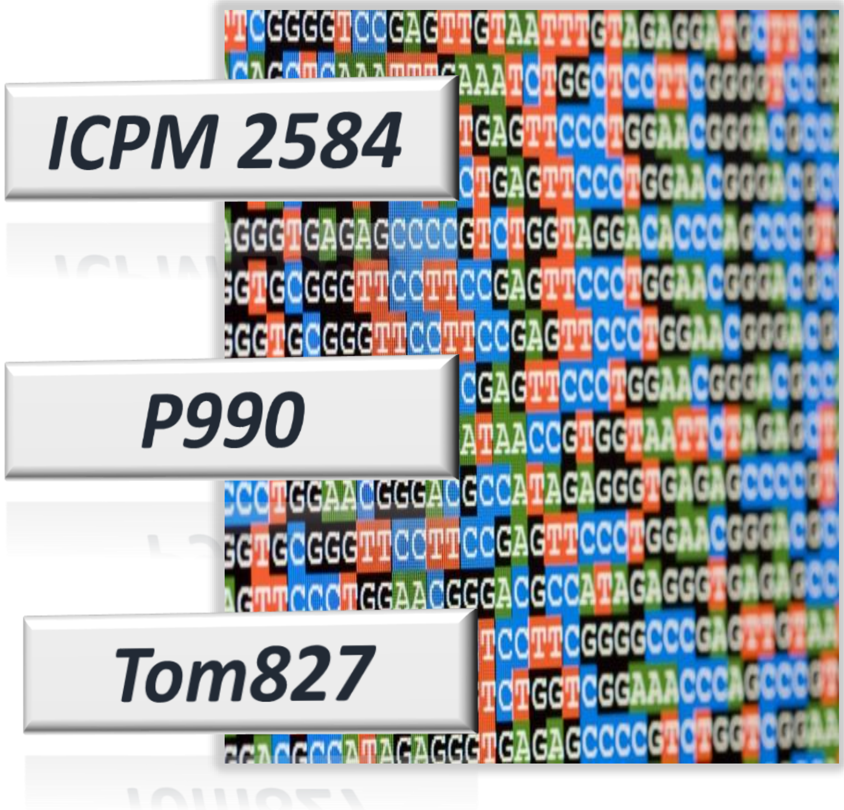
Population Analysis

Phenotypic and Molecular-Phylogenetic Analysis Provide Novel Insights into the Diversity of *Curtobacterium flaccumfaciens*

Ebrahim Osdaghi,† **S. Mohsen Taghavi**, **Silvia Calamai**, **Carola Biancalani**, **Matteo Cerboneschi**, **Stefania Tegli**, and **Robert M. Harveson**

First and second authors: Department of Plant Protection, College of Agriculture, Shiraz University, Shiraz 71441-65186, Iran; third, fourth, fifth, and sixth authors: Dipartimento di Scienze delle Produzioni Agroalimentari e dell'Ambiente, Laboratorio di Patologia Vegetale Molecolare, Università degli Studi di Firenze, Via della Lastruccia 10, 50019 Sesto Fiorentino, Firenze, Italy; and seventh author: University of Nebraska, Panhandle Research & Extension Center, 4502 Ave. I., Scottsbluff 69361.

Genomic Studies



Population Analysis of *Curtobacterium flaccumfaciens*

Isolated from dry beans

→ **Virulent on dry beans**

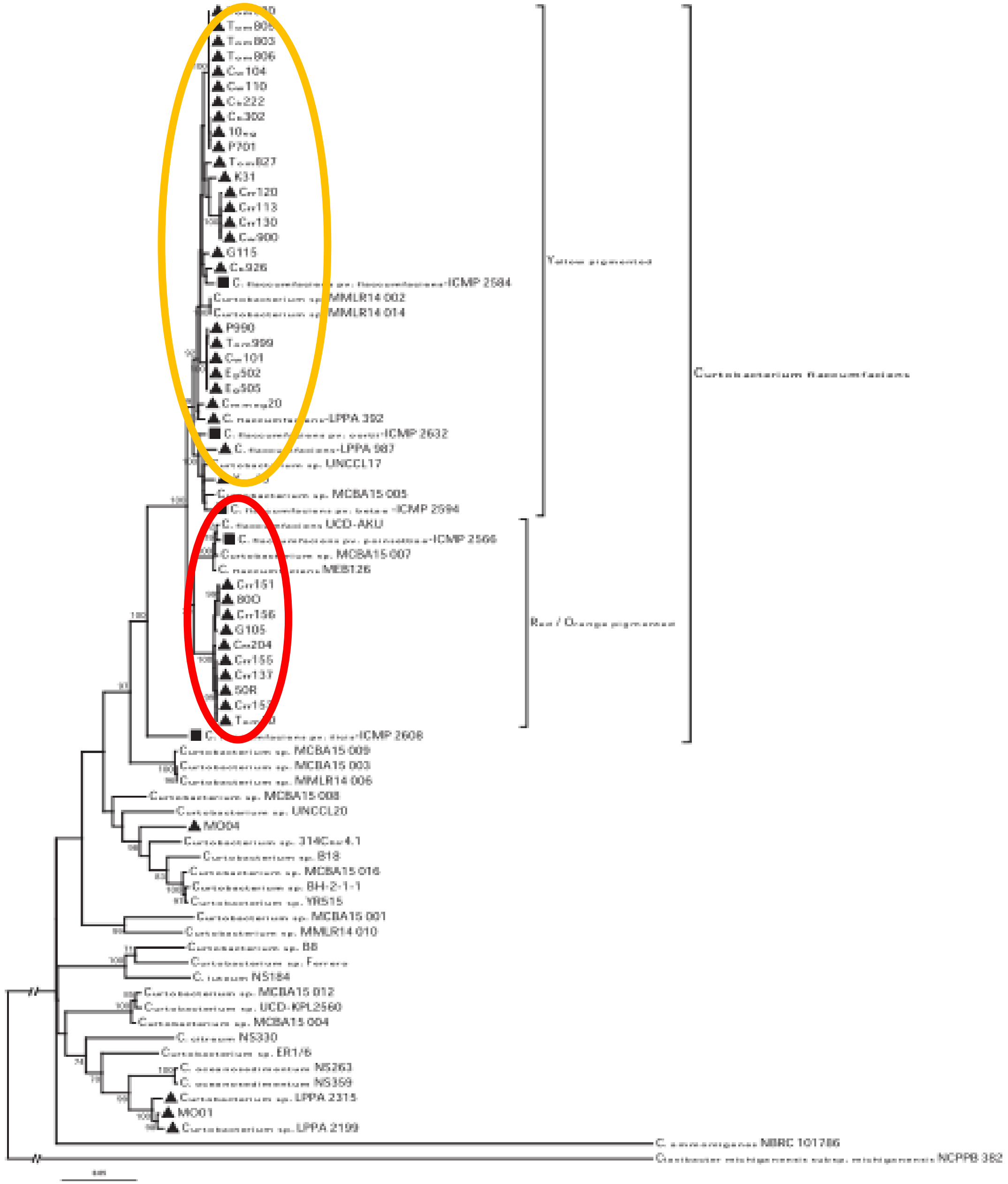
Isolated from solanaceous

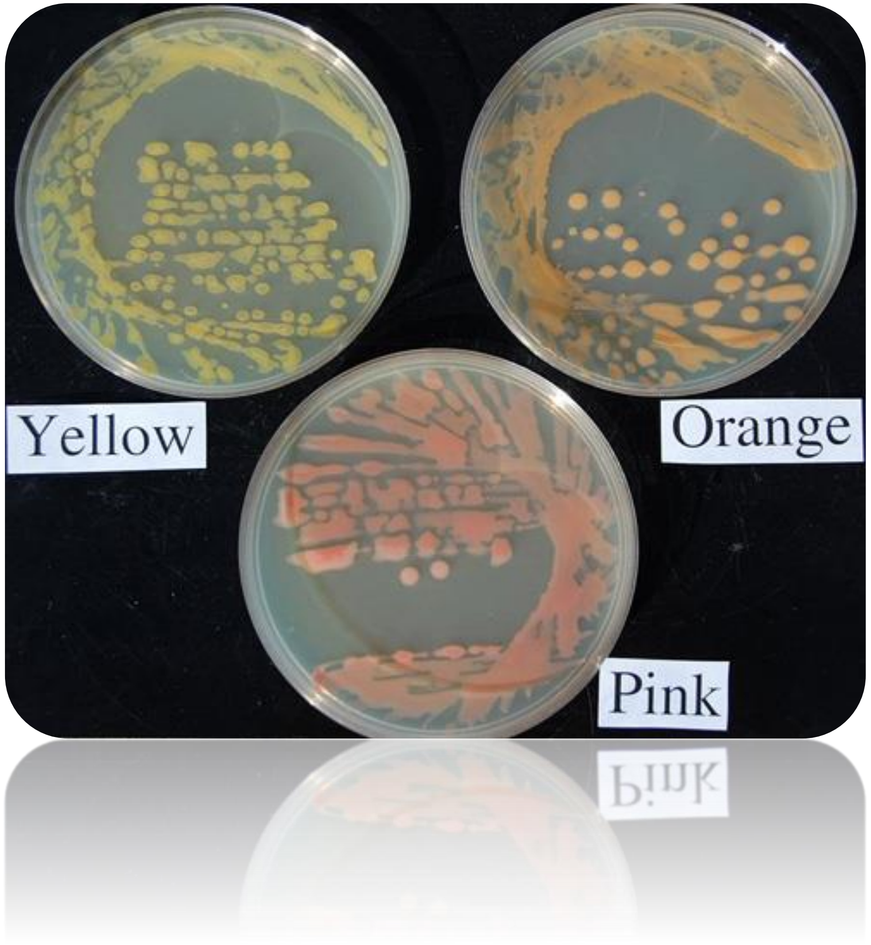
→ **Virulent on dry beans**

→ **No virulent on dry beans**

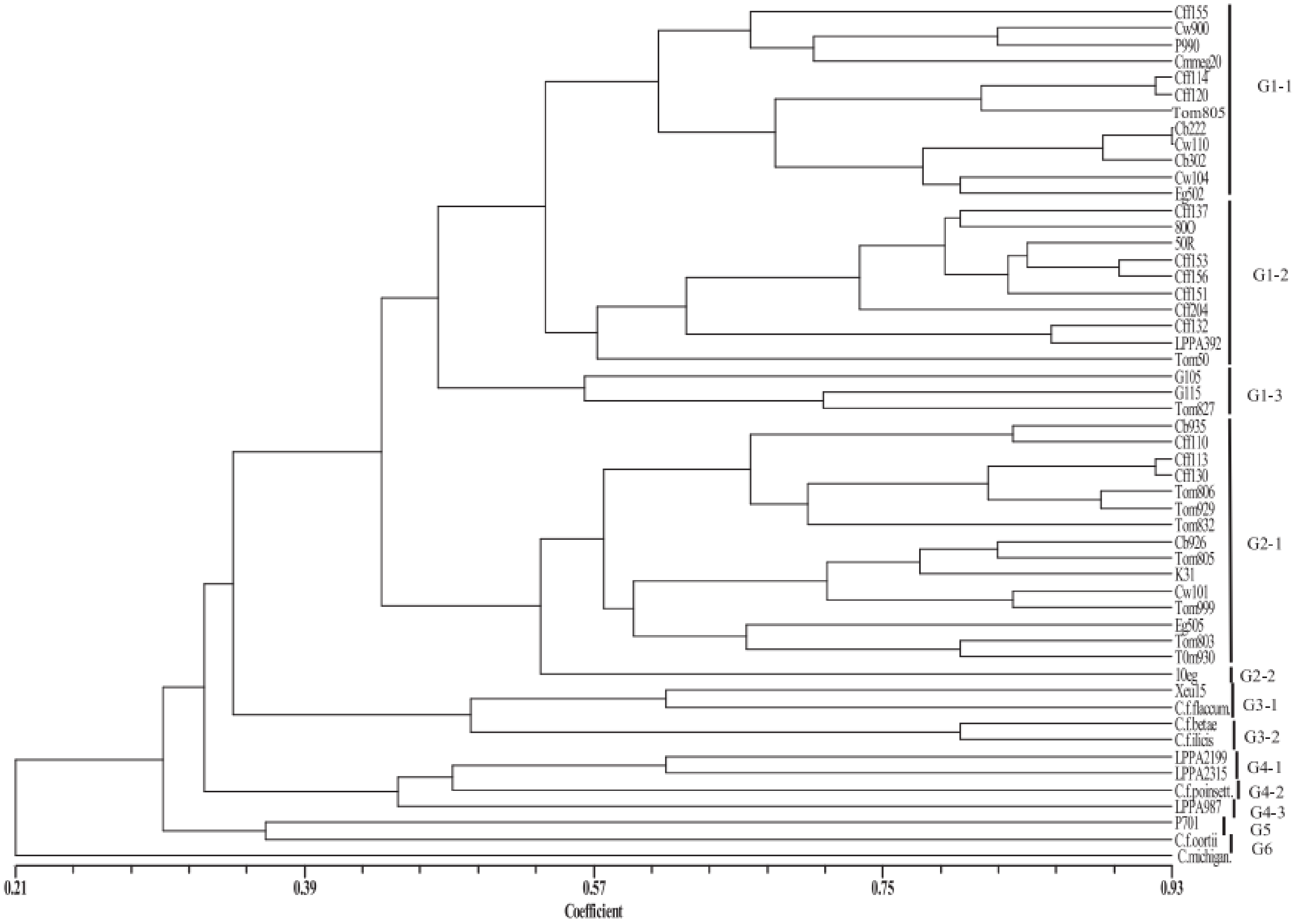
- ✓ ***Curtobacterium flaccumfaciens*** **pathovars**
- ✓ ***Clavibacter michiganensis*** **subsp. *michiganensis***

Phylogenetic Analysis





Genetic Diversity



No genetic diversity between strains isolated from dry beans and solanaceous plants

Screening for Arsenite Resistance

TABLE 3. Growth rate of *Curtobacterium flaccumfaciens*, *Curtobacterium*-like, and *Clavibacter michiganensis* strains used in this study on different concentrations of sodium arsenite ($NaAsO_2$) and sodium arsenate (Na_3AsO_4)[a]

Strain		Resistance to: Sodium arsenite 2 mM^S	Sodium arsenite 5 mM^S	Sodium arsenite 7 mM^S	Sodium arsenate 80 mM^S	Sodium arsenate 100 mM^S	Sodium arsenate 130 mM^S	Pathogenicity on common bean
C. flaccumfaciens pv. *flaccumfaciens*	10eg	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	50R	10^4–10^6	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	80O	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cb222	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cb302	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cb926	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cff110	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cff137	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cff151	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cff153	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cff155	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cff156	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	ICMP 2584^T	$\leq 10^2$	–	–	$\leq 10^2$	$\leq 10^2$	$\leq 10^2$	+
C. flaccumfaciens pv. *flaccumfaciens*	Cw101	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Cw110	10^4–10^6	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Eg502	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Eg505	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Mo11	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	P701	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	P990	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Tom50	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Tom803	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Tom806	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *flaccumfaciens*	Tom930	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	$\leq 10^2$	+
C. flaccumfaciens pv. *flaccumfaciens*	Tom999	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^2–10^4	+
C. flaccumfaciens pv. *oortii*	ICMP 2632^T	10^2–10^4	$\leq 10^2$	$\leq 10^2$	10^4–10^6	10^4–10^6	10^4–10^6	
C. flaccumfaciens	Cmmeg20	–	–	–	–	–	–	–
C. flaccumfaciens	G105	–	–	–	–	–	–	–
C. flaccumfaciens	Tom827	–	–	–	–	–	–	–
C. flaccumfaciens	Xeu15	–	–	–	–	–	–	–
Curtobacterium spp.	Mo04	–	–	–	–	–	–	–
Clavibacter michiganensis subsp. *michiganensis*	ICMP 2550^T	–	–	–	–	–	–	–
Clavibacter michiganensis subsp. *michiganensis*	NCPPB 382	–	–	–	–	–	–	–
Clavibacter michiganensis subsp. *michiganensis*	Tom835	–	–	–	–	–	–	–
Clavibacter spp.	Tom495	–	–	–	–	–	–	–

[a] All strains, which were pathogenic on common bean, were able to grow on different concentrations of both compounds, while nonpathogenic strains were sensitive. *Clavibacter michiganensis* strains were sensitive to both the compounds regardless of their pathogenicity on tomato. S = data statistically significant (ANOVA and Tukey's test, $P < 0.05$).

Genomic and Phenotypic Metal Resistance Profile

	CHEMICAL ELEMENT	*CHEMICAL COMPOUND*	*TOLERANCE LEVEL*		
			SENSITIVE[A]	MODERATELY TOLERANT[B]	RESISTANT[C]
METALS	**Al**	Aluminum sulfate		x[D]	
	Cd	Cadmium chloride	x		
	Co	Cobalt chloride		x	
	Cr	Potassium chromate		x	
		Sodium dichromate		x	
		Chromium chloride		x	
	Cs	Cesium chloride			x
	Cu	Cupric chloride		x	
	Fe	Ferric chloride		x	
	Li	Lithium chloride		x	
	Mn	Manganese(II) chloride		x	
	Ni	Nickel chloride		x	
	Tl	Thallium(I) acetate		x	
	V	Sodium metavanadate		x	
		Sodium orthovanadate		x	
	W	Sodium Tungstate		x	
	Zn	Zinc chloride		x	
METALLOIDS	**As**	Sodium m-arsenite		x (D)[E]	
		Sodium arsenate		x (D)	
	B	Boric acid		x	
		Sodium metaborate		x	
	Sb	Antimony(III) chloride		x (D)	
	Si	Sodium metasilicate			x
	Te	Potassium tellurite		x (D)	

ICPM 2584

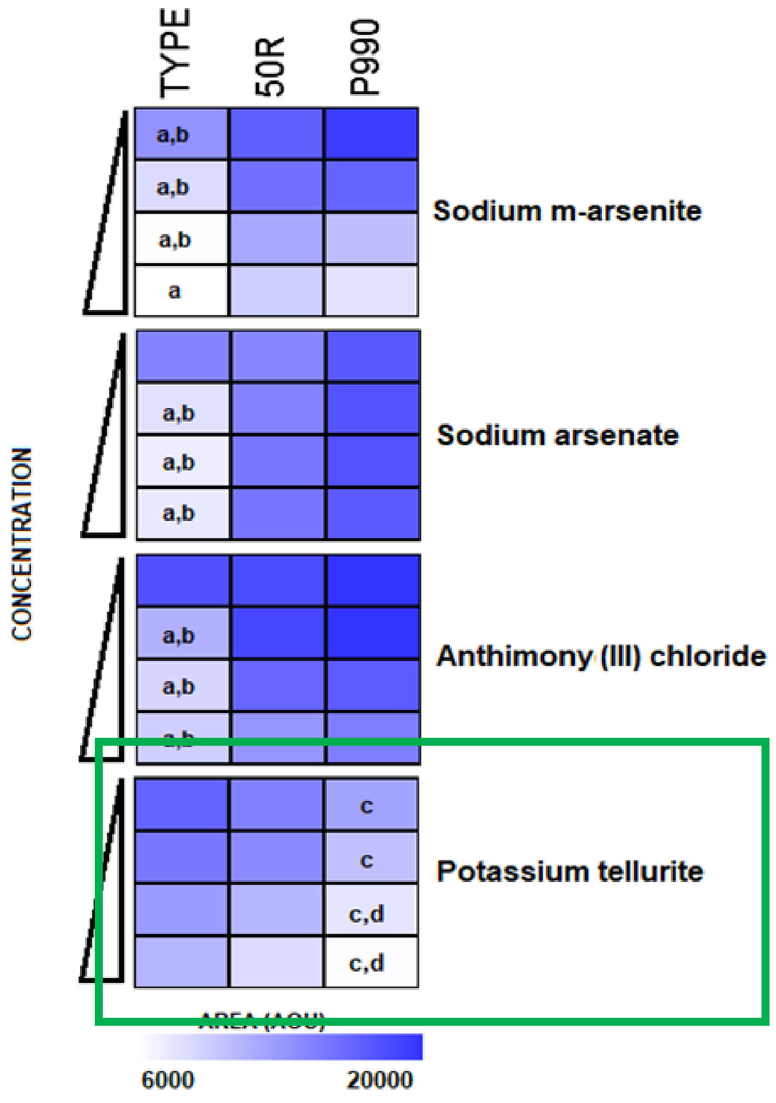
P990

50R

[D]X: the three showed overlapping kinetic curves

[E]X(D): the three strains showed different kinetic curves

Potassium Tellurite Tollerance



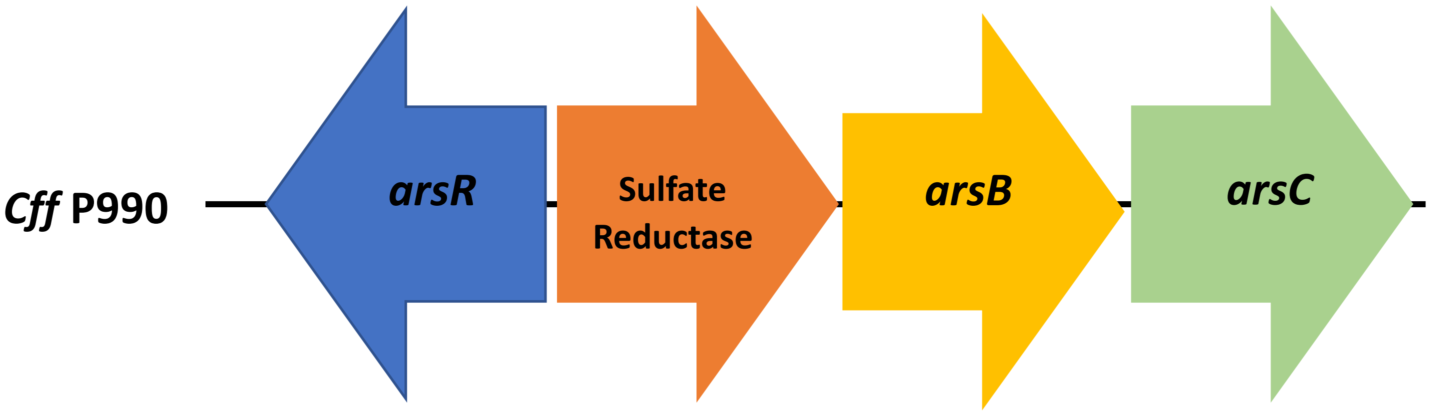
Screening for metal and metalloid resistance

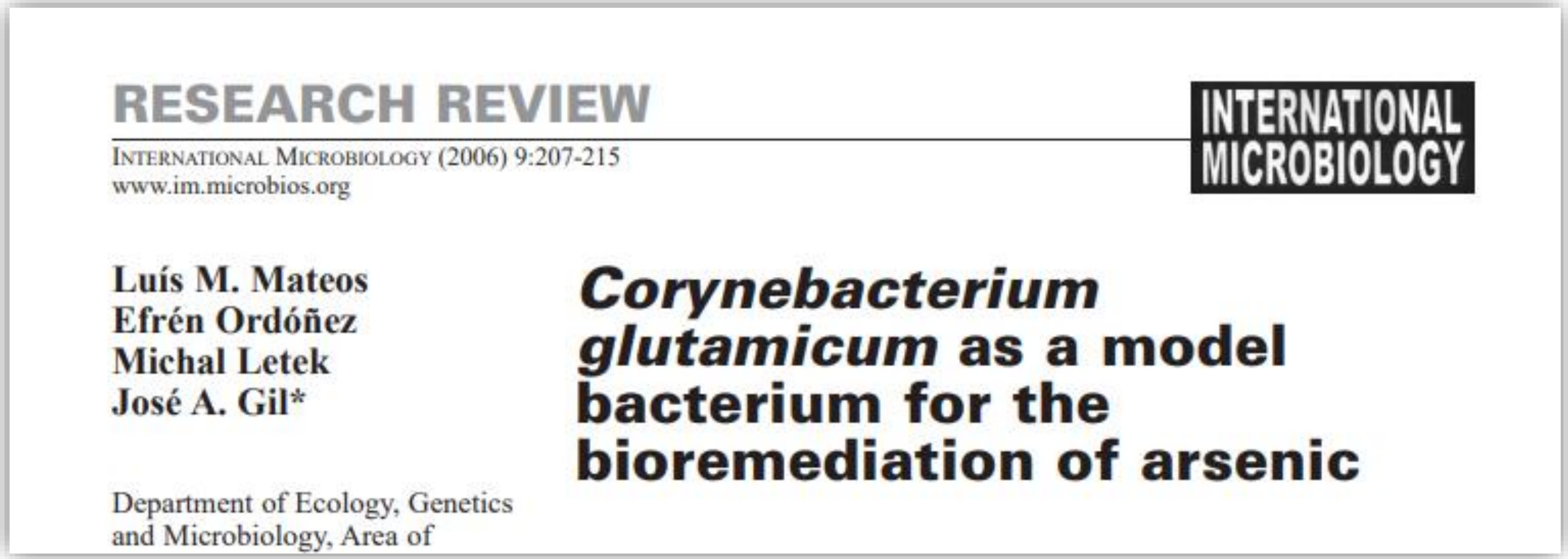
	Resistance to								
	Caesium Chloride			Sodium Metasilicate			Potassium Tellurite		
	75 mM	50 mM	25 mM	8 mM	6.5 mM	5 mM	0.3 mM	0.2 mM	0.1 mM
ICPM 2584	10^6-10^7	10^7-10^8	10^7-10^8	10^5-10^6	10^6-10^7	10^6-10^7	10^5	10^6	10^6
50R	10^6-10^7	10^7-10^8	10^7-10^8	10^5-10^6	10^6-10^7	10^6-10^7	10^5	10^6	10^6
P990	10^6-10^7	10^7-10^8	10^7-10^8	10^5-10^6	10^6-10^7	10^6-10	10^4	10^5	10^5
Tom827	10^6-10^7	10^7-10^8	10^7-10^8	10^5-10^6	10^6-10^7	10^6-10	10^4	10^5	10^5

Isolated from Fabaceae

Isolated from Solanaceae

Comparative Gene analysis





RESEARCH REVIEW
INTERNATIONAL MICROBIOLOGY (2006) 9:207-215
www.im.microbios.org
INTERNATIONAL MICROBIOLOGY

Luís M. Mateos
Efrén Ordóñez
Michal Letek
José A. Gil*

Department of Ecology, Genetics
and Microbiology, Area of

Corynebacterium glutamicum as a model bacterium for the bioremediation of arsenic

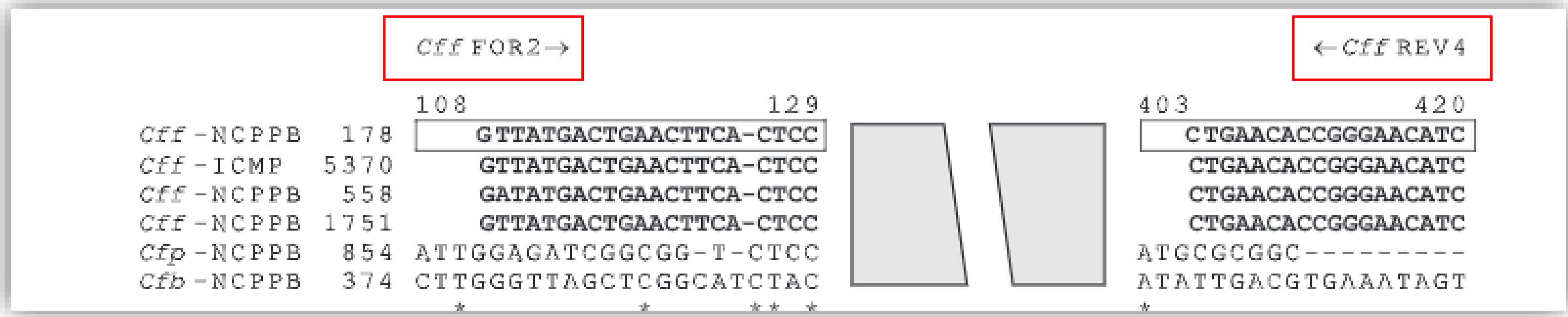
Comparative Genome Analysis of *Curtobacterium flaccumfaciens*

Letters in Applied Microbiology 2002, **35**, 331–337

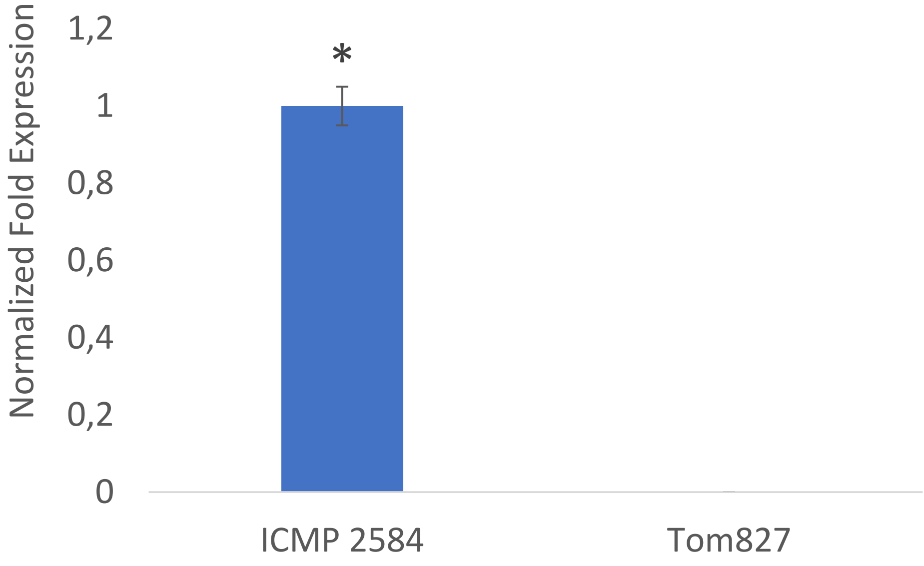
PCR-based assay for the detection of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* in bean seeds

S. Tegli, A. Sereni and G. Surico
Dipartimento di Biotecnologie Agrarie (DiBA) – Sezione di Patologia Vegetale, Università degli Studi di Firenze, Firenze, Italy

2002/31: received 23 January 2002, revised 1 March 2002 and accepted 25 June 2002



Gene Expression



Comparative genome analysis

CDS identifiers P990 strain	CDS identifiers Type strain	Annotation
p990_03611	type.fna_03759	trypsin-like serine protease
p990_03612	type.fna_03758	trypsin-like serine protease
p990_03613	type.fna_03757	serine protease
p990_03614	type.fna_03756	putative Serine/cysteine peptidase protein
p990_03615	type.fna_03755	pectate lyase
p990_03652	type.fna 03718	trypsin-like serine protease

p990_03610	type.fna_03760	transposase
p990_03627	type.fna_03743	transposase
p990_03648	type.fna_03722	transposase
p990_03649	type.fna_03721	integrase
p990_03650	type.fna_03720	integrase

Comparative genome analysis

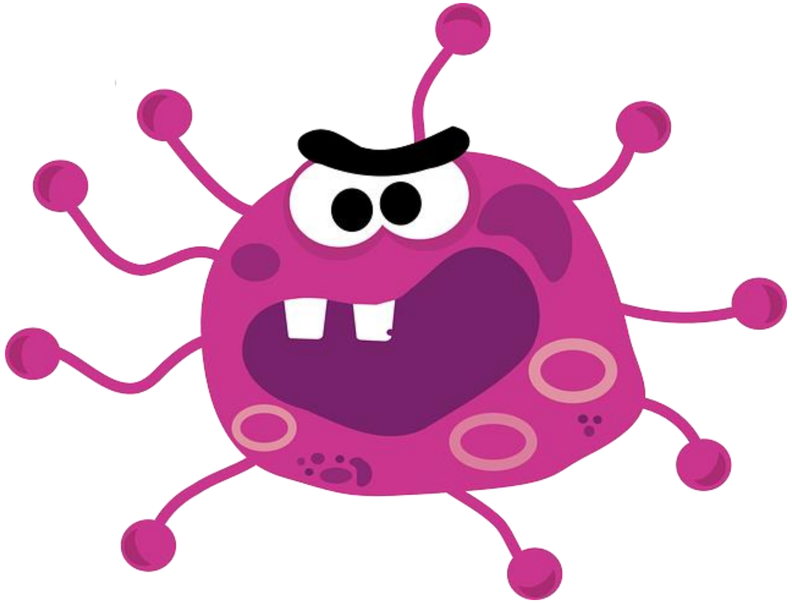
P990

ICPM 2584

~~Tom827~~

SERINE PROTEASE

PECTATE LYASE



New Phytologist
Research

Multiple plasmid-borne virulence genes of *Clavibacter michiganensis* ssp. *capsici* critical for disease development in pepper

In Sun Hwang[1], Eom-Ji Oh[1], Donghyuk Kim[2] and Chang-Sik Oh[1]
[1]Department of Horticultural Biotechnology, Kyung Hee University, Yongin 17104, Korea; [2]Graduate School of Biotechnology, Kyung Hee University, Yongin 17104, Korea

MPMI Vol. 22, No. 7, 2009, pp. 809–819. doi:10.1094/MPMI-22-7-0809.

The Putative Secreted Serine Protease Chp-7 Is Required for Full Virulence and Induction of a Nonhost Hypersensitive Response by *Clavibacter michiganensis* subsp. *sepedonicus*

Riitta Nissinen,[1] Yunjian Xia,[1] Laura M
Susan E. Knudson,[3] Mary Metzler,[4] ar

MOLECULAR PLANT PATHOLOGY (2008) **9**(5), 599–608 DOI: 10.1111/J.1364-3703.2008.00484.X

A family of serine proteases of *Clavibacter michiganensis* subsp. *michiganensis*: *chpC* plays a role in colonization of the host plant tomato

INES STORK, KARL-HEINZ GARTEMANN, ANNETTE BURGER AND RUDOLF EICHENLAUB
Fakultät für Biologie, Lehrstuhl für Mikrobiologie/Gentechnologie, Universitaetsstr. 25, D-33615 Bielefeld, Germany

Comparative genome analysis

P990

ICPM 2584

~~Tom827~~

TRASPOSASE

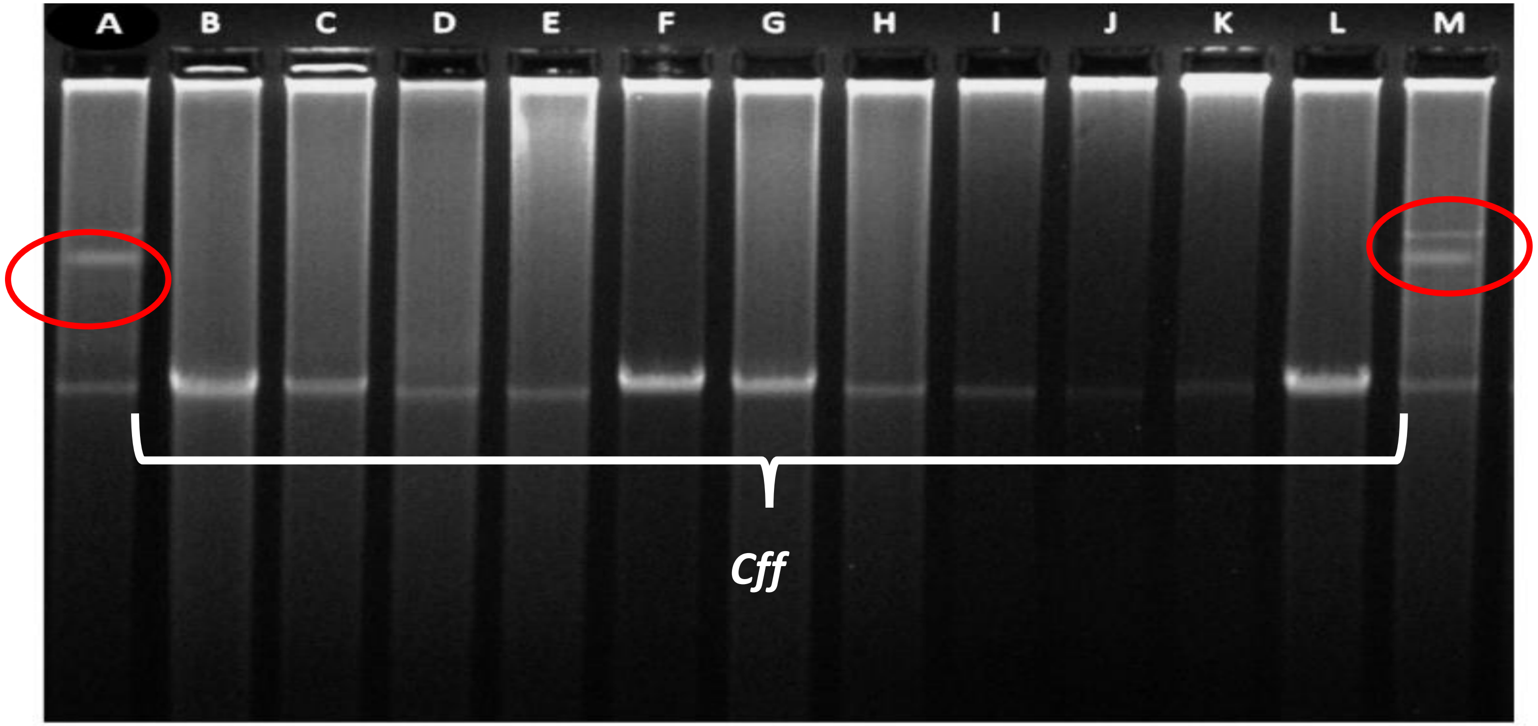
INTEGRASE

CONJUGATIVE GENES

Conjugative Relaxase, Pilus assembly protein, VirB4…

ICE ?

Plasmid Isolation



Conclusion

- ✓ Advance in epidemiology → CONTROL STRATEGY
- ✓ *ArsRBC* operon in P990
- ✓ Detect virulence determinant → NEW TARGETS

THANKS!

Silvia Calamai
silvia.calamai@unifi.it