

Evolutionary and Functional Genomics of Plant-associated Bacteria



植物暨微生物學研究所

Institute of Plant and Microbial Biology

Chih-Horng Kuo

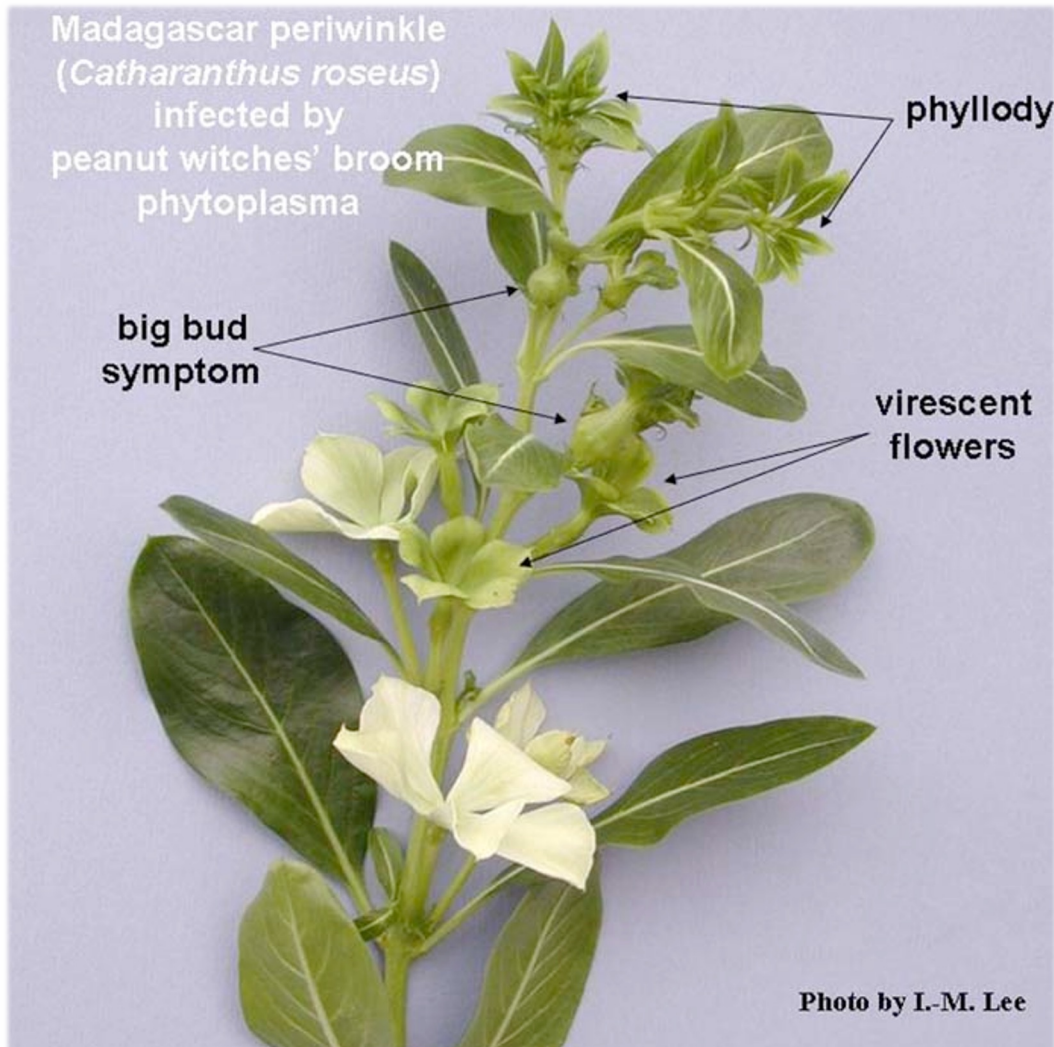
Evolutionary and Functional Genomics of Plant-associated Bacteria

- Questions
 - Biodiversity: evolutionary history and processes?
 - Functional consequences of genetic changes?
- Approaches
 - Phenotyping: infection experiments
 - Genotyping: genome sequencing and comparisons
 - Validation: molecular genetics, mutants, etc.



Phytoplasmas

Uncultivated bacteria that manipulate plants and insects



Difficulties in applying
conventional
microbiology tools



Genome sequencing &
comparative analysis



Identify key genes for
functional studies

Phytoplasmas

International collaborations: Brazil, Croatia, Poland, UK, etc.



GENOME SEQUENCES
August 2020 Volume 9 Issue 35 e00760-20
<https://doi.org/10.1128/MRA.00760-20>

Complete Genome Sequence of “*Candidatus* Phytoplasma asteris” RP166, a Plant Pathogen Associated with Rapeseed Phyllody Disease in Poland

Shu-Ting Cho^a, Agnieszka Zwolińska^b, Weijie Huang^c, Roland H. M. Wouters^c, Sam T. Mugford^c, Saskia A. Hogenhout^c, and Chih-Horng Kuo^{id}^a

^aInstitute of Plant and Microbial Biology, Academia Sinica, Taipei, Taiwan

^bVirology and Bacteriology Department, Institute of Plant Protection, National Research Institute, Poznań, Poland

^cDepartment of Crop Genetics, John Innes Centre, Norwich Research Park, Norwich, Norfolk, United Kingdom



Systematic and Applied Microbiology

Volume 42, Issue 2, March 2019, Pages 117-127



The genome of ‘*Candidatus* Phytoplasma solani’ strain SA-1 is highly dynamic and prone to adopting foreign sequences

Martina Seruga Music^a ✉, Ivana Samaržija^a ✉, Saskia A. Hogenhout^b ✉, Mindia Haryono^c ✉, Shu-Ting Cho^c ✉, Chih-Horng Kuo^c ✉

^a Department of Biology, Faculty of Science, University of Zagreb, Marulicev trg 9A, HR-10000 Zagreb, Croatia

^b Department of Crop Genetics, John Innes Centre, Norwich Research Park, Colney Ln, Norwich NR4 7UH, UK

^c Institute of Plant and Microbial Biology, Academia Sinica, 128 Sec. 2, Academia Rd., Taipei 11529, Taiwan

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ANNALS OF
BOTANY
FOUNDED 1887

PART OF A SPECIAL ISSUE ON PLANT IMMUNITY

A few sequence polymorphisms among isolates of Maize bushy stunt phytoplasma associate with organ proliferation symptoms of infected maize plants

Zigmunds Orlovskis¹, Maria Cristina Canale^{1,2,†}, Mindia Haryono³, João Roberto Spotti Lopes², Chih-Horng Kuo^{3,*} and Saskia A. Hogenhout^{1,*}

¹John Innes Centre, Department of Cell and Developmental Biology, Norwich Research Park, Norwich NR4 7UH, UK, ²Luiz de Queiroz College of Agriculture, University of São Paulo, Department of Entomology and Acarology, Piracicaba 13-418-900, Brazil and ³Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan

[†]Present address: Agricultural Research Company of Santa Catarina State (Epagri), Chapecó 89809-450, Brazil.

*For correspondence. E-mail saskia.hogenhout@jic.ac.uk or chk@gate.sinica.edu.tw

Cell

Volume 184, Issue 20, 30 September 2021, Pages 5201-5214.e12



Article

Parasitic modulation of host development by ubiquitin-independent protein degradation

Weijie Huang¹, Allyson M. MacLean^{1,6}, Akiko Sugio^{1,7}, Abbas Maqbool², Marco Busscher^{3,4}, Shu-Ting Cho⁵, Sophien Kamoun², Chih-Horng Kuo⁵, Richard G.H. Imminck^{3,4}, Saskia A. Hogenhout^{1,8} ✉

¹ Department of Crop Genetics, John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK

² The Sainsbury Laboratory, University of East Anglia, Norwich Research Park, Norwich NR4 7UH, UK

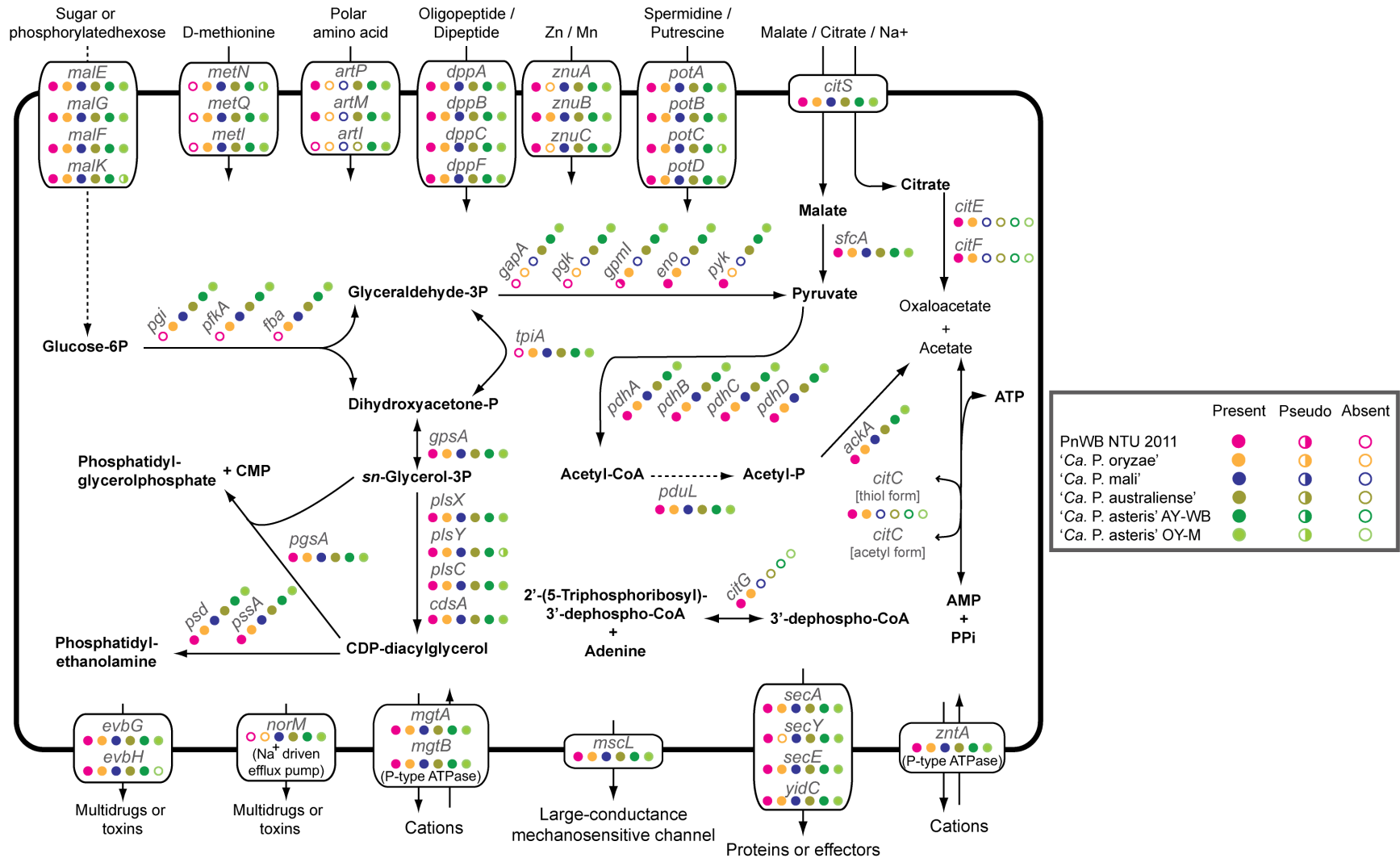
³ Laboratory of Molecular Biology, Wageningen University and Research, Wageningen 6708 PB, the Netherlands

⁴ Plant Developmental Systems, Bioscience, Wageningen University and Research, Wageningen 6708 PB, the Netherlands

⁵ Institute of Plant and Microbial Biology, Academia Sinica, Taipei 11529, Taiwan

Phytoplasmas

Comparison of gene content



Phytoplasmas

Transgenic expression of effector genes in *Arabidopsis*



B 35S::Opt(eGFP-SAP54^{PnWB}) WT



C 35S::Opt(eGFP-SAP54^{PnWB})

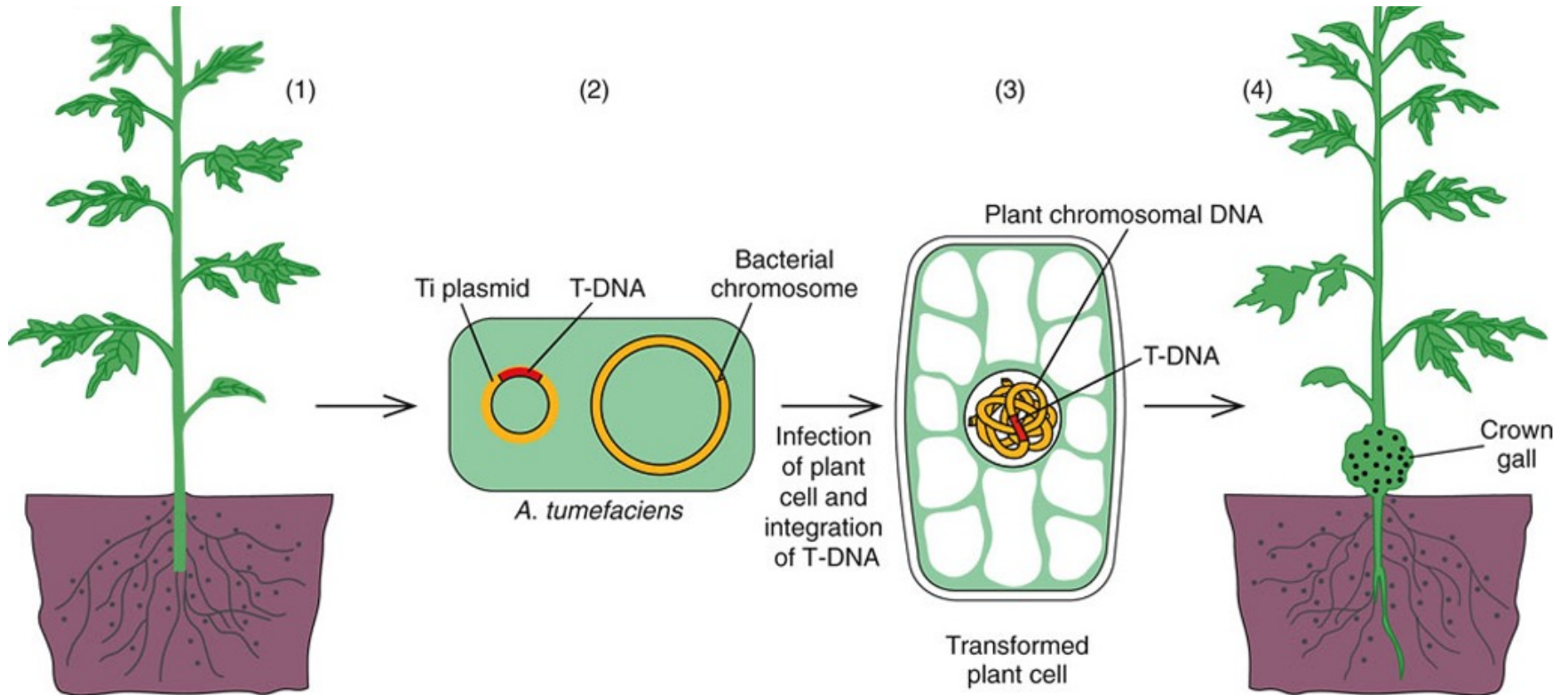


D WT



Agrobacterium

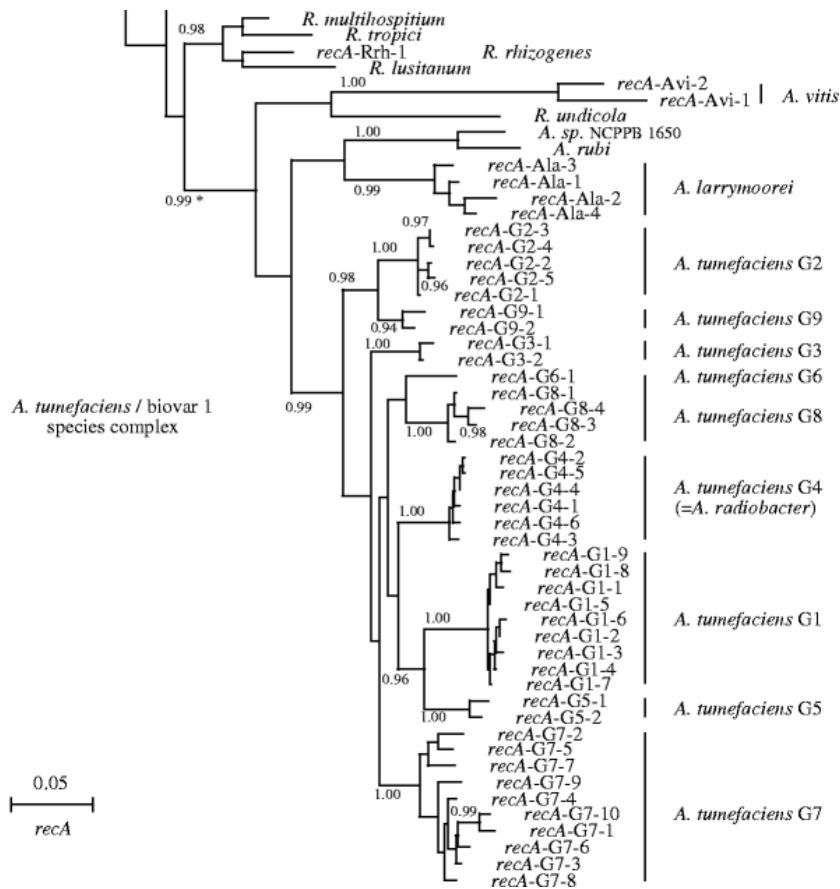
Nature's genetic engineer



Agrobacterium

Extant diversity

Phylogenetic & genetic

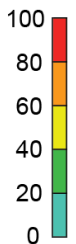


Costechareyre et al. (2010) *Microb Ecol*

Phenotypic

Host plant		Agrobacterium strains					
Family	Common name	C58 (N/G8)	1D1478 (N/G8)	1D1460 (N/G4)	1D1108 (N/G1)	Ach5 (O/G1)	1D1609 (O/G7)
Brassicaceae	Chinese cabbage	100	58	85	100	28	43
	Brown mustard	79	62	87	92	11	22
	White radish	98	80	98	97	57	0
	Head mustard	35	2	85	72	11	6
	Ching chiang pai-tsai	30	20	34	44	0	3
	Pai-tsai	34	12	45	19	5	0
Asteraceae	Sweet alyssum	18	53	39	6	28	10
	Garden cosmos	82	93	100	45	100	100
	Loose leaf lettuce	68	12	41	62	65	70
	Antler shape leaf lettuce	97	63	53	89	86	72
	Romaine lettuce	43	66	73	75	56	72
	White leaf lettuce	66	68	94	73	100	86
Solanaceae	Chicory	9	3	8	10	48	36
	Tomato	97	100	97	100	50	97
	Green pepper	65	25	11	27	0	10
Apiaceae	Egg plant	3	53	3	0	17	91
	Celery	31	12	59	91	91	98
	Carrot	11	6	43	59	36	51
Amaranthaceae	Cilantro	36	42	43	30	24	62
	Spinach	87	92	98	98	75	92
	Amaranth	12	21	43	6	8	10
Cucurbitaceae	Plumed cockscomb	2	19	2	6	6	57
	Bottle gourd	4	17	8	8	44	56
	Balsaminaceae	100	100	100	100	100	100
Balsaminaceae	Balsam/Impatiens	100	100	100	100	100	100
Apocynaceae	Vinca	100	100	54	100	98	80
Plantaginaceae	Snapdragon	52	69	71	89	15	71
Caryophyllaceae	Carnation	90	68	49	70	34	52
Leguminosae	Asparagus bean	71	88	97	97	83	100
	Pea	73	98	100	83	89	100
	Lima bean	22	59	61	92	52	46
	Kidney bean	75	69	58	58	19	100
	Sweet pea	100	100	78	44	92	100
	Mung bean	24	43	37	57	47	35
	White dutch runner bean	34	10	4	18	0	7
	Azuki bean	0	36	31	8	0	19
	Snap bean	53	21	0	39	6	0
	Soybean CWRD	100	82	75	98	60	79
	Soybean Tainan No. 7	10	42	73	100	2	92
	Soybean Gao-Gai No. 5	51	36	92	15	26	100
	Soybean Kaohsiung No. 5	11	49	24	92	5	40
	Cowpea Bai-Pi	44	61	33	86	71	70
	Cowpea 131 Farmers	44	43	19	4	78	84

Tumor formation efficiency (%)

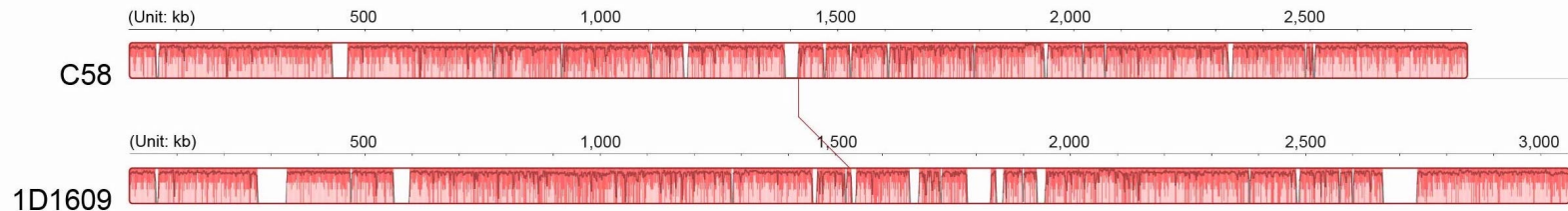


Hwang et al. (2013) *Plant Pathol*

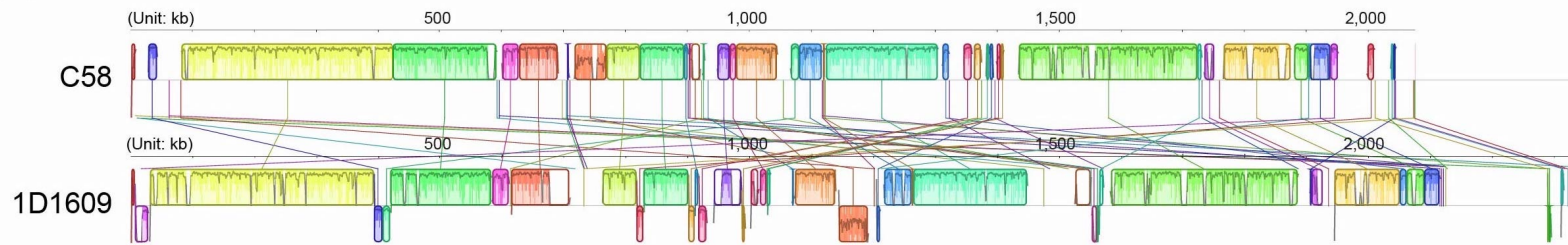
Agrobacterium

Diversity in genome organization

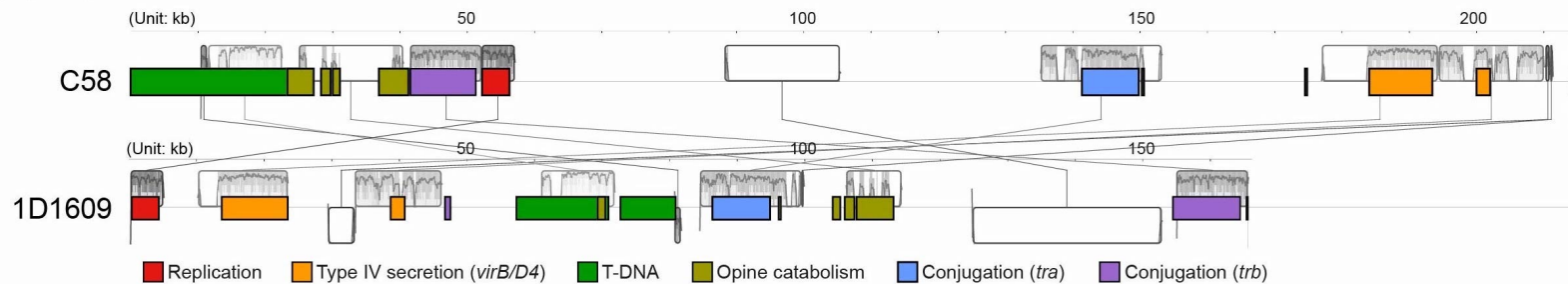
(A) Circular chromosome



(B) Linear chromosome



(C) Ti plasmid

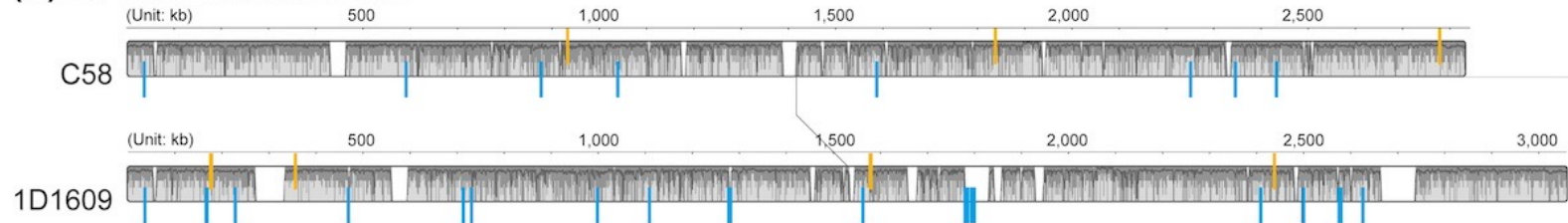


These two strains share ~4,000 genes
Each has ~1,000 unique genes

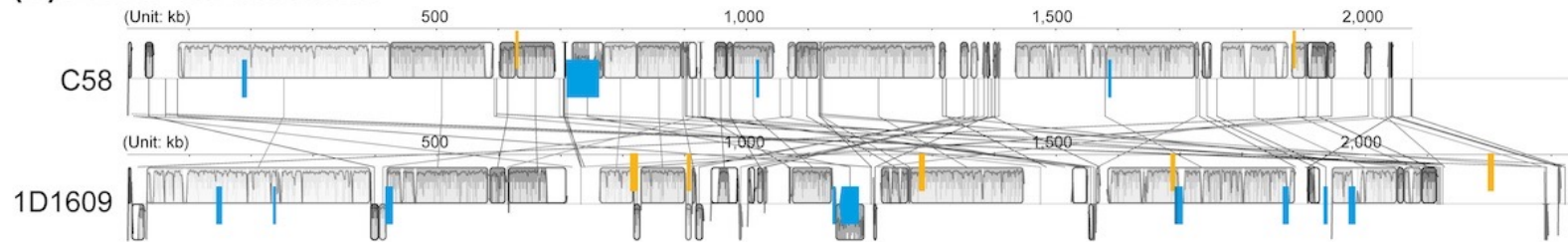
Agrobacterium

Diversity in gene expression regulation

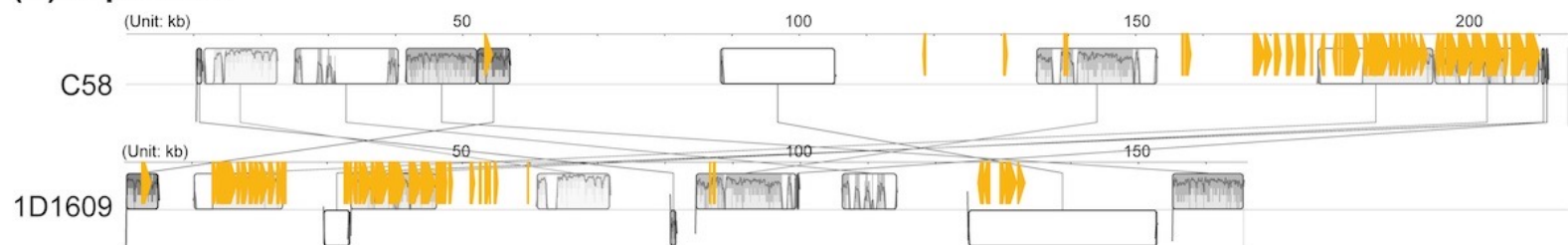
(A) Circular chromosome



(B) Linear chromosome



(C) Ti plasmid



■ Up-regulated by induction
 ■ Down-regulated by induction

	C58	1D1609
Up-regulated	52	74
Down-regulated	36	81

Evolutionary and Functional Genomics of Plant-associated Bacteria

- Our strength
 - Genomics, transcriptomics, and molecular evolution
- For collaborations
 - Organismal biology
 - Microbial diversity, ecology, physiology, symbiosis, etc.
 - Plant pathology
 - Molecular genetics
 - Others

