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## ICPPB2014 Abstracts

genes by stabilizing the 5' UTR of *hrpG*, which encodes the T3SS master regulator in Xcc.

### S4-K2 From the ecology of *Pseudomonas syringae* to probable scenarios of future disease emergence

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Since the beginning of this century, for woody crops alone there have been over 50 reports of new diseases or new outbreaks of diseases caused by *Pseudomonas syringae*. These have occurred in at least 25 countries and have concerned over 20 different plant species [1]. This and other series of outbreaks beg the question of the origin of new plant diseases, and in particular when previously unknown variants of a pathogen are involved such as in the case of canker of kiwifruit and bleeding canker of European horse chestnut. Increasing efforts are being dedicated to understanding the specific mechanisms underlying the history of such emergences. A next important step in apprehending disease emergence is to attempt to anticipate the probable nature of future epidemics.

The metapopulation of *P. syringae* constitutes a myriad of genetic lineages, many of which have been found in 'natural' environments and most of which have never been reported to be in association with plants – diseased or otherwise [2]. Yet many of these lines of *P. syringae* are clearly armed to be pathogens based on their genomic profiles of effectors and their aptitude to incite symptoms under conditions of artificial inoculation [3, 4]. Furthermore, the genomes of the various genetic lines in the *P. syringae* metapopulation represent a surprising variety of combinations of Type 3 Secretion System configurations and of relative abundances of genes for effectors and non-effector virulence factors (toxins, etc.), illustrating that there are multiple profiles of traits that confer evolutionary success of this bacterium [2]. This raises questions about the essential traits that are requisite for a strain to be pathogenic and how these traits are maintained by the bacterium across its varied habitats. By analyzing the vast repertory of information we have garnered on the ecology of *P. syringae*<sup>[5]</sup> – as a saprophyte, a commensal and a pathogen – and knowledge of traits seemingly involved in pathogenicity across a broad spectrum of diversity of this species complex, we are building a framework to construct probable scenarios of future disease emergence and to develop the diagnostic targets to anticipate such outbreaks and mitigate their negative impacts.

### References:

- [1] J.R. Lamichhane, et al. (2014). Advances in Agronomy, 126: 231-291.
- [2] O. Berge, et al. A user's guide to a data base of the diversity of *Pseudomonas syringae* and its application to classifying strains in this phylogenetic complex. (under review)
- [3] C.L. Monteil, et al. (2013). New Phytologist, 199 :800-811.
- [4] C. Bartoli, et al. A framework to gauge the epidemic potential of plant pathogens in environmental reservoirs: the example of kiwifruit canker (under review)
- [5] C.E. Morris, et al. (2013). Annu. Rev. Phytopath. 51:85-104.

### S4-K3 The essential nature of type and pathotype strains of plant pathogenic bacteria

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Typification is a fundamental concept in taxonomy and is essential to all biological disciplines. A type specimen is one with which a name of a particular taxon is associated. Typification of bacteria is prescribed in the Bacteriological Code [1] (the Code) and the Standards for Naming Plant Pathogenic Bacteria [2] (the Standards). For phytobacteriology the type of a family is a genus, the type of a genus is a species, the type of a species is a strain and the pathotype of a pathovar is a strain. Because classification, nomenclature, and identification are interdependent and interrelated, imperatives of one branch of taxonomy are relevant to the others. Thus, although typification is required by the Code and the Standards, typification is also essential in classification and identification of previously described and named pathogens. Types and pathotypes provide the fundamental framework and "fixed points for comparison" in classification and identification as well as nomenclature. Although type and pathotype strains are essential to the understanding the taxonomy and diversity of plant pathogenic bacteria, a few problems have arisen due to the lack of understanding of the essential nature of these strains and poor understanding of the relationship between the Code and the Standards by researchers, reviewers and editors [3,4]. Pathotype strains with identical specific and pathovar epithets also serve as the type strains for the species. For example, the pathotype of *Pseudomonas syringae* pv. *syringae* van Hall 1902 strain NCPPB 281 is also the type strain of *P. syringae*. This is not universally true due to misunderstandings about the relationship between the Code and the Standards. For example, *Xanthomonas campestris* sp. *hederae* was elevated to *X. hortorum* with the type strain of this species serving as the pathotype of *X. hortorum* pv. *hederae* [4,5]. In other examples pathotype swere

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# PROGRAM & ABSTRACTS

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