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## **Pervasive reservoirs, long distance aerial spread, variable host range: integrating the challenges of anticipating disease caused by *Pseudomonas syringae***

Cindy E. Morris, Odile Berge, Christelle Lacroix, Ghislain Geniaux, A.S. Eddine, Maria Choufany, Davide Martinetti, Samuel Soubeyrand

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Abstract N.  
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## **Pervasive reservoirs, long distance aerial spread, variable host range: integrating the challenges of anticipating disease caused by *Pseudomonas syringae***

Morris Cindy E.<sup>1</sup>, Berge O.<sup>1</sup>, Lacroix C.<sup>1</sup>, Geniaux G.<sup>2</sup>, Eddine A.S.<sup>2</sup>, Choufany M.<sup>3</sup>, Martinetti D.<sup>3</sup>, Soubeyrand S.<sup>3</sup>

<sup>1</sup> INRAE, Pathologie Végétale, F-84140, Montfavet, France

<sup>2</sup> INRAE, Ecodéveloppement, F- 84914 Avignon, France

<sup>3</sup> INRAE, Biostatistiques & Processus Spatiaux, F- 84914 Avignon, France

E-mail: cindy.morris@inrae.fr

*Pseudomonas syringae* is more frequently reported as causing new diseases than are any other group of plant pathogenic bacteria and even certain fungi [1]. Management of emerging plant diseases has been, up to present, a post-hoc effort involving development of diagnostics deployed in agricultural contexts to find traces of the emerging strains. Many plant pathogens can survive and multiply as saprophytes, although little research has been devoted to understanding the extent to which saprophytic phases impact pathogen evolution and disease emergence. *P. syringae* is found in a multitude of habitats within and beyond agricultural contexts. Habitats outside of agriculture harbor the greatest genetic diversity including strains with the greatest potential for aggressiveness as plant pathogens [1]. All these strains are disseminated by water – including major rivers used for irrigation – and by wind until they are deposited with precipitation [2]. To develop a surveillance system that accounts for a more comprehensive scope of *P. syringae* reservoirs and dissemination we have i) produced maps of the trajectories of its air and water dissemination in a French river basin based on network analyses of meteorological and hydrological data that we superimposed on land use for this region, and ii) conducted comprehensive pathogenicity tests of strains in the *P. syringae* complex to identify indicators of its host range within and beyond angiosperms. Detection of environmental reservoirs and natural long distance movement of *P. syringae* raises questions about agronomic practices for management of plant health that will be discussed in the presentation.

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[1] Morris et al., 2019. BMC Phytopathology Research 1 :4 doi.org/10.1186/s42483-018-0010-6

[2] Morris et al. 2013. Annu. Rev. Phytopath. 51:85-104.