



**HAL**  
open science

# Beyond host-pathogen co-evolution: the search for drivers of the evolution of a ubiquitous bacterium that impacts crop health and rain formation in clouds

Cindy E. Morris, Christelle Lacroix

## ► To cite this version:

Cindy E. Morris, Christelle Lacroix. Beyond host-pathogen co-evolution: the search for drivers of the evolution of a ubiquitous bacterium that impacts crop health and rain formation in clouds. *Empirisme et Théorie en Écologie et Évolution (ETEE 2015)*, Sep 2015, Gif-sur-Yvette, France. hal-02742568

**HAL Id: hal-02742568**

**<https://hal.inrae.fr/hal-02742568v1>**

Submitted on 3 Jun 2020

**HAL** is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

**Mardi 29 septembre 2015**

**9h30 – 10h40 : Traits d’histoire de vie**

**Beyond host-pathogen co-evolution: the search for drivers of the evolution of a ubiquitous bacterium that impacts crop health and rain formation in clouds**

**Cindy E. Morris and Christelle Lacroix**

Cindy E. MORRIS and Christelle LACROIX INRA, UR0407 Pathologie Végétale, F-84143 Montfavet cedex, France  
cindy.morris@avignon.inra.fr, christelle.lacroix@paca.inra.fr

The bacterium *Pseudomonas syringae* has been historically recognized as an important plant pathogen [1-3]. However, the description of its ecology is moving away from that of a ubiquitous epiphytic plant pathogen to one of a multifaceted bacterium sans frontières that can survive in various ecosystems linked to the water cycle [4-5]. Discovery of the aquatic facet of its ecology has led to a vision of its life history that integrates temporal scales spanning billions of years; and spatial scales traversing catchment basins, continents and the whole planet. Phenotypic and molecular characterization of about 800 strains from a wide range of substrates revealed a diversity of traits and abilities, including subverting the attacks and defense responses of the cohabitants of the various environments they occupy and setting off major environmental processes (e.g. rain and snowfall) that influence climate. This new ecological perspective has also yielded insights into epidemiological phenomena linked to disease emergence and into potential conflicts between its beneficial role in climate processes and its negative impact on the health of crops. Overall, it sets the stage for the integration of more comprehensive contexts of ecology and evolutionary history to elucidate the selective pressures that have shaped the biology of *P. syringae* into a highly diversified metapopulation of strains. We will present our current approach at elucidating the ecology and evolutionary history of this bacterial species and we will solicit discussions to further assess the drivers of its evolution.

Lamichhane J.R., et al. 2015. J. Gen. Plant Pathol. (in press). Lamichhane J.R., et al. 2014. Advances in Agronomy 126:235-295. Mansfield J., et al. 2012. Mol. Plant Pathol. 13 :614–629. Morris C.E., et al. 2014. Global Change Biol. 20:341-351. Morris C.E., et al. 2013. Annu. Rev. Phytopathol. 51:85-104.

Mots-clés : plant pathogen, ice nucleation, aerobiology, biogeography