



HAL
open science

Genome-scale investigation of the metabolic determinants generating bacterial fastidious growth

Leo Gerlin, Ludovic Cottret, Sophie Cesbron, Géraldine Taghouti,
Marie-Agnès Jacques, Stéphane Genin, Caroline Baroukh

► To cite this version:

Leo Gerlin, Ludovic Cottret, Sophie Cesbron, Géraldine Taghouti, Marie-Agnès Jacques, et al.. Genome-scale investigation of the metabolic determinants generating bacterial fastidious growth. Symposium on Synthetic and Systemic Biology, Nov 2019, Bordeaux, France. hal-03350558

HAL Id: hal-03350558

<https://hal.inrae.fr/hal-03350558>

Submitted on 21 Sep 2021

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.

Genome-scale investigation of the metabolic determinants generating bacterial fastidious growth

Leo Gerlin * ¹, Ludovic Cottret ¹, Sophie Cesbron ², Géraldine Taghouti ², Marie-Agnès Jacques ², Stéphane Genin ¹, Caroline Baroukh ¹

¹ LIPM – Université de Toulouse, INRA, CNRS – Chemin de Borde-Rouge - BP 27 31326 CASTANET TOLOSAN CEDEX, France

² Institut de Recherche en Horticulture et Semences – Université d'Angers, Institut National de la Recherche Agronomique : UMR1345, Agrocampus Ouest – AGROCAMPUS OUEST, UMR1345 IRHS, F-49045 Angers, France, France

High proliferation rate and robustness are vital characteristics of bacterial pathogens to successfully colonize their hosts. The observation of drastically slow growth in some pathogens is thus paradoxical and remains unexplained. In this study, we sought to understand the strikingly slow, designated as fastidious, growth of the plant pathogen *Xylella fastidiosa*. Using genome-scale metabolic network reconstruction, modeling and experimental validation, we explored its metabolic capabilities. Despite genome reduction and slow growth, the pathogen's metabolic network is complete but strikingly minimalist and lacking robustness. Most alternative reactions were missing, especially those favoring a fast growth, replaced by less efficient paths. We also unraveled that the production of virulence factors is inefficient and imposes a heavy burden on growth. Interestingly, some specific determinants of fastidious growth were also found in other slow-growing pathogens, enriching the view that these metabolic peculiarities are a pathogenicity strategy to remain at low population level.

*Speaker