



**HAL**  
open science

## Evolution and control of host-microbe symbiosis in arthropods: an RNAseq-based transcriptomic analysis

Yves Moné, F. Chevalier, M.C. Carpentier, N. Kremer, Patrick Mavingui, V. Raquin, Abdelaziz Heddi, Carole Vincent-Monégat, Christine Braquart-Varnier, P. Greve, et al.

### ► To cite this version:

Yves Moné, F. Chevalier, M.C. Carpentier, N. Kremer, Patrick Mavingui, et al.. Evolution and control of host-microbe symbiosis in arthropods: an RNAseq-based transcriptomic analysis. 7. International Wolbachia conference, Jun 2012, St Pierre d'Oléron, France. hal-02747908

**HAL Id: hal-02747908**

**<https://hal.inrae.fr/hal-02747908v1>**

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.

## Organizing Committee

Myriam BADAWI, Nicolas BECH, Sophie BELTRAN, Joanne BERTAUX, Didier BOUCHON, Christine BRAQUART-VARNIER, Yves CAUBET, Richard CORDAUX, Catherine DEBENEST, Carine DELAUNAY, Jessica DITTMER, Sandrine GENIEZ, Lise GENTY, Clément GILBERT, Isabelle GIRAUD, Frédéric GRANDJEAN, Pierre GREVE, Monique JOHNSON, Alexandra LAFITTE, Tiffany LAVERRÉ, Winka Le CLEC'H, Jérôme LESOBRE, Isabelle MARCADÉ, Christelle MIREBEAU, Bouziane MOUMEN, Elmina MOTTIN, Maryline RAIMOND, Roland RAIMOND, Freddie-Jeanne RICHARD, Mathieu SICARD, Catherine SOUTY-GROSSET

from UMR CNRS 7267 Ecologie et Biologie des Interactions,  
équipe Ecologie Evolution Symbiose POITIERS

With the participation of UMR CNRS 5558 Laboratoire de Biométrie et  
Biologie Évolutive LYON, UMR5557- Ecologie Microbienne LYON, UMR INRA/  
INSA Biologie Fonctionnelle Insectes et Interactions LYON, Institut des  
Sciences de l'Evolution MONTPELLIER

## Scientific Committee

Didier BOUCHON (University of Poitiers, FRANCE), Kostas BOURTZIS (University of Western Greece, GREECE), Sylvain CHARLAT (University of Lyon, FRANCE), Richard CORDAUX (University of Poitiers, FRANCE), Stephen DOBSON (University of Kentucky, USA), Olivier DURON (University of Montpellier, FRANCE), Takema FUKATSU (National Institute of Advanced Industrial Science and Technology, JAPAN), Pierre GREVE (University of Poitiers, FRANCE), Abdelaziz HEDDI (INSA of Lyon, FRANCE), Patrick MAVINGUI (University of Lyon, FRANCE), Barton SLATKO (New England Biolabs, USA), Einat ZCHORI-FEIN (Agricultural Research Organization, ISRAEL)

This book was designed by  
Christelle Mirebeau, EBI, UMR CNRS 7267, Poitiers  
and edited by Atlantique  
Editions de l'Actualité scientifique Poitou-Charentes,  
Espace Mendès France - 1 place de la Cathédrale, 86000 Poitiers  
Imprimerie Copy-Media - Mérignac  
ISBN 978-2-911320-44-6

## Evolution and control of host-microbe symbiosis in arthropods: an RNAseq-based transcriptomic analysis

Moné Y.<sup>1</sup>, Chevalier F.<sup>4</sup>, Carpentier M.C.<sup>1</sup>, Kremer N.<sup>1</sup>, Mavingui P.<sup>2</sup>, Raquin V.<sup>2</sup>, Heddi A.<sup>3</sup>, Vincent-Monégat C.<sup>3</sup>, Braquart-Varnier C.<sup>4</sup>, Grève P.<sup>4</sup>, Bouchon D.<sup>4</sup>, Vavre F.<sup>1</sup>

<sup>1</sup>Université de Lyon, F-69000, Lyon; Université Lyon 1; CNRS, UMR5558, Laboratoire de Biométrie et Biologie Evolutive, F-69622, Villeurbanne, France

Yves Moné: yves.mone@univ-lyon1.fr

<sup>2</sup>Université de Lyon, F-69000, Lyon; Université Lyon1; CNRS, VetAgro Sup, UMR 5557, Ecologie Microbienne, F-69622, Villeurbanne, France

<sup>3</sup>INSA-Lyon, UMR203 BF2I, INRA, Biologie Fonctionnelle Insectes et Interactions, Bat. Louis-Pasteur 20 ave. Albert Einstein, F-69621 Villeurbanne, France

<sup>4</sup>Université de Poitiers, UMR CNRS 7267, équipe Ecologie, Evolution, Symbiose, Poitiers 86022, France

Symbiotic interactions between microbes and eukaryotic organisms are widespread in nature and exhibit different features ranging from parasitism to mutualism. However, despite their different outcomes, parasites and mutualists microbes share mechanisms of infection, proliferation and defense within hosts: the molecular dialog between microbial mutualists or parasites and their hosts appears to have common bases.

To decipher common but also specific molecular mechanisms underlying the functioning of intimate interactions, we have developed a comparative transcriptomic approach using RNAseq in four symbiotic systems exhibiting different features, but all involving arthropod hosts associated with endosymbiotic vertically-transmitted bacteria. Three species are associated with *Wolbachia*: the hymenopteran wasp *Asobara tabida*, where *Wolbachia* appears necessary for oogenesis completion, the mosquito *Aedes albopictus*, where cytoplasmic incompatibility-inducing *Wolbachia* are close to commensal and the isopod *Armadillidium vulgare* where *Wolbachia* induces feminization generating a strong nucleo-cytoplasmic conflict. The fourth species is the cereal weevil *Sitophilus oryzae*, which shares an obligate trophic relationship with a gamma-proteobacteria called SPE (*Sitophilus* primary endosymbiont).

RNAseq analyses have been performed on ovaries of infected and uninfected individuals. In this talk, we will present the bioinformatics pipeline that has been set up for exploitation of transcriptomics data on these non-conventional organisms. The identification of genes differentially expressed between infected and uninfected individuals and their comparison across four invertebrate species will permit to unravel common and distant molecular mechanisms involved in symbiotic interactions.

**Keywords:** Bacterial-arthropod symbioses, Functional pathways in symbiosis, RNA sequencing