

The Fourth European Whitefly Symposium

September 11th – 16st, 2011, Rehovot, Israel

[Evidence of diversity and recombination in *Arsenophonus* symbionts of the *Bemisia tabaci* species complex]

L. Mouton^{1*}, M. Thierry^{2*}, H. Henri¹, R. Baudin², O. Gnankine⁴, B. Reynaud², E. Zchori-Fein⁵, N. Becker^{3}, F. Fleury^{1**} and H. Delatte^{2**}**

¹ Université Claude Bernard Lyon 1, Laboratoire de Biométrie et Biologie Evolutive, UMR CNRS 5558, 43 Bd du 11 Novembre 1918, 69622 Villeurbanne Cedex, France

² CIRAD, UMR Peuplements Végétaux et Bioagresseurs en Milieu Tropical, 3P, 7 chemin de l'IRAT 97410 Saint Pierre La Réunion, France

³ Museum National d'Histoire Naturelle, UMR CNRS 7205 Origine, Structure et Evolution de la Biodiversité, CP 50, 57 rue Cuvier, 75231 Paris Cedex 05, France.⁴ Université de Ouagadougou, Unité de Formation et de Recherche en Sciences de la Vie et de la Terre (UFR-SVT), Laboratoire d'Entomologie Fondamentale et Appliquée, 09 848 Ouagadougou 09, Burkina Faso

⁵ Agricultural Research Organization, Department of Entomology, Newe Ya'ar Research Center, PO Box 1021, Ramat Yishay, 30095, Israel

(*co-first authors, **co-last authors)

Background

Maternally inherited bacterial symbionts infecting arthropods have major implications on host ecology and evolution. Among them, the genus *Arsenophonus* is particularly characterized by a large host spectrum and a wide range of symbiotic relationships (from mutualism to parasitism), making it a good model to study the evolution of host-symbiont associations. The recently developed method of multilocus sequence typing (MLST) has provided the opportunity to accurately explore the diversity and distribution of *Arsenophonus* within host lineages. Here, this approach was used to survey *Arsenophonus* diversity in whitefly species (Hemiptera), in particular the *Bemisia tabaci* species complex. This polyphagous insect pest is composed of genetic groups that differ in many ecological aspects. They harbor specific bacterial communities, among them several

lineages of *Arsenophonus*, enabling a study of the evolutionary history of these bacteria at a fine host taxonomic level, in association to host geographical range and ecology.

Results

Among 152 individuals, our analysis identified 19 allelic profiles and 6 phylogenetic groups, demonstrating this bacterium's high diversity. These groups, based on *Arsenophonus* phylogeny, correlated with *B. tabaci* genetic groups with two exceptions reflecting horizontal transfers. None of three genes analyzed provided evidence of intragenic recombination, but intergenic recombination events were detected. A mutation inducing a STOP codon on one gene in a strain infecting one *B. tabaci* genetic group was also found. Phylogenetic analyses of the three concatenated loci revealed the existence of two clades of *Arsenophonus*. One, composed of strains found in other Hemiptera, could be the ancestral clade in whiteflies. The other, which regroups strains found in Hymenoptera and Diptera, may have been acquired more recently by whiteflies through lateral transfers.

Conclusions

This analysis of the genus *Arsenophonus* revealed a diversity within the *B. tabaci* species complex which resembles that reported on the larger scale of insect taxonomy. We also provide evidence for recombination events within the *Arsenophonus* genome and horizontal transmission of strains among insect taxa. This work provides further insight into the evolution of the *Arsenophonus* genome, the infection dynamics of this bacterium and its influence on its insect host's ecology.

Keywords: *Arsenophonus*, evolution, diversity, recombination

Acknowledgements: This study was partly funded by CNRS (IFR41-UMR5558), the CIRAD and the “Conseil Regional de La Reunion”. M. Thierry is a recipient of a PhD fellowship from the Conseil Regional de La Reunion and the EU (European Social Fund).

Preferred Topic Number 5. Whiteflies and their Symbionts
Corresponding Author: Laurence Mouton
Email address: laurence.mouton@univ-lyon1.fr