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



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Mouton, Thierry et al., BMC Microbiology (in press)

INTRODUCTION

Maternally inherited bacterial symbionts infecting arthropods have major implications on host ecology and evolution. Among them, the genus Arsenophonus has particular characteristics (large host spectrum, wide range of symbiotic relationships), making it a good model to study the evolution of host-symbiont associations. We realized a survey of Arsenophonus diversity in whitefly species, especially the Bemisia tabaci species complex. This polyphagous pest, composed of genetic groups that differ in many ecological aspects, harbor several lineages of Arsenophonus. The evolutionary history of these bacteria at a fine host taxonomic level was studied in association to geographical range and ecology.

Figure 1. Sampling sites and prevalence of *Arsenophonus* (blue) among whiteflies (KM) Ms **Q2** (ES) (MG) Ms **Q3** (BF) (SC) Ms ASL (BF) (RE) Ms (RE) **Q2** AnSL (TG) (RE) T. vaporariorum AnSL (BJ) (MU) Ms (RE) B. afer

Q2, Q3, AnSL, ASL and Ms indicate the genetic groups of Bemisia tabaci. Samples were collected in mainland France (FR), Spain (ES), Israel (IL), Burkina Faso (BF), Togo (TG), Benin (BJ), Tanzania (TZ), Seychelles (SC), Comoros Grande Comore (KM), Mayotte (YT), Madagascar (MG), Mauritius (MU) and Reunion (RE).

MATERIALS AND METHODS

- Samples were screened for Arsenophonus infection by amplification of the 23s rRNA gene. B. tabaci genetic groups were identified based on the mtCOI gene.
- Arsenophonus diversity was investigated on three genes, ftsK, yaeT and FbaA.
- Phylogenetic analyses were performed using maximum-likelihood (ML) and Bayesian inferences (BI) for the concatenated data set.
- Putative recombinant regions were searched using methods available in RDP3.

Figure 2. Phylogeny of *Arsenophonus* from whitefly species

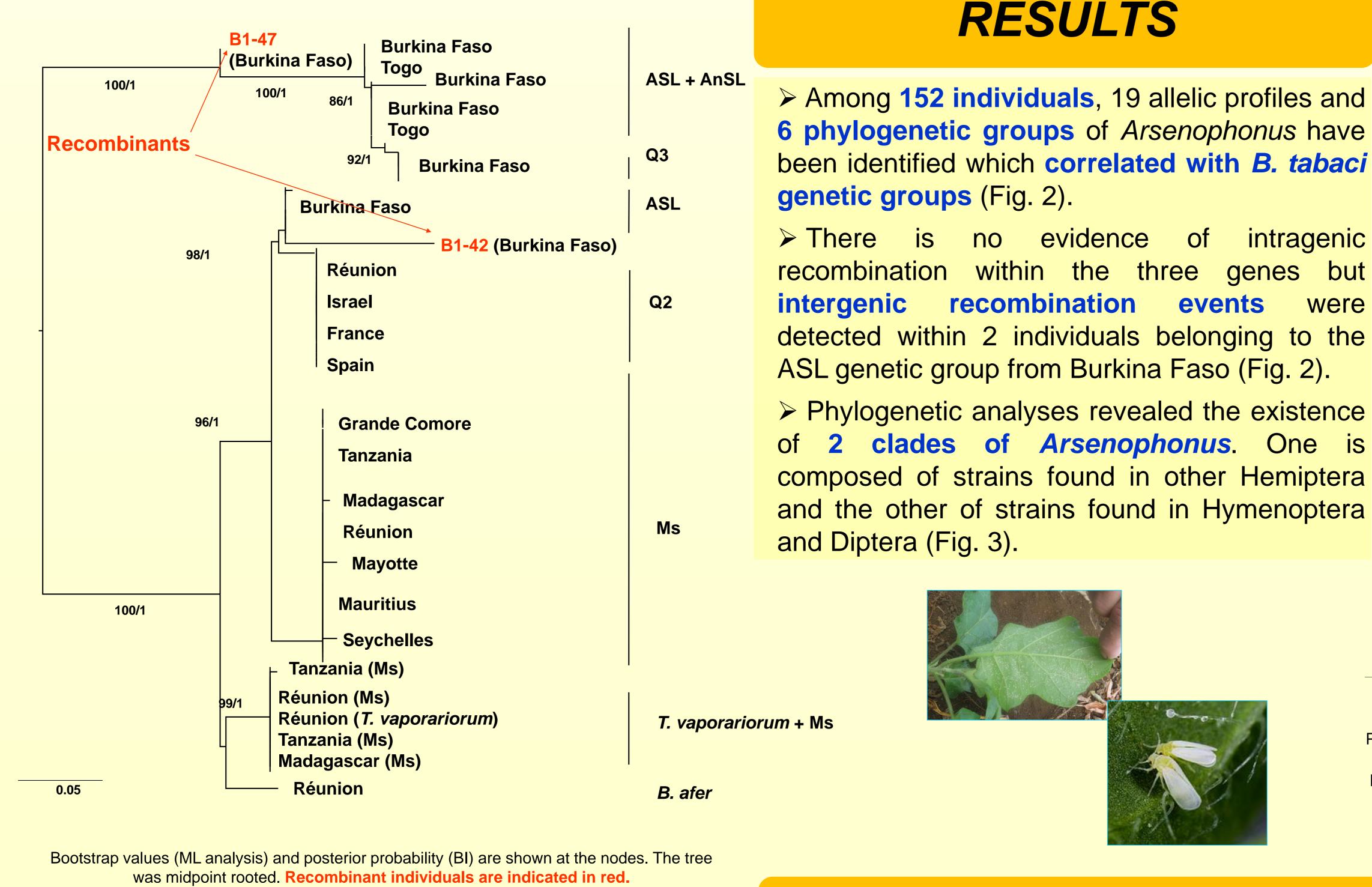
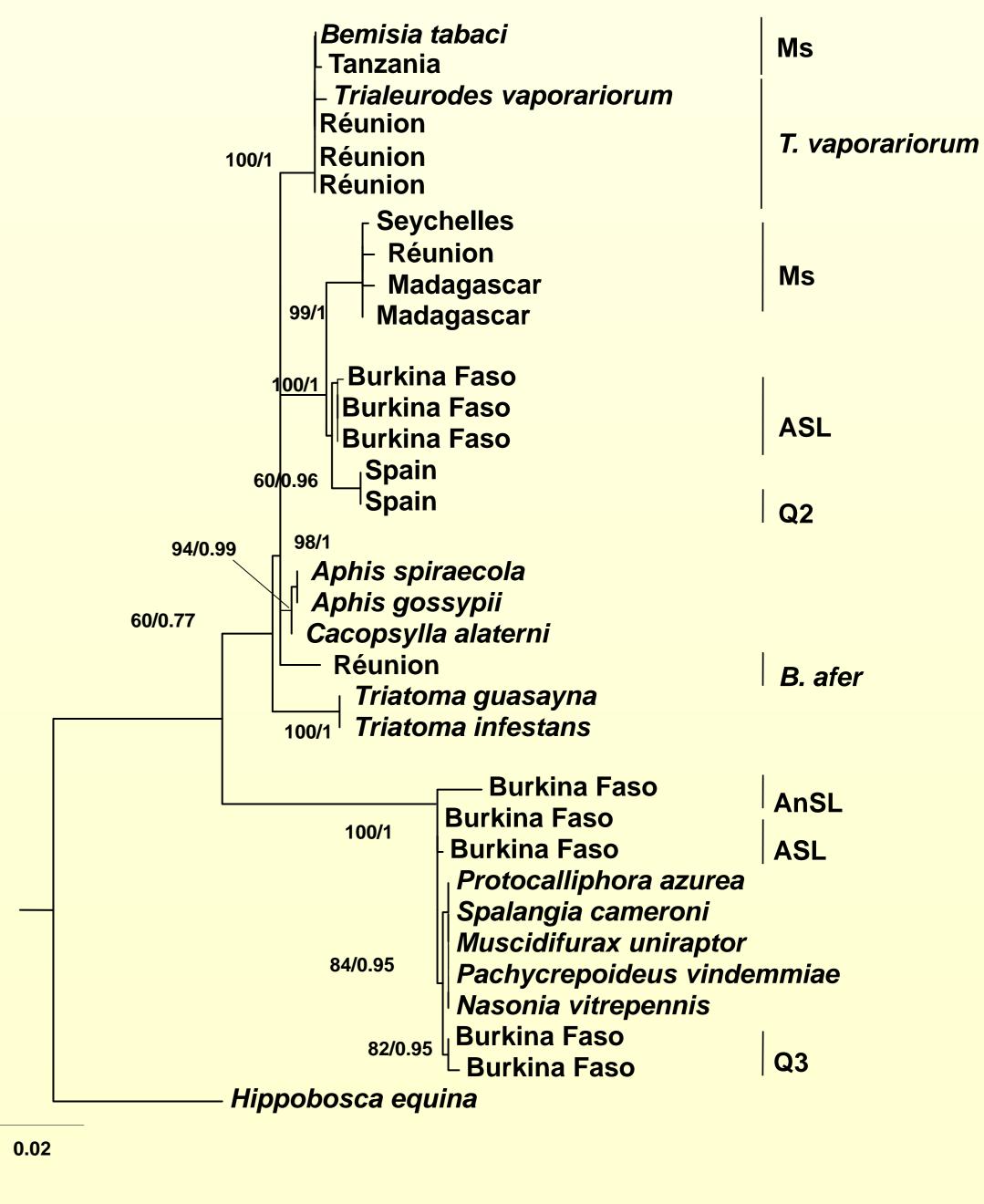


Figure 3. Phylogeny of symbiotic Arsenophonus of arthropods



Phylogeny constructed with representative sequences of this study and sequences from Duron et al., 2010*. Recombinants were discarded. Bootstrap values (ML analysis) and posterior probability (BI) are shown at the nodes. Arsenophonus from H. equina was used as outgroup. Strains retrieved from the literature are named by their host species and are in italics.

*Duron, O., T. Wilkes, and G. Hurst. 2010. Interspecific transmission of a male-killing bacterium on an ecological timescale. Ecology Letters 13: 1139-1148.

CONCLUSION

- > **High diversity** of *Arsenophonus* symbionts in *B. tabaci*.
- > Intergenic recombination events suggested that Arsenophonus is not a strict clonal bacterium.
- > Some strains were found in other Hemiptera and could be the ancestral clade in whiteflies while others were found in Hymenoptera and Diptera and may have been acquired more recently by whiteflies through horizontal transfers.













