

ABSTRACT

Phylogeny and Distribution of *Wolbachia pipientis* in *Bemisia tabaci* and its Effect on Host Reproduction

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A total of 671 whiteflies representing 76 populations of *B. tabaci* were screened for *Wolbachia* infection using 16S rDNA and *Wolbachia* surface protein (*wsp*) gene primers. Of the 76 populations studied, 16 were found to be infected with *Wolbachia*. PCR and phylogenetic analysis were used to type these *Wolbachia* strains. Fourteen of the sixteen *Wolbachia* strains analysed belonged to the B-supergroup of *Wolbachia*, while only two strains belonged to the A-supergroup. All the strains belonging to the B-supergroup, with the exception of the strain found in the *Jatropha* biotype, were further subtyped into the Con group. The *Wolbachia* strain found in the *Jatropha* biotype formed a separate and distinct subgroup known as Tab1.

Fitness traits of *B. tabaci* (B-biotype) infected with *Wolbachia*, were compared with a *B. tabaci* (B-biotype) population that was uninfected with *Wolbachia*. The traits measured were egg-to-adult viability, fertility, productivity and fecundity. Mating studies were also conducted to determine the phenotype of this *Wolbachia* strain. It was noted that whiteflies infected with *Wolbachia* were more fertile, more fecund, and more productive than the whiteflies that were not infected with *Wolbachia*.

No embryonic lethality was observed in the crosses between infected males and uninfected females. In all the traits measured, our results showed the absence of any negative effects of *Wolbachia* on its host. These results could explain

effects caused by these *Wolbachia* might result from a trade-off, where a relatively low bacterial density would be advantageous to the *Wolbachia*, in that it would suppress any deleterious effects on the female host, at the cost of a weaker maternal transmission rate of infection.