ABSTRACT

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

Sherline E. Brown

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 Wolbachia's evolution as naturally transmitted parasites keep a strong selective pressure to maintain their parasitic forms.
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.