## *BEMISIA TABACI* SECONDARY SYMBIONTS: THEIR FUNCTIONAL ROLES IN VIRUS TRANSMISSION AND WHITEFLY BIOLOGY

Murad Ghanim

*Institute of Plant Protection, Department of Entomology, the Volcani Center, Bet Dagan 50250, Israel. ghanim@agri.gov.il*

The whitefly *Bemisia tabaci* is an extremely devastating insect pest that harbors several symbiotic bacteria, including *Portiera aleyrodidarum*, the primary obligatory symbiont, as well as several secondary symbionts, including *Rickettsia*, *Hamiltonella*, *Wolbachia*, *Arsenophonus*, *Cardinium* and *Fritschea*, the function of which is unknown. The distribution of these secondary symbionts is biotype-dependent. In Israel, the B biotype harbors *Hamiltonella* while the Q biotype harbors *Wolbachia* and *Arsenophonus.* Both biotypes harbor *Rickettsia.* Examples of ongoing studies in our lab, aimed at deciphering functional roles for some of these secondary symbionts in their whitefly host will be presented. A first example includes the recent finding that a GroEL protein produced by *Hamiltonella* in the B biotype, but not other GroELs from other symbionts in the Q biotype, interacts with, and safeguards the *Tomato yellow leaf curl virus* (TYLCV) while circulating in the whitefly's body. This interaction contributes to the ability of the B biotype to be a much more efficient TYLCV vector than the Q biotype that lacks *Hamiltonella.* Other examples include the involvement of *Rickettsia* in the response to stress including chemical insecticides and heat shock, and the unique distribution of *Rickettsia* in the pathway of circulative viruses including stylets, midgut, hemolymph and salivary glands, its horizontal transmission between the reproductively isolated B and Q biotypes through the plant host, and its rapid establishment in *Rickettsia*-free whiteflies. Such unique interactions and possible roles for *B. tabaci* secondary symbionts might be employed in developing novel strategies for whitefly control.