

ABSTRACT

Bemisia tabaci is a species complex that is one of the largely destructive agricultural pests globally. It causes damage to its broad range of plant hosts through serious feeding. Among, other the most economically important emergent plant virus vectors, this one is well recognized. It transmits plant viruses of different groups to important agricultural crops. *Bemisia tabaci* shows high genetic variability and its genetically variable populations have been differentiated as races or biotypes. The term biotype for the first time was proposed in 1950s to describe whitefly with unique host associations and virus-vector capabilities. A number of commonly reported biotypes are, biotype Q, biotype B, biotype B2, biotype M, biotype L, biotype A, biotype H, biotype C, biotype K, biotype N, biotype R, biotype E, biotype P, biotype J, biotype S, biotype AN. Although the current report based on the Bayesian study of mitochondrial cytochrome oxidase gene1 (COI) DNA sequences has classified the different populations of whiteflies into twelve genetic groups which are Mediterranean, Sub-Saharan Africa silverleafing, Indian Ocean, Asia II, Asia I, Australia, New World, Italy, China, Sub-Saharan Africa non-silverleafing, Mediterranean/Asia Minor/Africa and Uganda sweet potato. Begomoviruses in *Geminiviridae* is the largest group of viruses transmitted by *B. tabaci*. All major diseases of crops such as tomato and chili leaf curl disease, cassava mosaic disease, yellow mosaic disease of legumes and cotton leaf curl disease are caused by begomoviruses. Amongst the main crops of Pakistan cotton is one, which is largely effected by ability of *B. tabaci* as a virus vector. All these factors make the study of *B. tabaci* economically more important and scientifically more informative. The main objective of current study is to inculcate knowledge regarding genetic diversity of whitefly in cotton fields across Pakistan and it is based upon phylogenetic analysis of partial DNA sequence of mitochondrial gene Cytochrom Oxidase I (mtCOI). Samples were collected from nine different geographical areas (Arifwala, Multan, Muzafargarh, Sahiwal, Kabirwala, Tiba sultan pur, T.T singh, Okara, Faisalabad) are found closely related with genetic group *B. tabaci* (Asia II) which includes biotypes H, K and P. Importance of this genetic group of whitefly along with other groups and their significance in spread of viral diseases have been discussed in this thesis.