

# First International Whitefly Symposium

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## Population genetics of the *Bemisia tabaci* Med species from Mediterranean countries

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Within the *Bemisia tabaci* species complex, the Middle East-Asia Minor I (MEAMI) and the Mediterranean (Med) species are the most invasive and widespread. These last years, Med has become the predominant, or even the only species, in the Mediterranean basin- its presumed area of origin- and has spread to many other parts of the world.

Combining mitochondrial (COI gene) and nuclear (microsatellite loci) markers, an extensive survey of Med *B. tabaci* (i.e. more than 3500 females studied) collected from five Mediterranean countries was undertaken to infer the genetic diversity and the possible role of ecological and environmental factors in shaping the population genetic structure observed.

Based on sequence polymorphism of a 676-bp fragment of the COI gene, eighteen haplotypes were obtained which delineated two mitochondrial groups (named Q1 and Q2 which also correspond to Western and Eastern Mediterranean countries, respectively). Simple PCR/RFLP-based molecular assays were used to examine the geographic distribution of these two mitochondrial types by monitoring approximately 1000 individuals: both Q1 and Q2 were found in Spain and France, in sympatry in the field or not respectively, whereas in Greece, Morocco and Tunisia only Q1 was observed.

Based on nuclear markers, Bayesian analysis of seven microsatellite loci polymorphism revealed three genetic clusters (France, Spain, Morocco \_ Greece \_ Tunisia) and a high level of genetic differentiation even between neighbouring samples belonging to the same mitochondrial group within a country. In some cases, subsequent Bayesian analysis within each genetic cluster disclosed additional sub-clusters, as in Greece where two genetic groups were found: the first with populations from South Crete, and the second with populations from continental Greece and North Crete. In this country, genetic differentiation is rather explained by differences in landscape structure than host plant species or habitat type. In *B. tabaci* from Tunisia, however, host plant species seems to play a role in the Q1 population structure. In France and Spain, where both Q1 and Q2 were observed, comparison with an Israeli Q2 provided confirmation of hybridization and evidence for asymmetrical gene flow between the two mitochondrial types.

Overall, our findings suggest that the Med *B. tabaci* species is more diverse and structured in its original geographic area than reported so far.

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