

**321 - *Brevipalpus* mites of economic and quarantine importance – integrating morphology and molecular information to advance their systematics**

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*Brevipalpus* mites are considered the most important pests within the Tenuipalpidae. The three main species, *B. californicus* (Banks), *B. obovatus* Donnadieu and *B. phoenicis* (Geijskes), have been incriminated as vectors of phyto virus. Dissemination of *Brevipalpus* mites associated to plant material and viruses represent an imminent threat to agriculture and ornamental industries. Systematics and phylogeny of *Brevipalpus* mites is of concern. The three mentioned species have been consistently confused and misidentified. The hypothesis that *B. phoenicis* represents a species complex has been analyzed. The quarantine species, *B. chilensis* Baker, is morphologically very close to *B. obovatus*, a species found worldwide, and taxonomists have discussed their possible synonymy. In order to advance with the understanding of *Brevipalpus* systematics, a phylogenetic analysis based on mitochondrial Cytochrome Oxidase I (COI) sequences and a detailed morphological study were conducted on *Brevipalpus* mites of the same populations. A total of 102 COI sequences of *Brevipalpus* mites from Brazil (65 sequences, 9 states; 11 hosts), Chile (33 sequences, 13 localities, 6 hosts) and the USA (4 sequences, 2 states, 2 hosts) were obtained. These data were analyzed together with other 41 sequences retrieved from GenBank from *Brevipalpus* originated from mites collected in Brazil (20, 3 states, 6 hosts); USA (16, 2 states, 6 hosts) and The Netherlands (6, 6 hosts). While a 430bp fragment was sequenced, the best alignment included 374 bp and was selected for further analysis which detected a total of 45 haplotypes. A *Cenopalpus pulcher* COI sequence was used as outgroup. About 30 specimens from the sequenced samples were mounted for morphological identification. Phylogenetic results support the present taxonomy of *B. obovatus* and *B. chilensis* as distinct taxa as well as the hypothesis of a species complex hidden in *B. phoenicis* phenotypes. Jointly, phylogenetic and morphological analyses support the presence of two *Brevipalpus* aff. *phoenicis* species among the studied populations: 1) from *Alnus subcordata* and *Ligustrum japonicum* from Colombo, Paraná, and *Ligustrum* sp. from Brasília, DF, Brazil; 2) from coconut, Janaúba, Minas Gerais, Brazil. In addition to the genetic distance of these species with other *B. phoenicis* populations, the distinctive morphological character was the median dorsal ornamentation pattern. A detailed taxonomic study of these aff. species is under way, and includes immature stages and morphometric characters. Because their role as vector and pest of economic importance there is an urgent need to advance in *Brevipalpus* systematic; matching morphological and molecular information will be extremely helpful.