

M. Navajas\*, J. Gutierrez\*, D. Fournier#, and P. Boursot°

\*Laboratoire d'Acarologie, INRA-ENSAM-ORSTOM, Place P. Viala, 34060 Montpellier (France)

#Laboratoire de Biologie des Invertébrés, INRA, B.P. 2078, 06606 Antibes (France)

°Laboratoire Genome et Population, URA 1592 CNRS, Université Montpellier II, Montpellier (France)

MOLECULAR PHYLOGENY AND MORPHOLOGICAL EVOLUTION IN  
PHYTOPHAGOUS MITES (Acari: Tetranychidae)

Although molecular tools are widely used in research on the evolution and phylogeny of organisms, few data of this kind are available for Acari or even for Arachnida. The molecular phylogeny of 19 Tetranychidae species (spider mites) is described; they belong to 7 different genera, including some of the best-represented of the family consisting entirely of phytophages. Several of the species are cosmopolitan and dangerous crop pests. Phylogeny is compared with a number of morphological and biological features.

The phylogeny of the considered genera was drawn up by analysis of the sequences of a 350 bp. fragment of the mitochondrial gene for sub-unit I of Cytochrome C Oxidase (COX I). However, a more variable region had to be used within the genus *Tetranychus*: the ribosomal DNA internal non-transcribed spacer (ITS2). Phylogeny at family levels is compatible with directional evolution of habitat and the spinning behaviour of species (habitat on one side of leaves or the other, silk quantity, appearance of the webs) and with the evolution of the related morphological characters, e.g. ambulacrum and the empodium shape. The Tetranychidae family has two reproduction modes: arrhenotoky (haploid parthenogenetic males and diploid non-parthenogenetic females) and thelytoky (parthenogenetic females). An evolutionary trend for thelytoky to become rarer has operated since the origin of the family. Altogether there is good agreement between morphological and molecular data, the latter have made it possible to clarify certain obscure points concerning the systematics of the group. Comparison of the results of the two approaches makes it possible to define morphological characters forming good phylogenetic and taxonomic clues.

Furthermore, these data enable analysis of the mitochondrial genome of Acari, about which nothing is known. Taking advantage of the heterogeneity that occurs primarily at silent sites of COXI sequences, codon amino acid assignments were deduced. We detected no inconsistency with the mitochondrial genetic code of insects. Base composition was strongly biased towards A+T (around 75%) so that most mutations were A-T transversions. However, this constraint appeared to be relieved to a certain extent in one of the lineages analysed, posing problems for the use of the phylogeny reconstruction methods available.



18 JUL. 1995

ORSTOM Fonds Documentaire

N° 42.078 ep 1  
Cote : B