

Presence of ant transposons in the genome of the silverfish *Atelura formicaria* (Zygentoma, Ateluridae)

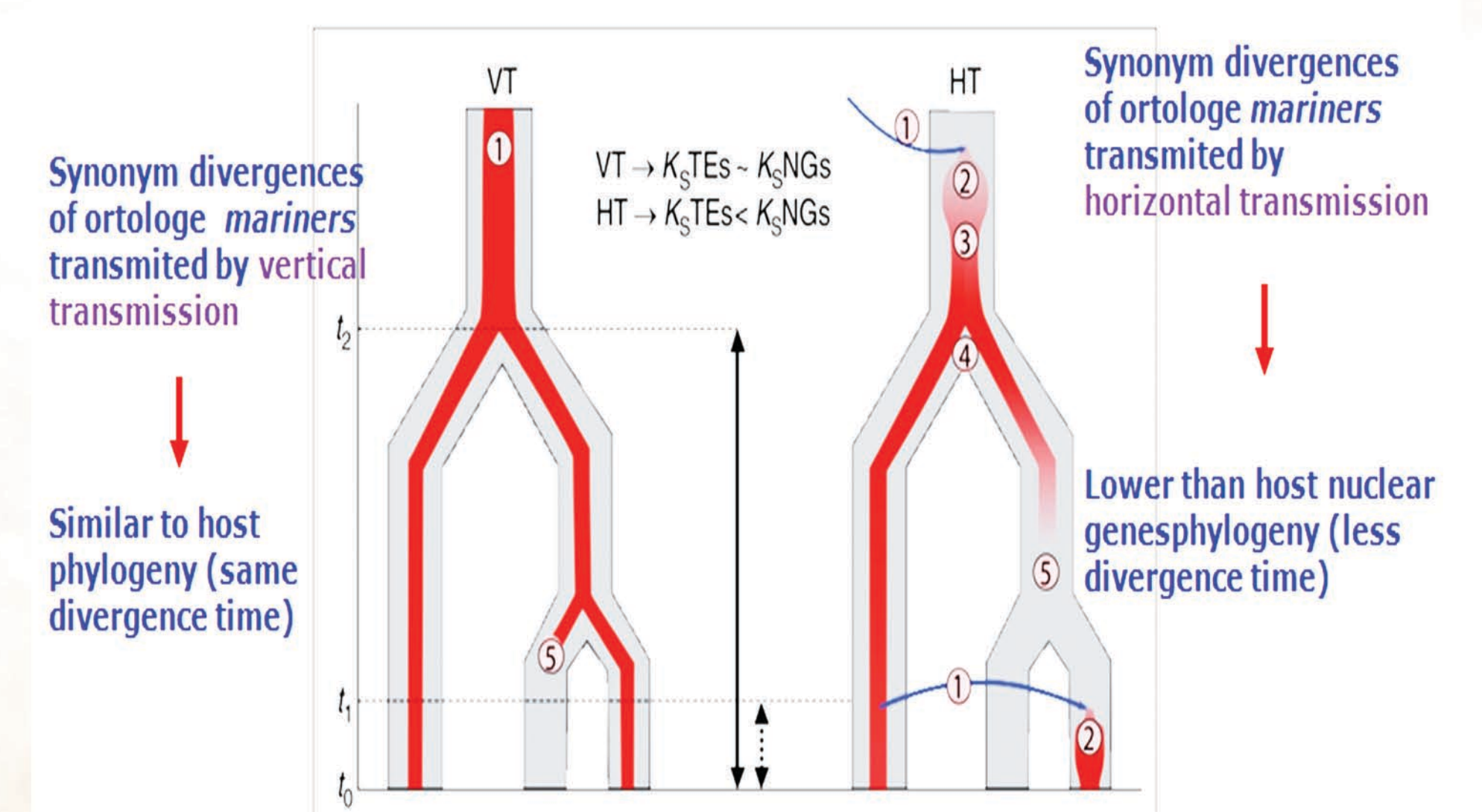
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INTRODUCTION

Mariner elements are the most frequent and extended transposons of type II (DNA transposons) in the genome of Eukaryotes. Active transposons are able to move along their host genome in an autonomous way. This trait enables their horizontal transmission (HT), which is evidenced when: (1) there is a high similitude in transposons from hosts phylogenically distant, (2) there are phylogenetic incongruencies between transposons and their hosts and (3) there is a discontinuous distribution of transposons among related taxa. Under HT the nucleotide divergence of the *mariners* is much lower than the average divergence among nuclear genes of the hosts. In ants there are four *mariner* elements known: *Mboumar*, *Sinvmar*, *Myrmar* and *Azteca*, that have been detected in several ant subfamilies. Previous studies support the existence of *mariner* HT among ants. Here we show the existence of two of the *mariners* *Mboumar* and *Azteca* in the genome of the silverfish *Atelura formicaria* (Zygentoma, Ateluridae), a small myrmecophilous insect as well as the possible existence of HT between ants and the silverfish.



MATERIAL AND METHODS

A nest of *Formica cunicularia* containing *Atelura formicaria* was sampled in Tours (France) during autumn 2013. The presence of the *Mboumar* and *Azteca* *mariners* were studied by PCR amplification with specific primers. The sequences obtained were aligned with other *mariner* sequences from different ant species (obtained from PCR or searched within published ant genomes) and then a phylogenetic tree of each *mariner* was performed with the Neighbour-Joining (NJ) method. Clones from *A. formicaria* would be expected to appear clustered together and well differentiated from those of ants, as silverfishes belong to a different insect order.

RESULTS AND DISCUSSION

PCRs resulted in the positive amplification of the *mariners* like *Mboumar* and *Azteca* in the *A. formicaria* genome. Also *mariners* like *Mboumar* were amplified in *Formica cunicularia*. The existence of HT of *Mboumar* *mariner* have been proposed for the ants *Messor bouvieri* (Myrmicinae subfamily) and *Tapinoma nigerrimum* (Dolichoderinae) as their *Mboumar* *mariners* are very similar and in the phylogenetic analysis they appear mixed. The *Mboumar* *mariners* of *F. cunicularia* (Formicinae) are also mixed with the previously analyzed *mariners*. (Fig. 1). The *Mboumar* sequences from *A. formicaria* show different results: three of them are separated but in a low supported clade whereas another one (*Atelura Mb-7*) is closely similar to the *Mboumar* *mariner* isolated in ants. Although the analysis of new *Mboumar* sequences in other species of ants and more *A. formicaria* sequences are necessary, the obtained results support the hypothesis of a possible process of HT between *A. formicaria* and ants.

As for *Azteca* in ants, HT cannot be neglected as their *mariner* clones are not differentiated according to ant subfamilies (Fig. 2). The phylogenetic inconsistencies and the analysis of the nucleotide divergence of the *mariners* and the nuclear genes of the hosts also support the existence of HT among ants. However in the *Azteca* phylogeny (Fig. 2) ant sequences appear clearly separated from those of *A. formicaria*, which points vertical transfer as the most probable transmission mechanism between both insect orders.

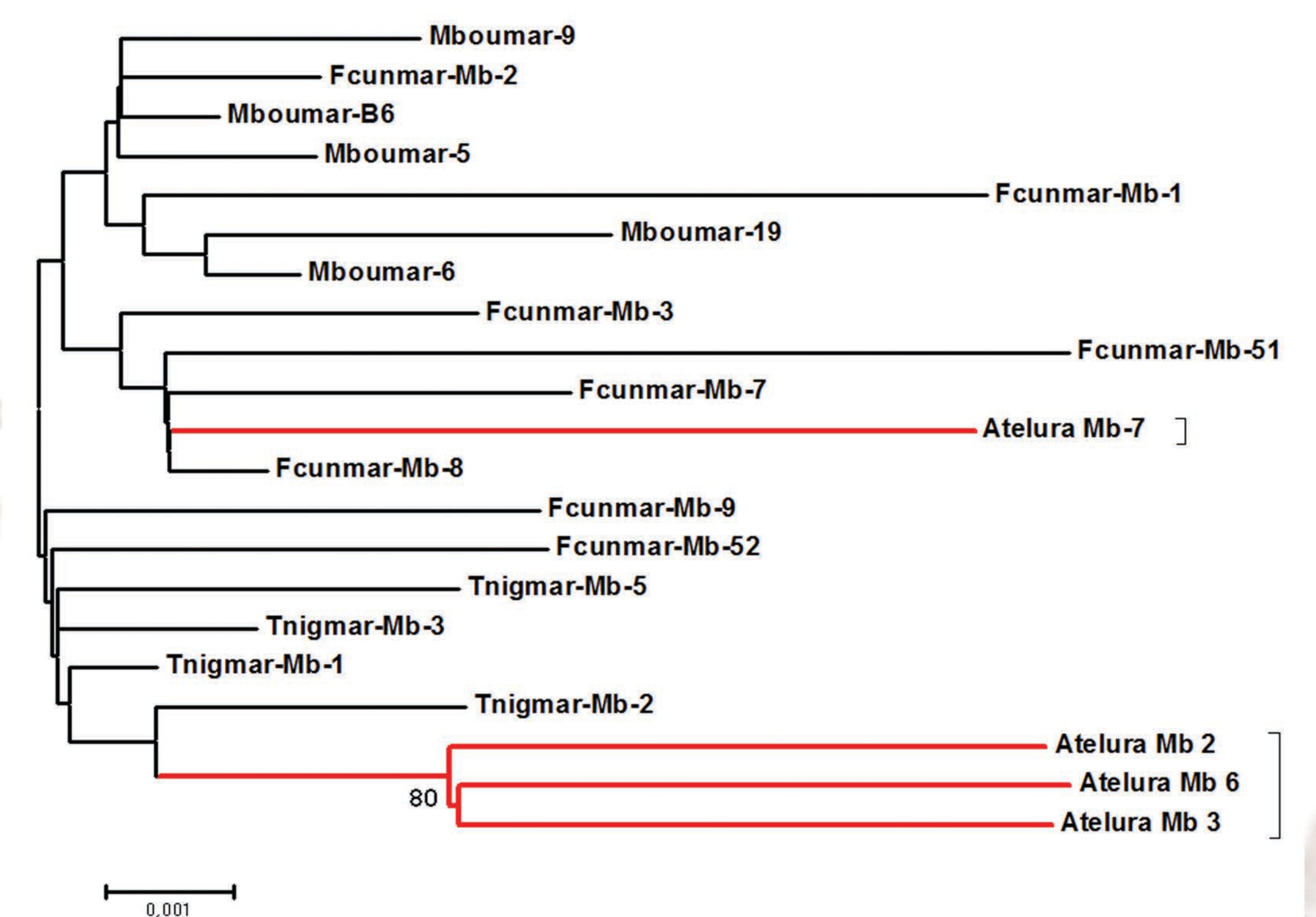


Fig. 1. Phylogenetic tree of *Mboumar* copies in *A. formicaria* (*Atelura-Mb*) and in the ant species: *Messor bouvieri* (*Mboumar*) from Myrmicinae subfamily, *Formica cunicularia* (*Fcunmar-Mb*) from Formicinae subfamily and *Tapinoma nigerrimum* (*Tnigmar-Mb*) from Dolichoderinae subfamily.

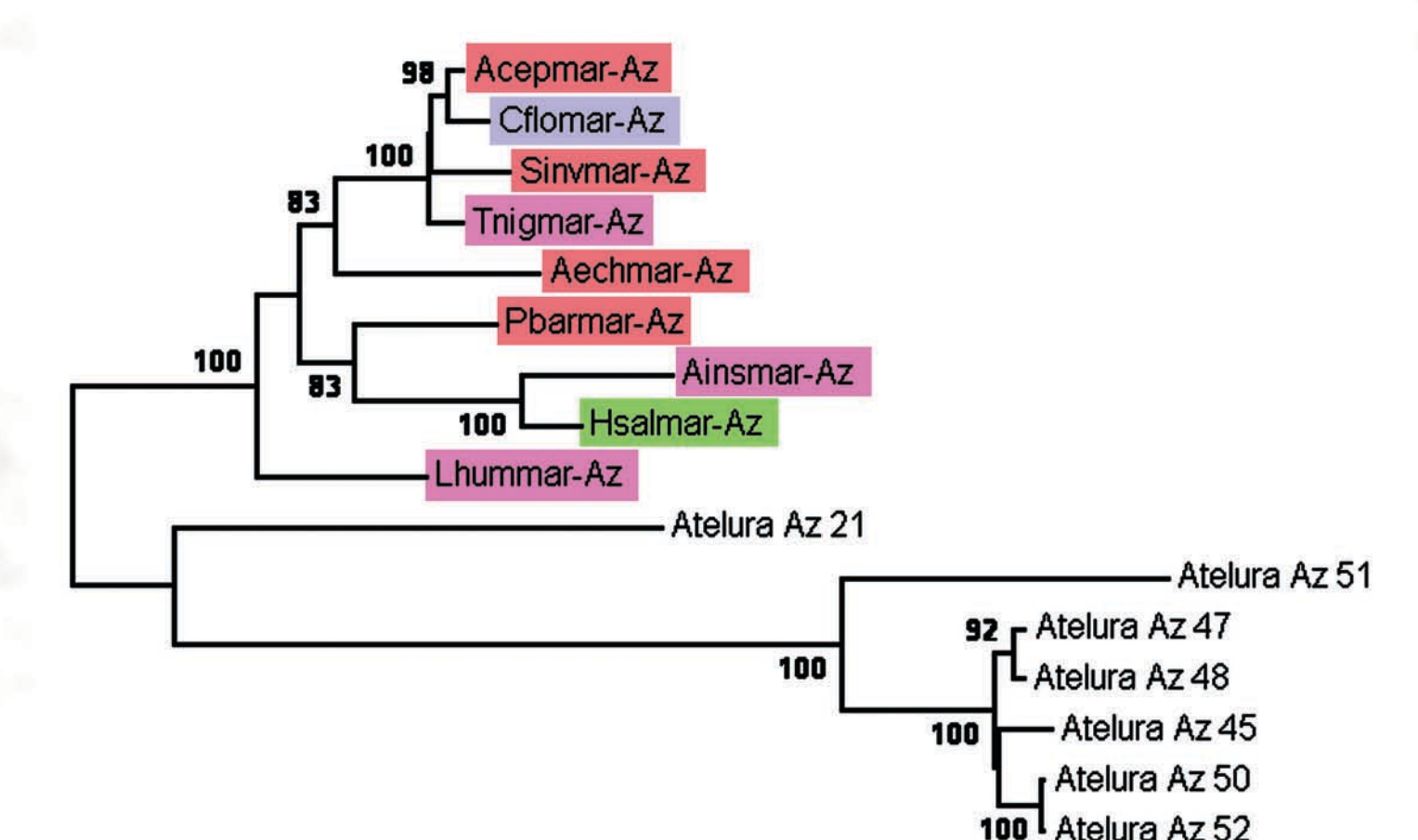


Fig. 2. Phylogenetic tree of *Azteca* copies in *A. formicaria* (*Atelura-Az*) and in the ant species: *Atta cephalotes* (*Acepmar-Az*), *Acromyrmex echinatior* (*Aechmar-Az*), *Solenopsis invicta* (*Sinvmar-Az*) and *Pogonomyrmex barbarus* (*Pbarmar-Az*) from the Myrmicinae subfamily, *Camponotus floridanus* (*Ctiomar-Az*) from Formicinae subfamily, *Tapinoma nigerrimum* (*Tnigmar-Az*), *Azteca instabilis* (*Ainsmar-Az*) and *Linepithema humile* (*Lhummar-Az*) from Dolichoderinae subfamily and *Harpegnathos saltator* (*Hsalmar-Az*) from Ponerinae subfamily.