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

Transposons are able to move along their host genome (with a "cut and paste" mechanism) 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. Here we study the possibility of HT between insect orders: the mariners Mboumar and Azteca described in ants are detected in the silverfish *Atelura formicaria* (Zygentoma, Ateluridae), a small myrmecophilous insect sampled in a *Formica cunicularia* nest. 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. This is what we found for the Azteca sequences, which suggests its vertical transmission between both orders although not among ants given that ant subfamilies are not differentiated for their Azteca clones. On the other hand, the phylogeny of Mboumar showed incongruencies with that of its hosts as evidenced by the random distribution of the *A. formicaria* clones within ants. These differences between mariner and host phylogenies point to horizontal transfer as the most probable mechanism of transmission.