

Abstract

In contrast to other eukaryotes, the telomeres of Arthropoda, the most diversified phylum, are composed of a specific motif (TTAGG)_n. The presence of this sequence is conserved within the phylum, yet alternative sequences derived from the ancestral have evolved. Diversity of short motifs has been found especially in the orders Coleoptera, Hymenoptera and Hemiptera. In addition, TRAS and SART retroelements transpose between telomeric sequences in many representatives of different orders. In arthropods, there are still numerous groups whose telomeres do not contain the (TTAGG)_n motif, but alternatives have not been proposed yet. One of them is the order Araneae (spiders), as well as some orders of insects. An interesting exception is the order Diptera, where a telomerase-independent telomere elongation mechanism has evolved. The genera *Anopheles* and *Chironomus* have telomeres composed of long repeats (up to 350 bp). *Drosophila melanogaster* relies on a mechanism based on transposition of the telomere-specific retroelements HeT-A, TART and TAHRE. The diversity of telomeric repeats in Diptera can be considerable even in closely related species, which may complicate the identification of novel telomeric sequences in unstudied species.

Key words

Drosophila, insects, retroelements, telomere, (TTAGG)_n