

INCREASED RATE OF GENE REARRANGEMENT IN THE MITOCHONDRIAL GENOMES OF THREE ORDERS OF HEMIPTEROID INSECTS (LICE, BARK LICE AND THRIPS)

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Prior to this study, the entire DNA sequence of mitochondrial (mt) genome was known for 12 species of insects, and part of mtDNA sequence was known for over 400 species of insects. The arrangements of all of the 13 protein-coding genes and two rRNA genes, and most of the 22 tRNA genes are the same in these genomes.

After sequencing the mt genome of the wallaby louse, *Heterodoxus macropus* (Phthiraptera), we have also sequenced the entire mt genomes of the plague thrips, *Thrips imaginis* (Thysanoptera) and a lepdopsocid species (Psocoptera), and partial mt genomes of another 20 species of hemipteroid insects. We found that rearrangements of protein-coding genes and tRNA genes have occurred in all of the species from the orders Phthiraptera (lice), Psocoptera (bark lice) and Thysanoptera (thrips), but not in species from the order Hemiptera (bugs).

Compared with the ancestral gene arrangement of insects, nine protein-coding genes and all of the 22 tRNA genes have translocated and/or inverted in the mt genome of the wallaby louse; six protein-coding genes, two rRNA genes and 16 tRNA genes have translocated and/or inverted in the mt genome of the plague thrips; and one protein-coding gene and seven tRNA genes have translocated in the mt genome of the lepidopsocid species. In addition, the arrangements of genes also vary between different families of the suborder Amblycera (Phthiraptera), and between two suborders of Psocoptera. Our results suggest that rearrangement of genes has evolved in a faster rate in the mt genomes of three of the four orders of hemipteroid insects.