

**NUMEROUS GENE REARRANGEMENTS IN THE MITOCHONDRIAL GENOME
OF THE WALLABY LOUSE, *HETERODOXUS MACROPUS* (PHTHIRAPTERA:
BOOPIDAE)**

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Prior to this study, the complete arrangement of genes was known for the mitochondrial (mt) genomes of 12 species of insects, and partial arrangement was known for over 400 other species of insects. The arrangement of genes in the mt genome was thought very conserved in insects, since all of the 13 protein-coding genes and two rRNA genes and most of the 22 tRNA genes are arranged in the same way in the mt genomes of the insects previously studied.

We sequenced the entire mitochondrial genome of the wallaby louse, *Heterodoxus macropus*. This genome is circular, 14670 bp long, and encodes all of the 37 genes typical for animal mt genomes. However, the arrangement of genes in this genome is unlike that of any other animals studied. All of the 22 tRNA genes have translocated and/or inverted relative to the ancestral gene arrangement of insects. At least nine protein-coding genes have translocated; moreover, four of these genes have also inverted. The largest non-coding region in this genome is 73 bp long and the second largest is 47 bp long; both of them are among the shortest non-coding regions observed so far in animals.

The wallaby louse is the first species from the Hemipteroid Assemblage for which the entire mt genome has been sequenced. This louse is also the first species of insect from which rearrangements of protein-coding genes or rRNA genes in mt genome have been observed. In addition, the large number of genes which have translocated and/or inverted in the mt genome of this louse is unprecedented for an arthropod.