

Comparative Analyses of Mitochondrial Genome Among *Bombyx mori*, *B. mandarina*, and Saturniidae Silkmoths

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We characterized the complete organization of the mitochondrial genomes (mt genome) of a sample of Japanese *Bombyx mandarina* (15,928 bp) and the *Bombyx mori* C108 strain (15,656 bp) and examined how the mt genomes of the two species have been diversified. Comparing these two mt genomes, sequence rearrangements in noncoding regions as well as significant levels of sequence variation were detected between them, although gene numbers, gene arrangement, translation initiation and translation termination sites were highly conserved. Regional bias of nucleotide differences was detected. Biased mutational changes were also confirmed: preferential occurrence of T/C transitional changes was observed in protein-coding genes on the major strand, whereas A/G transitions were observed more frequently in genes on the minor strand. Noncoding sequences including the A+T-rich region have undergone sequence rearrangements, including insertion or deletion. These results strongly indicate that, although *B. mandarina* is a close relative to *B. mori*, a sufficient degree of genetic isolation has occurred between Japanese *B. mandarina* and the population from which *B. mori* has been domesticated. We further analyzed parts of Saturniidae mt genomes, which share a common gene order so far we examined. Nevertheless, large variation in tRNA sequences as well as usage of translation initiator was confirmed.