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Genetic Homogeneity in the Domestic Silkworm, *Bombyx mori*, and phylogenetic relationship between *B. mori* and the wild silkworm, *B. mandarina* using mitochondrial COI gene sequences

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Genetic variation in the domestic silkworm strains (*Bombyx mori*) and phylogenetic relationships between domestic silkworms and wild silkworms (*B. mandarina*) were investigated by using a portion of mitochondrial COI gene sequences. Ten geographic strains of *B. mori* we sequenced were identical in the 410 bp-section of mitochondrial COI gene. This sequence was also identical to the homologous sequence of the four GenBank-registered strains, but one strain of *B. mori* differed a single nucleotide (0.2%) from others. MtDNA homogeneity in the *B. mori* strains appears to be resulted from fixation into the most frequent mtDNA type during the course of breeding for new strains, in which an extensive indoor rearing and removal of unwanted individuals were accompanied. In the comparisons between domestic and wild silkworms, some wild silkworms were closely related to domestic silkworms (0.2%-1.2% of divergence), but the others were not (2.7%-3.7% of sequence divergence). This result was also reflected in the phylogenetic analyses, showing two independent phylogenetic groups: one including all *B. mandarina* sequences and the other including both *B. mandarina* and *B. mori* sequences. Thus, domestic silkworms may have been derived from the ancestor of *B. mandarina*, which belongs to this group, although more extensive study will provide better understanding on this issue.