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EXCHANGE BETWEEN NUCLEAR AND MITOCHONDRIAL GENOMES
(BASED ON THE ANALYSIS OF NUCLEAR AND CYTOPLASMIC COPIES
OF MITOCHONDRIAL GENES — *numts* AND *cymts*)

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The opinion of strict cloning of mitochondrial DNA appears to be untrue. The mechanism of recombination that changes the nucleotide composition of the mitochondrial chromosome is not yet known, but many data indicate that nuclear copies of mtDNA (*numts* — nuclear sequence of mitochondrial origin) are involved. The old mtDNA haplotypes stored in the nucleus chromosomes in the form of *numts* can, after a time, be transferred back to the mitochondria. Such a return to the ancestral state disrupts the beauty of phyletic reconstructions. Horizontal gene transfer (HGT), which is widely spread in prokaryotes, also plays some role in the evolution of highly organized organisms. In both cases, nonclonal inheritance of molecular markers leads to the fact that the phylogenetic reconstruction carried out with their use contradict the schemes based on the characters of morphology and comparative anatomy. Most often this happens when trying to improve the classification of lower invertebrates using modern molecular methods. The conception on the inheritance of the mitochondrial haplotype solely on the maternal line, without the participation of recombination, has long been challenged by authoritative specialists, but it is still adopted in the making of phylogenetic reconstructions and serves as a source of many errors.

Key words: cloning and recombination of mtDNA, circular and linear fragmented mt-chromosomes, nuclear sequence of mitochondrial origin, molecular phylogenetics