Update of AMmtDB: a database of multi-aligned metazoa mitochondrial DNA sequences.

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The present paper describes AMmtDB a database collecting the multi-aligned sequences of Vertebrate mitochondrial genes coding for proteins and tRNAs, as well as the multiple alignment of the Mammalian mtDNA main regulatory region (D-loop) sequences. The genes coding for proteins are multi-aligned based on the translated sequences and both the nucleotide and aminoacid multialignments are provided. As far as the genes coding for tRNAs are concerned, the multi-alignments based on the primary and the secondary structures are both provided; for the Mammalian D-loop multialignments we report the conserved regions of the entire D-loop (CSB1, CSB2, CSB3, the Central region, ETAS1 and ETAS2) as defined by Sbis? et al. (1). A flatfile format for AMmtDB has been designed allowing its implementation in SRS (2) (http://bio-www.ba.cnr.it:8000/BioWWW/#AMMTDB). Data selected through SRS can be managed using GeneDoc (3) or other programs for the management of multi-aligned data depending on the userís operative system. The multiple alignments have been produced with CLUSTALV (4) and PILEUP (5) programs and then carefully optimized manually.