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Genetic similarities and phylogenetic analysis of human and farm animal species based on mitogenomic nucleotide sequences

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ABSTRACT

Mitochondrial genome (mitogenome) is a small and extra-chromosomal DNA, located in cytoplasm and presents an ideal model to study evolution and genetic similarity due to genomic rearrangement. In the present study, mitochondrial DNA sequences of 14 farm animal species including, *Bos indicus*, *Bos taurus*, *Ovis aries*, *Capra hircus*, *Equus caballus*, *Camelus bactrianus*, *Camelus dromedaries*, *Sus scrofa domesticus*, *Gallus gallus*, *Meleagris gallopavo*, *Struthio camelus*, *Anser anser*, *Anas platyrhynchos* and *Oncorhynchus mykiss* were retrieved from NCBI databases and compared with the sequence of *Homo sapiens*. Sequence distance analysis showed a high similarity (74.4%) between *Homo sapiens* and *Equus caballus*, while the *Oncorhynchus mykiss* had the lowest similarity (64.1%) to the *Homo sapiens*. The highest similarities among the studied species were observed between *Anser anser* and *Anas platyrhynchos* (100%) and *Bos taurus* and *Bos indicus* (98.5%). In phylogenetic analysis, the *Homo sapiens* fell in a same cluster with *Equus caballus*, *Bos indicus*, *Bos taurus*, *Ovis aries*, *Capra hircus*, *Camelus bactrianus*, *Camelus dromedaries* and *Sus scrofa domesticus*. Poultry species (*Gallus gallus*, *Meleagris gallopavo* and *Struthio camelus*, *Anser anser* and *Anas platyrhynchos*) and rainbow trout (*Oncorhynchus mykiss*) formed a distinct cluster with the lowest similarity to the human. The D-loop regions showed the most obvious differences, while other parts including tRNA, rRNA, STSs and CDSs for different genes, had more similarities. Based on the results of the present study, the mitogenomic sequences could be used for accurate phylogenetic analysis and clustering of different species. Moreover, use of mitogenomic sequence in mammalian farm animals, as biomedical model species would not be far-fetched for genetic control of zoonotic diseases.

Keywords: Mitochondrial genome; Human; Livestock; Phylogenetic analysis

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