

## Cytochrome B Diversity and Phylogeny of Egyptian Sheep Breeds

**Authors :** Othman E. Othman, Agn s Germot, Daniel Petit, Abderrahman Maftah

**Abstract :** Threats to the biodiversity are increasing due to the loss of genetic diversity within the species utilized in agriculture. Due to the progressive substitution of the less productive, locally adapted and native breeds by highly productive breeds, the number of threatened breeds is increased. In these conditions, it is more strategically important than ever to preserve as much the farm animal diversity as possible, to ensure a prompt and proper response to the needs of future generations. Mitochondrial (mtDNA) sequencing has been used to explain the origins of many modern domestic livestock species. Studies based on sequencing of sheep mitochondrial DNA showed that there are five maternal lineages in the world for domestic sheep breeds; A, B, C, D and E. Because of the eastern location of Egypt in the Mediterranean basin and the presence of fat-tailed sheep breeds- character quite common in Turkey and Syria- where genotypes that seem quite primitive, the phylogenetic studies of Egyptian sheep breeds become particularly attractive. We aimed in this work to clarify the genetic affinities, biodiversity and phylogeny of five Egyptian sheep breeds using cytochrome B sequencing. Blood samples were collected from 63 animals belonging to the five tested breeds; Barki, Rahmani, Ossimi, Saidi and Sohagi. The total DNA was extracted and the specific primer allowed the conventional PCR amplification of the cytochrome B region of mtDNA (approximately 1272 bp). PCR amplified products were purified and sequenced. The alignment of Sixty-three samples was done using BioEdit software. DnaSP 5.00 software was used to identify the sequence variation and polymorphic sites in the aligned sequences. The result showed that the presence of 34 polymorphic sites leading to the formation of 18 haplotypes. The haplotype diversity in five tested breeds ranged from 0.676 in Rahmani breed to 0.894 in Sohagi breed. The genetic distances (D) and the average number of pairwise differences (Dxy) between breeds were estimated. The lowest distance was observed between Rahmani and Saidi (D: 1.674 and Dxy: 0.00150) while the highest distance was observed between Ossimi and Sohagi (D: 5.233 and Dxy: 0.00475). Neighbour-joining (Phylogeny) tree was constructed using Mega 5.0 software. The sequences of the 63 analyzed samples were aligned with references sequences of different haplogroups. The phylogeny result showed the presence of three haplogroups (HapA, HapB and HapC) in the 63 examined samples. The other two haplogroups described in literature (HapD and HapE) were not found. The result showed that 50 out of 63 tested animals cluster with haplogroup B (79.37%) whereas 7 tested animals cluster with haplogroup A (11.11%) and 6 animals cluster with haplogroup C (9.52%). In conclusion, the phylogenetic reconstructions showed that the majority of Egyptian sheep breeds belonging to haplogroup B which is the dominant haplogroup in Eastern Mediterranean countries like Syria and Turkey. Some individuals are belonging to haplogroups A and C, suggesting that the crosses were done with other breeds for characteristic selection for growth and wool quality.

**Keywords :** cytochrome B, diversity, phylogeny, Egyptian sheep breeds

**Conference Title :** ICASVM 2016 : International Conference on Animal Science and Veterinary Medicine

**Conference Location :** London, United Kingdom

**Conference Dates :** August 25-26, 2016