

## Genomic Diversity and Relationship among Arabian Peninsula Dromedary Camels Using Full Genome Sequencing Approach

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**Abstract :** The dromedary camels (*Camelus dromedarius*) are single-humped even-toed ungulates populating the African Sahara, Arabian Peninsula, and Southwest Asia. The genome of this desert-adapted species has been minimally investigated using autosomal microsatellite and mitochondrial DNA markers. In this study, the genomes of 33 dromedary camel samples from different parts of the Arabian Peninsula were sequenced using Illumina Next Generation Sequencing (NGS) platform. These data were combined with Genotyping-by-Sequencing (GBS) data from African (Sudanese) dromedaries to investigate the genomic relationship between African and Arabian Peninsula dromedary camels. Principle Component Analysis (PCA) and average genome-wide admixture analysis were conducted on these data to tackle the objectives of these studies. Both of the two analyses conducted revealed phylogeographic distinction between these two camel populations. However, no breed-wise genetic classification has been revealed among the African (Sudanese) camel breeds. The Arabian Peninsula camel populations also show higher heterozygosity than the Sudanese camels. The results of this study explain the evolutionary history and migration of African dromedary camels from their center of domestication in the southern Arabian Peninsula. These outputs help scientists to further understand the evolutionary history of dromedary camels, which might impact in conserving the favorable genetic of this species.

**Keywords :** dromedary, genotyping-by-sequencing, Arabian Peninsula, Sudan

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