

Analysis of Genetic Variations in Camel Breeds (*Camelus dromedarius*)

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Abstract : Camels are substantial providers of transport, milk, sport, meat, shelter, security and capital in many countries, particularly in Saudi Arabia. Inter simple sequence repeat technique was used to detect the genetic variations among some camel breeds (Majaheim, Safra, Wadah, and Hamara). Actual number of alleles, effective number of alleles, gene diversity, Shannon's information index and polymorphic bands were calculated for each evaluated camel breed. Neighbor-joining tree that re-constructed for evaluated these camel breeds showed that, Hamara breed is distantly related from the other evaluated camels. In addition, the polymorphic sites, haplotypes and nucleotide diversity were identified for some camelidae *cox1* gene sequences (obtained from NCBI). The distance value between *C. bactrianus* and *C. dromedarius* (0.072) was relatively low. Analysis of genetic diversity is an important way for conserving *Camelus dromedarius* genetic resources.

Keywords : camel, genetics, ISSR, neighbor-joining

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