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The Thesis Submitted for the Degree of Master of Science
(In the Field of Genetics and Animal Breeding)

**Diversity analysis of mitochondrial HVR¹ ecotypes
in some Iranian native goats breeds (*Capra hircus*)**

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Abstract

Iranian native goats considered as a valuable genetic resources and protection of genetic diversity of them is very important. Mitochondrial genome have been considered as a suitable index to replicate population diversity within and between ecotypes. Therefore, the aim of the current study was to evaluate of genetic structure and phylogenetic study of mitochondrial HVR1 region of four Iranian native goat populations and compare them with other goat breeds from Genbank information (NCBI). Blood samples have been randomly taken from 4 heads of each Sistani, Pakistani, Black Lori and Adani ecotypes from Sistan and Baluchistan, Kohkiloye and Boirahmad and Bushehr provinces, respectively. DNA was extracted through *chloroform* method and used as template for extension and sequencing of mitochondrial HVR1 region. PCR reaction have done using a pair of private primers. Then, PCR products were sequenced after purification. Sequences compared with 20 extra sequences of other goat breeds mitochondrial genome and 45 sequences of other species from NCBI and phylogenetic tree was drawn. Evaluation of mitochondrial HVR1 region of goats in the current study revealed 123 polymorphic loci and 16 haplotypes. Molecular variance analysis shown that 15 % of variants were between populations and 85 % were within populations. All of the studied goats was categorized in haplotype A which commonly found in all continents. The between population magnitude of dN/dS was 1.17 which demonstrate positive trend of selection for HVR1 gene in the four studied ecotypes during evolution. D and Fs values from Tajima test were negative and insignificant which may be due to small sample size in the current study. Result of this study illustrated high levels of genetic diversity and existence of genetic resemblance for some of goat breeds. Therefore, for protection of native ecotypes, it could be recommended controlled mating between populations.

Keywords: Sequencing, Genetic Diversity, D-loop, Phylogenetic relationships