

## STUDY OF GENETIC DIVERSITY IN POPULATIONS OF IRANIAN NATIVE BUFFALOS THROUGH MICROSATELLITES MARKERS

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**Objective:** Genetic diversity has been found in all species on the protein and DNA levels that acting as a vital role in the survival, adaptability, decreasing extinction of a species and mating programs in animal breeding. In this regard, Microsatellites, so-called Simple Sequence Repeats (SSRs) polymorphisms are plentiful and highly polymorphic in the genome of eukaryotes both in coding and non-coding regions of DNA that used commonly in the genetic diversity studies in many species of animal (Hoshino et al., 2012). Therefore, the aim of this study was to identify genetic variability and drawing phylogenetic tree in between three populations of Iranian native buffalos (khuzestan, Azarie and North), based on ten microsatellites markers.

**Materials and Methods:** The total numbers of animals sampled were 200, and collected from khuzestan, Azarie and North populations (70, 70 and 60, respectively). Genomic DNA was extracted from their hair by the modified salting-out method (Miller et al., 1988) and quantitative and quality of DNA was determined with spectrophotometer and 1% agarose gel, respectively. A total of ten different primer pairs (CSSM047, CSSM033, BM1824, BM1818, BoLA-DRB3, ILSTS089, ILSTS061, ILSTS058, ILSTS033, ILSTS017) were optimized for polymerase chain reaction to amplify microsatellite loci in total hair genomic DNA. The PCR fragments from each locus was loaded on 9% poly acrylamide gel and then visualized by staining with silver-nitrate method. All genotypic data analyzed by GenAEx and Popgene software. Genetic distances among populations were estimated using standard genetic distance of Nei (Nei et al., 1972), and then were used for drawing phylogenetic tree according to unweighted pair group method with arithmetic means (upgma) method.

**Results and Discussions:** The results showed that, all the microsatellites were highly polymorphic, with mean allelic number of 5.9, 5.9 and 5.6 for Khuzestan, Azarie and North populations. Also high genetic diversity in these populations observed, nevertheless, genetic diversity in Azarie population is greater than the populations of Khuzestan and North buffalos. On the other side, the phylogenetic tree revealed that the Khuzestan and Azarie population is placed in a sub-branch which forms a clade beside the North population (Fig. 1). Finally, this study confirms that, the high polymorphism of this selected loci and its benefits for identification of population structure in Iranian native buffalos. This research indicated, high variation within and between studied Iranian buffalo populations and also proved that microsatellite genotyping is an useful tool to assessing of Genetic variation and a prerequisite in developing strategies for conservation and utilization of Iranian buffalo genetic resources.



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