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Graduate school
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Thesis Submitted for Degree of Ph.D
In Genetic and Animal Breeding

Investigation of Population Structure and Selection Signature of Iranian Sarabi and Najdi Cattle using Genomic Data

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Abstract

By selecting new and effective mutations in some populations, symptoms appear at the genome level. Identifying and tracking selection signature is an important topics in animal genetics. Recent advances in genomics and access to genomic information have led to the development of various methods and models for examining population structure and identifying selection signature in various species of domestic animals. The present study was conducted to evaluate homozygosity rate based on SNP containing sites and to assess run of Homozygosity (ROH) positions in Iranian Sarabi and Najdi Cattle's, using genomic data of 424 cattle including 213 Sarabi and 211 Najdi cattle. The data were provided by the National Livestock Breeding Center. After checking the accuracy of the sequences and determining the FDR using plink software version 9/1, the quality control of SNPs was performed with 85% in each animal and 95% in each marker. In order to prevent error in the calculation of inbreeding, the cow population was divided by the SPIN software version 2. Also, the inbreeding coefficient was performed by four methods; genomic homozygous inbreeding Coefficient (F_{HOM}), the inbreeding coefficient of ROH by length of more than 4Mb ($F_{ROH>4Mb}$), estimate by plink software, the inbreeding coefficient of genomic relationships matrix (F_{GRM}) using R software and the pedigree inbreeding coefficient (F_{Ped}) was calculated by the CFC software and the correlation between them were calculated for all animals with genomic data. The effective population size (N_e) was calculated by SNeP software version 2. Also, the selection Signatures in Sarabi and Najdi were evaluated using F_{st} statistic by HierFstat software R programming environment version 2.1.1, ROH hotspots and hapFLK were calculated. According to the results, the highest correlation between $F_{ROH>4Mb}$ and F_{Ped} was 0.581 in Sarab ($P<0.001$). The correlation between $F_{ROH>4Mb}$ and other estimated inbreeding coefficients was generally low, from 0.465 ($F_{ROH>4Mb}-F_{GRM}$) in Sarabi ($P<0.001$) to 0.028 ($F_{ROH>4Mb}-F_{Ped}$) in Najdi ($P<0.05$), and the correlations in Sarabi were higher than Najdi. According to the results of the inbreeding coefficient, the ROH components observed are more than 4Mb, expected that inbreeding would be related to the five generations ago. Also, identified that SUMO3, RF00001, and H3F3B genes ($P<0.05$), associated with genetic changes in carcasses and meat quality and animal behavior.

Keywords: Genomic Inbreeding Coefficients, Single Nucleotide polymorphism, Pedigree ,Run of Homozygosity, Native Cow and Genetic Drift.