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## **Genomic Selection of Dromedary Camel in Yazd Province**

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### **Abstract**

In order to Development of camel husbandry for protein production in desert climate, attention to genetic improvement is very important. Traditional camel breeding is difficult because of recording difficulty and staff injures. Therefore, genomic selection is necessary. We assessed genome-wide diversity, linkage disequilibrium (LD), effective population size ( $N_e$ ) and relatedness in 96 dromedaries originating from five different regions of the central desert of Iran using genotyping-by-sequencing (GBS). The genome-wide association studies of the birth weight, daily gain, and body weight were determined. The Genomic selection was performed with the BGLR package. A total of 14,522 Single Nucleotide Polymorphisms (SNPs) with an average minor allele frequency (MAF) of 0.19 passed quality control and filtering steps. The mean of LD at distances shorter than 40 kb was low ( $r^2 = 0.089 \pm 0.234$ ). Recent  $N_e$  of Iran's camels was estimated to be 89. Predicted Tajima's D (1.28) suggested a bottleneck or balancing selection in dromedary camels in the central desert of Iran. A general decrease in effective and census population size poses a threat for Iran's dromedaries. twenty-eight SNPs were associated with birth weight, gain/ day, and body weight ( $p$ -value  $< 0.001$ ) and located the 36 candidate genes. A total of 99 SNPs was associated with birth weight, gain/ day, and body weight ( $p$ -value  $< 0.002$ ). The accuracy of GEBVs was more than 0.65 based on all 14,522 SNPs, but the regression coefficients for birth weight, gain/ day, and body weight were 0.39, 0.20, and 0.23, respectively. Because of low sample size, the GEBVs were predicted using the associated SNPs from GWAS. The accuracy of GEBVs based on the 99 associated SNPs was 0.62, 0.82, and 0.57 for birth weight, gain/day, and body weight. Because of low sample size, the GEBVs were predicted using the associated SNPs from GWAS. The accuracy of GEBVs based on the 99 associated SNPs was 0.62, 0.82, and 0.57 for birth weight, gain/day, and body weight. This report is the first GWAS using GBS on dromedary camels and identifies the associated markers with growth traits that could help to plan breeding program to genetic improvement. Further researches using larger sample size and collaboration of the camel farmers and more profound understanding will permit verification of the associated SNPs identified in this project. The genomic selection could be the appropriate way to genetic

improvement of body weight in dromedary camels due to long generation interval, seasonal reproduction, and lack of records and pedigrees.

**Key words:** Dromedary camel, Genomic Selection, Genome Wide Association Study, Body Weight