Abstract

In the modern breeding programs that was based on the use of genomic data, The most important tool is the imbalance or LD by various factors including the mating system between animals during past and present generation. The aim of this study is to assess the accuracy of breeding values in different scenarios including of different heritabilities, the number if QTLs and effective population size in the simulated data for beef cattles. The trait of carcass weight based on the average of standard deviation phenotypic were simulated in beef cattles. In the recent study were used from four scenarios for heritability of trait. Genomic data simulated for five chromosomes in the length of 500 cM with different dense markers includings four scenarios 500, 1000, 1500 and 2000 SNP markers that was seprated in random on the each chrosomes. The results showed that the accuracy of estimated breeding values for animales were improved for trait with high heritability, high-dense markers, increasing the number of QTL and increase the effective population size.

Keywords: breeding values, reference population, controlling quantitative trait position,markers

University of Zabol
Graduate School
Faculty of Agriculture

Department of Animal Science

The Thesis Submitted for the Degree of M.sc in the field of Genetics
and Animal Breeding

Effect of population size, heritability of trait, density of QTL and markers on accuracy of genomic selection in simulated populations.

Supervisor:

Dr.G. R. Dashab

Advisors:

Dr.M. Rokouei

Dr.M. Asadi

BY:

S. Askarzadeh

2016