



Estimation of Akkaraman sheep in genomic heritability and genome wide association in blood parameters

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DESCRIPTION

Sheep (*Ovis aries*) were one of the first animals that humans domesticated. This domestication has spread over numerous continents and different geographic regions. Native sheep breeds are significant genetic resources because of their long history of adaptation and outstanding gene-environment interactions for survival. Due to characteristics that make it suitable for dry regions and the use of low-quality pastures like several other fat-tailed sheep, the Akkaraman sheep is one of the most common domestic sheep breeds. Complete Blood Counts (CBCs) are frequently used to learn about the general health state of mammals and allow for the evaluation of blood parameters. Changes in baseline CBC values are one of the most often used diagnostic techniques by veterinarians and offer crucial information on the diagnosis of various diseases in farm animals. Additionally, blood cells carry out crucial functions related to animal life and disease resistance. Erythrocytes, leukocytes, and platelets are the three main cell groupings that are assessed by measured blood parameters.

Environmental elements such local infections, diet, and altitude are known to have a big impact on sheep's blood parameters. In addition to this, genetics is a significant factor in sheep blood parameters. Quantitative trait loci are genomic areas that influence the determination of quantitative phenotypic characteristics, such as blood values. The availability of a sheep reference genome allowed scientists to pinpoint the genetic loci underpinning variations in CBC values at the whole-genome level, despite the fact that research on the genetic mechanisms causing changes in blood parameters in sheep is still fairly limited. A substantial Single Nucleotide Polymorphism (SNP) was shown to be associated with mean corpuscular haemoglobin concentration in one of these studies' completed genome-wide association studies for red blood cell characteristics in three domestic sheep breeds. Further

investigation revealed that the Red Blood Cell (RBC) abnormalities observed in study lambs were most likely caused by mutations in the *MYADM*-like gene family¹⁵. Two specific genes were discovered to be connected with hematopoiesis, or the formation of blood cells, in a different Genome-Wide Association Study (GWAS) of erythrocyte-related features in Alpine Merino sheep. This study's objective was to look at the genetics of 18 phenotypes in Akkaraman sheep related to erythrocytes, leukocytes, and platelets. Using phenotypes from CBCs and genotypes from a 50 K ovine SNP panel, genetic parameter estimations, a genome-wide association analysis, and regional heritability mapping study were carried out for this aim.

The assembling of reference genome sequences from many species has contributed the most to the identification of genes linked to complex traits, followed by the acceleration of scientific progress in the field of genomics. The genetic basis of economically significant livestock features like disease resistance, milk yield, meat yield, and haematological parameters has also been discovered by linking phenotype and genotype data using a linear mixed model based analysis, which is a frequent technique in GWAS⁷. In this study, genetic heritability estimates for 19 blood parameters in the common indigenous sheep breed known as Akkaraman were obtained. Genome-wide association analyses for each trait were used, and the results suggested 19 particular genes and 3 unknown sites. We can expect different heritabilities for the same trait in populations exposed to these natural and artificial causes over different time periods and in diverse ways. Although these studies used different breeds, the heritability estimates of several features in our analysis were remarkably close to the findings of earlier investigations. However, the very small sample size of our study resulted in the heritability estimates having quite high standard errors, which may make it more difficult to detect discrepancies across estimates. In any event, one can assume that no

systematic selection has been applied to these parameters that might have changed the amount of genetic variance in the phenotypic features of these animals given the concordant moderate heritability estimates of several blood parameters in many sheep breeds. Therefore, it is entirely feasible to genetically increase these parameters using selection techniques. In addition to the single step GWAS method, a regional heritability mapping strategy was utilised to look for any associations between particular genomic areas derived from the genome and blood parameters. The frequently used technique for identifying potentially significant genomic areas. It has been reported that this can be used as a selection criterion in sheep breeding

approaches because it is reportedly a more effective method than the SNP-based GWAS method in detecting genomic regions containing multiple and rare allele with relatively moderate and small effects or epistatic effects in the genome. Erythrocytes and leukocytes are strongly associated to sheep adaption and survival, so the resulting breeding techniques may result in more resilient and long-lasting animals. Finally, it is strongly advised that these and comparable studies be carried out on bigger numbers and in diverse groups in order to get more complex understanding on the genetic causes of blood parameters and convert this knowledge to applications.