S03(T)-PP-1

Genetic identification, of beef and dairy cattle breeds in four regions of Russia Alexandr Kalashnikov¹, Yana Kabitskaya², Lubov Kalashnikova¹, Elena Boyko², Valentin Prozerin³, Vladimir Yaluga³, Nina Furaeva⁴, Evgenva Zvereva⁵, Alexej Novikov¹

¹Laboratory of Immunogenetics, VNIIPLEM, MA Russia, Lesnye Polyany, Russian Federation

²Tyumen State Agrarian University of Northern Ural, Tyumen, Russian Federation

³Arkhangelsk Scientific Research Institute of Agriculture of the RAS, Arkhangelsk, Russian Federation

⁴Yaroslavl State Agricultural Academy, Yaroslavl, Russian Federation

⁵Yaroslavl tribal association, Yaroslavl, Russian Federation

Genetic identification of cattle is carried out in Russia using immunogenetic analysis and various identification methods. No organization, other than the institutions of the Russian Ministry of Agriculture, does not carry out the identification process in accordance with international ISAG rules. The issue of harmonization of microsatellite analysis and analysis by gene chips is a prerequisite for determining the credibility of the origin of bulls for calculating the breeding value (from 2018). The aim of the study was the genetic identification of animals and the definition of their relationship by parents. In the Moscow, Arkhangelsk, Tyumen and Yaroslavl regions genotyping of bull sperm was carried out at analysis of 11-15 microsatellite loci, which are fully complied with the standard ICAR panel. The analysis involved the breeds - Yaroslavl, Kholmogory, Holstein, Black-and-white, Salers, Abrac, Aberdeen Angus, Hereford, (351, 150, 95, 302, 125, 1600, 175, 222 heads respectively). In the middle of the matching of triples {father-mother-offspring} (n = 799), 5 errors for the mother and 2 for the father were identified. The match was 88.8%. As a result of checking the records for parents were found out with mother counting errors of 0.8%, and for the father 0.3%. The discrepancy for the black-and-white breed of dairy cattle was 3.0%, the detected errors for the father were 1.5%, for the mother there were no errors. For the rest of dairy cattle, the magnitude of errors in the loci was 0.2-11% and was the highest for the locus tgla53 for 7-11%. A transition is underway to the ICAR and ISAG standards in the field of genetic identification of animals in three regions of Russia for competent management of breeding and breeding work, as well as the sale of genetic material and breeding animals at farms in the framework of genetic expertise testing. This work was supported by the grant of the Ministry of Agriculture of the Russian Federation No. 082-03-1290.

Keywords: genomic selection, microsatellites, genetic identification, genetic diversity, locus variability, accounting errors