ABSTRACT

of the dissertation work by Bekova Gulmira on the topic «Study of the productive qualities of the Kazakh horse of the Jabe type based on genome-wide coverage SNP genotyping» submitted for the degree of Doctor of Philosophy (PhD) under the education programme 8D08201- Technology of Livestock Production

Relevance of the study. The relevance of the study is due to the fact that ensuring food security of the population is one of the priority tasks of the Republic of Kazakhstan and the production of horse breeding products in our country is a powerful tool for solving this problem in our country. Kazakhstan is the second largest producer of horse meat in the world after China, but it is mainly limited to the domestic market, since the country is not among the significant exporters of horse meat in the world.

With the growing interest in horse meat as a safe and nutritious alternative to beef, Kazakhstan has the potential to become an important supplier to the global horse meat market. This requires large-scale modernization of horse breeding to meet internationally recognized standards. An important aspect of such modernization is the widespread introduction of modern molecular genetics and genomics methods into breeding practices to better understand the genetic structures of horse lines and breeds, improve the classification and management of horse genotypes, promote selection using molecular markers associated with valuable traits, etc.

Commercial animal microarray genotyping panels contain tens or hundreds of thousands of SNP markers selected to reflect common genetic variation, helping to scan genomes for potentially important polymorphisms without expensive whole-genome sequencing. In Kazakhstan, SNP microarray genotyping has previously been used to characterize the genetic structures of local sheep breeds, another animal of significant importance to the country. For horses, the EquineSNP50 panel has been developed and has proven useful for genome-wide association studies and equine diversity studies.

One of the most popular horse breeds in Kazakhstan is the Kazakh breed of the Jabe type, whose representatives are the largest and are bred for the meat and dairy industry, since they have a strong constitution with pronounced meaty forms.

The Kazakh Jabe type horse is unique because it represents populations that are less manageable than popular breeds in Europe and America, occupy a variety of habitats, and has been bred to select animals with the qualities needed for meat and milk production, in addition to being used for transport.

To date, the Kazakh Jabe type horse remains unstudied on a genome-wide scale. There has been no comparison of genetic diversity in the world, either within the Kazakh Jabe type breed or with other breeds, no study of the phylogenetic relationships between the Jabe and other breeds, and the development of DNA chipping methodology provides researchers with a powerful tool.

Completion of the reference genome has taken equine genomics to a new level. The EquCab 2.0 equine reference genome has facilitated the discovery of millions of sequence polymorphisms across horse breeds, leading to the development of three generations of SNP arrays. In 2011, first- and second-generation DNA genotyping arrays became available. These SNP arrays have identified a range of phenotypic traits and genetic diseases, including lavender foal syndrome, alternative gait, iris color variation, and squamous cell carcinoma of the eye. These resources have been used to identify breed-specific selection biases that help to understand the biology underlying performance and other equine traits.

The genome of the modern horse shows regions with signs of selective pressure. The most notable are the MSTN gene for muscle fibers in racing breeds, the DMRT3 gene for performing alternative gaits. Candidate genes for racing qualities in horses have been identified: COX4I2 and PDK4, involved in cellular respiration.

There is evidence of the contribution of some genes to horse growth traits. Makvandi-Nejad S. et al. using a 50,000 SNP array identified loci including the LCORL/NCAPG, HMGA2, ZFAT and LASP1 genes that explain most of the size differences between breeds. Additional studies have confirmed the association of the LCORL/NCAPG9], ZFAT and HMGA2 genes with growth in various other horse populations.

Another aspect that determines the relevance of the study is the national need to preserve and improve the unique genomic characteristics of aboriginal horse breeds in general and Jabe horses in particular..

Purpose of the work: to characterize the genome features of Jabe horses based on wide-coverage SNP genotyping data and to identify SNPs associated with growth and development rates to improve the animal selection method and use in marker selection.

Objectives of the work:

1. To characterize the intrabreed genetic diversity of populations of the Kazakh aboriginal horse type Jabe in different regions of the Republic of Kazakhstan by genotyping with wide genome coverage.
2. To conduct a comparative analysis of the genomes of the aboriginal horse type Jabe and other traditionally defined types and breeds of aboriginal Kazakh horses.
3. To establish single nucleotide substitutions in the coding regions of the genome, significantly associated with the productive qualities of the Kazakh breed of the Jabe type (QTL- associated SNP).
4. To evaluate the phenotypic effects of QTL-associated SNPs on economically significant productivity traits of the Kazakh aboriginal horse of the Jabe type.
5. To develop a DNA panel for early assessment of performance potential in Jabe horses.

Object of study: horses of the Kazakh breed of the Jabe type, bred in different regions of the Republic of Kazakhstan (Almaty, Pavlodar, East Kazakhstan regions, etc.).

Subject of research: polymorphic regions of the genome of aboriginal horses of the Jabe type.

Methodology and research methods. Whole-genome SNP genotyping of the Kazakh Jabe breed was carried out using the Equine 80k HTS biochip and reagent kit manufactured by Illumina Inc. SNP genotyping of DNA of the Kazakh Jabe breed is carried out according to the methodology of reagent and equipment manufacturers, the principle of which is to bind DNA sections to certain SNPs on the chip and their fluorescence at different wavelengths of light, which allows obtaining reliable data on the manifestation of SNPs in a particular DNA section. The studies were conducted in the accredited laboratory of biotechnology and diagnostics of infectious diseases (No. KZ.T.09.E0858) of the Testing Center of the West Kazakhstan Agrarian and Technical University named after Zhangir Khan. The scope of accreditation of the laboratory is genotyping of farm animals, including horses. The laboratory staff developed and certified by RSE KazInMetr the "Methodology for the analysis of amplified fragment length polymorphism (AFLP) for conducting molecular genetic examination of farm animals" (Certificate No. 1176 dated 17.02.2017), as well as the "Methodology for performing measurements. Determination of the genetic profile of animals by the method of studying nuclear DNA" (Certificate No. 314 dated 11/24/2021).

Scientific novelty of the research. The scientific novelty of the work is that the genetic diversity of the Jabe has been characterized for the first time, the data of the whole-genome SNP genotyping of the Jabe have been compared with an international sample of various horse breeds, and informative genetic markers in the coding sequences of the genome associated with productive qualities have been identified. This study can be considered as the first step in deepening our knowledge of the genomic diversity of the Jabe.

The theoretical significance of the project is that the data obtained will help clarify the relationship between the Jabe and breeds around the world with applications for conservation, management and breeding of horses. The implementation of the proposed project will help explain the history of the Kazakh breed of the Jabe type, determine the uniqueness of the breed, and serve as a starting point for further monitoring of the diversity of the breed.

Practical significance of the study. The practical significance of the research lies in the development of a new approach to the breeding of domestic horse breeds. The research results can be used by specialists in the development of technologies for effective management of the breeding process in horse breeding, by students to improve their educational level, by scientists to deepen their knowledge and use new methods in their research. The work will increase the intellectual potential for performing molecular genetic research in the Republic of Kazakhstan and will contribute to the further development of genomic technologies in the livestock industry.

The social and economic effect is determined by the fact that the conducted research expands the in-depth understanding of the genetic architecture of the Kazakh Jabe breed, allows improving the process of breed conservation and breeding.

The obtained data on the presence of SNPs associated with productive qualities in the genome of the Kazakh breed of the jabe type give breeders specific marker sequences that will allow assessing the potential of economically useful traits without spending money on cultivation and time to obtain offspring. This will accelerate breeding activities for the selection of animals with desirable economically useful characteristics of the Kazakh breed of the jabe type and contribute to the intensification of horse breeding.

The main points to be defended:

1. Zootechnical assessment of Kazakh populations of Jabe horses
2. Intra-breed genetic structure of populations of the Kazakh aboriginal horse of the Jabe type in different regions of the Republic of Kazakhstan.
3. Comparative genomic characteristics of populations of the Kazakh aboriginal horse of the Jabe type with other Kazakh horse breeds and with foreign ones.
4. QTL-associated SNPs in the coding sequences of the genome of the Kazakh breed of the Jabe type.
5. DNA panel to improve selection of high-yielding Jabe horses.

Approbation of the work. The main results of the dissertation work were presented at the international scientific and practical conferences "State and development of horse breeding in Kazakhstan and other adjacent states" (2022) and "Modern innovative technologies in herd horse breeding in Kazakhstan and other adjacent states" (2023) held at the NJSC "Toraigyrov University" in Pavlodar.

Implementation of the research results. The results of the study are implemented in the work of LLP «Akzhar Ondiris», Pavlodar region and are used in practical and theoretical activities by employees.

Degree of reliability of results. The reliability of the research results is confirmed by a sufficient sample of animals of the studied breeds, the use of a set of statistical methods that allow confirming the correctness of the findings. The work was carried out in accredited laboratories according to "GOST ISO/IEC 17025-2009. General requirements for the competence of testing and calibration laboratories».

Publications. Based on the results of the dissertation, 6 scientific papers were published, including 1 article in a peer-reviewed foreign scientific publication indexed in the Scopus database, 3 articles in publications recommended by the Committee for Quality Assurance in the field of Education and Science of the Ministry of Education and Science of the Republic of Kazakhstan, 2 scientific publications in the materials of international conferences. 1 measurement methodology was developed and registered in the State System of Surveys of the Republic of Kazakhstan. 2 methodological recommendations were published.

The structure and scope of the dissertation. The dissertation work consists of an introduction, literature review, research materials and methods, research results, conclusion, proposals for production, a list of references, including 281 sources, including 250 in foreign languages. The work contains 115 pages of computer text, 16 tables, 14 figures, 8 appendixes.