

Scientific events

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RECENT ACHIEVEMENTS AND CHALLENGES IN FARM ANIMAL BIOTECHNOLOGY (10th Anniversary Scientific Conference with international participation — analytical review)

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Abstract

10th All-Russian scientific conference and school «Recent achievements and challenges in farm animals biotechnology — BioTechZh-2015» (<http://www.vij.ru/index.php/ru/konferentsii/>) was held on December 8–11, 2015 at the L.K. Ernst All-Russian Research Institute of Animal Husbandry (Moscow Province, Russia) with the support of the Federal Agency of Scientific Organizations of the Russian Federation, Russian Foundation for Basic Research (RFBR) and the Ministry of Innovations and Investments of the Moscow region. A series of these scientific conferences dates back to 2001, when on the basis of the All-Russian Research Institute of Animal Husbandry (VIZh) a scientific event on farm animal biotechnology as a new research area in biology of that time has been initiated due to Professor Lev K. Ernst, the Vice-President of the Russian Academy of Agricultural Sciences. In 2015, the anniversary conference brought together experts and young scientists (207 young scientists, graduate students and students of a total of 281 participants) to discuss promising and rapidly developing areas in biotechnology of farm animals. The conference was attended by scientists from 16 Russian regions as well as scientists from Austria, Belarus, Kazakhstan, Kyrgyzstan, Tajikistan.

Keywords: farm animals, game animals, gene pool, molecular and genetic research, molecular genetic studies, genetic profiling, genetic engineering.

The conferences BioTehZh started in 2001, when the innovative event on farm animal biotechnologies was first held in All-Russian Research Institute of Livestock (VIZH) on the initiative of Vice-President of the RAAS professor Lev K. Ernst. Research areas discussed then and there and reflected in the resolutions of the first conference today became a priority of science and technology development of the country [1, 2].

The next 15 years were characterized by the rapid development of molecular genetics, making it possible to study not only individual genes but entire genomes. Full genome sequencing have been reported in animals, from Btau 4.0 whole-genome resequencing in cattle (*Bos taurus*) in 2009 [3] to CHIR_1.0 domestic goat (*Capra hircus*) genome assembly in 2013 [4]. SNPs were identified in comparative studies of different animal breeds to be further used in genomic analysis. A genotyping technology was developed based on BeadArray platform enabling researchers to assay simultaneously several hundreds to several hundred thousands SNPs [5]. To date, it is the most informative to study species domestication and phylogeny, the structure and dynamics of a population, QTL mapping in farm animals [6–10]. Significant progress has been achieved in genome engineering, in which further development is associated with active transgenesis strategy [11, 12].

The 10th Anniversary Scientific Conference, which has become a platform

for discussing the prospects in farm animal biotechnology, has brought together both 207 junior scientists, graduate and undergraduate students, and 84 senior scientists from 16 Russian regions, and also from Austria, Belarus, Kazakhstan, Kyrgyzstan and Tajikistan.

All current aspects of farm and game animal's biotechnology were considered at the plenary session. Professor Dr. Gottfried Brem, the Member of the German and the Austrian Academy of Sciences, a foreign member of the Russian Academy of Sciences (Institut für Tierzucht und Genetik, VMU, Vienna, Austria) made a presentation «Y-chromosomal markers in the study of the origin of stallions» giving a new view of the process of horse domestication and genealogy.

Dr. M.E. Mikhailova (Institute of Genetics and Cytology of the National Academy of Sciences of Belarus, Minsk, Republic of Belarus), in the report «Investigation of gene pools of domesticated and wild species in the Republic of Belarus» told about the experience of studying the gene pool of bison population of the Bialowieza Forest with the use of molecular-genetic methods.

In the reports «Genetic resources of Tajikistan animals» (Dr. F.S. Amirshoev, TAAS Institute of Animal Husbandry, Dushanbe, Republic of Tajikistan), and «The state of livestock genetic resources of the Kyrgyz Republic» (Dr. E.M. Luschihina (Kyrgyz Research Institute of Animal Husbandry, Bishkek, Kyrgyz Republic) the aspects of gene pool of the local animal breeds were considered.

The genomic approach in cattle breeding were discussed by Dr. T.N. Karymsakov (Kazakh Research Institute of Husbandry and Forage Production, Astana, Republic of Kazakhstan) in the report «Perspectives of molecular genetic methods for breeding meat cattle in Kazakhstan», and Dr. K.V. Plemyashov (All-Russian Research Institute of Animal Genetics and Breeding, St. Petersburg) in the report «Verification of breeding value of Holstein Black-and-White sires and cows in Leningrad region».

The current state of species populations and breed populations of farm animals characterized with the use of DNA markers was considered by Dr. Yu.A. Stolpovskii (N.I. Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow) who summarized data on domesticated species with special attention to gene pool evaluation and effective use. Dr. M.I. Selionova (Stavropol Research Institute of Animal Husbandry and Forage Production, Stavropol) reviewed sheep and goat genetic resources in Russia with regard to the most prospective biotechnologies, and in the presentation of Dr. A.M. Zaitsev (All-Russian Research Institute of Horse Breeding, Ryazan) the intra- and interbreed genetic variability in horses used for molecular genetic certification was considered.

Characterization of pedigree resources, strategy of biodiversity preservation, and gene pool standards were considered by Dr. L.A. Kalashnikova (All-Russian Research Institute of Animal breeding, Moscow Province) in the report «Management and methodology of genetic examination and certification of pedigree animals».

Studies of gene pools of reindeer and bighorn sheep attracted special interest of the participants. These animals are essential in the ecosystems of the North and an integral part of life and culture of indigenous peoples in the region. These presentations were «The current state of bighorn *Ovis nivicola* and *Rangifer tarandus* populations in Yakutia and perspectives of their use» (Dr. I.M. Okhlopkov, Institute of Biological Problems of Cryolithozone, the RAS Siberian Branch, Yakutsk) and «Genetic monitoring of Nenets Breed reindeer in the Nenets Autonomous Okrug» (Dr. T.M. Romanenkova, Naryan-Mar Agricultural

Experimental Station, Naryan-Mar).

Recent achievements in poultry biotechnology was summarized by Dr. N.F. Volkova (L.K. Ernst VIZh) in the presentation «Modern approach to poultry genetic modification».

In the presentation «Actual problems in cryopreservation of cattle oocytes and embryos» (Dr. G.P. Malenko from the Center of Experimental Embryology and Reproduction Biotechnologies, Moscow) the methodological aspects of cryotechnologies with regard to farm animal germplasm were under consideration.

Based on the competition the best nine presentations of junior scientists were chosen for publication in two journals, the Agricultural Biology and the Achievements in Science and Technology in Agro-industrial Complex.

D.V. Beloglazov (<http://www.agrobiology.ru/6-2015beloglazov-eng.html>) studied cell proliferation in hen oviduct during ontogenesis to optimize a retrovirus-mediated gene transfer. The efficiency of local transgenesis in an oviduct was shown to be increased more than 3.3-fold due to epithelial cell stimulation using estrogens [13]. T.E. Deniskova obtained whole-genome SNP profiles of local Russian sheep breeds and evaluated the informativeness of an international reference SNPs panel (<http://www.agrobiology.ru/6-2015deniskova-eng.html>) [14]. O.V. Kostyunina found out a quantitative effect of DNA marker genotype *IGF2* on meat production and nutrient utilization in pigs. The marker genotypes were also gender-influenced (<http://www.agrobiology.ru/6-2015kostyunina-eng.html>) [15]. A.A. Sermyagin conducted a study of whole-genome SNP associations with breeding value in the Holstein sires (<http://www.agrobiology.ru/2-2016sermyagin-eng.html>). It was found out that a whole-genome analysis allowed to map quite precisely the productivity and reproduction trait QTLs of heritability from low to moderate [16]. M.S. Fornara compared an informativeness of morphometric parameters and high polymorphic microsatellite DNA markers in evaluation of diversity and differentiation of mountain grey Caucasian honeybees (*Apis mellifera caucasica*) (<http://www.agrobiology.ru/6-2015fornara-eng.html>) [17]. V.P. Kharzinova (<http://www.agrobiology.ru/6-2015kharzinova-eng.html>) has developed the world's first multilocus panel for STR-marker analysis of reindeers (*Rangifer tarandus*). Its functionality was shown both in origin authentication and biodiversity study of Russian reindeer population [18].

M.A. Zhilinskii found out (<http://agroapk.ru/70-archive/12-2015/1204-2015-12-27-ru>) the variations in qualitative and quantitative semen parameters in cocks due to integration of recombinant DNA that should be considered when creating transgenic chicken lines [19]. O.S. Pomanenkova has developed the system for direct molecular genetic testing of *LoF* mutations in *SMC2* gene associated with HH3 haplotype impacting fertility (<http://agroapk.ru/68-archive/11-2015/1136-2015-11-27-ru>) and causing early embryonic death in cows. The HH3 wide spreading among Russian Holsteins was shown [20]. Comparative data on metabolism in heifers as influenced by ovarian function depression during the first third of lactation were presented by A.A. Solomakhin (<http://agroapk.ru/68-archive/11-2015/1137-2015-11-28-ru>) [21].

All these young scientists presented the results of their research at sessions or workshops of the conference.

The conference helped identifying the world's research priorities in farm animal biotechnology and cell technologies. It has become an information platform for sharing relevant experience among Russian agrobiotechnologists. It should be especially noted that the conference presented and discussed the results of the research projects supported by Russian Science Foundation (14-36-00039, 15-16-00020), Russian Foundation for Basic Research (№ 13-04-01888,

№ 14-48-03681, № 15-08-99473), Ministry of Education and Science of the Russian Federation (14.604.21.0141, 14.604.21.0062). The conference contributed to establishing alliances between Russian and foreign researchers' teams to address fundamental problems in such a dynamic field of science as biotechnology.

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