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INHERITED DISORDERS INDAIRY AND BEEFCATTLE

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Abstract.

The article presents the overview of genetically determined abnormalities of cattle, the most common in highly productive livestock.

The most significant scientific results of foreign scientists to identify and prevent the data of anomalies are presented.

A collection of information on the composition of breeding beef and diary cattle from the farms of different ownership forms of Akmola, Kostanai and North Kazakhstan regions has been done.

Keywords: cattle, breed, genotype, diseases, recessive alleles.

At the present stage of veterinary science and practice development, the problems of congenital pathology are of special interest that is directly connected with thelivestock breeding intensification, on one hand, and growth of anthropogenic load on environment, on the other hand.

One of the etiological factors of embryonic mortality, abortions, still births and congenital anomaly is existence of lethal, sub lethal, semi-lethal and sub vital genes in animal genotypes.

Mutations result the various hereditary abnormalities which can be shown as genetic anomalies or to have character of hereditary insufficiency. Genetic anomaly is the caused hereditary abnormality having an adverse effect on viability of health state and breeding value of animals. Hereditary anomalies may not come out in all individuals with an identical genotype. This phenomenon was called as a penetrance – relative frequency.

Penetrance of other recessive mutation – a congenital tremor (shakes) at chickens is 40%by the Hut and Wilde data. The second phenomenon – expressivity or sign expressiveness degree is closely connected with the concept of a penetrance.

Inherited disorders can be groupedas those that are definitely due to the action of just one gene, those that are due to the combined action of many genes and many non-genetic (environmental) factors. And many traits and disorders that appear to run in families, but insufficient information about them makes difficulties inunderstanding about whether one or more genes are involved.

At the present stage of veterinary science development it is marked that the following genetically caused anomalies in cattle are mostly met: hairlessness (hypotrichosis), congenital absence of extremities (acroteriasiscongenita), paralysis of back extremities, epitheliogenesis imperfecta —perodermia or "frog skin", an achondroplasia (dwarfism), truncation of the lower jaw (brachygnathia) and mass scale in combination with exophthalmus, the general dropsy, the general anchylosis, congenital dropsy of a brain (hydrocephaly), lengthening of periods of cows'pregnancy, congenital umbilical hernias, spastic paresis, symphalangia (whole-hoofed), congenital blindness, probatocephalia (sheep's-head), parakeratosis, porphyria, hypoplasiaof gonads, BLAD (Bovine leukocyte adhesion deficiency), CVM (Complex vertebral malformation)

From the beginning of industrialization of livestock breeding branch,the number of separate population and the general livestock beganto considerably increase, therefore, there were objective conditions for accumulation of recessive mutation and their transition to a homozygous status. This process was promoted mainly by widespread introduction of artificial insemination (AI) and transplantation of embryos. Implementation of AI led to that the number of the progeny received from one sirehas been increased fromten tothousands or evenhundreds of thousands. Even if 90% of the progenyis not used for a reproduction, the remaining herd stable enough to save this or that mutation in half of them.

Therefore, distribution of mutation in herds is the phenomenon which is inevitably accompanying selection and technological progress in livestock breeding. The fact that 43 sires from 166 in Czechoslovakia were carriers of lethal genes shows a wide distributionof various mutations among animals. Frequency of hereditary anomalies can be unequal in different breeds and herds. According to (ZhigachevA.I. and others, 1989)[1], shortening of a jaw (31%) are met among abnormal calves in the Kostromskaya breed,symphalangia – in the Yaroslavl breed, a muscular contracture –at Holmogorsky and umbilical hernia is met at black and white breed.

In the USA 25% of red Danish breed animals areheterozygous on allelic gene, responsible for paralysis of back extremities, and 11% are mutation carriers connected with an anchylosis of joints. Among Holsteinbulls registered in the first volume of the catalog of the USA, 17 were heterozygous carriers of a symphalangia, 9 – porphyria, 1 – bulldog like.

To the present moment about 101inherited disorderswith a known causal mutation are describedin cattle.[2]They cause morphological and functional anomalies, negatively influence on health and animal productivity. In particular the diagnostics accuracy of Complex vertebral malformation (CVM) and Bovine leukocyte adhesion deficiency (BLAD)have been considerably increased due to the establishment of the genetic nature of these molecular diseases [3,4]. In the developed countries of Europe and North America a special program on elimination of mutant CV and BL alleles in populations of black and white breed has been created [5].

The wide exchange of genetic material between the countries promotes the distribution of other mutant genes, in particular the gene causing a BLAD mutation. For the first time the BLAD mutation (Bovine Leukocyte Adhesion Deficiency) was described in cattle in 1983 entitledas "granulocytic syndrome", inherited by autosomal-recessive type.

In the USA 15% of Holstein breed herd bulls of are carriers of BLAD mutation, among cows this index around 6% (Boichard D., 1995). All animals with this mutation are progeny of one sireCarlin-M Ivanhoe Bell, whose semen was widely used in 50-60 in Western Europe and in the former USSR (Shuster D.E., 1992) [5].

The ancestor of this mutation is Osborndale Ivanhoe1189870 who was born in Holland in 1952 (Kalashnikova L.A. and others, 1999) [6].

MarzanovN.S. and others [7] exploring the bulls livestock of AI central office (Moscow region) confirmed that Holsteinbulls– carriers of a BLAD mutation were also progeny of this sire. In France in a homozygous status the gene was appeared at 6% of newborn calves of Holsteinbreed. In Ukraine, the total quantity of carriers from the analyzed livestock made 3,2%, in Germany – to 30% (Glazko V. I., 1998), in Argentina – 2,88% (Poli M.A., 1996), in Japan –16% (Nagahata H., 1997), in Brazil – 2,8% (Ribeiro L.A, 2000), in Iran – 3,3% (Norouzy A., 2005),in India – 1,59% (Roy A., 2012), in Poland – 3% (Czarnik U., 2004) [8,9, 10,11,12,13,14].

Due to the fast distribution of a BLAD mutation and the economic damage caused by it,the special national programs for an exception of BLAD mutations carriers have been created in the countries with developed dairy cattle breeding (including rejection of Carlin-M Ivanhoe Bell progeny) from reproduction systems and MOET systems (embryotransplants) (Islamova S., 2007; Kalashnikova L.A. 1999). Such selection allowed selectors in US and other countries to reduce the number of heterozygous carriers of this hereditary syndrome (A.I. Zhigachyov, 2002) [15].

The modern technologies allowed to revealepy other lethal gene causing a CVM mutation. For the first time this defect was opened in Denmark in 1999 (Agerholm J.S., 2001) and within the next years it was also found in the USA (Duncan R.B., 2001), Great Britain (Revell S., 2001), Netherlands (Wouda W., 2000), Japan (Nagahata H., 2002), Germany (Konersmann Y., 2003), Sweden (Berglund B., 2004), Denmark (Thomsen B., 2006) andIndia (Mahdipour M., 2010).

Complex vertebral malformation (CVM) causes deformity of calves (Agerholm J.S., 2001) and abortions at cows during the period from 56 to 260 days of pregnancy (Agerholm1 J.S., 2004).

It is characterized by deformation of vertebrae in cervical, thoracic and lumbar regions, sternum anomalies, abnormality of ribs, anomalies of joints and anomalies of heart (Agerholm J.S., 2004).

Conducted genomic researches showed that a syndrome isautosomal-recessive (Bendixen C., 2002).

According to Yakovlev A. (2004), the distribution frequency of this defect in heterozygous state can reach 20,0% and above. In the breeding organizations of Russia the ratio of CVM carriersiresinaverageis 2,77% (Ernst L.K., 2011, P.28). In Denmarkthe carriers of this mutant allele are 31% of animals (Thomsen B., 2006), inPoland – 24,8% (Rusc A., 2007), in Japan-32,5% (Nagahata H., 2002), in Sweden – 23% (Berglund B., 2004), in Germany – 13,2% (Konersmann Y., 2003). Thus, this genetic anomaly is widespread in Holsteindairy breed and in case of crossing with other cattle breeds it promotes the distribution of a mutant allele among them.

If to provide an economic justification of the main genetically hereditary anomalies, the following is be discernible: for example, economic losses of Krasnoyarskregion farms from distribution of lethal genes in brood stocks made 165 931 thousand rubles. Semen on the amount of 7 928 thousand rubles was not received during the period of 2005-2012 due to the early leaving of bulls of red and white breed because of spastic paresis.

American scientists of Agricultural research service (ARS) Roman L. and Hrusk Y.S. (Research and Development Meat Animal Research Center (USMARC) in the center of Clay, the State of Nebraska) found the point on the 20th chromosome of a bull connected to the appearance level of the most widespread bacterial diseases –sharp infectious conjunctivitis, radical decay of hoofs and a respiratory disease of bulls (pneumonia) directly influencing on a loss of cattle.

ARS is the principal research and development service of the Ministry of Agriculture of the USA. On a priority of the Ministry of Agriculture of the USAon the assistance of the international food safety.

Among the beef cattle breeds, 75% of all diseases and 70% of all loss fall on respiratory diseases, thus the economic damage to agricultural producers exceeds $1 billion a year. Budget expenditures on prevention and treatment of conjunctivitis make $150 million a year, and losses in dairy production because of hoofed decay in the range from $120 to $350 per one animal.

In foreign countries there are services whose task is to monitor the genetic health of farm animalspopulations, but such researchhave not conducted in our country. Absence ofsuch program promotes uncontrolled distribution of such disorders in livestock.

In general 65 967 heads of cattle were imported from foreign countries into the Republic of Kazakhstan from 2010 to 2014, among them 11 163 are dairy breedanimals, 49 069 arebeefcattle, 5 725 heads of double direction.

According to the data of the Ministry of Agriculture of the Republic of Kazakhstan it was set that farms of Akmola, Kostanay and North Kazakhstan regionstotally contain 47 514 animals of meat cattle of the above-mentioned breeds, including: in Akmolaregion – 18 700 animals (Aberdeen - Angus – 7 843, Hereford – 4 053, Kazakh-white-headed – 6 804 heads), in the Kostanay region – 17 646 heads (Aberdeen - Angus – 6 537, Hereford – 1 559, Kazakh-white-headed – 9 550 heads) and in the North Kazakhstan region – 11 168 heads (Aberdeen - Angus – 2 843, Hereford – 1 627, Kazakh-white-headed – 6 698 heads). Regarding the dairy breed animalsit was established that 5 722 animals of Holstein breed were imported to the regionover the last 5 years. The highly productive breeding cattle was imported to the region generally from 13 countries of Europe, North America and Australia; data are presented in a figure 1.

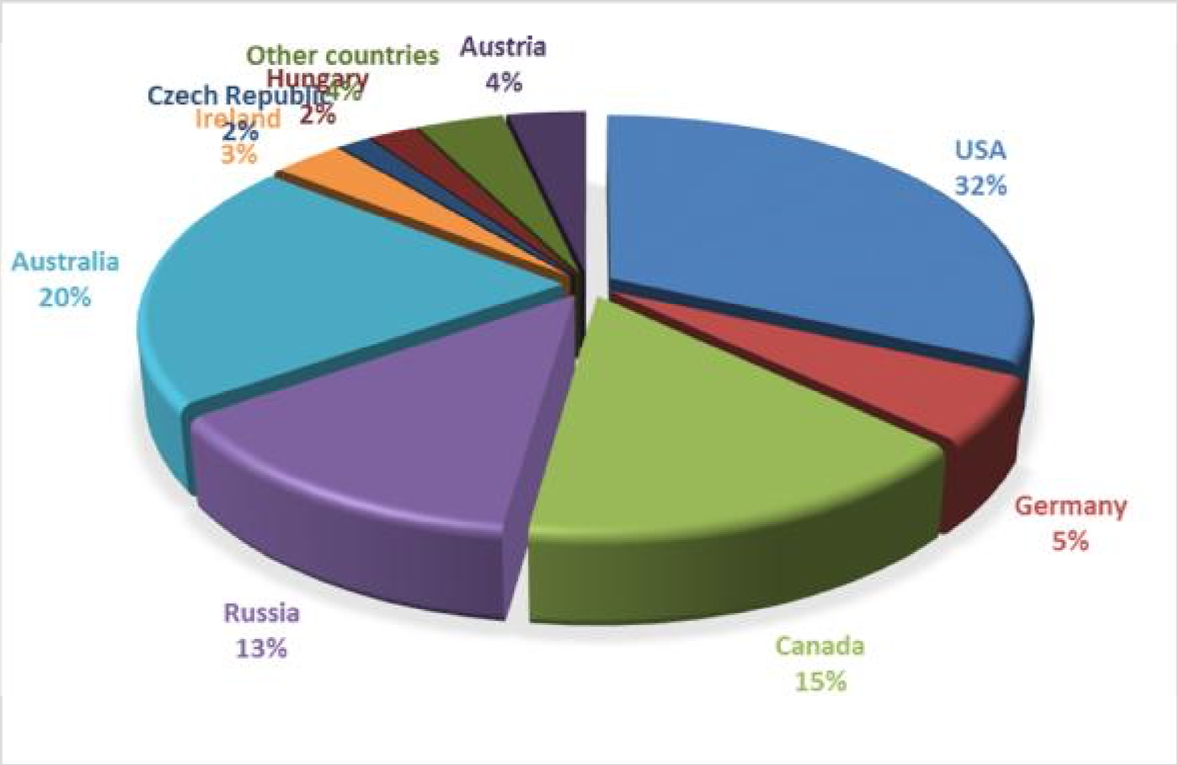

Figure 1 –Countries-exporters of breeding cattle to the Republic of Kazakhstan for 2010-2014.

The mains and large exporters of cattle to the region are the USA, Australia, Canada, Russia, Germany and Austria. It is also worth pointing out that the livestock of breeding cattle in farms is filled and increased due to the selection activities of domestic reproducer.

Taking into account the high level of prevalence hereditary anomalies in foreign countries and in connection with import from abroad of a large livestock of animals, the issues of genetic diseases study represent a huge interest and are undoubtedly topical. As monitoring of pathology data aren't carried out in the Republic of Kazakhstan, in case of further cultivation of cattle there will be considerable problems concerning hereditary anomalies.

According to the research

project on thetopic: "Research of genetic diseases heritability in cattle of foreign and domestic selection" and its main researchdirection, the data collectionwas carried out on the quantitative composition of a beef and dairy breedcattle in the farms of different forms of ownership of Akmola, Kostanay and North Kazakhstan regions. As research objects were animals ofbeef breeds: Aberdeen-Angus, Hereford, Kazakh-white-headed and dairyHolsteinbreed. Animals and semen of sireswere selected for carrying out genetic researches. Biological samples of these animals were taken and sent to laboratory for DNA extraction.

During the clinical studies of cattle in economic entities of different forms of ownership, the existence of vision organs defeat at animals was found out by us whose symptoms indicate thenatureof infectious bovine keratoconjunctivitis.

On the basis of the collected database and taking into account their breeding and economic activity 2 farms in Akmola region and by one in Kostanay and North Kazakhstan regions were determined where further researches on study of genetic diseases and determination of carriers of their genes will be conducted. Animalsfrom these farms were selected tostudyfor a carriage of recessive alleles of genetic diseases of cattle. At the moment biological samples from 30 sires and 7 calves of Holstein breed, 10 sires and 10 calves of Kazakh-white-headed breed, 6 sires of Hereford breed, 7 sires and 67 calves of Aberdeen - Angus breedhave been collected and sent to the laboratories for DNA extraction and genotyping. During sampling pedigree of animals, data their productivity and parents, an origin and a birth place were studied and analyzed,alsothey were analyzed for a case of presence of the information on a carriage of genetic anomalies.

In order to detect and exclude the paratypical factors influencing on the appearance of different disturbance at breeding animals, the preliminary estimate of their production activity was carried out in the studied farms. Such parameters as the contents, feeding, ration, insemination methods, zoohygienic, veterinary and sanitarian parameters were evaluated (microclimate, density of animals placemen, temperature, gas contamination and a dust content location, ultra-violet radiation, existence of carriers of infectious diseases, physical exercise, etc.).

For an assessment of feeding quality and full value of animals ration in the studied farms all types of the forages consumed at the moment were selected (different types of hay, silage, silo, concentrated forages, premixes, etc.) which are tested on biochemical composition and nutrient density.

We note finally that the considerable information material is provided on spread of the main hereditary diseases of cattle in the near and far abroad countries as well as the data on economic justification of their damage. For the first time these researches on existence of recessive alleles of genetic anomalies are conducted in Kazakhstan.

Further investigation and following necessary steps in our opinion could decrease and prevent distribution of undesired traits in livestock of Kazakhstan. First of all, documents on genetic status of each bull used in AI should be provided. Also, survey of local breeds must be conducted. And of course, establishing national lab to control and communicate to breeding organizations or farmers is important.

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References

1. Жигачев, А.И. Эколого-генетический мониторинг в животноводстве / А.И. Жигачев, Т.В. Богачева, Н.И. Хороших // Зоотехния. – 2000. – №3.– С. 2-4.

2.http://omia.angis.org.au

3.Kehrli M.E., Schmalstieg C., Anderson D.C., Van Der Maaten M.J., Hughes B.J., Akermann M.R., Wilhemsen C.L., Brown G.B., Stevens M.G., Whetstone C.A. Molecularidentification of deficiency of the Mac-1 (CD11b/CD18) glycoprotein // Am. J. Vet. Res. – 1990. – Vol.51. – P.1826-1836.

4.Tammen I. Weiterentwicklung des DNA-Tests auf BLAD(Bovine Leukozyten Adhasions defizienz) fur den Einsatz in Rinderzucht und klinischer Diagnostik. Hannover, 1994. – 128 p.

5. Shuster D.E., Kehrli M.E.Jr., Ackermann M.R., Gilbert R.O. Identification and prevalence of a genetic defect that causes leukocyte adhesion deficiency in holstein cattle // Proc. Nat. Acad. Sci. USA. – 1992a. – Vol.89. – P.9225-9229.

6. Калашникова Л.А. ДНК-технологии оценки сельскохозяйственных животных/Л.А. Калашникова, И.М. Дунин, В.И. Глазко, Н.В. Рыжова, Е.П.Голубина. ВНИИплем, 1999. – 148 с.

7. Марзанов Н.С. Отчет по Разделу 2: «Изучить приемлемость полиморфизма ДНК для оценки биоразнообразия и хозяйственно-биологических качеств сельскохозяйственных животных». – Дубровицы, 2006. – 27 с.

8. Глазго В.И. Мутация BLED (иммунодефицита) у крупного рогатого скота / В.И. Глазго//Зоотехния. – 1998. - №8. – С. 5-7.

9.PoliM.A.,DeweyR.,SemorileL., LozanoM.E., AlbarinoC.G., RomanowskiV., GrauO. PCRscreeningforcarriersofbovineleukocyteadhesiondeficiency (BLAD) andUridinemonophosphatesynthase (DUMPS) inArgentineHolsteincattle. ZentralblVetA, 1996. 43(3): 163-168.

10.NagahataH, MiruraT., TagakiK., OhtakeM., HodaH., YasudaT., R. Nioka. Prevalenceandallelefrequencyestimationofbovineleukocyteadhesiondeficiency (BLAD) inHolstein-FriesiancattleinJapan.JVetMedSei, 1997. 59(4): 233-238.

11.RibeiroL.A., BaronE.E., MartinezM.L., CoutinhoL.L., PCRscreeningandallelefrequencyestimationofbovineleukocyteadhesiondeficiencyinHolsteinandGircattleinBrazil.GenetMolBiol, 2000. 23(4): 831-834.

12.NorouzyA., NassiryM.R., EftekharishahrodyF., JavadmaneshA., MohammadM.R., Abadi, SulimovaG.T., Identificationofbovineleukocyteadhesiondeficiency (BLAD) carriersinHolsteinandBrownSwissALbullsinIran. RussJGen, 2005. 41(12): 1697-1701.

13. RoiA., KotikalapudiR., PatelR.K., AnantaneniR., KatragaddaS., NewcasesofBovineLeukocyteAdhesionDeficiency (BLAD) carriersinIndianHolsteincattle. InterJVetSci, 2012.1(2): 80-82.

14. CzarnikU., ZabolewiczT., GalinskiM., PareekC.S., WalawskiK. SilentpointmutationpolymorphismofthebovineCD18 encodinggene. JApplGenet 2004, 45:73-76.

15. Жигачев А.И. Наследственные аномалии и их контроль у КРС/А.И. Жигачев, И.Л. Суллер // Практик.2002. – 2 – 4: 46-53.

Резюме

Во всех зарубежных странах с интенсивным ведением животноводства, изучение распространения генетических аномалии у крупного рогатого скота, является неотъемлемой частью науки и практики, так как главная его цель, контроль за генетическим здоровьем популяций разводимых сельскохозяйственных животных. Поэтому и в нашей стране данные исследования актуальны не только с научной точки зрения, но необходимы всем координирующим и контролирующих органам в сфере животноводства для формирования здорового генофонда высокопродуктивных животных

Түйін

Қарқынды мал шаруашылығымен айналысатын барлық шетел мемлекеттерінде, ірі қара мал арасында генетикалық аномалиялардың таралуын зерттеу, ғылым мен тәжірибенің ажыратылмас бөлігі болып саналады. Үйткені оның негзігі мақсаты, өсірілетін ауыл шаруашылық жануарлар популяциясының генетикалық денсаулығын бақылау. Сондықтан біздің елімізде де бұндай зерттеулер тек ғылыми тұрғыдан ғана өзекті емес, сонымен қатар мал шаруашылығы саласындағы барлық

үйлестіруші және бақылаушы органдарға, дені сау жоғары өнімді жануарлардың генофондын құру үшін қажет.