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PROCEDURE OF CUSTOM MATING AND GENOMIC ANALYSIS OF BULL-CALVES IN DAIRY CATTLE BREEDING

Abstract. The research has been carried out on the formation of bull-producing cows, the production of replacement bulls from custom mating, the system work has been done to obtain the primary data of pedigree records with the entry of data into the information and analytical system (IAS) and on automatic calculation of estimated breeding value (EBV) of cows. Also, the work was carried out on the formation of first-calf heifers groups in order to organize targeted selection work with the dairy cattle. In total, 609 cows from 3 regions were formed. It was established that the dairy productivity of mothers the formed groups for lactation has significant fluctuations (3413...9611 kg), but the productivity of the mothers of their fathers is much higher (5000...14850 kg), which predetermines the genetic potential of the cows of the formed groups.

As a result of the custom mating, there was obtained 18 bull-calves, whose genomic analysis determined their breeding value in the laboratory for genomic analysis of the Holstein Association (Vermont, USA). Of the 18 bulls, the most valuable were 5 heads with a breeding value (TPI) of more than 1600 according to the American system, including 1 bull with TPI = 2169. The average index (TPI) of genetically estimated bull-calves of domestic reproduction was 1512.6 that allows to assert about a sufficiently high genetic potential of dairy cattle in the RK.

Keywords: dairy cattle, custom mating, genomic analysis, estimated breeding value.

Introduction. A promising alternative in the existing system of assessing breeding value is a genomic selection program that solves a wider range of issues, starting with the bulls' mothers, the type, and extent of the bulls assessment, their use based on the results of the genomic breeding value estimation. Economic efficiency and advantages of using genomic selection are based on the fact that genomic breeding value can be calculated for calves at the earliest age. If we compare genomic selection and traditional selection, in terms of the level of reliability of the quality of offspring, it is almost the same that is reliable, but faster due to a shorter interval between generations. Genomic selection can not only save costs, accelerate genetic progress by 50%, but also increase the selection pressure[1].

Estimation of the breeding value of dairy cattle is one of the links in the practical implementation of selective programs in herds and populations with the aim of directional formation in animals of the intended hereditary traits and the selection of animals in determining the breeding value of bulls. The need for a detailed study of the exteriors of cows arises because of the active use of the Holstein breed, which introduces changes to the existing type of animals [2,3].

Along with this, there is a process of approbation of the methods of linear evaluation of the exterior and the determination of genetically determined interrelationships between the exterior characteristics with such indicators as the duration of economic use. Identification in the shortest possible periods of time of the best genotypes of animals and their subsequent use for breeding and selective work with the herd is the basis of genetic progress in modern cattle breeding. At the same time, it is important to take into account the data on the exteriors, the lifetime productivity and the health status of the estimated livestock.

The cornerstone of achievement of the identified selective priorities is the accuracy of the evaluation of genetically determined economic traits of animals. In this regard, a need arises to accumulate the information obtained by creating electronic databases and their corresponding software. The use of linear statistical models using computer modeling of the breeding process in dairy herds in an accelerated mode will help to provide an objective assessment of the breeding value of dairy cattle and the selection of animals with a high genetic potential of productivity. The use of pedigree bulls with high indices of breeding value in generations will allow to increase the productivity of dairy cattle [4,5].

It should be noted that genomic studies are an improved method of selecting young bulls, the reliability of which is confirmed by a subsequent estimation of the offspring. Since 2009, genomic evaluation has become the official assessment system in the US and Canada, and since August 2011 in Germany and Austria. The only difference from the current evaluation is that the reliability indicators reflect the additional accuracy of genomic data [6,7,8].

Thanks to modern information technologies, the selection was made possible remotely. Improvement of the functions of the Information and Analytical System "The Republican Livestock System" in terms of monitoring, analyzing the accumulated data on the livestock of animals, analytical tools, as well as tools that automate the collection of data on the quality of milk, will significantly improve the quality of the recorded information and more fully use an existing base for breeding and selective work in farms. The collected data, improved by an additional control system, in combination with modern analytical tools will allow to conduct economic and scientific research work at a qualitatively new level [9].

Currently, a definite priority is to increase the economic efficiency of production and improve its quality characteristics by improving the breeding qualities of animals and the rational use of genetic resources. In solving this problem, the main role is played by the optimization of the general system of pedigree work at the level of breeds and animal populations. The programs of breeding and selective work in dairy cattle are based on three components: the evaluation of breeding qualities of animals, the formation of breeding groups and their intensive use in the reproductive system of the genetic material of the selected population. At the same time, the accuracy and objectivity of assessing the tribal (genetically conditioned) qualities of animals belong to the priority in the overall complex of tribal activities. In countries with developed animal breeding (the USA, Canada, Germany, Sweden, the Netherlands, etc.), the most theoretically substantiated methods are used to predict the genetic traits of individuals (primarily bulls): the best linear unbiased prediction (BLUP method) and the Animal Model (an improved version of BLUP). However, to date, the practice of dairy cattle breeding in the Republic of Kazakhstan officially uses the evaluation of producers by offspring based on a direct comparison of the productivity of daughters of test bulls with their peers within individual herds, which often leads to a bias in the results. In the end, in practically all breeds of domestic dairy cattle, the rates of genetic improvement in populations are far from optimal ones [10].

The set tasks for the development of a management system for the selection process in dairy cattle breeding are promising and effective for obtaining servicing bulls of domestic breeding. A comprehensive assessment of the phenotypic indicators and the classification evaluation of the cows' exteriors, along with pedigree, genetic analysis, will allow for better selection when forming bull-producing groups. New methods for assessing breeding value, taking into account the linear profile and genetic analysis of cows, will contribute to the intensification of breeding and selective work with dairy herds.

Aim of the research. Selection of farms and organization of custom mating with carrying out of the genomic analysis of bull-calves, obtained from custom mating.

Materials and methods. Objects of the research were brood stocks, as well as servicing bulls. The materials for research were the documents of primary zootechnical and pedigree accounting (from the IAS system), as well as the results of experimental studies, visual assessment, weighing, measurements, control milking of animals. In addition, biochemical studies of milk were carried out.

The calculation of the estimated breeding value was carried out according to the methodology developed by the co-workers of the Kazakh Scientific Research Institute of Animal Breeding and Fodder Production LLP [11].

Results of the study. The traditional system of determining the breeding value of animals and the selection based on it require patience: often from six to seven years from the selection of parents to the completion of the productivity tests of their offspring. Genomic selection allows to "jump" through the

barrier of the generation interval: when selecting bulls at the age of four to six weeks, specialists have access to the breeding value (BV) based on genomic analysis.

A year later bulls with higher genomic value can be realized for stud purpose. Scientists have calculated that even with reliability (accuracy of determination) the BV is 75%, due to the use of the estimated "genomically" young bulls, the breeding efficiency will double.

Table 1 shows that the composition of bull-producing cows is represented by almost all the main breeds in the Republic of Kazakhstan. A total of 162 heads were formed, of which the smallest number of livestock was formed in a black-and-motley manner. It should be noted that animals of the black-and-motley breed are direct descendants of bulls of the Holstein black-and-motley breed, if we combine these two breeds, it turns out that the livestock of the Holstein and Holsteinized animals composes the greatest specific weight - 43.8 %, which corresponds to a given number of bulls. So if from 71 cows half of the bulls will be received ie. 35 heads of which will be evaluated 3-4 heads, then this will be fuller enough for the brood stock of the black-and-motley population.

Evaluation of the breeding value of dairy cattle is one of the links in the practical implementation of selection programs in herds and populations with the aim of directional formation in animals of the intended hereditary traits and the selection of animals in determining the breeding value of bulls.

During the formation of bull-producing cows, their own production was taken into account according to the highest lactation from 7.0 thousand kg and more.

Table 1 - Information on the formed bull-producing cows

Farm	Breed	Number of the formed bull-producing cows			Total by breeds
		II	III	IV	
Almaty integrated agricultural production centre	Alatau	7	3	2	45
Mamed farm		17	6	2	
Mezhdurechensk LLP		4	2	2	
EsilAgroLLP	Holstein	2	2	1	40
AF«Rodina»LLP		1	3	1	
Sadchikovskoe LLP		2	1	2	
Aidarbayev farm		16	6	3	
Kamyshinskoye farm	Simmental	14	8	4	46
Kamyshinskoye LLP		14	4	2	
Mezhdurechensk LLP	Black-and-motley	7	5	4	31
K. Marx LLP		5	3	2	
Sheminovka LLP		2	2	1	
TOTAL		91	45	26	162

It has been established that the limits of bulls-producing cows range from 7.0 to 10.3 thousand kg of milk (Table 2).

In order to obtain high-quality offspring from these cows, some of them were inseminated by servicing bulls of the North American breeding (table 3).

Table 3 shows that 72 heads are now inseminated, mostly by American and Canadian breeds, while the breeding value of these bulls is quite high, according to the TPI from 1600 to 2300, the remaining animals will be inseminated as they come in heat.

Of 18 bulls, 15 are representatives of the Holstein breed of domestic reproductions, two bulls of the Alatau breed and two bulls of the "Ertis" intra-breed type of the Simmental breed. (Table 4).

Table 2- Average productivity of bull-producing cows

Breed	n	Average milk yield of bull-producing cows, kg	
		$\bar{X} \pm m_x$	Limit
Alatau	45	7824±207	7000-10131
Holstein	40	8279±194	7044-10191
Simmental	46	8584±261	7122-9105
Black-and-motley	31	8109±244	7012-10373

Table 3 - Information on custom mating of bull-producing cows

Breed	Servicing bulls (fathers)	Bullmother's productivity, kg	BV of bull (TPI, LPI)	Number of the inseminated cows, heads
Alatau	Emergency 199362	11598	2100	3
	Popstar 68101680	12475	1900	2
	Diego CAN M 11014268	13714	1800	1
Black-and-motley	AltaVITTEK 11HO10909	11386	2321	1
	AltaGREATEST 011HO10928	11903	2370	1
	AltaJOEL 011BS00644	10314	1681	2
	Eaton 69710369	15518	2279	3
	Murray 72436573	11314	2233	3
	Enrich 69710405	17550	1973	4
	Kano 69742883	12563	2114	2
	Alta Fire 07667	14108	1513	3
Simmental	Mazda 136722780	12062	1696	4
	Colley 63026616	14736	1664	5
	Artve 342516	10848	1720	7
	Skyfire 231465	10814	1840	6
	Brayday 50803818	16113	1650	1
Holstein	EATON HO00600656	10982.5	1884	6
	AltaGoalman USA000063449647	14751	2103	5
	BOMAZ SHTL USA63262902	14660	2141	2
	ZIMMERVIEW USA62510183	11122	1960	3
	Altasamurai09861	14840	1940	2
	AltaRoss 09703	14438	1877	3
Swiss	MVP 7BCF00828	10637.5	1730	3

It was established that out of 15 bulls that have passed the stage of determining the authenticity of origin, 14 bull-calves did not confirm their origin by father, and according to mother (belonging to mother was determined by mother's father), they were confirmed (table 5).

Table 4 - List of bulls selected for genomic analysis

No	Identitynumber	Breed	Farm
1	2	3	4
1	KZP157866611	Holstein black-and-motley	Sheminovka LLP
2	KZP157866636	Holstein black-and-motley	Sheminovka LLP
3	KZP157923541	Holstein black-and-motley	Sadchikovskoe LLP
4	KZP157923775	Holstein black-and-motley	Sadchikovskoe LLP
5	KZP157923673	Holstein black-and-motley	Sadchikovskoe LLP
6	KZP157923561	Holstein black-and-motley	Sadchikovskoe LLP
7	KZC158746855	Holstein black-and-motley	AF«Rodina»LLP
8	KZB157778956	Holstein black-and-motley	Mezhdurechensk-Agro LLP
9	KZB157507262	Alatau	Mamed farm
10	KZB157507352	Alatau	Mamed farm
11	516271	"Ertis" intra-breed type	Kamyshinskoye LLP/farm
12	516441	"Ertis" intra-breed type	Kamyshinskoye LLP/farm
13	KZT183231895	Holstein black-and-motley	Taiynsha-AstyKLLP
14	KZT183231897	Holstein black-and-motley	Taiynsha-AstyKLLP
15	KZT183231857	Holstein black-and-motley	Taiynsha-AstyKLLP
16	KZB158174418	Holstein black-and-motley	ZKAPAmiranLLP
17	KZB158174428	Holstein black-and-motley	ZKAPAmiranLLP
18	KZB158174438	Holstein black-and-motley	ZKAPAmiranLLP

Genomic analysis was carried out in the Laboratory for Genomic Research of the Holstein Association (USA). The process of genomic analysis consists of several stages, one of which is the determination of the authenticity of origin (Table 6).

From the data in Table 6 it can be seen that 1 bull, born in Amiran LLP, received GTPI of more than 2000, this bull may become a superbull in the future. The average index of genetically estimated bull-calves of domestic reproduction was 1512.6, which allows us to confirm the sufficiently high genetic potential of the dairy cattle of the Republic of Kazakhstan. It was also established that all bull-calves were not confirmed by fathers. Since in the Laboratory for Genomic Research of the Holstein Association (USA), where the genomic analysis of bull-calves was conducted, there is a computer data bank on the genome of 80-90% of the Holstein servicing bulls, whose seeds are used all over the world, according to this fund, they found the real fathers of our bull-calves and the genome of the identified fathers served as the material for calculating the GTPI of our bull-calves. Three bull-calves did not have a genome analysis, because they were representatives of other breeds.

Table 5 - Name of farms from which the bulls were selected

No	Name of the farm	Breed	Number of heads	Confirmation of origin by	
				father	mother
1	2	3	4	5	6
1	Sheminovka LLP	Holstein black-and-motley	2	-	+
2	Sadchikovskoe LLP	Holstein black-and-motley	4	-	+
3	AF«Rodina» LLP	Holstein black-and-motley	1	-	+
4	Mezhdurechensk-Agro LLP	Black-and-motley	1	-	+
5	Mamed farm	Alataublack-and-motley	2	-	+
6	Kamyshinskoye LLP/farm	Holstein red-and-motley	1	-	+
		Ayrshire	1	-	+
7	Taiynsha-Asty LLP	Holstein black-and-motley	3	-	+
8	ZKAP Amiran LLP	Holstein black-and-motley	3	+1 and -2	+

Table 6 - Results of the genomic analysis

Name of the farm	Identity number of bull-calves	GTPI	Confirmation of origin by	
			father	mother
1	2	3	4	5
Sheminovka LLP	KZP157866611	1293	-	+
Sheminovka LLP	KZP157866636	1478	-	+
Sadchikovskoe LLP	KZP157923541	1503	-	+
Sadchikovskoe LLP	KZP157923775	1397	-	+
Sadchikovskoe LLP	KZP157923673	1609	-	+
Sadchikovskoe LLP	KZP157923561	1573	-	+
AF«Rodina» LLP	KZC158746855	1421	-	+
Mezhdurechensk-Agro LLP	KZB157778956	1475	-	+
Mamed farm	KZB157507262	not determined	n/a	n/a
Mamed farm	KZB157507352	not determined	n/a	n/a
Kamyshinskoye LLP/farm	516271	1340	-	+
Kamyshinskoye LLP/farm	516441	not determined	n/a	n/a
Taiynsha-Asty LLP	KZT183231895	1666	-	+
Taiynsha-Asty LLP	KZT183231897	1276	-	+
Taiynsha-Asty LLP	KZT183231857	1167	-	+
ZKAP Amiran LLP	KZB158174418	1718	-	+
ZKAP Amiran LLP	KZB158174428	1604	+	+
ZKAP Amiran LLP	KZB158174438	2169	-	+
Average		1512.6	X	X

It was found that the average estimated breeding value (EBV) for all breeds was 81.4. Among all breeds, the highest EBV level was determined in Holstein cows (84.3) of imported breeding. The EBV level of cows of other breeds does not have a significant difference (Table 6).

Conclusion. The traditional system of determining the breeding value of animals and the selection based on it require patience: often from six to seven years starting from the selection of parents to the completion of the productivity tests of their offspring. The genomic selection allows to "jump" through the barrier of the generation interval: when selecting bulls at the age of four to six weeks, specialists have access to a breeding value (BV) assessment based on genomic analysis. A year later bulls with higher genomic value can be realized for stud purpose. It is proved that even with reliability (accuracy of determination) of the BV at 75%, due to the use of estimated "genomically" young bulls, the breeding efficiency will double.

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СҮТТІ СИЫР ШАРУАШЫЛЫҒЫНДА ТАПСЫРЫСПЕН ШАҒЫЛЫСТЫРУДЫ ЖӘНЕ ГЕНОМДЫҚ ТАЛДАУДЫ ҰЙЫМДАСТЫРУ

Аннотация. Тапсырыспен шағылыстырылып алынған табын толықтыратын бұқаларды өндіретін сиырлар тобын қалыптастырылды, ғылыми-зерттеу жұмыстары жүргізіліп, алынған алғашқы мәліметтер ақпараттық-аналитикалық жүйеге (АТЖ) енгізілді және сиырлардың асыл тұқымды құндылықтарының (ТБИ) индекстерін автоматты түрде есептеледі. Сүтті ірі қара малының сиырларын максатты түрде асылдандыру жұмыстарын ұйымдастыру үшін бірінші тума сиырларының топтары құрылды. Барлығы 3 облыстан 609 сиыр топтары құрылды. Құрылған топтағы аналықтардың сауын маусымында сүт өнімділік көрсеткіштері (3413 ... 9611 кг) елеулі ауытқуларға ие екендігі анықталды, бірақ әкелерінің аналарының өнімділігі (5000 ... 14850 кг) едәуір жоғары, бұл қалыптасқан топтардағы сиырлардың генетикалық әлеуетін алдын -ала анықтайды.

Тапсырыспен шағылыстырудан 18 бас бұқа алынды, Гольштейн Ассоциациясының (Вермонт, АҚШ) геномдық талдау лабораториясында генетикалық талдауда асылтұқымдық құндылығы анықталды. 18 бұқаның ішінде 5 бастың асылтұқымдық құндылығы 1600-ден астам (ТPI) жоғыры АҚШ жүйесі бойынша, оның ішінде 1 бұқа ТPI = 2169. Отандық репродукцияда бұқалардың геномды бағалаудың орташа индексі (ТПИ) 1512,6 құрады, бұл Қазақстан Республикасының сүтті сиырларының генетикалық әлеуетінің жеткілікті түрде жоғары екендігін білдіреді.

Түйін сөздер: сүтті ірі қара мал, тапсырыспен шағылыстыру, геномдық талдау, асыл тұқымды құндылық индексі.

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ОРГАНИЗАЦИЯ ПРОВЕДЕНИЯ ЗАКАЗНОГО СПАРИВАНИЯ И ГЕНОМНОГО АНАЛИЗА БЫЧКОВ В МОЛОЧНОМ СКОТОВОДСТВЕ

Аннотация. Проведены научные исследования по формированию быкопроизводящих коров, получению ремонтных бычков от заказного спаривания, проведена системная работа по получению первичных данных племенного учета с занесением данных в информационно-аналитическую систему (ИАС) и автоматическому расчету индексов племенной ценности (ИПЦ) коров. Проведена работа по формированию групп коров-первотелок для того, чтобы организовать целенаправленную селекционную работу с молочным скотом. Всего было сформировано 609 коров из 3 областей. Установлено, что молочная продуктивность матерей за лактацию сформированных групп имеет значительные колебания (3413...9611 кг), но продуктивность матерей их отцов значительно выше (5000...14850 кг), что и предопределяет генетический потенциал коров сформированных групп.

От заказного спаривания были получены бычки в количестве 18 гол, у которых посредством геномного анализа была определена их племенная ценность в лаборатории геномного анализа голштинской ассоциации (штат Вермонт, США). Из 18 бычков наиболее ценными оказались 5 голов с племенной ценностью (ТPI) более 1600 по по американской системе, в т. ч. 1 бычок с ТPI= 2169. Средний индекс (ТPI) геномно оцененных бычков отечественной репродукции составил 1512,6 что позволяет утверждать о достаточно высоком генетическом потенциале молочного скота РК.

Ключевые слова: молочный скот, заказное спаривание, геномный анализ, индекс племенной ценности.

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