

Comparative evaluation of the breeding value of Holstein bulls-producers

O.V. Gorelik¹, M.Yu. Sevostyanov^{1}, and F.A. Sagitdinov¹*

¹Ural Research Institute of Agriculture - branch of the Federal State Budgetary Scientific Institution "Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences" (Ural Research Institute is a branch of the URFANITS Ural Branch of the Russian Academy of Sciences), 620061, Yekaterinburg, Russia

Abstract. Modern dairy cattle breeding efficiency is largely determined by the strategy of choosing a producer for herd reproduction, which determines the growth rate of herd productivity for the next 3 to 5 years. According to the results of 2022, there are 20 organisations in the Sverdlovsk region with milk production per feed cow of more than 9 thousand kg, including 10 farms with milk production of more than 10 thousand kg. The best farm in the region, APC "Kilachevsky", produced an average of 12829 kg of milk for each of 3000 cows. Two record-breaking cows were milked there, each of which yielded more than 21 tonnes of milk for a standard lactation. Thirty-four breeding bulls were included in the study. As a result of their evaluation, it was found that in bulls whose genomic breeding value for milk yield exceeded 1000 kg of milk 80.0% of producers were actual improvers for this trait, and in bulls with low genomic breeding value for milk yield (0-99 kg) only 25.0% of producers were actual improvers. Bulls with a negative breeding value for milk production in 66.6 percent of cases turned out to be actual improvers. In terms of protein content in milk, the dependence is similar, the higher the genomic value of the sire according to MDB, the more bulls actually have a positive effect on the protein-milk content of daughters (Tables 3,4). However, the number of sires that confirmed genomic breeding value for protein-milk yield is much less than for milk yield. For milk yield, 17 sires out of 34 (50.0%) received confirmation of breeding value, and for protein-milk yield only 11 (32.0%).

1 Introduction

The efficiency of modern dairy cattle breeding is largely determined by the strategy of choosing a producer for herd reproduction, which determines the growth rate of herd productivity for the next 3-5 years. The basis for selection of a producer is information about his breeding value, which is calculated by various methods, the most accurate of which is considered to be the traditional method of determining the breeding value of a producer by the quality of offspring. Along with this method of determining the breeding value of a sire, the method of genomic evaluation, based on the study of the genome of an individual, is now

* Corresponding author: sevamiha@yandex.ru

actively used. This method makes it possible to significantly increase the intensity of breeding by reducing the generation interval. However, genomic determination of breeding value of producers is carried out in foreign international cattle breeding centres and is based on phenotypic data obtained outside the Russian Federation [1-4].

In the world dairy cattle breeding at present, it is impossible to do without intensive mutual exchange of genetic material in order to minimise the negative impact of inbreeding and obtain maximum genetic progress, for which the semen production of bulls-producers from different world breeding centres is used. This practice also takes place in the Sverdlovsk region, where along with semen products of domestic production of Urapplemcentre JSC, foreign breeding bulls from various semen suppliers are intensively used. And, if the breeding value of domestic producers is determined by the traditional method on the quality of offspring in Russia, the breeding value of imported producers, as a rule, is determined by the genomic method, based on the study of the genome of the individual and its relationship with phenotypic traits in the conditions of foreign countries [5-12]. In this connection, it is of great practical importance to study the degree of realisation of genomic breeding value of imported Holstein bulls in the conditions of the Sverdlovsk region.

In the article by V.S. Mymrin and M.Y. Sevostyanov "Influence of genetic trend and environmental factors on the breeding value of bulls-producers" published in the journal *Agrarny Vestnik Urala*) it was concluded that the results of evaluation of bulls-producers on the quality of offspring, carried out in other regions, do not always coincide with the results of actual use of producers in specific conditions of the Sverdlovsk region. At that time, the level and adequacy of feeding of cattle, especially new cows and cows of the first half of lactation were much worse than at present. The next important difference of dairy cattle breeding at the beginning of the century was the fact that the process of interbreed crossing of Ural black-and-spring cattle with Holstein cattle was still in progress, and the breeding population was a motley mixture of genotypes of different bloodlines on Holstein breed with not yet consolidated heredity. In 2008, the productivity of black-spring cattle in the Sverdlovsk region was 4119 kg of milk, and in breeding organisations - 5897 kg. Over the past 14 years, the average milk yield in the region increased more than 2-fold to 8310 kg, and in breeding reproducers and breeding plants it reached 9453 kg of milk (Fig. 1).

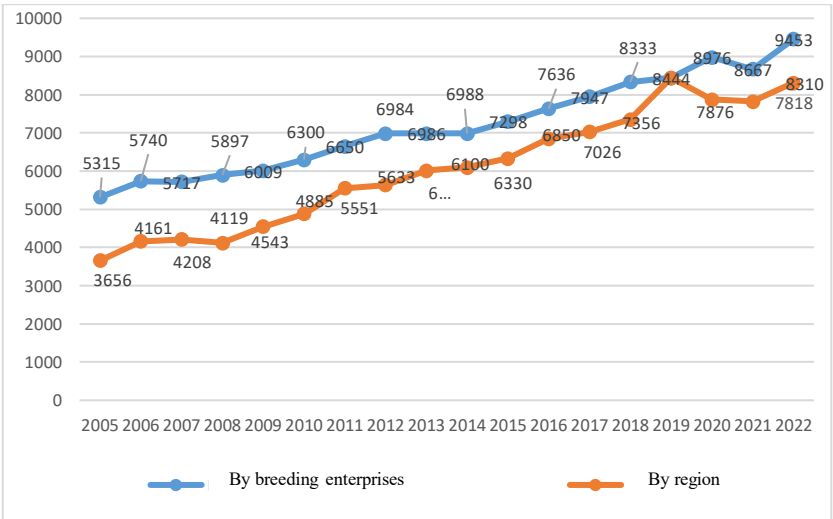


Fig. 1. Dynamics of milk productivity of cows in the Sverdlovsk region

According to the results of 2022, there are 20 organisations in the Sverdlovsk Region with milk yield per feed cow of more than 9 thousand kg, including 10 farms with milk yields of more than 10 thousand kg. The best farm in the region - APC "Kilachevsky" produced an average of 12829 kg of milk for each of 3000 cows. Two record-breaking cows were milked there, each of which yielded more than 21 tonnes of milk for a standard lactation. This is the result of purposeful use of the genetic potential of the Holstein breed to improve the Ural black-and-brown cattle, significant improvement of the level and quality of feeding, active introduction of modern protocols of dairy cattle breeding into production.

The above-mentioned data testify to a significant formed and largely realised genetic potential of productivity of the bred cattle, which according to the data of breed inventory of 2021-2022 and researches of scientific workers of the Ural Research Institute of Agricultural Sciences - branch of the Federal State Biological Institute of the Urals Federal Academy of Sciences (Modorov M.V. et al., 2021) is currently purebred Holstein cattle.

Thus, modern cattle and conditions of dairy cattle breeding in the Sverdlovsk region have changed dramatically compared to 2008 and differ little from modern dairy cattle breeding in developed European countries.

As part of the development of breeding plans for breeding plants and reproducers in the Sverdlovsk region in 2021-2022, we compared the genomic evaluation of the breeding value of a Holstein bull breeder with its actual breeding value determined in a particular farm in the Sverdlovsk region by the quality of offspring.

The aim of this work was to conduct a comparative evaluation of bulls-producers by genomic evaluation with the evaluation by progeny quality in a particular farm.

2 Methods and Materials

The research involved 34 Holstein bulls used for herd reproduction in 2 breeding reproducers and 4 breeding plants of the Sverdlovsk region. Producers with data on the first completed lactation of at least 20 daughters were included in the processing. Data on breeding value of bulls-producers determined by genomic method were taken from breeding certificates provided by semen suppliers. The results of breeding value assessment by progeny quality were calculated by IAS Sellex programme and generated in Table 12 "Results of using bulls-producers". Breeding value was considered by three traits of the first lactation: milk yield for 305 days, fat and protein content in milk. According to the level of genomic breeding value, all producers were distributed into groups with different levels from negative to maximum breeding value. For example, by milk yield the producers were distributed into 5 groups: a group of producers with negative breeding value, breeding value 0-99 kg, 100-499 kg, 500-1000 kg and more than 1000 kg of milk. Similar distribution of producers was carried out by fat and protein content in milk. Coincidence of the results of genomic evaluation with the evaluation of progeny quality was considered as obtaining the same positive or equally negative evaluation result.

3 Results

Comparison of actual influence of Holstein sires on daughter milk yield calculated by IAS Sellex programme with genomic breeding value shows that not all types have genomic evaluation of breeding value to some extent coincides with actual one (Table 1).

Table 1. Breeding value of Holstein bulls by milk yield, kg

Bull-Producer		Breeding value	
Name	Ind. No.	Genomic	Progeny quality
Genomic breeding value for milk yield over 1000 kg			
Bently	924557855	1581	346
Piledriver	3126539652	1212	571
Ferdy	921967107	1130	319
Newpoint	357545442	1113	-4
Silver	70358050	1031	376
Genomic breeding value by milk yield 500-1000 kg			
Renigheid	3011816312	765	52
Altacarnival	69474074	698	-77
Altaclaim	3133630023	547	853
Genomic breeding value by milk yield 100 - 499 kg			
Seo	69177565	482	-371
Altaichelon	537222111	444	-8
Altaeverglade	3008559787	399	-129
Altajake	72395545	392	243
Horizon	71060382	372	-299
R. Altadoni	63031811	368	-112
Skoda	69169948	367	264
Altasanford	707154747	332	-259
Altaalfa	70346650	318	51
Altarevolver	641883561	278	156
Millard	137633111	267	-273
Thorne	56438534	245	608
Ledgendery	3125066436	240	-511
Manny	74307908	220	220
Jenix	64410464	161	-189
Magiste	3129037660	120	-624
Genomic breeding value by milk yield 0-99 kg			
Trouble	3125479393	83	343
Loveboat	108568399	67	-347
Altabac	55618727	45	-153
L. Casual	56265391	6	-541
Negative genomic breeding value for milk yield			
Altasanford	70715474	-36	-315
Black Jack	3129037702	-64	-235
Altapilsner	70344827	-64	178
David	141367055	-136	-687
Eivenger	74072229	-179	-640
Charmant	53774748	-282	16

Moreover, the number of sires whose genomic evaluation partially coincides with the actual one is in direct correlation with the level of genomic breeding value of the bull. The higher the genomic breeding value, the greater the number of sires has a positive influence on the milk yield of daughters. In bulls whose genomic breeding value for milk yield exceeded 1000 kg of milk 80.0% of sires were actual improvers for this trait, and in bulls with low genomic breeding value for milk yield (0-99 kg) only 25.0% of sires were actual improvers. Bulls with negative breeding value for milk yield in 66.6% of cases were actually improved (Table 2).

Table 2. Coincidence of the results of evaluation of breeding value determined by different methods depending on the value of genomic breeding value by milk yield

Genomic evaluation of breeding value by milk yield, kg	Total bulls, heads	including with the coincidence of the results of the breeding value assessment	
		heads	%
More than 1,000	5	4	80.0
500-1000	3	2	66.6
100-499	16	6	37.5
0-99	4	1	25.0
Negative breeding value	6	4	66.6

The use in breeding herds with milk yields of more than 8-9 thousand kg of milk of quite a large number of bulls with low and negative breeding value for milk yield is a cause for concern. In this study, out of 34 producers, 10 (29.4%) belonged to this category.

In modern market conditions, there is a large number of semen suppliers offering a wide range of sires with different pedigree values, among which it is possible to choose a sire with a complex, including milk yield, which improves the quality of offspring. This fact testifies to insufficient demandingness of zootechnicians-breeders to the breeding value of sires assigned to the herd.

With regard to protein content in milk, the dependence is similar, the higher the genomic value of the sire according to MDB, the more bulls actually have a positive effect on protein-milk content of daughters (Tables 3,4). However, the number of sires that confirmed genomic breeding value for protein-milk yield is much less than for milk yield. For milk yield, 17 sires out of 34 (50.0%) received confirmation of breeding value, and for protein-milk yield only 11 (32.0%).

Table 3. Breeding value of Holstein bulls by protein content in milk, %

Bull-producer		Breeding value determined by different methods, %	
Name	Ind. No.	Genomic	Progeny quality
Genomic breeding value by protein more than 0.10%			
Newpoint	357545442	0.21	0.03
Altapilsner	70344827	0.12	0.01
Genomic breeding value for protein 0.05-0.10%			
Altaeverglade	3008559787	0.09	0.05
Altabac	55618727	0.09	0.14
Black Jack	3129037702	0.08	-0.01
Charmant	53774748	0.07	0.01
David	141367055	0.07	-0.04
Renigheid	3011816312	0.06	-0.01
Ferdy	921967107	0.06	-0.07
Loveboat	108568399	0.06	0.01
Eivenger	74072229	0.05	0.01
Horizon	71060382	0.05	0.00
Genomic breeding value for protein 0.00 - 0.05%			
Magiste	3129037660	0.04	0.03
Trouble	3125479393	0.04	-0.01
Millard	137633111	0.03	-0.16
Altasanford	707154747	0.03	-0.04
R. Altadoni	63031811	0.03	0.00
Manny	74307908	0.03	-0.02
Skoda	69169948	0.02	-0.01
Altasanford	70715474	0.02	-0.03
Seo	69177565	0.02	0.00
L. Casual	56265391	0.02	-0.05
Altaalfa	70346650	0.01	0.01

Altarevolver	641883561	0.01	0.00
Negative genomic breeding value for protein			
Altacarnival	69474074	-0.01	0.00
Silver	70358050	-0.01	0.00
Ledgendery	3125066436	-0.01	-0.01
Jenix	64410464	-0.02	0.01
Thorne	56438534	-0.02	0.00
Piledriver	3126539652	-0.02	0.02
Altaichelon	537222111	-0.02	0.01
Altaclaim	3133630023	-0.02	0.05
Altajake	72395545	-0.05	0.06
Bently	924557855	-0.05	-0.19

According to this trait 10 producers also had negative breeding value, the use of which is absolutely inexpedient in breeding herds.

Table 4. Coincidence of results of breeding value assessment by different methods depending on the value of genomic breeding value by milk protein content

Genomic evaluation of breeding value by protein content, %	Total bulls, heads	including the coincidence of the results of breeding value assessment by different methods	
		heads	%
More than 0.10	2	2	100.0
0.05-0.10	10	5	50.0
0.00-0.04	12	2(3)	16.7 (41.6)
Negative breeding value	10	2	20.0

Comparison of genomic and actual breeding value of the studied bulls by fat content in milk of daughters does not fit into the revealed regularity in milk yield and protein-milk yield. Out of 34 bulls-producers 18 or 52,9% confirmed their genomic pedigree value by fat content in milk of daughters by the daughter-female method (Table 5). But at the same time the value of genomic pedigree value did not influence the number of bulls-producers who actually confirmed their pedigree value by this trait (Table 6).

Table 5. Breeding value of Holstein bulls by milk fat content, %

Bull-Producer		Breeding value determined by different methods, %	
Name	Ind. No.	Genomic	Progeny quality
Genomic breeding value by fat more than 0.10%			
Newpoint	357545442	0.36	0.01
Black Jack	3129037702	0.23	0.00
Renigheid	3011816312	0.17	0.02
Altaeverglade	3008559787	0.16	0.02
Millard	137633111	0.17	-0.01
Horizon	71060382	0.12	-0.01
Magiste	3129037660	0.12	-0.01
Trouble	3125479393	0.11	0.03
Ferdy	921967107	0.11	-0.08
Altapilsner	70344827	0.11	0.02
Genomic breeding value by fat 0.05 – 0.10%			
Eivenger	74072229	0.10	0.00
Thorne	56438534	0.09	0.01

Altabac	55618727	0.10	0.04
Charmant	53774748	0.10	-0.03
Loveboat	108568399	0.08	-0.03
Seo	69177565	0.06	0.01
Altaalfa	70346650	0.05	-0.01
Genomic breeding value by fat 0.00-0.04%			
L. Casual	56265391	0.02	0.01
Altasanford	707154747	0.02	0.03
Jenix	64410464	0.02	-0.03
David	141367055	0.01	-0.06
Negative genomic breeding value for fat			
Altacarnival	69474074	-0.01	0.00
Altaclaim	3133630023	-0.02	-0.01
Manny	74307908	-0.01	-0.01
Bently	924557855	-0.05	0.02
R. Altadoni	63031811	-0.01	-0.01
Skoda	69169948	-0.02	-0.06
Piledriver	3126539652	-0.05	-0.02
Altaichelon	537222111	-0.03	0.02
Altarevolver	641883561	-0.02	0.02
Altasanford	70715474	-0.02	-0.05
Silver	70358050	-0.12	0.00
Altajake	72395545	-0.08	-0.03
Ledgendery	3125066436	-0.09	-0.03

The largest number of bulls-producers used in the controlled breeding herds with negative genomic breeding value was by milk fat content 13 out of 34 producers or 38.2%, of which 8 (61.5%) confirmed their negative genomic breeding value by actual breeding value determined by the quality of offspring, which once again proves the inexpediency of using such producers, especially in breeding herds.

Table 6. Coincidence of the results of breeding value assessment by different methods depending on the value of genomic breeding value by milk fat content

Genomic evaluation of breeding value by fat content, %	Total bulls, heads	including with the coincidence of the results of the breeding value assessment	
		heads	%
More than 0.10	10	5	50.0
0.05-0.10	7	3	43.8
0.00-0.04	4	2	50.0
Negative breeding value	13	8	61.5

4 Conclusions

Thus, in the transitional period of creation of the domestic genomic index and the system of genomic evaluation of breeding value of domestic producers it is possible to use the data of genomic evaluation of breeding value of domestic producers of Holstein breed made abroad and imported producers with genomic evaluation of breeding value.

When selecting Holstein bulls-prodecers for herds in the Sverdlovsk region with milk yield more than 9,000 kg of milk, it is necessary to use producers with genomic breeding value for milk yield not less than 1000 kg of milk, protein-milk yield not less than 0,05%, and with a positive evaluation for fat-milk yield.

It is unacceptable to use in breeding herds producers with negative breeding value for milk productivity traits.

References

1. Genomic selection - present and future of livestock breeding / <https://www.agroyug.ru/news/id-33102>
2. O.I. Leshonok, I.V. Tkachenko, M.Yu. Sevostyanov, et al., Current state of pedigree work with black-and-white cattle in the Urals region - results of 2021 (monograph). (Ekaterinburg, 2022)
3. Methodical recommendations on carrying out breed inventory of pedigree stock of cattle of dairy direction/<https://mcx.gov.ru/upload/iblock/b07/b07ebe....pdf>.
4. M.V. Modorov, I.V. Tkachenko, A.A. Grin, et al., Genetics **57**, 4, 437-444 (2021)
5. S.V. Mymrin, V.S. Mymrin, I.M. Donnik, Agrarny vestnik Urala **4**, 28 (2014)
6. V. Mymrin, O. Loretts, *Contemporary trends in the formation of economically-beneficial qualities in productive animals*. Digital agriculture - development strategy Proceedings of the International Scientific and Practical Conference(ISPC 2019) Advances in Intelligent Systems Research 511-514 (2019)
7. S. Gridina, V. Gridin, O. Leshonok, Advances in Engineering Research, 253-256 (2018)
8. N. Bogolyubova, et.al., OnLine Journal of Biological Sciences **17(2)**, 121-27 (2017)
9. N. Bogolyubova, et.al., Asian Journal of Pharmaceutical and Clinical Research **10(10)**, 117-20 (2017)
10. O.V. Gorelik, et al, IOP Conf. Ser.: Earth Environ. Sci. **548**, 082009 (2020) doi:10.1088/1755-1315/548/8/082009
11. O.V. Gorelik, et al, *The use of inbreeding in dairy cattle breeding* IOP Conf. Ser.: Earth Environ. Sci. (2020) /10.1088/1755-1315/548/8/082013
12. O.V. Gorelik, et al, AIP Conference Proceedings **2207** 020012 (2020) doi 10.1063/5.0000317