Use of Genomic Evaluation of Cattle in Breeding Work (A Case Study from The Udmurt Republic, Russia)

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Abstract

The task of increasing milk productivity faced by every livestock enterprise necessitates continuous efforts to enhance the genetic potential of animals. This endeavor entails a comprehensive approach, encompassing the integration of innovative biotechnologies, efficient methods of animal care and feeding, and comprehensive breeding and selection programs. Research on the genomic selection of dairy cows under specific natural and climatic conditions has gained particular relevance. This article presents the results of a comprehensive analysis of the genetic profile of the Kalinin Agricultural Production Cooperative's cattle herd in the Debessky District of the Udmurt Republic, Russia, based on genomic assessment. The study encompassed 1,557 individuals, including heifers, non-lactating cows, and lactating cows of the Holstein breed. The findings showed significant variations in milk yield evaluations across different generations of cows. The findings provided valuable insights into the genetic characteristics of the cattle herd at the Kalinin Agricultural Production Cooperative, shedding light on milk productivity dynamics and genetic fertility defects, which can inform future breeding and management strategies for improved dairy cattle production.

Keywords: genomic assessment, breeding value, fertility haplotypes, line, branch.

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1. Introduction

Over the past 40-50 years, average milk productivity has more than doubled in many countries as a result of the growth of genetic potential in several economically significant parameters [1]. This became possible as a result of an integrated approach: the introduction of innovative biotechnologies, effective technologies for keeping and feeding [2, 3], and integrated breeding programs [4, 5]. In breeding programs for the improvement of farm animals, an important point is the development and practical use of effective methods for assessing the breeding qualities of animals, which allows ranking them by breeding value and selecting the most valuable [6, 7]. The essence of genomic breeding is the selection of cows that ensures their breeding value according to markers that regularly replenish the entire genome [8].

Many authors summarize information about current trends in the field of genomic breeding of dairy cattle and the use of new technologies to improve the efficiency of breeding [5, 9, 10, 11]. Important fields in the development of genomic breeding methods are the increase in the accuracy of breeding evaluation by comparing different genotypes of cows, including genotyping of individuals in breeding programs, predicting the genotypes of missing single nucleotide polymorphisms (SNPs) based on chips with a lower density of markers and predicting the genotypes of dairy cattle based on the genotypes of parents [12, 13]. Together with modern methods, genotype breeding can potentially bring higher profitability [5, 9, 14].

Quantitative traits refer to characteristics that differ in the degree of expression and can be attributed to polygenic effects. That is, they are the product of two or more genes and depend on the number of cows evaluated in the herd (group). Based on this, genomic breeding has a greater effect when working with breeds that are common globally, such as the Holstein [8, 15]. Therefore, the increase in the reliability of genomic estimates depends on the number of individuals added to the study population, the reliability of their phenotyping, and their kinship relationships [9]. Research on genomic breeding of dairy cows in certain natural and climatic conditions is becoming particularly relevant. In this regard, the purpose of this work was to analyze the results of the genomic evaluation of cattle and determine the possibility of their use in further breeding work at one of the enterprises of the Udmurt Republic, Russia, the Kalinin Agricultural Production Cooperative (SPK) (Collective Farm) of the Debessky district.

Objectives of the study:

- To analyze the genetic profile of the herd based on the results of genomic evaluation.
- To identify the distribution of fertility haplotypes of Holstein cattle among the genotyped livestock.

- To determine the indicators of the level of milk productivity in cows that are carriers of fertility haplotypes.
- To assess the influence of origin on the results of genomic evaluation of animals.

2. Materials and Methods

The study was carried out at the Kalinin SPK in 2023. The number of cows in the farm was 1,105 heads with an average level of dairy productivity for the herd equaling 9,153 kg of milk with a 4.37% mass fraction of fat and 3.03% of protein. Heifers, non-lactating cows, and lactating cows of the Holstein breed with the results of genomic evaluation served as the material for the study. The total sample size was 1,557 heads, including 1,037 lactating cows, 257 non-lactating cows, and 263 heifers. The fathers of the analyzed livestock were 24 bulls of the Holstein breed, belonging to five main lines: R. Sovereign (nine bulls), V.B. Ideal (eight bulls), M. Chieftain (five bulls), and one bull each of the Pabst Governor and S.T. Rocket lines. The values of the breeding estimates of the main selected traits and the results for carriers of cattle fertility haplotypes were taken from the KSITEST database.

Genotyping for genomic evaluation was carried out based on a molecular genetic study of cattle on Bovine Versa SNP 50k v1.3 chips (50 thousand SNPs). To determine the estimates of the breeding value of animals, the BLUP Sire Model and BLUPG methodology were used, considering the complex factor "herd – year – calving season".

The study methodology included statistical data processing using the Data Analysis package in Microsoft Excel.

3. Results and Discussions

The Kalinin SPK is one of the first farms that took part in the republican breeding program for the genomic evaluation of animals and the creation of a reference group of animals in the Udmurt Republic (since 2019). As of April 8, 2023, there were 1,557 heads of cattle from the analyzed farm in the unified database of genetic assessments, including 1,037 lactating cows, 257 non-lactating cows, and 263 heifers. Figures 1 and 2 show the growth rates of estimates of the value of milk yield and the distribution of the estimated herd animals by milk yield, depending on the year of birth. Analyzing the indicators, it can be noted that the results of the assessment of milk yield are steadily increasing. Thus, the milk yield estimate for cows born in 2014 was -218 kg, and for cows born in 2022 +784 kg. Starting from 2019, the growth of the analyzed indicators has been more systematic and high. The estimate for milk yield increases annually by 109 to 192 kg.

When evaluating animals by genome, several haplotypes (defects) were identified, the presence of which must also be identified and considered in breeding work with the herd. In the herd of the Kalinin SPK, 196 disease carriers were identified among the breeding stock. This is 8.7% of the total livestock or 12.6% of the number of genotyped animals (Table 1). Thus, in the population of the analyzed herd, the following haplotypes of the fertility of the Holstein cattle breed were identified: HH1 (frequency in the livestock 6.2%),

HH3 (3.7%), BLAD (1.3%), HCD (0.5%), HH7(0.4%) and HH4 (0.06%). Some animals identified in the herd were carriers of two fertility haplotypes in different combinations at once (0.4%). These defects were found among different age and sex groups. All haplotypes were found among lactating cows, with the most carriers of HH1, HH3, and BLAD. Among heifers, there were carriers of haplotypes HH1, HH3, HH7, and BLAD, and among non-lactating cows, carriers of HH1, HH3, and BLAD were found.

When planning breeding work with animals carrying fertility haplotypes, it is necessary to consider their value and importance for the effectiveness of selection. The value of milk yield and quality indicators of milk in carrier cows are high (Table 2). If we compare the value of milk yield for the maximum lactation, then in cows with the haplotypes HH7, BLAD, and HCD in the genotype, this indicator was higher compared to the defect-free animals by 1,187.5, 386.5, and 402 kg, respectively. However, in the groups of cows with HH7 and HCD defects, there were only four and eight heads. In the groups of cows that were carriers of haplotypes HH1 and HH3, the milk yield for maximum lactation was lower by 282 and 860 kg, respectively.

A similar trend is observed in the amount of milk yield for the LFL of these animals. These were mainly young cows: first-calf cows (54.6% of the total number of carriers with completed lactation) and two-calf cows (21.3%), while the rest of the animals were mature (from the 3rd to the 8th lactation). The value of milk yield in carriers of haplotypes HH1 and HH3 was lower than in defect-free cows by 264 and 757 kg, respectively. For the remaining groups, there was an excess of milk productivity of 341.5 to 1,057 kg. This once again confirms that an individual approach is necessary when planning selection and breeding with these animals. In terms of milk yield for the first lactation, defect-free cows were inferior only to BLAD carriers by 450 kg. In the remaining groups of haplotype-bearing cows, this indicator was higher by 61 to 1,053 kg. Moreover, the greatest excess in the level of milk yield after the first lactation was observed in carriers of HH1 (1,053 kg).

Table 3 shows the influence of lines and branches on the breeding value of offspring according to the results of genomic evaluation. According to Table 3, the greatest contribution to the structure of the herd was made by descendants of the V.B. Ideal (56%) and R. Sovereign (29%) lines. The results of genomic evaluation are the highest in animals of the V.B. Ideal line. Thus, the values of the breeding value in terms of milk yield and the MFF in cows of this line are +390.8 kg and +0.04%. In animals of the R. Sovereign line, the evaluation indicators are +270.2 kg and +0.02%. Less numerous lines (Pabst Governor and S.T. Rocket) have a negative assessment of the value of milk yield (-143.1 and -142.1 kg, respectively). According to the MFF in milk, the assessment of breeding value is positive and high (+0.09%). The MPF in cows of the Pabst Governor line is negative (-0.01%), and in cows of the S.T. Rocket line, it is low positive (+0.009%). In the section of branches, the best indicators were obtained in animals of the V.B. Ideal line (Manfred and Mogul branches) and M. Chieftain line (O. Ivanhoe branch). Their milk yield estimate ranged from +202.8 to +699.4 kg, MFF from +0.05 to +0.11%, and MPF from +0.02 to +0.04.
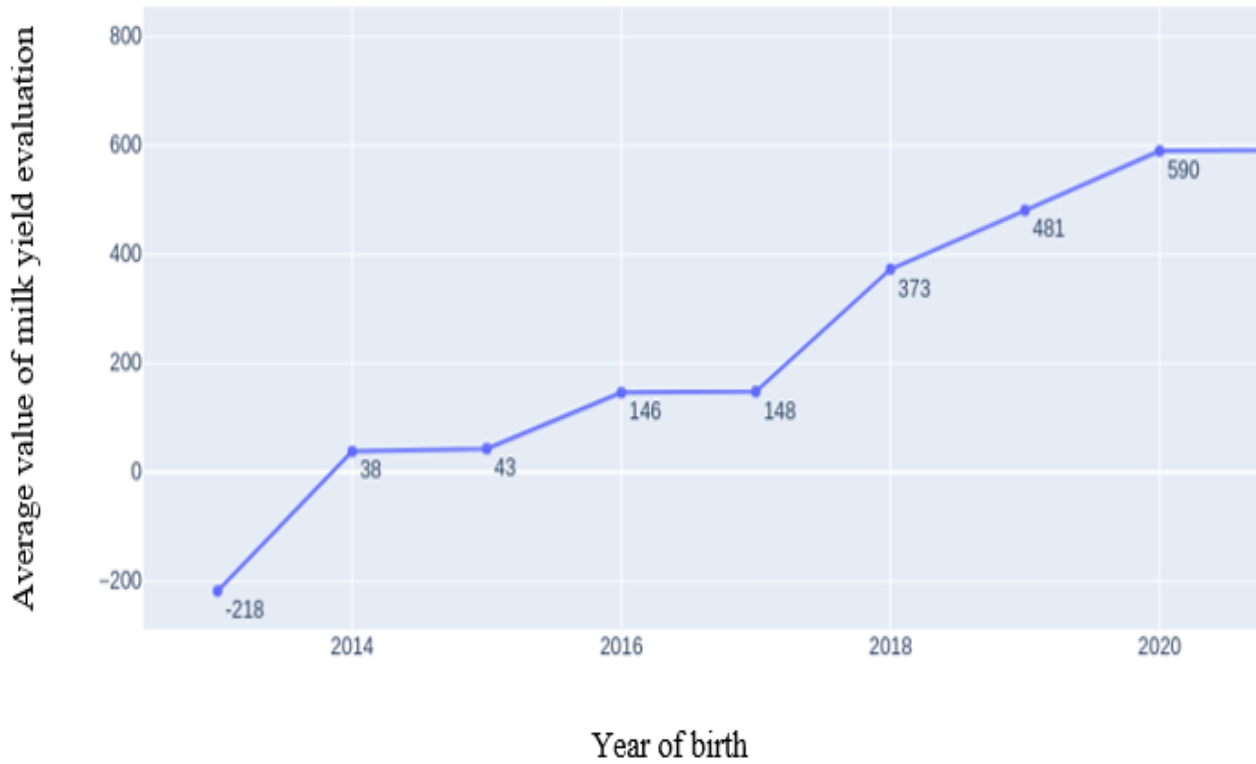
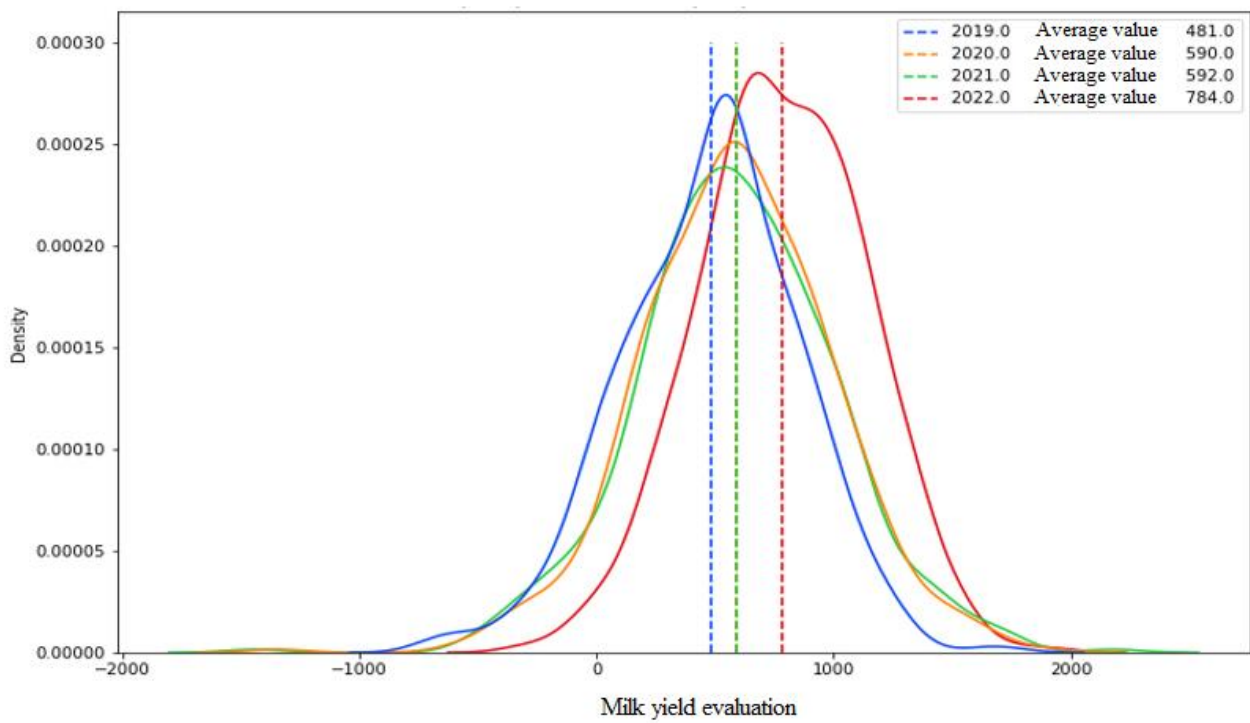**Figure 1.** The growth of the evaluation of milk yield of cows by year

Figure 2. Distribution of yield estimates by year

Table 1. Distribution of fertility haplotypes

Haplotype (defect)	Number of carriers, heads				Frequency in livestock (from the number of genotyped animals), %
	lactating cows	non-lactating cows	heifers	total	
HH1	75	13	8	96	6.2
HH3	45	2	10	57	3.7
HH4	1	-	-	1	0.06
HH7	4	-	3	7	0.4
Bovine leukocyte adhesion deficiency(BLAD)	15	1	4	20	1.3
Haplotype for cholesterol deficiency (HCD)	8	-	-	8	0.5
BLAD, HCD	1	-	-	1	0.06
BLAD, HH1	1	-	-	1	0.06
BLAD, HH3	1	-	-	1	0.06
HH1, HH3	1	-	-	1	0.06
HH1, HH7	1	-	-	1	0.06
HH3, HH7	1	-	-	1	0.06
Bovine dilated cardiomyopathy (BDCMP), HH1	-	1	-	1	0.06
Total carriers, heads	154	17	25	196	12.6

Table 2. Indicators of milk productivity of cows that are carriers of fertility haplotypes

Haplotype (defect)	Average age in lactation	Milk yield for 305 days of maximum lactation, kg	Milk yield for 305 days of the 1st lactation, kg	Milk yield for 305 days of the last finished lactation (LFL), kg	Fat in dry matter (FDM) during the LFL, %	Protein in dry matter (PDM) during the LFL, %
HH1	1.6 (1-8)	9,023±192	8,397±218	8,938±208	4.20±0.05	3.06±0.01
HH3	1.7 (1-3)	8,445±194	7,628±234	8,445±244	4.27±0.07	3.05±0.01
HH7	3.3 (2-4)	10,492.5±758	7,645.5±1018	10,259±849	4.49±0.15	2.92±0.04
BLAD	3.2 (1-6)	9,691.5±375	6,894±471	9,543.5±421	4.48±0.11	3.02±0.01
HCD	2.6 (1-3)	9,707±246	7,405±358	9,656±261	4.33±0.14	2.99±0.01
Defect-free	2.5 (1-9)	9,305±157	7,344±176	9,202±184	4.38±0.01	3.04±0.01
On average in the genotyped animals	2.4 (1-9)	9,257±146	7,406±163	9,168±170	4.37±0.01	3.04±0.01

Table 3. Influence of lines and branches on the breeding value of offspring according to the results of genomic evaluation

Line	Branch	Number of daughters	Breeding value by		
			milk yield, kg	MFF, %	MPF, %
Vis Back Ideal 1013415	Aerostar	61	+164.0	+0.06	+0.013
	Cleitus	42	+337.6	+0.01	+0.004
	Lidman	9	+210.4	+0.05	0
	Manfred	287	+407.9	+0.05	+0.02
	Mogul	29	+699.4	+0.11	+0.04
	Prelude	131	+419.9	+0.009	+0.007
On average in the line		559	+390.8	+0.04	+0.01
Montvik Chieftain 95679	Bar Lee	19	-1	+0.12	+0.01
	O. Ivanhoe	33	+202.8	+0.05	+0.02
	W. Bell	15	+38.8	+0.08	+0.004
On average in the line		67	+108.3	+0.07	+0.02
Pabst Governor	Ned Boy	20	-143.1	+0.09	-0.01
On average in the line		20	-143.1	+0.09	-0.01
Reflection Sovereign 198998	Bellwood	12	+286.5	+0.002	+0.008
	Blackstar	109	+334.8	+0.03	-0.02
	Valian	65	+238.5	+0.04	+0.01
	Melwood	23	+121.8	+0.01	-0.008
	Robust	26	+140.7	-0.04	-0.06
	Chief Mark	55	+299.3	+0.03	+0.03
On average in the line		290	+270.2	+0.02	-0.004
Siling Trijun Rocket 252803	Rockman	55	-142.1	+0.09	+0.009
On average in the line		55	-142.1	+0.09	+0.009

4. Conclusions

The results of genomic evaluation are of some interest in further breeding work with the herd, in particular for the selection of the most valuable animals. Since 2019, the use of breeding estimates of animals in the selection of the analyzed herd has allowed us to increase the results of the breeding value of cows in terms of milk yield by 303 kg. In addition, the timely detection of animals that are carriers of defects will allow for improving the herd in what concerns the undesirable haplotypes of Holstein cattle.

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