

Perspectives for the use of genomic selection for genetic improvement of dairy cattle in Ukraine

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Abstract. An important problem in modern dairy cattle breeding is the achievement of a high level of genetic progress in economically important traits through the implementation of effective breeding programs. For this purpose, genomic selection is currently used in many countries of the world. The aim of the study was to investigate possibilities of use of genomic selection in dairy cattle breeding in Ukraine. On the basis of analysis of "Catalogue of sires of dairy and dual-purpose breeds for reproduction of cows in 2020" (sperm of these sires was used in Ukraine) two methods of breeding value estimation were compared: 1) traditional method based on pedigree and performance of progeny; 2) genomic method based on effects of SNPs. Considerable advantage of sires with genomic evaluations was proved. These sires excel sires with traditional evaluation for milk yield by 1.6 times, for fat percentage by 2.2 times, for fat yield by 1.7 times, for protein percentage by 2.1 times and for protein yield by 1.7 times. Using estimates of breeding values of sires pair-wise genetic correlations between main genetic traits were computed. The negative genetic relationship between milk yield and fat and protein percentages was revealed. Values of energy corrected milk (ECM) of daughters and dams of sires across breeds and countries of origin were calculated. It was shown that dams of sires of Holstein and Jersey breeds had highest values of energy corrected milk (9,132.0 kg and 8,041 kg, respectively) while dams of sires of Ukrainian Black-and-White dairy breed had lowest values of this trait (5,848.1 kg). According to country-of-origin daughters of sire's form USA, Canada and the Netherlands had highest values of energy corrected milk. Values of response to selection using traditional breeding program and genomic selection were compared. It was proved that by means of shortening generation intervals on pathways of genetic improvement "sires of bulls", "sires of cows" and "dams of bulls" using genomic selection it is possible to increase rate of genetic progress for milk yield from 100.1 kg to 180.0 kg that is by 80%

Keywords: dairy breed; energy corrected milk; genetic improvement; genetic correlation; response to selection; genomic evaluation

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INTRODUCTION

Traditional breeding programs for dairy cattle are based on progeny testing of young bulls. However, such programs require 6-7 years to obtain reliable estimates of breeding values and are very expensive (it is necessary to obtain 60-100 daughters for each bull while most of progeny tested bulls are not used for reproduction).

Genomic selection allows shorten time period necessary to obtain reliable breeding values of young bulls and is more cost-effective compared to progeny testing schemes. Breeding programs based on genomic selection are currently used in many countries of the world.

The effectiveness of breeding programs depends on their profitability. In implementing such a program, it is important to predict the expected genetic progress that is associated with the response to selection (Ruban & Danshin, 2019).

At the beginning of the 21st century the possibility of predicting the breeding values of animals in the early stages of ontogenesis using multiple markers that cover the entire genome was proved (Weller, 2019). This led to the formulation of what is known now as “genomic selection” (Misztal *et al.*, 2020). But at that time this approach was not implemented due to the lack of sufficient number of genetic markers. In 2009,

after sequencing the genome of cattle, the features of polymorphism of individual nucleotides (SNP – Single Nucleotide Polymorphism), and relationship of SNPs with the important traits were revealed. Later use of technology of micro-panels of DNA (DNA – microarray) has made genomic selection more widely used in the breeding programs of many species of farm animals and especially in dairy cattle (VanRaden, 2020).

In 2009-2011 breed associations in a number of countries around the world implemented genomic selection using DNA micro-panel technology (BovineSNP50 BeadChip), and the overall profitable effect of such programs increased the application of genomic testing in other countries. Number of genotyped animals permanently increases. For example, number of genotyped animals in USA and Canada increased from 22,344 in 2009 to more than 6.5 million in 2022 (Wiggans & Carrillo, 2022).

Widespread implementation of genomic selection is associated with considerable development of methodology of genomic prediction used for evaluation of genomic breeding values (Ahmadi & Bartholomé, 2022).

Figure 1 presents a general scheme of organization of selection in dairy cattle.

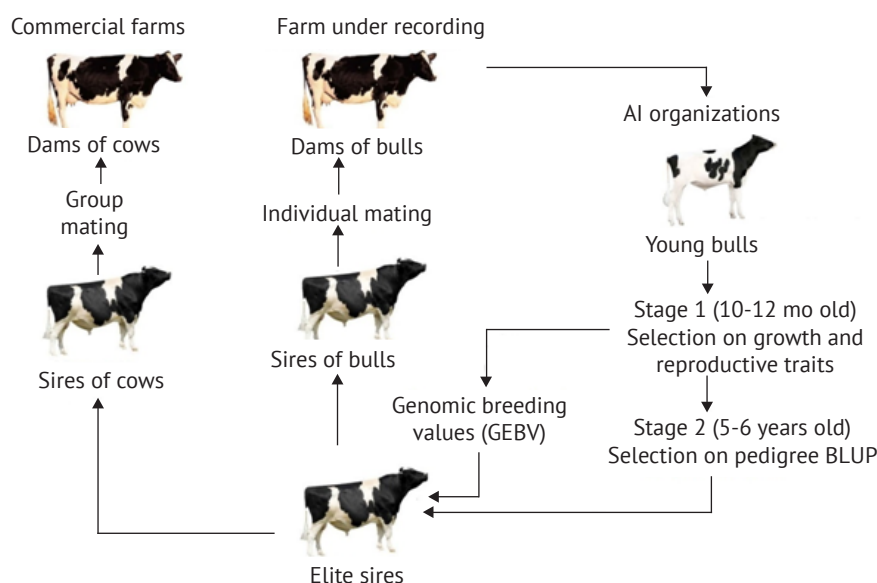


Figure 1. General scheme of breeding program in dairy cattle using two methods of evaluation of breeding values: traditional (pedigree BLUP) and genomic (genomic BLUP)

Source: S. Ruban & V. Danshin (2019)

On farms under recording individual data on productivity, product quality, health status and level of reproduction are collected with the determination of the best animals for selection. From these animals' young bulls are selected to AI organization, and best of them pass to group of elite sires or “sires of bulls”.

Selection of this category of animals can be carried out in two ways: 1) traditional two-stage selection, when at the first stage bulls are selected at the age of 10-12 months on growth and reproductive traits, and at the second stage, at the age of 5-6 years, they are selected on estimates of breeding values (pedigree BLUP) using

progeny testing; 2) bulls are genotyped out at the age of 6-10 months, selected on genomic breeding values (genomic BLUP) and the best of them are used since the age of 10-12 months (time of start of accumulation of sperm for artificial insemination) in individual mating programs to obtain the best cows to form the next generation (Fig. 1). Most of the frozen sperm from sires is used for artificial insemination of cows and heifers. The main purpose of selection is to obtain healthy offspring capable to produce a certain amount of milk with a certain composition and quality (Ruban & Danshin, 2019).

The base of the organizational scheme of genomic selection is a reference population with known genotypes of animals for SNPs and the corresponding phenotypes. Based on these data, the prediction equation is constructed, which allows to calculate genomic estimates of breeding value for animals – candidates for selection (young bulls and heifers). According to these estimates, in accordance with the breeding objectives, animals of next generation are selected. This is two-step procedure. Recently, single-step genomic BLUP combining information on both genotyped and non-genotyped animals is widely implemented (Lourenco *et al.*, 2020; Mäntysaari *et al.*, 2020; Bermann *et al.*, 2022).

A good example of the practical use of genomic selection in dairy cattle is the HD Genomics program for the Norwegian Red breed. The total population of this breed is 200,000 cows, so about 100,000 bulls and the same number of heifers are born annually. Data on performance, health, and pedigree are collected for each animal. Annually, 8,000 young bulls and 12,000 young heifers are selected for genotyping in order to calculate the genomic breeding values on a set of traits. From the evaluated animals, 50-60 elite bulls are selected to obtain sperm, which is used for artificial insemination, and from the evaluated heifers 120 elite heifers are selected for the production of embryos (Norwegian Red breeding program, 2021).

The use of genomic estimates of breeding value causes significantly reduce of generation intervals. B.O. Makanjuola *et al.* (2020) investigated the changes in the intervals on the four pathways of genetic improvement in the populations of Holstein and Jersey breeds in the United States for the period from 1990 to 2018. On four pathways of selection due to the introduction of genomic selection the average generation interval reduced from 6-6.5 years (traditional selection) to 2.5-3 years, i.e., 2 times. At the same time, the largest reduction in the generation interval occurred in the category of sires of bulls – from 8 to 2-3 years. The reduction of generation intervals on the main pathways of selection led to a corresponding acceleration of the rate of genetic progress (Wiggans & Carrillo, 2022). For example, genetic gain in fat yield for Holstein bulls increased 6 times since 2009 (Guinan *et al.*, 2023). Generally, genomic selection program for dairy cattle has doubled the rate of genetic gain in the United States (Wiggans & Carrillo, 2022). At the same time, an increase in the rate of inbreeding is observed (Lozada-Soto *et al.*, 2022). Mitigation of the negative effects of inbreeding depression on different traits also requires use of genomic information (Gutierrez-Reinoso *et al.*, 2021).

The aim of the study was to investigate possibilities of use of genomic selection in dairy cattle breeding in Ukraine.

MATERIALS AND METHODS

Material of the study were estimated breeding values of 937 sires for milk production traits (milk yield, fat percentage, fat yield, protein percentage and protein yield) taken from the catalogue of dairy and dual-purpose service sires of Ukraine (39 AI organizations) in 2020 (Polupan *et al.*, 2020). Table 1 contains descriptive statistics of milk production traits of daughters of sires used in the study.

General level of milk production was estimated as energy corrected milk (ECM) according to N.G. Hossein-Zadeh (2017):

$$ECM = \frac{fat\ yield, kg \cdot 38.3 + protein\ yield, kg \cdot 24.2 + milk\ yield, kg \cdot 0.7832}{3.14} \quad (1)$$

Annual response to selection (R) was calculated as (Simm *et al.*, 2021):

$$R = \frac{S_{SB} + S_{SC} + S_{DB} + S_{DC}}{L_{SB} + L_{SC} + L_{DB} + L_{DC}}, \quad (2)$$

where $S_{SB} = i_{SB} \cdot r_{gISB} \cdot \sigma_a$ – genetic superiority of sires of bulls; $S_{SC} = i_{SC} \cdot r_{gISC} \cdot \sigma_a$ – genetic superiority of sires of

cows; $S_{DB} = i_{DB} \cdot r_{gIDB} \cdot \sigma_a$ – genetic superiority of dams of bulls; $S_{DC} = i_{DC} \cdot r_{gIDC} \cdot \sigma_a$ – genetic superiority of dams of cows; $i_{SB}, i_{SC}, i_{DB}, i_{DC}$ – corresponding values of selection intensity; $r_{gISB}, r_{gISC}, r_{gIDB}, r_{gIDC}$ – corresponding values of selection accuracy; σ_a – additive genetic standard deviation; $L_{SB}, L_{SC}, L_{DB}, L_{DC}$ – corresponding values of generation interval.

Table 1. Descriptive statistics (Mean±SD) of milk production traits of daughters of sires used in the study

Breed	n	Milk yield, kg	Fat percentage, %	Fat yield, kg	Protein percentage, %	Protein yield, kg
Holstein	446	10,104±3,331	3.82±0.17	386.0±129.6	3.13±0.08	316.3±77.6
Jersey	29	9,810±674	4.79±0.16	469.9±31.6	3.63±0.07	356.1±22.1

Table 1, Continued

Breed	n	Milk yield, kg	Fat percentage, %	Fat yield, kg	Protein percentage, %	Protein yield, kg
Montbeliard	11	5,699±1,608	3.90±0.21	222.3±74.2	3.58±0.16	204.0±37.8
Simmental	37	5,663±1,605	3.84±0.17	217.5±62.2	3.27±0.17	185.2±37.7
Ukrainian Black-and-White dairy breed	55	5,246±1,675	3.75±0.13	196.7±74.2	3.11±0.09	163.2±71.4
Ukrainian Red dairy breed	23	5,410±1,674	3.78±0.11	204.5±65.5	3.18±0.12	172.0±39.1
Ukrainian Red-and-White dairy breed	39	4,831±1,389	3.73±0.12	180.2±51.1	3.08±0.11	148.8±45.7

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan *et al.*, 2020)

Statistical analysis was carried out using program IBM® SPSS 17.0 that offers advanced statistical analysis and is ease of use, flexible and scalable.

Analysis of variance was conducted using linear model:

$$y = \mu + a + e, \quad (3)$$

where y – estimated breeding value of a sire, a – effect of method of breeding value evaluation, e – error.

Genetic correlations between milk production traits (milk yield, fat percentage, fat yield, protein percentage and protein yield) were computed as Pearson correlations between corresponding estimates of breeding values of sires.

All procedures were carried out in accordance with the ethical considerations regarding the involvement of animals according to the recommendations of ARRIVE (n.d.). The authors of this study assure compliance with all ethical standards in research involving animals.

RESULTS AND DISCUSSION

Based on the data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan *et al.*, 2020), traditional (pedigree BLUP) and genomic (GBLUP) estimates of breeding values of sires for milk production traits were compared (Table 2). A considerable advantage of sires with genomic estimates of breeding values was observed.

Table 2. Estimated breeding values sires with traditional and genomic evaluations for milk production traits

Trait	Traditional evaluation (pedigree BLUP), 462 sires	Genomic evaluation (GBLUP), 475 sires
	Mean±s.e.	Mean±s.e.
Milk yield, kg	+783.37±25.71	+1,220.75±25.36
Fat percentage, %	+0.089±0.010	+0.197±0.010
Fat yield, kg	+39.87±1.10	+69.05±1.09
Protein percentage, %	+0.056±0.005	+0.120±0.05
Protein yield, kg	+31.01±0.81	+53.25±0.80

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan *et al.*, 2020)

Table 3 contains results of analysis of variance of influence of method of breeding value evaluation on estimated breeding values of sires for milk production traits.

For all milk production traits, the influence of method of breeding value evaluation on estimated

breeding values of sires was significant. Thus, the genomically evaluated sires are superior to the sires with the traditional estimates.

Using estimates of breeding values of sires genetic correlations between milk production traits were calculated (Table 4).

Table 3. Analysis of variance of influence of method of breeding value evaluation (traditional versus genomic) on estimated breeding values of sires for milk production traits

Source of variation	Trait	Sum of squares	df	Mean square	F	p
Method of breeding value evaluation	Milk yield	4.480E7	1	4.480E7	146.723	0.000
	Fat percentage	2.755	1	2.755	58.811	0.000

Table 3, Continued

Source of variation	Trait	Sum of squares	df	Mean square	F	p
Method of breeding value evaluation	Fat yield	199,481.990	1	199,481.990	354.736	0.000
	Protein percentage	0.958	1	0.958	93.832	0.000
	Protein yield	115,882.651	1	115,882.65	382.178	0.000
Error	Milk yield	2.855E8	935	305,356.432		
	Fat percentage	43.795	935	0.047		
	Fat yield	525,786.785	935	562.339		
	Protein percentage	9.547	935	0.010		
	Protein yield	283,507.123	935	303.216		
Total	Milk yield	1.277E9	937			
	Fat percentage	65.945	937			
	Fat yield	3,525,259.000	937			
	Protein percentage	17.838	937			
	Protein yield	2,074,931.000	937			

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan et al., 2020)

Table 4. Genetic correlations (r_g) between milk production traits

Traits	n	r_g
Milk yield – fat percentage	1,195	-0.200**
Milk yield – protein percentage	972	-0.195**
Fat percentage – protein percentage	972	+0.705**
Fat yield – protein yield	1,067	+0.791**
Protein percentage – fat yield	969	+0.398**
Fat percentage – fat yield	1,193	+0.580**
Milk yield – fat yield	1,243	+0.658**
Milk yield – protein yield	1,070	+0.836**
Fat percentage – protein yield	1,031	+0.126**
Protein percentage – protein yield	969	+0.352**

Note: ** – $p < 0.01$

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan et al., 2020)

There is a negative genetic relationship between milk yield and fat and protein contents in milk (-0.200 between milk yield and fat percentage and -0.195 between milk yield and protein percentage), which confirms the risk of reduction of the last two traits as a result of selection on milk yield. In all other cases the relationships were positive. Highest positive genetic

correlations were between milk yield and fat yield (+0.658) and between milk yield and protein yield (+0.836). All genetic correlation coefficients were significant ($p < 0.01$).

Based on the catalog data (Polupan et al., 2020) the values of energy corrected milk (ECM) of daughters and dams of sires according to breeds were calculated (Table 5).

Table 5. Genetic Energy corrected milk (ECM) of dams and daughters of sires according to breed

Breed	Dams	Daughters
Ukrainian Red-and-White dairy breed	6,279.3	3,789.9
Ukrainian Red dairy breed	6,719.5	4,200.7

Table 4, Continued

Breed	Dams	Daughters
Ukrainian Black-and-White dairy breed	5,848.1	4,227.6
Simmental	6,871.8	4,439.3
Montbeliard	7,384.0	4,651.9
Holstein	9,132.0	7,509.6
Jersey	8,041.0	8,531.9

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan *et al.*, 2020)

This trait makes it possible to comprehensively assess the level of milk production, taking into account fat and protein contents. The highest values of ECM have dams of Holstein and Jersey sires (9,132.0 kg and 8,041 kg, respectively), the lowest – sires of the Ukrainian Red-and-White dairy breed (5,848.1 kg). Other breeds occupy an intermediate position in terms of the value of this trait. Regarding the high values of ECM for the daughters of sires, the leading place is occupied by the Jersey breed (8,531.9 kg), and the second – Holstein breed (7,509.6 kg). Daughters of sires of Ukrainian

Red-and-White dairy breed, Ukrainian Red dairy breed and Ukrainian Black-and-White dairy breeds have values of ECM is in the range from 3,789.9 to 4,651.9 kg, which indicates the possibility of improvement of this trait by means of selection. Given the fact that up to 80% of frozen sperm of sires is imported to Ukraine (Polupan *et al.*, 2020) ECM values of the daughters of sires depending on their country of origin were analyzed (Fig. 2). Daughters of sires from the USA, Canada and the Netherlands, where genomic selection has been intensively used recently, have the highest values of ECM.

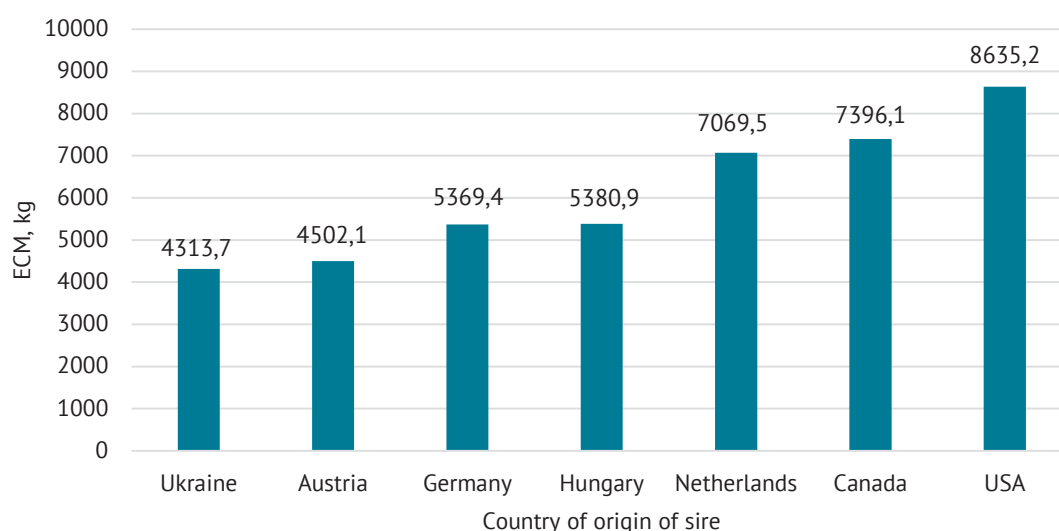


Figure 2. Energy corrected milk (ECM) of daughters of sires according to country of origin

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan *et al.*, 2020)

In order to determine the potential effectiveness of genomic selection in dairy cattle breeding in Ukraine the average annual responses to selection (R) in milk yield in the population of Ukrainian Black-and-White dairy cows using traditional selection and genomic selection were compared (Table 6).

The calculations showed that by reducing the generation intervals on such pathways of genetic improvement as “sires of bulls”, “sires of cows” and “dams of bulls”, it is possible to increase the level of genetic progress in milk yield from 100.1 kg up to 180.0 kg, i.e., by 80%.

Recently genomic selection became conventional method of dairy cattle breeding in many countries, replacing traditional breeding programs based on expensive and time-consuming progeny testing (VanRaden, 2020). Genomic selection allows to obtain estimates of breeding values of animals at early age with relatively high accuracy. Urgent prerequisite of implementation of genomic selection is forming reference population (animals with known phenotypes and genotypes) to obtain prediction equation which is used to compute genomic breeding values of candidates of selection. Size of reference population to a great extent influences

the accuracy of genomic prediction (van den Berg *et al.*, 2019). As a result, genomic selection can be easily implemented in large dairy breeds (like Holstein).

According to A.-C. Doublet *et al.* (2019) in France genomic selection induced an increase in mean annual genetic gains of 50, 71 and 33% for Montbéliarde, Normande and Holstein bulls, respectively; in the same time the generation intervals were reduced by a factor of 1.7, 1.9 and 2, respectively. In Australia the rates of genetic gain for the national economic index (Balanced Performance Index) has increased by ~160% in Holstein females and ~100% in Jersey females (Scott *et al.*, 2021).

F. Lembeye *et al.* (2022) estimated genetic progress from selection on the VEL (Valor Económico Lechero) selection index developed for Chilean dairy cattle

based on selection schemes using progeny testing (PT) and genomic selection (GS). Authors concluded that compared to PT, a more profitable alternative might be the implementation of a GS-scheme, that would result in a faster genetic gain in the aggregate breeding value or merit for all the traits included in the selection objective (0.323-0.371 vs. 0.194 σ_g /year).

Use of genomic selection in small local breeds is difficult because a limited number of animals can be included to reference population. Nevertheless, in several studies it was shown that under certain conditions (for example, use of combined reference populations from closely related breeds) genomic selection still may be implemented in such breeds (Marjanovic *et al.*, 2021).

Table 6. Comparison of annual genetic response of milk yield (R) in Ukrainian Black-and-White dairy breed depending on method of selection

Pathway of selection	Proportion of selected animals, %	Selection intensity, i	Accuracy of selection, r _{gl}	Genetic superiority, (S=i·r _{gl} ·σ _a)	Generation interval (L), years
Traditional selection (σa = 562.5 kg)					
Sires of bulls	3	2.27	0.90	1,149	6
Sires of cows	15	1.55	0.70	610	7
Dams of bulls	1	2.67	0.40	601	5
Dams of cows	85	0.27	0.40	61	6
Sum				2,421	24
R		2,421/24 = 100.1kg			
Genomic selection (σa = 542.8 kg)					
Sires of bulls	3	2.27	0.75	924	3
Sires of cows	15	1.55	0.75	631	3.5
Dams of bulls	1	2.67	0.75	1087	2.5
Dams of cows	85	0.27	0.40	59	6
Sum				2,701	15
R		2,701/15 = 180.0 kg			

Source: data of the catalog of dairy and dual-purpose sires used for reproduction of cattle in 2020 (Polupan *et al.*, 2020)

Until now no research on possible effectiveness of use of genomic selection in breeding of Ukrainian dairy cattle was done. It should be noted that genetic progress in the Ukrainian dairy breeds is very small. The main reasons are small numbers of cows, lack of comprehensive and regular recording and out-of-date methods of genetic evaluation. One of the advantages of genomic selection is possibility to apply recording only to reference population and so reduce costs of phenotyping (Obšteter *et al.*, 2021). So, investigating possible implementation of genomic selection in dairy cattle breeding in Ukraine seems to be reasonable.

Results of the study indicate that genomically evaluated sires used in Ukraine have significantly higher breeding values for milk production traits than sires with traditional evaluations. Reason is faster genetic progress resulting from shorter generation intervals with genomic selection (Hagan & Cue, 2019).

Analysis of energy corrected milk showed that both dams and daughters of sires of Ukrainian dairy breeds generally have lower total milk production than dams and daughters of imported sires.

Comparison of expected annual genetic gain in milk yield in Ukrainian Black-and-White dairy breed for

traditional and genomic selection suggests that use of genomic selection can considerably accelerate genetic progress and this result is similar to results of other authors (Lee *et al.*, 2020; Scott *et al.*, 2021; Guinan *et al.*, 2023).

It should be noticed that can genomic selection can be implement in any dairy breed without increasing the level of investment (Obšteter *et al.*, 2021). Reliability of genomic estimated breeding values in small dairy populations can be considerably increased by using multi-trait single step genomic BLUP (Zhang *et al.*, 2022).

Further investigations are needed to study possible effects of implementation of genomic selection on economically important traits (milk quality, longevity, fertility etc.) of dairy cattle as well as genetic diversity in local dairy breeds in the Ukraine.

CONCLUSIONS

Analysis of variance showed significant influence of method of breeding value evaluation on estimated breeding values of sires. Genomically evaluated sires had higher estimated breeding values for milk production traits than sires with the traditional estimates.

There is a negative genetic correlation between milk yield and fat and protein contents in milk (-0.200 between milk yield and fat percentage and -0.195 between milk yield and protein percentage). Highest positive genetic correlations were between milk yield and fat yield and between milk yield and protein yield.

The highest values of energy corrected milk had dams of Holstein and Jersey sires, the lowest – sires of the Ukrainian Red-and-White dairy breed, while other breeds occupied an intermediate position in terms of the value of this trait. The high values of energy corrected milk had daughters of Jersey and Holstein sires. Daughters of sires of Ukrainian Red-and-White dairy breed, Ukrainian Red dairy breed and Ukrainian Black-and-White dairy breeds have values of energy corrected milk is in the range from 3,789.9 to 4,651.9 kg. With regard to country of origin daughters of sires from the USA, Canada and the Netherlands had the highest values of energy corrected milk.

The use of genomic selection in breeding of dairy cattle in Ukraine can substantially increase genetic progress by means of shortening generation intervals. Reducing the generation intervals on such pathways of genetic improvement as “sires of bulls”, “sires of cows” and “dams of bulls”, it is possible to increase the level of genetic progress in milk yield from 100.1 kg up to 180.0 kg, i.e., by 80%.

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CONFLICT OF INTERESTS

None.

REFERENCES

- [1] Ahmadi, N., & Bartholomé, J. (Eds.). (2022). *Genomic prediction of complex traits. Methods and protocols*. Totowa: Humana Press.
- [2] ARRIVE guidelines. (n.d.). Retrieved from <https://arriveguidelines.org/>.
- [3] Bermann, M., Cesarani, A., Misztal, I., & Lourenco, D. (2022). Past, present, and future developments in single-step genomic models. *Italian Journal of Animal Science*, 21(1), 673-685. doi: 10.1080/1828051X.2022.2053366.
- [4] Doublet, A.-C., Croiseau, P., Fritz, S., Michenet, A., Hozé, C., DanchinBurge, C., Laloë, D., & Restoux, G. (2019). The impact of genomic selection on genetic diversity and genetic gain in three French dairy cattle breeds. *Genetics Selection Evolution*, 51, 52. doi: 10.1186/s12711-019-0495-1.
- [5] Guinan, F.L., Wiggans, G.R., Norman, H.D., Dürr, J.W., Cole, J.B., Van Tassell, C.P., Misztal, I., & Lourenco, D. (2023). Changes in genetic trends in US dairy cattle since the implementation of genomic selection. *Journal of Dairy Science*, 106(2), 1110-1129. doi: 10.3168/jds.2022-22205.
- [6] Gutierrez-Reinoso, M.A., Aponte, P.M., & Garcia-Herreros, M. (2021). Genomic analysis, progress and future perspectives in dairy cattle selection: A review. *Animals*, 11(3), 599. doi: 10.3390/ani11030599.
- [7] Hagan, B.A., & Cue, R. (2019). Generation intervals in Canadian dairy cattle herds. *Canadian Journal of Animal Science*, 100(1), 175-183. doi: 10.1139/cjas-2019-0053.
- [8] Hossein-Zadeh, N.G. (2017). Application of growth models to describe the lactation curves for test-day milk production in Holstein cows. *Journal of Applied Animal Research*, 45(1), 145-151. doi: 10.1080/09712119.2015.1124336.
- [9] Lee, Y.-M., Dang, C.-G., Alam, M.Z., Kim, Y.-S., Cho, K.-H., Park, K.-D., & Kim, J.-J. (2020). The effectiveness of genomic selection for milk production traits of Holstein dairy cattle. *Asian-Australasian Journal of Animal Science*, 33(3), 382-389. doi: 10.5713/ajas.19.0546.
- [10] Lembeye, F., López-Villalobos, N., & Uribe, H. (2022). Potential response from selection schemes based on progeny testing and genomic selection for the Chilean dairy cattle under pastoral systems: A deterministic simulation. *Journal of Dairy Research*, 89(3), 231-235. doi: 10.1017/S0022029922000504.

- [11] Lourenco, D., Legarra, A., Tsuruta, S., Masuda, Y., Aguilar, I., & Misztal, I. (2020). Single-step genomic evaluations from theory to practice: Using SNP chips and sequence data in BLUPF90. *Genes*, 11(7), 790. doi: [10.3390/genes11070790](https://doi.org/10.3390/genes11070790).
- [12] Lozada-Soto, E.A., Tiezzi, F., Jiang, J., Cole, J.B., VanRaden, P.M., & Maltecca, C. (2022). Genomic characterization of autozygosity and recent inbreeding trends in all major breeds of US dairy cattle. *Journal of Dairy Science*, 105(11), 8956-8971. doi: [10.3168/jds.2022-22116](https://doi.org/10.3168/jds.2022-22116).
- [13] Mekanjuola, B.O., Miglior, F., & Abdalla, E.A. (2020). Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle populations. *Journal of Dairy Science*, 103(6), 5183-5199. doi: [10.3168/jds.2019-18013](https://doi.org/10.3168/jds.2019-18013).
- [14] Mäntysaari, E.A., Koivula, M., & Strandén, I. (2020). Symposium review: Single-step genomic evaluations in dairy cattle. *Journal of Dairy Science*, 103(6), 5314-5326. doi: [10.3168/jds.2019-17754](https://doi.org/10.3168/jds.2019-17754).
- [15] Marjanovic, J., Hulsege, B., & Calus, M.P.L. (2021). Relatedness between numerically small Dutch Red dairy cattle populations and possibilities for multibreed genomic prediction. *Journal of Dairy Science*, 104(4), 4498-4506. doi: [10.3168/jds.2020-19573](https://doi.org/10.3168/jds.2020-19573).
- [16] Misztal, I., Lourenco, D., & Legarra, A. (2020). Current status of genomic evaluation. *Journal of Dairy Science*, 98(4), 1-14. doi: [10.1093/jas/skaa101](https://doi.org/10.1093/jas/skaa101).
- [17] Norwegian Red breeding program. (2021). Retrieved from <https://www.norwegianred.com/about-norwegian-red/norwegian-red-breeding-program/>.
- [18] Obšteter, J., Jenko, J., & Gorjanc, G. (2021). Genomic selection for any dairy breeding program via optimized investment in phenotyping and genotyping. *Frontiers in Genetics*, 12, 637017. doi: [10.3389/fgene.2021.637017](https://doi.org/10.3389/fgene.2021.637017).
- [19] Polupan, Y.P., Gladiy, M.V., Basovskiy, D.M., Germanchuk, S.G., Biriukova, O.D., Pryima, S.V., Podoba, B.E., & Romanova, O.V. (2020). *Catalogue of dairy and dual-purpose service sires of Ukraine*. Kyiv: NAASU.
- [20] Ruban, S. & Danshin, V. (2019). *Modern methods of animal breeding*. Kyiv: NUELS.
- [21] Scott, B.A., Haile-Mariam, M., Cocks, B.G., & Pryce, J.E. (2021). How genomic selection has increased rates of genetic gain and inbreeding in the Australian national herd, genomic information nucleus, and bulls. *Journal of Dairy Science*, 104(11), 11832-11849. doi: [10.3168/jds.2021-20326](https://doi.org/10.3168/jds.2021-20326).
- [22] Simm, G., Pollott, G., Mrode, R., Houston, R., & Marshall, K. (2021). *Genetic improvement of farmed animals*. Wallingford: CAB. doi: [10.1079/9781789241723.0000](https://doi.org/10.1079/9781789241723.0000).
- [23] van den Berg, I., Meuwissen, T.H.E., MacLeod, I.M., & Goddard, M.E. (2019). Predicting the effect of reference population on the accuracy of within, across, and multibreed genomic prediction. *Journal of Dairy Science*, 102(4), 3155-3174. doi: [10.3168/jds.2018-15231](https://doi.org/10.3168/jds.2018-15231).
- [24] VanRaden, P.M. (2020). Symposium review: How to implement genomic selection. *Journal of Dairy Science*, 103(6), 5291-5301. doi: [10.3168/jds.2019-17684](https://doi.org/10.3168/jds.2019-17684).
- [25] Weller, J.I. (2019). Genetic evaluation: Use of genomic data in large-scale genetic evaluations in dairy cattle breeding. In J. van der Werf, & J. Pryce (Eds.), *Advances in breeding of dairy cattle* (pp. 441-474). Cambridge: Burleigh Dodds Science Publishing Limited.
- [26] Wiggans, G.R., & Carrillo, J.A. (2022). Genomic selection in United States dairy cattle. *Frontiers in Genetics*, 13, 994466. doi: [10.3389/fgene.2022.994466](https://doi.org/10.3389/fgene.2022.994466).
- [27] Zhang, M., Luo, H., Xu, L., Shi, Y., Zhou, J., Wang, D., Zhang, X., Huang, X., & Wang, Y. (2022). Genomic selection for milk production traits in Xinjiang brown cattle. *Animals*, 12(2), 136. doi: [10.3390/ani12020136](https://doi.org/10.3390/ani12020136).

Перспективи застосування геномної селекції для генетичного покращення молочної худоби в Україні

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Анотація. Важливою проблемою в сучасному молочному скотарстві є досягнення високого рівня генетичного прогресу по економічно важливим ознакам шляхом впровадження ефективних селекційних програм. Задля цього нині в багатьох країнах світу використовують геномну селекцію. Метою дослідження було вивчення можливостей застосування геномної селекції в розведенні молочної худоби в Україні. На основі аналізу «Каталогу плідників молочних і комбінованих порід для відтворення корів у 2020 р.» (сперму цих плідників використовували в Україні) порівнювали два методи оцінки племінної цінності: 1) традиційний метод, заснований на родоводі і продуктивності потомства; 2) геномний метод, заснований на ефектах SNP-маркерів. Доведено значну перевагу плідників з геномними оцінками. Ці плідники перевершують плідників з традиційною оцінкою за надоєм молока в 1,6 рази, за відсотком жиру в 2,2 рази, за виходом жиру в 1,7 рази, за відсотком білка в 2,1 рази і за виходом білка в 1,7 рази. На основі оцінок племінної цінності плідників були розраховано генетичні кореляції між основними селекційними ознаками. Виявлено негативний генетичний зв'язок між надоєм та вмістом жиру та білка. Були розраховані значення скорегованого на енергію надою (ECM) дочок і матерів плідників для різних порід і країн походження. Показано, що найвищі показники скорегованого на енергію надою мали матері плідників голштинської та джерсейської порід (9132,0 кг та 8041 кг, відповідно), а найнижчі – матері плідників української чорно-рябої молочної породи (5848,1 кг). Відповідно до країни походження дочки бугаїв з США, Канади та Нідерландів мали найвищі значення скорегованого на енергію надою. Порівнювали значення відповіді на відбір за традиційною селекційною програмою та геномною селекцією. Доведено, що за рахунок скорочення генераційних інтервалів на шляхах генетичного покращення «батьки бугаїв», «батьки корів» і «матері бугаїв» за допомогою геномної селекції можна підвищити швидкість генетичного прогресу за надоєм від 100,1 кг. до 180,0 кг, тобто на 80 %

Ключові слова: молочна порода; скорегований на енергію надій; генетичне покращення; генетична кореляція; відповідь на відбір; геномна оцінка