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# Modern approaches and prospects for the genetic evaluation of dairy cattle in breeding programmes

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**Abstract.** The evaluation of breeding value for economically important traits is a key tool in modern systems of genetic improvement in dairy cattle. This analytical study aimed to describe the current algorithm for genetic evaluation in dairy cattle and to identify promising directions for potential improvement in the near future. Genetic evaluation methods have undergone significant development, evolving from mass daughter-dam comparisons, direct and improved herdmate comparisons, and modified contemporary comparison, to more complex approaches such as the Animal Model and genomic evaluation using mathematical techniques such as BLUP and REML. The implementation of modern genomic selection programmes required a substantial restructuring of the entire organisational system of breeding. The presence of reference populations, with ongoing monitoring of genetic and phenotypic traits, was a fundamental requirement. It was noted that a general trend in modern dairy farming was the increasing number of traits considered in selection to account for both observable traits (such as milk yield and composition) and "hidden" traits (such as health status, reproductive

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efficiency, productive longevity, and feed conversion efficiency), all of which significantly influence production economics. A comparative analysis of the monitored livestock population and productivity indicators in Ukraine and ICAR member countries was carried out, revealing key limitations within the national breeding system. It was established that genomic evaluation enables the shortening of generation intervals and the doubling of the rate of genetic progress in milk yield. The practical value of the study lies in providing scientifically grounded guidelines for developing an effective system of genetic evaluation and breeding resource management in Ukraine

**Keywords:** BLUP Animal Model; genomic selection; holo-omics; genome editing; biotechnology

## Introduction

An important challenge in modern dairy farming is achieving a high level of genetic progress in economically significant traits through the implementation of effective breeding programmes. The genetic improvement of livestock, including dairy cattle, traditionally comprises the following stages: (1) defining the breeding objective; (2) constructing a selection index aimed at achieving the breeding objective with maximum profitability; (3) organising regular monitoring of traits included in the selection index; (4) conducting genetic evaluation of animals for selected traits; (5) developing and implementing a breeding programme based on specific selection criteria; and (6) selecting potential parents to produce the next generation. The genetic evaluation of animals involves the use of mathematical methods designed to minimise estimation error (Simm *et al.*, 2021). In the early 21st century, it was demonstrated that the breeding value of animals could be predicted at early stages of ontogeny by using a large number of genetic markers distributed across the entire genome. This led to the development of the approach now known as genomic selection (Misztal *et al.*, 2020).

In the monograph by R.A. Mrode *et al.* (2023), methods for using linear models to evaluate the genetic merit of animals are described. The publication outlines approaches to genetic evaluation using various sources of information, genetic covariance among relatives, best linear unbiased prediction of breeding value, models incorporating maternal effects, animal models, models including social interactions between animals, methods for genomic prediction of genetic merit and forecasting selection response, as well as genetic and genomic models involving multiple breeds and crossbreeding analysis. It also presents methods for estimating genetic parameters.

The introduction of DNA microchip technology has led to the widespread use of genomic selection in livestock species, particularly in dairy cattle. Breeding values with higher reliability can now be estimated at early stages of life by combining DNA genotypes at tens of thousands of loci with existing databases on identity, pedigree, and phenotype for millions of animals. Genomic selection was initially applied to males to predict the performance of their offspring, but it is now widely used in females and even embryos to forecast their own future performance (VanRaden, 2020). Y.C.J. Wientjes *et al.* (2022) demonstrated that genomic selection outperforms pedigree-based selection in terms of long-term genetic progress, although it results in a comparable reduction in genetic variation. The genetic architecture of traits changed considerably over generations, particularly under selection pressure and in the presence of non-additive effects. In conclusion, non-additive effects had a significant influence on selection accuracy and the long-term response to selection, especially when selection was highly accurate. B.A. Scott *et al.* (2021) found that the implementation of genomic selection in Australian dairy cattle led to a 160% increase in genetic progress for national economic index values in the Holstein breed and a 100% increase in the Jersey breed. According to K. Weigel *et al.* (2024), genomic testing of young bulls and heifers provides greater accuracy in selection decisions for traditional fertility traits such as daughter pregnancy rate, while also enabling improvement in emerging traits such as pregnancy loss.

The monograph by N. Ahmadi & J. Bartholomé (2022) focused on genomic prediction of quantitative traits. It covers the non-genetic foundations of quantitative traits – from quantitative trait loci to genomic prediction – along with methods for genomic prediction, underlying principles, an overview of factors affecting the reliability of genomic prediction, and the algebra of its accuracy. The authors provide a comprehensive review of genomic prediction methods and the associated assumptions concerning marker effect variance and the genetic architecture of quantitative traits. The text also explores approaches that account for non-additive genetic effects, the inclusion of trait correlations in genomic prediction, and the prediction of quantitative traits in animals with a long history of selection, particularly in dairy cattle. Furthermore, the monograph assesses the economic efficiency of genomic selection in comparison with traditional breeding approaches. S. Ruban & V. Danshin (2023) conducted a comparative analysis of selection response under traditional breeding programmes versus genomic selection. Their findings demonstrated that by reducing generation intervals in genetic improvement pathways – such as "sire of bulls," "sire of cows," and "dam of bulls" – genomic selection can accelerate genetic progress in milk yield by between 100.1 kg and 180.0 kg, representing an increase of up to 80%.

This study aimed to analyse the potential of modern methods for the genetic evaluation of dairy cattle and to outline prospects for their further development under conditions specific to Ukraine.

## Materials and Methods

The research methodology was based on the principles of comparative analysis and systematic synthesis of empirical statistical data on the genetic evaluation of cattle in Ukraine and ICAR (International Committee for Animal Recording) member countries. The primary data source was the 2023 State Register of Breeding Entities in Animal Husbandry (Zhukosky *et al.*, 2024), which included information on the number, breed composition, and productivity of the monitored livestock of dairy and dual-purpose cattle.

Additionally, data from the ICAR Annual Report (2023a) for the years 2022-2023 were analysed. These materials reflect the status of performance recording and breeding systems in over twenty European countries. Aggregated indicators from the official ICAR statistical section (2023b) were also used, including data on the number of monitored livestock, average lactation productivity, frequency of genomic evaluation use, and breed distribution by country. The ICAR reports made it possible to identify key trends in the development of breeding record-keeping in leading dairy-producing countries such as the USA, Germany, France, Canada, and Italy. To gain a deeper understanding of the context, a systematic review of scientific publications (Misztal *et al.*, 2020; VanRaden *et al.*, 2021) was conducted, with a focus on genomic selection practices, the use of Single Nucleotide Polymorphism (SNP) markers, Best Linear Unbiased Prediction (BLUP) models, and the application of the Net Merit Dollar Index (NM$).

The comparative analysis included indicators such as milk yield, fat and protein content, the proportion of monitored livestock, the specific influence of individual breeds, and the degree of integration of genomic methods into breeding value assessment systems. Promising directions for the development of Ukraine's breeding system were identified through the extrapolation of effective international practices, particularly those from the USA, which was the first to introduce a genomic model for evaluating Predicted Transmitting Ability (PTA). Data processing methods involved elements of descriptive statistics, typological grouping, and interpretation of correlation relationships between traits (milk yield, fat, protein, fertility, longevity), based on findings from previous studies (V.O.Danshin *et al*., 2017). The study was analytical in nature and did not involve original experimental material. It aimed to synthesise existing practices and formulate scientifically grounded recommendations for improving the genetic evaluation of dairy cattle in Ukraine.

## Results and Discussion

As of the end of 2024, the total number of dairy cows in Ukraine was 1.156 million head, with an annual milk production of 7.2 million tonnes, indicating a relatively intensive development of the sector despite the ongoing martial law. A key component of this industry remains the focus on producing economically viable animals through methods of genetic evaluation and the implementation of selection programmes for dairy cattle. Table 1 presents the breed composition and productivity indicators of the monitored (controlled) livestock, which accounted for approximately 9.7% of the total dairy cow population – significantly lower compared to the corresponding figures in most European countries (Table 2).

Market conditions in Ukraine's dairy sector impose strict requirements on cattle breeds, with the Holstein breed increasingly coming to dominate in recent years. According to analytical data, up to 68% of the national breeding livestock can be classified as Holstein. It is worth noting that the two most numerous Ukrainian dairy breeds – the Ukrainian Red-and-White Dairy and the Ukrainian Black-and-White Dairy – were developed in the late 20th century through combination crossbreeding schemes involving local breeds and partial use of Holsteins.

***Table 1.*** *Breed composition and productivity of the breeding (monitored) livestock of dairy and dual-purpose cattle in Ukraine*

| **Breed** | **Livestock** | | | **Milk yield, kg** | **Percentage, %** | |
|---|---|---|---|---|---|---|
| | **total population, head** | **including cows, head** | **% of total cow livestock** | | **fat** | **protein** |
| Ayrshire | 969 | 420 | 0.37 | 7,402 | 4.00 | 3.03 |
| Holstein | 175,412 | 51,429 | 45.76 | 9,810 | 3.84 | 3.32 |
| Jersey | 2,497 | 1,064 | 0.95 | 6,004 | 5.98 | 4.15 |
| Lebedyn | 766 | 329 | 0.29 | 6,035 | 4.14 | 3.31 |
| Simmental | 9,200 | 3,563 | 3.17 | 7,051 | 4.06 | 3.32 |
| Ukrainian Brown Dairy | 1,299 | 466 | 0.41 | 6,995 | 4.13 | 3.53 |
| Ukrainian Red Dairy | 3,733 | 1,213 | 1.08 | 7,310 | 3.83 | 3.52 |
| Ukrainian Red-and-White Dairy | 32,361 | 11,439 | 10.18 | 7,689 | 3.82 | 3.45 |
| Ukrainian Black-and-White Dairy | 118,599 | 41,094 | 36.56 | 8,218 | 3.74 | 3.22 |
| Red Steppe | 737 | 256 | 0.23 | 6,318 | 4.19 | 3.20 |
| Brown Swiss | 3,809 | 1,115 | 0.99 | 8,718 | 3.95 | 3.40 |
| **Total** | **349,382** | **112,388*** | **100** | **7,623** | **4.19** | **3.42** |

**Source:** developed by the authors based on O.M. Zhukosky *et al.* (2024)

These breeds have been genetically improved mainly through the use of Holstein sires, with semen imported from the USA. The milk production market in European countries is highly dynamic and varies in terms of selection programme focus and the number of animals in the monitored (breeding) livestock (Table 2). This variation also contributes to a strong market for breeding resources (heifers, young bulls).

***Table 2.*** *Number and productivity of dairy cows in European countries, 2022-2023*

| Country | Total number of dairy cows | Monitored livestock | Proportion of monitored livestock, % | Milk yield, kg | Milk fat, % | Milk protein, % |
|---|---|---|---|---|---|---|
| Austria | 546,035 | 437,712 | 80.2 | 7,918 | 4.16 | 3.40 |
| Belgium | 351,583 | 202,275 | 56.8 | 9,606 | 4.27 | 3.51 |
| Croatia | 96,477 | 68,384 | 70.1 | 4,975 | 4.07 | 3.49 |
| Czech Republic | 352,557 | 339,272 | 96.1 | 9,266 | 3.89 | 3.42 |
| Denmark | 557,831 | 498,644 | 91.1 | 10,571 | 4.33 | 3.62 |
| Finland | 242,017 | 189,148 | 78.2 | 9,332 | 4.46 | 3.56 |
| France | 3,429,000 | 1,968,566 | 56.2 | 7,516 | – | – |
| Germany | 3,712,815 | 3,251,621 | 87.6 | 8,547 | 4.12 | 3.46 |
| Hungary | 173,618 | 177,430 | 100.0 | – | 3.96 | 3.48 |
| Ireland | 1,643,470 | 25,309 | 100.0 | 5,301 | 4.30 | 3.52 |
| Italy | 2,009,834 | 1,407,368 | 70.0 | – | – | – |
| Estonia | 83,700 | 81,020 | 96.8 | 10,655 | 3.90 | 3.40 |
| Latvia | 127,803 | 106,175 | 83.0 | 7,748 | – | – |
| Netherlands | 1,576,925 | 1,455,909 | 92.3 | 9,346 | 4.45 | 3.61 |
| Norway | 203,327 | 178,897 | 97.7 | 7,955 | 4.30 | 3.55 |
| Poland | 2,203,900 | 807,719 | 38.0 | 7,596 | – | – |
| Portugal | 218,840 | 92,149 | 42.1 | 8,643 |  |  |
| Romania | 133,438 | 133,438 | 100.0 | 7,149 | 3.83 | 3.45 |
| Serbia | 92,000 | 52,309 | 56.9 | 4,576 |  |  |
| Slovak Republic | 114,410 | 101,392 | 89.9 | 8,362 | 3.79 | 3.37 |
| Sweden | 289,182 | 179,681 | 74.2 | 9,747 | 4.26 | 3.53 |
| Switzerland | 542,927 | 416,068 | 76.6 | 6,989 | 4.14 | 3.36 |
| United Kingdom | 265,801 | 267,322 | 100.0 | 8,699 | 4.34 | 3.38 |
| Ukraine | 115,600 | 112,388 | 9.7 | 7,623 | 4.19 | 3.42 |

**Source:** developed by the authors based on ICAR (2023a; 2023b)

The majority of stakeholders in Ukraine's dairy industry have adopted the North American model of cattle farming. However, under current conditions – including the limited size of the monitored livestock, the need to reduce dependence on expensive imports (semen, embryos, heifers), global risks of epizootic outbreaks, and the specific economic circumstances of Ukraine's agricultural sector – there is a pressing need to develop a domestic system of genetic evaluation. The direction of such efforts, as outlined in various scientific publications, is based on modern methodologies for breeding value assessment (Ruban *et al.*, 2021).

According to H.D. Norman *et al.* (2022), the historical development of genetic evaluation methods for dairy cattle can be divided into the following stages:

1) Daughter–Dam Comparison (DDC). The breeding value of a bull is estimated as the difference between the performance of his daughters and their dams.

2) Herdmate Comparison (HC). The performance of a bull's daughters is compared to that of daughters of other bulls raised under similar environmental conditions (e.g. herd, age, year and season of calving).

3) Improved Herdmate Comparison (IHC). This method includes adjustments to bull evaluations based on the number of herds in which the daughters were assessed, the distribution of daughters across those herds, and the number of lactations per daughter.

4) Modified Contemporary Comparison (MCC). In this method, a bull's evaluation incorporates information about his ancestors as well as the genetic merit of the parents of his contemporaries. This allows for a more accurate adjustment of the bull's breeding value in line with the genetic trend.

5) BLUP Animal Model (AM). A simultaneous evaluation of all animals (both bulls and cows), taking into account environmental effects and all genetic relationships among animals.

6) Genomic Evaluation (GE). Breeding value assessment based on SNP markers, which represent a substitution of one pair of nucleotides in the DNA sequence with another.

In the study by V.O. Danshin *et al.* (2017), genetic correlations between economically important traits were assessed (Table 3).

Despite some breed-specific differences, the genetic correlations between traits generally indicate a significant unfavourable relationship between milk production and reproductive performance in cows. In contrast, productive longevity shows relatively weak correlations with both milk yield and calving interval. These findings highlight the need to include reproductive performance and productive longevity in the selection index used for choosing sire bulls.

***Table 3.*** *Estimates of genetic correlations between traits by breed*

| Trait | Genetic correlation | | | | |
|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| Holstein | | | | | |
| 1. Milk yield | 1 | | | | |
| 2. Milk fat | 0.95 | 1 | | | |
| 3. Milk protein | 0.75 | 0.74 | 1 | | |
| 4. Calving interval | 0.30 | 0.29 | 0.19 | 1 | |
| 5. Productive longevity | 0.01 | 0.05 | 0.06 | −0.01 | 1 |
| Ukrainian Black-and-White Dairy | | | | | |
| | 1 | 2 | 3 | 4 | 5 |
| 1. Milk yield | 1 | | | | |
| 2. Milk fat | 0.97 | 1 | | | |
| 3. Milk protein | 0.81 | 0.80 | 1 | | |
| 4. Calving interval | 0.28 | 0.25 | 0.21 | 1 | |
| 5. Productive longevity | 0.05 | 0.03 | 0.06 | 0.02 | 1 |
| Ukrainian Red-and-White Dairy | | | | | |
| | 1 | 2 | 3 | 4 | 5 |
| 1. Milk yield | 1 | | | | |
| 2. Milk fat | 0.92 | 1 | | | |
| 3. Milk protein | 0.77 | 0.79 | 1 | | |
| 4. Calving interval | 0.31 | 0.24 | 0.18 | 1 | |
| 5. Productive longevity | 0.07 | 0.07 | 0.08 | 0.03 | 1 |
| Ukrainian Red Dairy | | | | | |
| | 1 | 2 | 3 | 4 | 5 |
| 1. Milk yield | 1 | | | | |
| 2. Milk fat | 0.93 | 1 | | | |
| 3. Milk protein | 0.79 | 0.75 | 1 | | |
| 4. Calving interval | 0.29 | 0.27 | 0.23 | 1 | |
| 5. Productive longevity | 0.04 | 0.06 | 0.07 | 0.01 | 1 |

**Source:** V.O. Danshin *et al.* (2017)

Since 2007, countries with developed dairy industries – including Australia, Ireland, New Zealand, France, Germany, the Netherlands, Denmark, Sweden, Finland, the USA, and Canada – have adopted genomic selection based on genomic prediction methods (Simm *et al*., 2021; Xu, 2022). This is based on the method of genomic prediction (Ahmadi & Bartholomé, 2022). The theoretical basis for genomic selection was established in 2001 by T.H.E. Meuwissen *et al*. (2001). The most comprehensive system of genomic selection, as demonstrated in the U.S. dairy industry, is illustrated in Figure 1. This now-classic approach relies on a so-called reference (or training) population, consisting of animals with known phenotypes and genotypes for SNP markers, which is used to develop equations for predicting the genetic merit of each animal.

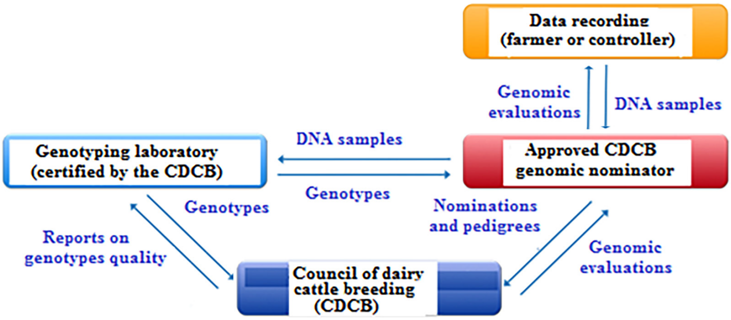
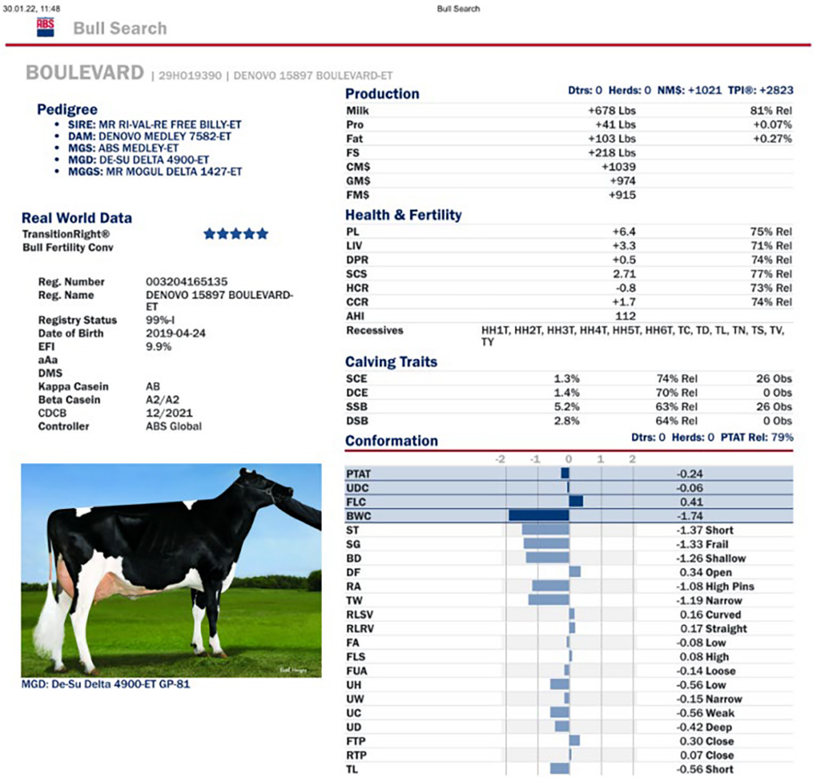


***Figure 1.*** *General scheme of genomic evaluation of dairy cattle in the USA*
**Source:** Council on Dairy Cattle Breeding (n.d.)

The first genomic evaluations of PTA (Predicted Transmitting Ability; PTA equals half the breeding value of an animal) in the USA were published in April 2008, although they gained official status in January 2009. Since then, approximately 700,000 animals have been genotyped each year. Genotyping laboratories accredited by the Council on Dairy Cattle Breeding (CDCB), in cooperation with breed associations and artificial insemination organisations, collect DNA samples and pedigree data, and notify the CDCB of their intent to obtain a genomic evaluation for a specific animal – a process known as nomination. Most animals are genotyped using SNP chips (platforms containing probes for identifying SNPs across the genome), with densities ranging from 9,000 to 30,000 SNP markers. These chips provide information on the sequence of nucleotide pairs in the animal's DNA. High-density microchips are primarily used for research and bull evaluation. Each animal's genotype is verified by comparing it with those of its parents and grandparents (Pal, 2022).

Genotypes obtained from chips of varying densities are included in the evaluation process through imputation, which involves inferring missing SNP markers to expand genomic information while reducing costs. Imputation is primarily used for animals genotyped with low-density chips. In this process, genomic information is "borrowed" from animals in the reference population that have been genotyped using higher-density chips (Klímová *et al*., 2020). For the genomic evaluation of dairy cattle in the USA, 79,294 SNP markers are used. The results of a bull's evaluation are presented in an electronic profile (Fig. 2) available on the ABS Genetics website, which includes the following information:

Since the development of the genomic selection system in the USA, efforts have been made to expand the size of the reference population. In genomic evaluations of Holstein cattle, genotype data are also used from animals in Canada, the United Kingdom, Switzerland, and Germany (Wiggans & Carrillo, 2022).



30.01.22, 11:48 Bull Search

Bull Search

BOULEVARD | 29H019390 | DENOVO 15897 BOULEVARD-ET

**Pedigree**

- SIRE: MR RI-VAL-RE FREE BILLY-ET
- DAM: DENOVO MEDLEY 7582-ET
- MGS: ABS MEDLEY-ET
- MGD: DE-SU DELTA 4900-ET
- MGGS: MR MOGUL DELTA 1427-ET

**Real World Data**

TransitionRight® ★★★★★
Bull Fertility Conv

| | |
|---|---|
| Reg. Number | 003204165135 |
| Reg. Name | DENOVO 15897 BOULEVARD-ET |
| Registry Status | 99%-I |
| Date of Birth | 2019-04-24 |
| EFI | 9.9% |
| aAa | |
| DMS | |
| Kappa Casein | AB |
| Beta Casein | A2/A2 |
| CDCB | 12/2021 |
| Controller | ABS Global |

MGD: De-Su Delta 4900-ET GP-81

**Production** Dtrs: 0 Herds: 0 NM$: +1021 TPI®: +2823

| | | |
|---|---|---|
| Milk | +678 Lbs | 81% Rel |
| Pro | +41 Lbs | +0.07% |
| Fat | +103 Lbs | +0.27% |
| FS | +218 Lbs | |
| CM$ | +1039 | |
| GM$ | +974 | |
| FM$ | +915 | |

**Health & Fertility**

| | | |
|---|---|---|
| PL | +6.4 | 75% Rel |
| LIV | +3.3 | 71% Rel |
| DPR | +0.5 | 74% Rel |
| SCS | 2.71 | 77% Rel |
| HCR | -0.8 | 73% Rel |
| CCR | +1.7 | 74% Rel |
| AHI | 112 | |
| Recessives | HH1T, HH2T, HH3T, HH4T, HH5T, HH6T, TC, TD, TL, TN, TS, TV, TY | |

**Calving Traits**

| | | | |
|---|---|---|---|
| SCE | 1.3% | 74% Rel | 26 Obs |
| DCE | 1.4% | 70% Rel | 0 Obs |
| SSB | 5.2% | 63% Rel | 26 Obs |
| DSB | 2.8% | 64% Rel | 0 Obs |

**Conformation** Dtrs: 0 Herds: 0 PTAT Rel: 79%

| | |
|---|---|
| PTAT | -0.24 |
| UDC | -0.06 |
| FLC | 0.41 |
| BWC | -1.74 |
| ST | -1.37 Short |
| SG | -1.33 Frail |
| BD | -1.26 Shallow |
| DF | 0.34 Open |
| RA | -1.08 High Pins |
| TW | -1.19 Narrow |
| RLSV | 0.16 Curved |
| RLRV | 0.17 Straight |
| FA | -0.08 Low |
| FLS | 0.08 High |
| FUA | -0.14 Loose |
| UH | -0.56 Low |
| UW | -0.15 Narrow |
| UC | -0.56 Weak |
| UD | -0.42 Deep |
| FTP | 0.30 Close |
| RTP | 0.07 Close |
| TL | -0.56 Short |

***Figure 2.** Example of a bull's electronic profile from ABS Genetics*

**Source:** ABS (n.d.)

As of June 2025, the number of genotyped Holstein animals totals approximately 9 million (Council on Dairy Cattle Breeding, n.d.). As a result of the implementation of genomic selection, the age of a sire at the time of a young bull's birth has decreased to two years (Wiggans & Carrillo, 2022). This reduction in generation interval has led to a twofold increase in the rate of genetic progress in the Holstein breed (Guinan *et al*., 2023). A characteristic trend in dairy cattle breeding is the continuous expansion of selection traits, as illustrated by one of the selection programmes in the USA (Table 4).

***Table 4.** Composition of economic selection indices used by the United States Department of Agriculture for dairy cattle evaluation and selection, 1971-2022*

| Trait | Relative economic weight, % | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | PD$ 1971 | MFP$ 1976 | NM$ 1994 | NM$ 2000 | NM$ 2003 | NM$ 2006 | NM$ 2014 | NM$ 2017 | NM$ 2018 | NM$ 2021 | NM$ 2025 |
| Milk yield | 52 | 27 | 6 | 5 | 0 | 0 | −1 | −1 | −1 | 0 | 3.2 |
| Milk fat | 48 | 46 | 25 | 21 | 22 | 23 | 22 | 24 | 27 | 22 | 31.8 |
| Milk protein | | 27 | 43 | 36 | 33 | 23 | 20 | 18 | 17 | 17 | 13.0 |

***Table 4.** Continued*

| Trait | Relative economic weight, % | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | **PD$ 1971** | **MFP$ 1976** | **NM$ 1994** | **NM$ 2000** | **NM$ 2003** | **NM$ 2006** | **NM$ 2014** | **NM$ 2017** | **NM$ 2018** | **NM$ 2021** | **NM$ 2025** |
| Productive longevity | | | 20 | 14 | 11 | 17 | 19 | 13 | 12 | 15 | 13.0 |
| Somatic cell concentration in milk | | | −6 | −9 | −9 | −9 | −7 | −7 | −4 | −3 | −2.6 |
| Body weight | | | | −4 | −3 | −4 | −5 | −6 | −5 | −9 | −11.0 |
| Udder conformation | | | | 7 | 7 | 6 | 8 | 7 | 7 | 3 | 1.3 |
| Leg and foot structure | | | | 4 | 4 | 3 | 3 | 3 | 3 | 1 | 0.4 |
| Conception rate | | | | | 7 | 9 | 7 | 7 | 7 | 5 | 2.1 |
| Calving ability | | | | | | 6 | 5 | 5 | 5 | 3 | 3.3 |
| Heifer conception rate | | | | | | | 1 | 1 | 1 | 1 | 0.5 |
| Cow conception rate | | | | | | | 2 | 2 | 2 | 1 | 1.8 |
| Cow livability | | | | | | | | 7 | 7 | 4 | 5.9 |
| Health | | | | | | | | | 2 | 2 | 1.5 |
| Residual feed intake | | | | | | | | | | −12 | −6.8 |
| Age at first calving | | | | | | | | | | 1 | 1.0 |
| Heifers livability | | | | | | | | | | 1 | 0.8 |

**Note:** PD$ – predicted difference in dollars; MFP$ – milk, fat and protein combined value in dollars; NM$ – Lifetime Net Merit in dollars
**Source:** P.M. VanRaden *et al.* (2021), Council on Dairy Cattle Breeding (n.d.)

In 1971, dairy cattle selection in the USA was based on just two traits – milk yield and milk fat content. Today, however, the NM$ index (Lifetime Net Merit in dollars) includes twelve economically important selection traits. Similar developments have taken place in other countries. As a result of implementing genomic evaluation and enabling early selection of breeding bulls, the generation interval – the age of the sire at the time of a young bull's birth – has decreased to two years (Wiggans & Carrillo, 2022). This reduction has led to a twofold increase in the rate of genetic progress in the Holstein breed (Guinan *et al.*, 2023). Furthermore, the availability of such detailed data enables the identification of new predictor traits (from the English predictor – a prognostic parameter or forecasting tool), which can simplify data collection procedures and improve the accuracy of genetic evaluations.

The study by S. Ruban & V. Danshin (2023) demonstrated that the use of genomic selection in dairy cattle breeding in Ukraine could significantly accelerate genetic progress by reducing generation intervals. Shortening generation intervals along the breeding pathways – sires of bulls, sires of cows, and dams of bulls – would increase milk yield gains from 100.1 kg to 180.0 kg, representing an 80% improvement. In a related study, S.W. Alemu *et al.* (2025) investigated the impact of functional DNA variants on the accuracy of genomic prediction for milk fat content, protein content, milk yield, and total milk fat and protein in lactating dairy cows. This was compared with predictions based on the Illumina 50k SNP chip (covering approximately 50,000 nucleotide sequences). Functional variants were identified through Genome-Wide Association Studies (GWAS) – which examine the likelihood or extent of genomic regions influencing a quantitative trait – as well as RNA sequencing (RNA-seq) and histone modifications (ChIP-seq), and were found to be coding variants. The authors concluded that incorporating functional variants can improve the accuracy of genomic prediction compared to relying solely on SNP markers.

According to D. Lourenco *et al.* (2020), the single-step genomic Best Linear Unbiased Prediction method is gaining popularity. This approach allows for the application of the BLUP method using a mixed linear model, where the relationship matrix between animals consists of three submatrices: 1) a submatrix for genotyped animals; 2) a submatrix for non-genotyped animals; 3) a combined submatrix linking both genotyped and non-genotyped animals. These matrices contain probes that identify SNP genotypes across the entire genome. This method enables the optimal integration of data from both genotyped and non-genotyped animals, increasing the overall dataset size and thereby improving the accuracy of predicted breeding values. M. Bermann *et al.* (2022) found that the single-step genomic BLUP method is widely used to estimate genomic breeding values across various livestock species, as well as in Genome-Wide Association Studies. In such contexts, there arises a need to establish information databases that reflect the phenotypic and genotypic characteristics of specific breeds across multiple generations, with verified pedigree information for each animal. Meeting these requirements is a key priority for Ukrainian breeders, particularly in the context of applying advanced genomic research methods, and depends heavily on the development of a robust reference population.

In the near future, advances in animal genetics and breeding will be closely linked to information and communication technologies. These encompass computer systems, software, programming languages, and data processing and storage – particularly within reference populations, which are increasingly integrated under the umbrella of omics technologies. The term omics derives from the suffix *-ome*, meaning whole or entire. In life sciences, omics typically refers to fields of study focused on large-scale data to understand biological processes, collectively referred to as the omes. One of the most promising directions for improving the genetic evaluation of dairy cattle is the application of holo-omics, which involves evaluating animals while accounting for the influence of the metagenome, or the genome of the microbial communities in specific organs. Key traits in this context include feed efficiency and methane emissions, both of which are significantly influenced by the rumen microbiota of ruminants (Ross & Hayes, 2022).

Another important area is the use of genome editing technologies in dairy cattle (Van Eenennaam, 2025). These technologies not only have the potential to enhance animal productivity but also to address diseases, including infectious ones. Below are examples of such applications:

1. Bovine Viral Diarrhoea (BVD) is one of the most significant diseases affecting the health and welfare of cattle worldwide. Using CRISPR/Cas9 technology combined with somatic cell nuclear transfer (SCNT), a live calf was produced with six altered amino acids in the BVDV-binding domain of the bovine CD46 gene. The calf exhibited markedly reduced susceptibility to infection, as evidenced by milder clinical symptoms and the absence of viral presence in its leukocytes (Workman *et al.*, 2023);

2. according to G.-M. Gim *et al.* (2023), the CRISPR-Cas9 technique was used to produce calves with edited PRNP genes (conferring resistance to bovine spongiform encephalopathy) and dairy calves with modified MSTN and BLG genes, resulting in the production of milk less likely to cause allergic reactions;

3. bovine herpesvirus type 1 (BHV-1), the causative agent of infectious bovine rhinotracheitis, has also been targeted. H. Dai *et al.* (2022) developed a line of cattle resistant to this virus using the CRISPR/Cas9 system;

4. M. Yuan *et al.* (2021) applied the CRISPR/Cas9 system to modify the ROSA26 locus, identified as a potential GSH in cattle, to develop animals with enhanced resistance to tuberculosis.

An important area in dairy cattle breeding is improving feed efficiency. There is growing scientific interest in the use of omics technologies in livestock selection. In addition to genomics, these include transcriptomics, proteomics, metabolomics, metagenomics, and epigenomics (Chakraborty *et al.*, 2022). Biotechnological methods of reproduction are also rapidly advancing, particularly in vitro fertilisation and the use of Sex-selected semen (Hopper, 2021). These approaches enable the evaluation of an embryo's genetic merit at early stages of development. Special attention is being paid to the application of artificial intelligence in dairy cattle breeding, which is now successfully used to address a wide range of tasks (De Vries *et al.*, 2023).

F. Monteiro *et al.* (2024) demonstrated, using artificial intelligence, that the composition of the rumen microbiome accounts for a significant portion of the variability in residual feed intake in dairy cows. Precision livestock farming, powered by artificial intelligence and sensor-based technologies, offers innovative solutions for advancing milk production. G. Koutouzidou *et al.* (2022) found that these technologies have enabled real-time monitoring and data-driven decision-making, resulting in improved animal welfare and increased productivity. A. De Vries *et al.* (2023) identified the main applications of artificial intelligence in dairy farming as follows: 1) development of expert systems for optimising feeding, culling, mastitis control, and individual sire bull selection; 2) meta-analysis for management strategies; 3) disease diagnosis; 4) detection of oestrus and prediction of successful insemination; 5) forecasting future milk yield; 5) estimation of individual feed intake based on productivity, behaviour, and metabolic indicators; 6) implementation of voluntary milking systems (robotic milking).

Thus, an analysis of the current state of genetic evaluation of dairy cattle in Ukraine has revealed positive trends in the adoption of advanced breeding approaches, particularly through the adaptation of genomic evaluation methods. At the same time, significant gaps remain in terms of the proportion of monitored livestock and the use of information technologies compared to leading countries. The findings confirm the effectiveness of reducing the generation interval and integrating SNP analysis to achieve significant genetic progress. Incorporating international experience and adapting promising tools – including artificial intelligence, omics technologies, and genome editing – will shape the future directions for improving breeding strategies in Ukrainian dairy farming.

## Conclusions

A significant proportion of the dairy cattle livestock in Ukraine consists of Holstein animals or local crossbreeds, with Holstein ancestry accounting for approximately 75%-87.5% of pedigrees. A key limiting factor in the breeding system is the relatively small number of animals under monitored livestock. Genetic evaluation methods for dairy cattle have evolved considerably – from relatively simple approaches such as daughter–dam comparisons to more advanced techniques like the BLUP Animal Model and genomic evaluation – greatly enhancing the effectiveness of selection programmes. The implementation of genomic selection requires a comprehensive organisational overhaul of the entire breeding system, particularly in the Ukrainian context. Such a system must not only include genetic laboratories and breeding information centres to maintain a continuous flow of data but also involve a revision of specialist training programmes at higher education institutions. A general trend in modern dairy farming is the increasing number of selection traits to better account for economic factors, with the effectiveness of breeding programmes being tested within a reference section of the population of a given breed.

Promising areas of research in this field include the use of genomic selection, holo-omics (evaluating genetic merit based on both the cow's genome and the associated metagenome), and genome editing techniques such as CRISPR-Cas9 in dairy cattle. These approaches, combined with extracorporeal fertilisation and sex-selected semen, offer new opportunities for advancing genetic evaluation methods and implementing effective breeding programmes. An important focus in dairy cattle breeding is the improvement of feed efficiency. The application of Omics technologies – such as transcriptomics, proteomics, metabolomics, metagenomics, and epigenomics – in livestock selection is considered highly promising. The integration of artificial intelligence into these processes further enhances precision and decision-making in breeding strategies.

To support research in these areas, it would be advisable to establish a dedicated breeding and genetic centre in Ukraine, closely collaborating with reference herds of leading breeds. This would reduce reliance on costly imports of genetic materials such as semen, embryos, and live animals.

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## Conflict of Interest

None.

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# Сучасні підходи та перспективи генетичної оцінки молочної худоби в селекційних програмах

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**Анотація.** Оцінка племінної цінності за економічно важливими ознаками є основним інструментом в сучасних системах генетичного покращення молочної худоби. Мета наведених аналітичних досліджень пов'язана з описом сучасного алгоритму генетичної оцінки молочної худоби та визначення перспективних напрямів можливого удосконалення на найближче майбутнє. Встановлено, що методи генетичної оцінки пройшли довгий шлях розвитку від масового порівняння «дочка – мати», прямого та покращеного порівняння з одностадницями, модифікованого методу порівняння з ровесницями до таких комплексних методів як «Модель тварини» і геномна оцінка з використанням математичних підходів BLUP та REML. Впровадження сучасних геномних програм відбору потребує суттєвої перебудови організаційної системи всієї племінної роботи де наявність референтних популяцій з постійним моніторингом генетичних та фенотипових характеристик є основною задачею. Зазначено, що загальною тенденцією в сучасному молочному скотарстві є збільшення числа селекційних ознак для повного врахування реальних (кількість та склад молока), та «прихованих» ознак (стан здоров'я, рівень відтворення, продуктивне довголіття, ефективність використанні корму) які суттєво впливають на економіку виробництва. Проведено порівняльний аналіз підконтрольного поголів'я і показників продуктивності в Україні та країнах-членах ICAR, що дозволило виявити ключові обмеження національної селекційної системи. Встановлено, що використання геномної оцінки дозволяє скоротити генераційні інтервали та подвоїти темпи генетичного прогресу за надоєм. Практична цінність дослідження полягає у формуванні науково обґрунтованих орієнтирів для створення в Україні ефективної системи генетичної оцінки та управління племінними ресурсами

**Ключові слова:** BLUP «Модель тварини», геномна селекція, голо-оміка, редагування геному, біотехнологія