https://doi.org/10.15407/animbiol26.01.003
UDC 636.2.034
Received 16.09.2023 ▪ Revision 09.02.2024 ▪ Accepted 13.03.2024 ▪ Published online 29.03.2024

Review

Feed efficiency of dairy cattle as genetic trait

S. Y. Ruban, V. O. Danshyn
rubansy@gmail.com

National University of Life and Environmental Sciences of Ukraine, 15 Heroiv Oborony str., Kyiv 03041, Ukraine

ORCID:
S. Y. Ruban https://orcid.org/0000-0002-8114-3665
V. O. Danshyn https://orcid.org/0000-0001-9012-6835

Authors' Contributions:
RSY: Conceptualization; Data curation; Formal analysis; Supervision.
DVO: Methodology; Project administration; Writing — review & editing.

Declaration of Conflict of Interests:
None to declare.

Ethical approval:
Not applicable.

Acknowledgements:
The authors acknowledge National University of Life and Environmental Sciences of Ukraine for financial support.

Attribution 4.0 International (CC BY 4.0)

This review article is devoted to the use of feed efficiency traits in dairy cattle breeding. An efficient cow is defined as the one that produces the same amount of milk and milk solids while consuming less feed and remaining healthy and fertile; thus, allowing to reduce costs without decrease in production. Improving feed efficiency is economically important due to the increasing price of fodder. Feed efficiency is a genetically complex trait that can be described as units of product output (e.g., milk yield) per unit of feed input. Nowadays genetic evaluation of dairy cattle for feed efficiency is routinely conducted in several countries, including Australia, USA, Canada, Netherlands, Denmark, Sweden, Finland, Norway and United Kingdom. Different countries use different measures of feed efficiency of dairy cows. The main feed efficiency traits are dry matter intake, gross feed efficiency, residual feed intake, energy balance and feed saved. Genome-wide association studies demonstrated that feed efficiency in polygenic trait. Nevertheless, several genes with large effects on feed efficiency were identified. Estimates of heritability of these traits vary from 0.07 to 0.49 and show the presence of considerable genetic variation of these traits and therefore, the possibility of their genetic improvement under the conditions of inclusion in breeding programs. Changes in diet and rumen microbiome substantially impact feed efficiency of dairy cows. Feed efficiency is related to methane emissions and excess nitrogen excretion. Genetic improvement of feed efficiency requires recording of individual data on feed intake in cows. Such data are limited. Two options exist to solve this problem: use of indirect predictors and genomic prediction. Accuracy of genomic prediction varies from 0.21 to 0.61 across countries. International cooperative projects such as *Efficient Dairy Genome Project* in Canada were launched to establish large databases and to increase accuracy of feed efficiency traits genomic prediction. Future directions of research are the use of novel technologies: mid-infrared spectroscopy, artificial intelligence, holo-omics.

Key words: dry matter intake, energy balance, residual feed intake, feed saved, heritability, genomic selection, holo-omics

Introduction

The purpose of this review is to describe use of feed efficiency in dairy cattle genetic improvement programs. The main tasks are to highlight the importance of reducing feed costs in milk production, to characterize traits of feed efficiency of dairy cows and their genetic architecture, to describe methods of measuring feed efficiency used in different countries, to focus on the importance of international collaboration for genomic prediction of feed efficiency of dairy cattle. The review refers to dairy cattle breeding and genetics and considers problems of genetic improvement of dairy cattle for the purpose of increasing economic efficiency of milk production.

Discussion

Feeds are the main cost item in milk production. For instance, according to the Agricultural Research Service of the US Department of Agriculture, in 2021 the share of the cost of feeds in the total costs of milk production was 57.8%.

According to calculations by M. Coffey [11] in UK, in a herd of 150 cows with an average milk yield of 9,000 liters, the average annual feed costs will be equal to £125,628 (£838 per cow). Saving 10% of this amount is a big prize. The UK national herd of 1.9 million lactating cows with an average milk yield of 7,600 kg consumes feeds for approximately £1.592 billion per year. If cows consumed 10% less feeds under the same conditions, the feed savings would be 159 million pounds per year.

In fig. 1 the dynamics of prices of feeds for farm animals in the USA is presented. For the period from 2000 to 2022, the feed price index increased from 100 to 250, i.e. by 1.5 times. Thus, reducing feed costs is an important lever from the point of view of increasing the profitability of milk production, especially given the rising feed prices.

From the point of view of the need to ensure sustainable milk production, it is important to reduce feed costs by increasing the share of feed used for milk production. Feed efficiency is an important genetic trait that has recently received considerable attention due to its economic importance [41, 42].

C. M. Richardson et al. [39] showed that increasing estimated breeding value of the feed performance (defined as a kg of more efficiently used feed) by one unit (i.e. 1 kg of more efficiently converted dry matter intake during the cow's first lactation) translates to a total lifetime saving of 3.23 kg in dry matter intake with the economic value of CAD $0.82.

K. Houlahan et al. [17] showed that the inclusion of feed efficiency in economic selection indices allows increasing significantly the efficiency of breeding programs of dairy cattle.

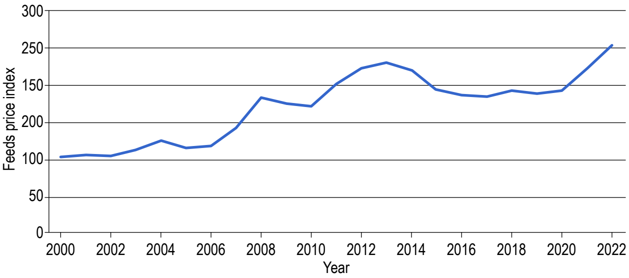

Fig. 1. Dynamics of prices of feeds for farm animals in the USA from 2000 to 2022 [36]

In dairy cattle breeding the following traits of feed efficiency are used [25]:

— **dry matter intake** (DMI) — the difference between the feed offered and that which remains uneaten;

— **gross feed efficiency** (GFE), also known as **feed conversion efficiency** — the amount of milk produced per 1 kg of dry matter of feed consumed;

— **residual feed intake** (RFI) — the difference between actual dry matter intake and predicted dry matter intake based on energy requirements for production and maintenance;

— **energy balance** (EB) — the difference between the consumed energy of feed and the output of total energy (milk, maintenance, growth and pregnancy);

— **feed saved** (FS), which takes into account the costs of milk production and maintenance.

Close to the residual feed intake is the **residual energy intake** (REI), which is defined as the difference between the required and actual consumption of the net lactation energy of a dairy cow [1].

The most expensive component of diet for dairy cows is protein [6]. Based on this, Y. Chen et al. [8, 9] developed Nitrogen Efficiency Index (NEI) that includes nitrogen intake, milk true protein nitrogen, and milk urea-nitrogen yield. The NEI showed positive genetic correlations with production traits (e.g., milk yield, protein yield) and has the advantage of large-scale prediction. Genome-wide association study showed that the largest explanatory genomic regions of NEI were *Bos taurus* autosomes 14, 26, 16, and 6; 16 key candidate genes were identified for NEI and its composition traits, which are mainly expressed in the milk cell, mammary, and liver tissues [10].

According to their genetic architecture feed efficiency traits are polygenic. B. Li et al. [23] conducted a genome-wide association study of residual feed intake of Holstein cows (fig. 2). It was shown that regions of the genome located on chromosomes 25 and 18 have the greatest influence on residual feed intake. Genes that determine this trait were identified and biological mechanisms of their action were determined.

N. Krattenmacher et al. [20] identified four quantitative trait loci (QTL) located on chromosomes 1, 10, 15 and 16 that affect energy balance in dairy cows.

S. M. Salleh et al. [44], using the gene co-expression network analysis [31], identified genes and regulators (ATP7b, IFNG, and IL10RA) that could potentially impact feed efficiency in dairy cows.

S. Lam et al. [21] based on RNA sequencing from the liver tissue of Holstein and Jersey cows found 9 genes (IN-SRR, CSK, DYNC1H1, GAB1, KAT2B, RXRA, SHC1, TRRAP, PIK3CB) that affect feed efficiency due to their participation in the processes of cell growth and regeneration, metabolism and immunity.

Estimates of the heritability of feed efficiency traits of dairy cows vary significantly between different countries, but in general the presented estimates indicate the possibility of successful genetic improvement of these traits (table 1).

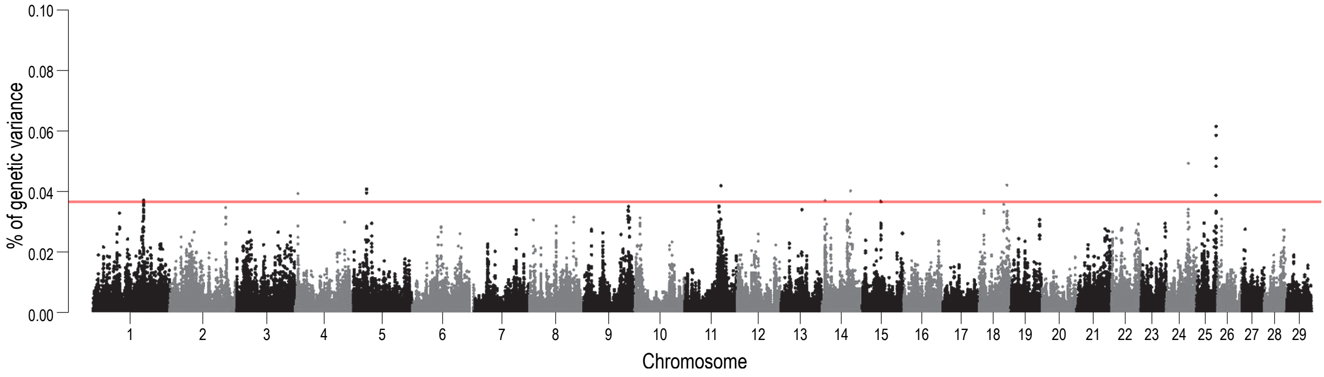

Fig. 2. Manhattan plot of the genetic variance (%) explained by each genome region for residual feed intake in Holstein dairy cattle [23]

P. Khanal et al. [19] using multiple-trait random regression model showed that heritability of daily residual feed intake and feed saved changed during lactation both for primiparous (0.05–0.07 and 0.11–0.17, respectively) and multiparous (0.03–0.13 and 0.10–0.17, respectively) cows. However, heritability estimates based on lactation averages were substantially higher, ranging from 0.17 to 0.25 for residual feed intake and from 0.35 to 0.41 for feed saved.

In different countries different approaches are used to measure feed efficiency of dairy cattle.

Australia was the first country in the world to use breeding value estimates for feed efficiency in dairy cattle breeding [2]. Feed efficiency is expressed by the **feed saved** (Feed Saved ABV). The goal is to produce animals that give the same amount of milk with reduced maintenance requirements. Feed Saved ABV includes residual feed intake (RFI) and maintenance requirements calculated on the basis of live weight. Feed Saved ABV is expressed in kilograms (dry matter) of feed saved per cow per year. The base (or average for breed) is zero: a positive value means saving feeds; a negative value represents additional feed consumed. Animals that are one standard deviation above the mean for the feed saved trait consume 65 kg less feed per year, while maintaining the same levels of production [37]. Feed Saved ABV is included to both selection indices used in Australian dairy farming: the Balanced Performance Index (BPI) and the Health Weighted Index (HWI), with higher weighting in the HWI.

Table 1. Estimates of heritability (h^2) of feed efficiency traits in dairy cows [25]

Trait	Country	Breed	h^2
Dry matter intake	Netherlands	Holstein	0.21–0.40
	Germany	Holstein	0.26–0.37
	Denmark and Sweden	Holstein	0.20–0.40
	Denmark	Jersey	0.17–0.42
		Holstein	0.32–0.49
	USA, Canada, UK, Netherlands	Holstein	0.23–0.32
	Canada	Holstein	0.28
	Denmark, Finland and Sweden	Holstein	0.30–0.55
Gross feed efficiency	USA	Holstein	0.43–0.47
Residual feed intake	Netherlands	Holstein	0.40
	Southern Australia	Holstein	0.27
	Australia and New Zealand	Holstein	0.22–0.38
	USA	Holstein	0.36
	Canada	Holstein	0.20
	Denmark	Holstein	0.23–0.36
	USA, Canada, UK, Netherlands	Holstein	0.13–0.14
Energy balance	Finland	Nordic Red	0.10
	USA	Holstein	0.07–0.22
	Germany	Holstein	0.29–0.49

In USA feed efficiency is expressed as **feed saved** (FSAV) based on estimates of predicted transmitting ability for residual feed intake (PTArfi) and body weight composite (PTAbwc) PTA for feed saved is calculated as [35, 47]:

$$\text{PTAfsav} = -1\ \text{PTArfi} - 151.8\ \text{PTAbwc} \qquad (1)$$

Data from the experimental farms of University of Wisconsin-Madison, Michigan State University, Iowa State University, University of Florida, and of Animal Genomics and Improvement Laboratory of the department of agriculture are used to estimate residual feed intake. The database contains more than 650,000 feed intake records (approximately 6,200 cows).

Body weight composite (BWC) is calculated based on linear appraisal traits of cows according to the formula:

$$\begin{aligned}\text{BWC} = {} & (0.23\ \text{Stature}) + (0.72\ \text{Strength}) + \\ & + (0.08\ \text{Bodydepth}) + (0.17\ \text{Rumpwidth}) - \\ & - (0.47\ \text{Dairyform})\end{aligned} \qquad (2)$$

The American Holstein Association uses the **Feed Efficiency** index (FE$), which is calculated using the formula:

$$\begin{aligned}\text{FE\$} = {} & (0.0008\ \text{PTAmilkyield}) + \\ & + (1.55\ \text{PTAmilkfat}) + (1.73\ \text{PTAmilkprotein}) + \\ & + (0.11\ \text{PTAfsav})\end{aligned} \qquad (3)$$

In Canada, in April 2021, Canadian Dairy Network began to publish official genetic evaluations based on

Feed Efficiency for Holstein sires. Feed efficiency includes three traits: dry matter intake (DMI) to estimate feed intake, metabolic body weight to determine energy requirements for maintenance, and energy corrected milk to account for performance level. Thus, feed efficiency is an expression of how much feed an animal eats regardless of its maintenance and productivity requirements.

Initially, only the data on the first lactation were used. Starting with the publication of genetic evaluations in December 2022, relative breeding values include second lactation data. An increase in the relative breeding value for every 5 points reduces the consumption of dry matter of feeds in daughters of sire by approximately 80 kg in the first lactation and by 120 kg in the second lactation. This corresponds to 2% reduction in feed intake.

In the Netherlands, the farmer organization CRV (https://crv4all.com) collects daily data on feed intake of more than 2,000 lactating cows on five commercial dairy farms. This gives four million feed intake records each year. CRV combines this information with data collected from 9,000 Dutch and Flemish cows, allowing for large reference population of cows and reliable estimates of breeding values. The reliability of estimated breeding values of feed efficiency for CRV sires is 85–90%.

The evaluation of the breeding value of bulls and cows is carried out in three stages [12]:

1. Evaluation of breeding values for dry matter intake is carried out separately for the first (BVdmi1), second (BVdmi2) and third and subsequent lactations (BVdmi3). The total evaluation of the breeding value for of dry matter intake (BVdmi) is calculated according to the formula:

$$\text{BVdmi} = 0.41\ \text{BVdmi1} + 0.33\ \text{BVdmi2} + 0.26\ \text{BVdmi3} \tag{4}$$

2. Estimated breeding values for feed saved for maintenance (FSM) in physical measurement are calculated according to the formula:

$$\text{FSM} = ((1000/940)\ (5.9\ \text{kg fat} + 3.0\ \text{kg protein} + 2.43\ \text{kg lactose})/301) - \text{BVdmi} \tag{5}$$

3. Estimated breeding values for **saved feed costs for maintenance** (SFCM) in monetary terms are calculated according to the formula:

$$\text{SFCM} = 60.20\ \text{EURO FCM} \tag{6}$$

In April 2023, CRV introduced *FeedExcel*, a breeding strategy that promises 25% increase in herd productivity or 25% less feed consumption by cows, as well as a 25% reduction in methane emissions by 2050.

The joint Danish-Finnish-Swedish consortium NAV (*Nordisk Avlsværdi Apskning* — Nordic Cattle Genetic Evaluation), which carries out genetic evaluation of dairy cattle in these three countries, to evaluate feed efficiency uses **Saved feed** index, which includes two components: maintenance efficiency and metabolic efficiency. Maintenance efficiency is calculated on the basis of data on live weight and type traits on linear scale (stature, body depth and chest width). The heritability of this trait is 0.58–0.65. Metabolic efficiency is defined as the difference between actual and predicted feed intake (that is, it equals residual feed intake) Data on feed intake come from the international database *Efficient Dairy Genome Project* (EDGP), experimental farms in Finland and from *VikingGenetics* farms equipped with the CFIT system.

In Norway feed efficiency is expressed by the *Feed$aved*™. The goal of Norwegian breeders is to reduce the amount of feeds needed to maintain body weight. The comprehensive system of recording in the Norwegian Red breed represents 93% of all cows in Norway. Live weight records of 1.2 million cows ensure high selection accuracy for *Feed$aved*™. *Feed$aved*™ calculations are based on dry matter intake. Top *Feed$aved*™ Norwegian Red sires produce smaller crossbred daughters compared to the average 700 kg mature Holstein cow weight, saving maintenance feed costs at $0.28 per day or saving of approximately 1 kg of feed per day (at a cost of 0.26 USD per 1 kg of dry matter of feed). On average, a Norwegian Red cow eats 0.6 kg less feed than a Holstein cow. In general, this saves about 101,000 US dollars on a farm with 1000 cows.

In United Kingdom, *Feed Advantage* is used — an index that is calculated as predicted transmitting ability (PTA) in kilograms of dry matter intake saved in each lactation. The development of the index is the result of over 30 years of researches and data collection at the award-winning Langhill herd in Dumfries. In researches carried out by the Scottish Rural College (SRUC) dry matter intake of Langhill cows throughout their lifetime was measured. Adjustments are made according to the size of the animal, as smaller cows require less feed than larger cows with the same level of milk production. The most efficient cows consume 400 kg less per lactation compared to the least efficient cows, meaning that the same level of performance can be achieved by reducing feed intake. The Feed Advantage index is a component of the *EnviroCow* index, which aims to reduce the negative impact of milk production on the environment.

Iranian scientists conducted a study on the possibility of including feed efficiency in the selection index [32]. Data from seven dairy herds were used. Calculated economic weights for traits at prices of $0.34 for 1 kg of milk, $6.93 for 1 kg of milk fat, $5.53 for 1 kg of milk protein, –$1.68 for 1 kg of consumed dry matter of feeds, –$1.70 for 1 kg of residual feed intake, $0.47 for 1 month of productive life and –$2.71 for 1 day of days open. The Iranian selection index was revised from the point of view of improving feed efficiency and the sub-index of feed efficiency (FE$), introduced by the Holstein Association of the USA, was adopted taking into account the characteristics of the economic and production system of Iran.

L. Cavani et al. [7] studied the relationship between feeding behavior traits of Holstein cows (number of feeder visits per day, number of meals per day, duration of each feeder visit, duration of each meal, total duration of feeder visits, intake per visit, intake per meal, feeding rate per visit, and feeding rate per meal) with residual feed intake. The authors found that feeding behavior traits of dairy cows can be useful indicators of feed efficiency and cows with lower feeding rate use feeds more efficiently. W. E. Brown et al. [5] concluded that slower feeding rate by more efficient cows was associated with lower dry matter intake.

In several studies it was shown that feed efficiency of dairy cows largely depends on the rumen microbiome — community of microorganisms that inhabit rumen [13, 24, 29]. In Holstein and Nordic Red lactating dairy cows, R. J. Wallace et al. [48] identified 39 heritable core microbial OTUs (operational taxonomic units), with microbiability (proportion of phenotypic variance explained by microorganisms) estimates ranging from 0.20 to 0.60. According to B. Hayes [16], the accuracy of predicting feed efficiency based on cow genome was 0.33, while the accuracy of predicting this trait based on rumen microbiome data was 0.49; combined prediction using both sources of information (cow genome and rumen microbiome) made it possible to achieve a prediction accuracy of 0.57. Therefore the perspective direction for increasing feed efficiency is application of holo-omics — analysis and prediction of feed efficiency based on simultaneous accounting for influence of both cow genome and metagenome (genome of microorganisms) of rumen [38]. Scheme of this approach is presented on fig. 3.

A. Fischer et al. [15] studied the dependence of feed efficiency of dairy cows (residual feed intake) on the diet. The authors found that feed efficiency was less reproducible across diets than within the same diet, and that it varied more after diet changes than during successive stages of lactation.

According to J. Karlsson et al. [18], dairy cows with high feed efficiency mobilized more of their body reserves both at the beginning of lactation and during full lactation.

It was shown that most feed efficient cows had improved reproductive performance compared with the least efficient cows [34].

S. Y. Ruban et al. [40] revealed significant influence of the “genetic group” factor on the main economic traits of dairy cows, including feed conversion.

An important aspect of improving feed efficiency is its relationship with methane emissions. The conducted studies show that genetic improvement of feed efficiency will contribute to the reduction of methane emissions in ruminants, and with the inclusion of both traits (feed efficiency and methane emission) in breeding goal, it is possible to achieve significant success both in terms of increasing the economic efficiency of milk production and reducing the negative impact on the environment [26, 27].

M. Nehme Marinho et al. [33] showed that the most feed-efficient cows were also characterized by less excess excretion of nitrogen which is related to environmental challenges.

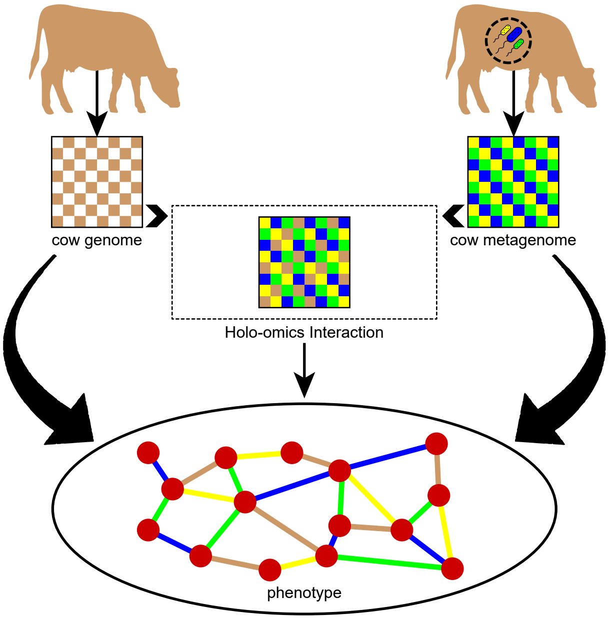

Fig. 3. Scheme of application of holo-omics in dairy cattle [37]

The main problem of using feed efficiency in breeding is the limitation of individual data on feed intake by cows [45]. Individual recording of feed intake requires the availability of appropriate equipment on the farm. There are two ways to solve this problem:

1) use of indirect (proxy) predictors,
2) genomic prediction [4].

As predictors can be used milk production traits, live weight, body condition scores, behavior traits, metabolites, etc. [28, 49].

J. R. R.Dórea et al. [14] using an artificial neural network approach developed models to estimate dry matter intake based on milk mid-infrared (MIR) spectral data.

Genomic prediction is based on the use of SNP markers and requires the definition of reference (training or predictor) population — group of animals for which their phenotypes and genotypes are known. Based on these data, the effects of the genotypes of each marker on quantitative trait are calculated, which are then used to obtain genomic estimates of breeding values (genomic estimated breeding values, GEBV) of genotyped animals [43].

The accuracy of genomic prediction depends on the number of animals in the reference population. The sizes of reference populations with data on traits, which are necessary for evaluating feed efficiency in each individual country, are quite limited; therefore, international cooperation for combining relevant data is of great importance.

The Global Dry Matter Initiative (gDMI) was established in 2014 to strengthen and coordinate the work on breeding dairy cattle for feed efficiency at the international level. Currently, it includes 15 participants from 10 countries. The main task of the organization is the collection and harmonization of data necessary for evaluating feed efficiency of dairy cows.

The Efficient Dairy Genome Project (EDGP, www.genomedairy.ualberta.ca) is an international research

Table 2. Accuracy of genomic predictions of feed efficiency traits in dairy cattle [25]

Trait	Country	Breed	Accuracy
Dry matter intake	UK, Netherlands and Australia	Holstein	0.35
	Europe, North America and Australia	Holstein	0.37
	Ireland, UK and Netherlands	Holstein	0.33
	Netherlands	Dutch dairy	0.21–0.38
	Germany	Holstein	0.33–0.61
Residual feed intake	Australia and New Zealand	Holstein	0.40
	Australia	Holstein	0.27
	USA, Canada, Netherlands and UK	Holstein	0.25–0.39
Energy balance	Netherlands	Holstein	0.29
	Germany	Holstein	0.27–0.47

project in Canada aimed at developing the strategic research, tools and infrastructure needed to implement genetic and genomic evaluations to improve feed efficiency and reduction of methane emissions in dairy cattle [30].

Values of accuracy of genomic prediction of feed efficiency traits in dairy cattle vary from 0.21 to 0.47 (table 2).

As part of this project, the Canadian Dairy Network (CDN) and the University of Guelph, together with international partners, created the EDGP database, which is located at the CDN (Guelph, Ontario, Canada). The database contains the following information: 1) pedigree, 2) calving, 3) performance, 4) events (including data on feed efficiency and methane emissions), 5) genotypes, 6) milk mid-infrared spectroscopy data.

As of February 1, 2023, the database contained information on 13,609 cows from the USA, Canada, Germany, Denmark, Switzerland, Spain, and Australia.

In the study of S. Bolormaa et al. [3] it was proved that the use of the international EDGP database allows to substantially increase the accuracy of genomic prediction of feed efficiency of dairy cows.

Genetic evaluation of dairy cattle for feed efficiency requires individual recording of feed intake. Usually this work is carried out using special equipment — automatic feeders. Such equipment is very expensive — approximately at the level of $220,000 for 24 feeders — and is installed only on experimental farms [11]. However, in recent years, individual feed intake recording systems have been developed for commercial farms, the most famous of which is the *Cattle Feed InTake* (CFIT) system. Such systems are based on the use of 3D video cameras and are much cheaper. In CFIT system artificial intelligence is used capable of both identifying individual cows in a herd and measuring individual feed intakes [22, 46].

Conclusions

Feed efficiency is an important genetic due to the significant share of feeds among the costs of milk production.

Feed efficiency traits are polygenic, i.e. determined by a large number of genes. Heritability estimates indicate the presence of significant genetic variability of these traits and, therefore, the possibility of their improvement under the conditions of inclusion in breeding programs. A number of gene were identified that considerably influence feed efficiency of dairy cows.

Feed efficiency depends on diet and to large extent on rumen microbiome of cows.

In different countries various approaches are used to determine feed efficiency of dairy cows.

Due to the limitation of amount of individual data on cows, necessary for genetic evaluation based on feed efficiency, the best tool for such work is the use of genomic selection. International cooperation plays an important role, the purpose of which is the creation of relevant databases, the use of which allows increasing the accuracy of genomic prediction.

Perspective research directions are the use of modern technologies, such as mid-infrared spectroscopy, artificial intelligence, as well as holo-omics (estimating genetic values with the simultaneous inclusion of information on both the cow genome and the metagenome, i.e. the genome of the rumen microbiota).

References

1. Becker VAE, Stamer E, Spiekers H, Thaller G. Genetic parameters for dry matter intake, energy balance, residual energy intake, and liability to diseases in German Holstein and Fleckvieh dairy cows. *J Dairy Sci.* 2022; 105 (12): 9738–9750. DOI: 10.3168/jds.2022-22083.
2. Bolormaa S, MacLeod IM, Khansefid M, Marett LC, Wales WJ, Nieuwhof GJ, Baes CF, Schenkel FS, Goddard M E, Pryce JE. Evaluation of updated Feed Saved breeding values developed in Australian Holstein dairy cattle. *JDS Commun.* 2022; 3 (2): 114–119. DOI: 10.3168/jdsc.2021-0150.
3. Bolormaa S, MacLeod IM, Khansefid M, Marett LC, Wales WJ, Miglior F, Baes CF, Schenkel FS, Connor EE, Manzanilla-Pech CIV, Stothard P, Herman E, Nieuwhof GJ, Goddard ME, Pryce JE. Sharing of either phenotypes or genetic variants can increase the accuracy of genomic prediction of feed efficiency. *Genet Sel Evol.* 2022; 54: 60. DOI: 10.1186/s12711-022-00749-z.
4. Brito LF, Oliveira HR, Houlahan K, Fonseca PAS, Lam S, Butty AM, Seymour DJ, Vargas G, Chud TCS, Silva FF, Baes CF, Cánovas A, Miglior F, Schenkel FS. Genetic mechanisms underlying feed utilization and implementation of genomic selection for improved feed efficiency in dairy cattle. *Canad J Anim Sci.* 2020; 100 (4): 587–604. DOI: 10.1139/cjas-2019-0193.
5. Brown WE, Cavani L, Peñagaricano F, Weigel KA, White HM. Feeding behavior parameters and temporal patterns in mid-lactation Holstein cows across a range of residual feed intake values. *J Dairy Sci.* 2022; 105 (10): 8130–8142. DOI: 10.3168/jds.2022-22093.
6. Cantalapiedra-Hijar G, Dewhurst RJ, Cheng L, Cabrita ARJ, Fonseca AJM, Nozière P, Makowski D, Fouillet H, Ortigues-Marty I. Nitrogen isotopic fractionation as a biomarker for nitrogen use efficiency in ruminants: A meta-analysis. *Animal.* 2018; 12 (9): 1827–1837. DOI: 10.1017/S1751731117003391.
7. Cavani L, Brown WE, Parker Gaddis KL, Tempelman RJ, VandeHaar MJ, White HM, Peñagaricano F, & Weigel KA. Estimates of genetic parameters for feeding behavior traits and their associations with feed efficiency in Holstein cows. *J Dairy Sci.* 2022; 105 (9): 7564–7574. DOI: 10.3168/jds.2022-22066.

8. Chen Y, Vanderick S, Mota RR, Grelet C, GplusE Consortium, Gengler N. Estimation of genetic parameters for predicted nitrogen use efficiency and losses in early lactation of Holstein cows. *J Dairy Sci.* 2021; 104 (4): 4413–4423. DOI: 10.3168/jds.2020-18849.
9. Chen Y, Atashi H, Grelet C, Vanderick S, Hu H, Gengler N. Defining a nitrogen efficiency index in Holstein cows and assessing its potential effect on the breeding program of bulls. *J Dairy Sci.* 2022; 105 (9): 7575–7587. DOI: 10.3168/jds.2021-21681.
10. Chen Y, Atashi H, Grelet C, Mota RR, Vanderick S, Hu H, GplusE Consortium, Gengler N. Genome-wide association study and functional annotation analyses for nitrogen efficiency index and its composition traits in dairy cattle. *J Dairy Sci.* 2023; 106 (5): 3397–3410. DOI: 10.3168/jds.2022-22351.
11. Coffey M. Advances in dairy cattle breeding to incorporate feed conversion efficiency in national genetic evaluations. In: *Advances in breeding of dairy cattle*. Ed. by J. van der Werf, J. Pryce. Burleigh Dodds Science Publishing Limited, 2020: 173–189. DOI: 10.19103/AS.2019.0058.11.
12. De Jong G, Bouwmeester-Vosman JJ, van der Linde C, de Haas Y, Schopen GCB, Veerkamp RF. Feed intake genetic evaluation: progress and an index for saved feed cost. Proceedings of the 2019 Interbull Meeting, Cincinnati, OH (USA), 23–26 June 2019. *Interbull Bull.* 2019; 55. Available at: https://journal.interbull.org/index.php/ib/article/view/171
13. Delgado B, Bach A, Guasch I, González C, Elcoso G, Pryce JE, Gonzalez-Recio O. Whole rumen metagenome sequencing allows classifying and predicting feed efficiency and intake levels in cattle. *Sci Rep.* 2019; 9: 11. DOI: 10.1038/s41598-018-36673-w.
14. Dórea JRR, Rosa GJM, Weld KA, Armentano LE. Mining data from milk infrared spectroscopy to improve feed intake predictions in lactating dairy cows. *J Dairy Sci.* 2018; 101 (7): 5878–5889. DOI: 10.3168/jds.2017-13997.
15. Fischer A, Dai X, Kalscheur KF. Feed efficiency of lactating Holstein cows is repeatable within diet but less reproducible when changing dietary starch and forage concentrations. *Animal*. 2022; 16 (8): 100599. DOI: 10.1016/j.animal.2022.100599.
16. Hayes B. *Genomes, phenomes and microbiomes to improve health, welfare and productivity of livestock*. The University of Queensland, Australia, 2019: 25 p.
17. Houlahan K, Schenkel FS, Hailemariam D, Lassen J, Kargo M, Cole JB, Connor EE, Wegmann S, Oliveira Júnior GA, Miglior F, Fleming A, Chud TCS, Baes CF. Effects of incorporating dry matter intake and residual feed intake into a selection index for dairy cattle using deterministic modeling. *Animals*. 2021; 11 (4): 1157. DOI: 10.3390/ani11041157.
18. Karlsson J, Danielsson R, Åkerlind M, Holtenius K. Full-lactation performance of multiparous dairy cows with differing residual feed intake. *PLoS ONE.* 2022; 17 (8): e0273420. DOI: 10.1371/journal.pone.0273420.
19. Khanal P, Parker Gaddis KL, Vandehaar MJ, Weigel KA, White HM, Peñagaricano F, Koltes JE, Santos JEP, Baldwin RL, Burchard JF, Dürr JW, Tempelman RJ. Multiple-trait random regression modeling of feed efficiency in US Holsteins. *J Dairy Sci.* 2022; 105 (7): 5954–5971. DOI: 10.3168/jds.2021-21739.
20. Krattenmacher N, Thaller G, Tetens J. Analysis of the genetic architecture of energy balance and its major determinants dry matter intake and energy-corrected milk yield in primiparous Holstein cows. *J Dairy Sci*. 2019; 102 (4): 3241–3253. DOI: 10.3168/jds.2018-15480.
21. Lam S, Miglior F, Fonseca PAS, Gómez-Redondo I, Zeidan J, Suárez-Vega A, Schenkel F, Guan LL, Waters S, Stothard P, Cánovas A. Identification of functional candidate variants and genes for feed efficiency in Holstein and Jersey cattle breeds using RNA-sequencing. *J Dairy Sci*. 2021; 104 (2): 1928–1950. DOI: 10.3168/jds.2020-18241.
22. Lassen J, Thomasen JR, Hansen RH, Nielsen GGB, Olsen E, Stentebjerg PRB, Hansen NW, Borchersen S. Individual measures of feed intake on in-house commercial dairy cattle using 3D camera technology. *Proc. World Congress on Genetics Applied to Livestock Production*. Auckland, New Zealand, 2018: 635.
23. Li B, Fang L, Null DJ, Hutchison JL, Connor EE, VanRaden PM, VandeHaar MJ, Tempelman RJ, Weigel KA, Cole JB. High-density genome-wide association study for residual feed intake in Holstein dairy cattle. *J Dairy Sci*. 2019; 102 (12): 11067–11080. DOI: 10.3168/jds.2019-16645.
24. Li F, Li C, Chen Y, Liu J, Zhang C, Irving B, Fitzsimmons C, Plastow G, Guan LL. Host genetics influence the rumen microbiota and heritable rumen microbial features associate with feed efficiency in cattle. *Microbiome*. 2019; 7: 92. DOI: 10.1186/s40168-019-0699-1.
25. Madilindi MA, Zishiri OT, Dube B, Banga CB. Technological advances in genetic improvement of feed efficiency in dairy cattle: A review. *Livestock Sci*. 2022; 258: 104871. DOI: 10.1016/j.livsci.2022.104871.
26. Manzanilla-Pech CIV, Løvendahl P, Mansan Gordo D, Difford GF, Pryce JE, Schenkel F, Wegmann S, Miglior F, Chud TC, Moate PJ, Williams SRO, Richardson CM, Stothard P, Lassen J. Breeding for reduced methane emission and feed-efficient Holstein cows: An international response. *J Dairy Sci*. 2021; 104 (8): 8983–9001. DOI: 10.3168/jds.2020-19889.
27. Manzanilla-Pech CIV, Stephansen RB, Difford GF, Løvendahl P, Lassen J. Selecting for feed efficient cows will help to reduce methane gas emissions. *Front Gen*. 2022; 13: 885932. DOI: 10.3389/fgene.2022.885932.
28. Martin MJ, Dórea JRR, Borchers MR, Wallace RL, Bertics SJ, DeNise SK, Weigel KA, White HM. Comparison of methods to predict feed intake and residual feed intake using behavioral and metabolite data in addition to classical performance variables. *J Dairy Sci*. 2021; 104 (8): 8765–8782. DOI: 10.3168/jds.2020-20051.
29. McGovern E, Kenny DA, McCabe MS, Fitzsimons C, McGee M, Kelly AK, Waters SM. 16S rRNA sequencing reveals relationship between potent cellulolytic genera and feed efficiency in the rumen of bulls. *Front Microbiol*. 2018; 9: 1842. DOI: 10.3389/fmicb.2018.01842.
30. Miglior F, Baes C, Cánovas A, Coffey M, Connor E, De Pauw M, Goddard E, Hailu G, Lassen J, Malchiodi F, Osborne V, Pryce J, Sargolzaei M, Schenkel F, Wall E, Wang Z, Wegman S, Wright T, Stothard PA. Progress report for the Efficient Dairy Genome Project. *J Anim Sci*. 2018; 96 (3): 123. DOI: 10.1093/jas/sky404.271.
31. Montenegro JD. Gene Co-expression network analysis. In: Edwards D. (ed.). *Plant Bioinformatics: Methods and Protocols. Method Mol Biol*. 2022; 2443: 387–404. DOI: 10.1007/978-1-0716-2067-0_19.
32. Nadri S, Sadeghi-Sefidmazgi A, Zamani P, Ghorbani GR, Toghiani S. Implementation of feed efficiency in Iranian Holstein Breeding Program. *Animals*. 2023; 13 (7): 1216. DOI: 10.3390/ani13071216.
33. Nehme Marinho M, Zimpel R, Peñagaricano F, Santos JEP. Assessing feed efficiency in early and mid lactation and its associations with performance and health in Holstein cows. *J Dairy Sci*. 2021; 104 (5): 5493–5507. DOI: 10.3168/jds.2020-19652.
34. Nehme Marinho M, Santos JEP. Association of residual feed intake with blood metabolites and reproduction in Holstein cows. *Front Anim Sci*. 2022; 3: 847574. DOI: 10.3389/fanim.2022.847574.
35. Parker Gaddis KL, VanRaden PM, Tempelman RJ, Weigel KA, White HM, Peñagaricano F, Koltes JE, Santos JEP, Baldwin RL, Burchard JF, Dürr JW, VandeHaar MJ. Implementation of Feed Saved evaluations in the U.S. Proceedings of the 2021 Interbull Meeting, Leeuwarden (Netherlands), April 26–30, 2021. *Interbull Bull*. 2021; 56: 147–152. Available at: https://journal.interbull.org/index.php/ib/article/view/72
36. Price of Feed. *IBISWorld*, published April 23, 2024. Available at: https://www.ibisworld.com/us/bed/price-of-feed/745
37. Pryce JE, Nguyen TTT, Axford M, Nieuwhof G, Shaffer M. Symposium review: Building a better cow — the Australian experience and future perspectives. *J Dairy Sci*. 2018; 101 (4): 3702–3713. DOI: 10.3168/jds.2017-13377.
38. Qadri QR, Zhao Q, Lai X, Zhang Z, Zhao W, Pan Y, Wang Q. Estimation of complex-trait prediction accuracy from the different holo-omics interaction models. *Genes*. 2022; 13 (9): 1580. DOI: 10.3390/genes13091580.
39. Richardson CM, Baes CF, Amer PR, Quinton C, Martin P, Osborne VR, Pryce JE, Miglior F. Determining the economic value of daily dry

matter intake and associated methane emissions in dairy cattle. *Animal*. 2020; 14 (1): 171–179. DOI: 10.1017/S175173111900154X.

40. Ruban SY, Perekrestova AV, Shablia VP, Bochkov VM. Feed conversion efficiency in different groups of dairy cows. *Ukr J Ecol*. 2018; 8 (1): 124–129. DOI: 10.15421/2018_196.
41. Ruban SY, Danshin VO, Fedota AM. Possibilities of application of feed efficiency and reproduction traits in dairy cattle breeding of Ukraine. *Anim Sci Food Tech*. 2019; 10 (3): 41–55. DOI: 10.31548/animal2019.03.041. (in Ukrainian)
42. Ruban SY, Danshin VO, Kyrii AA. Genetic improvement of dairy cattle for feed efficiency and fertility. *Dynamics of the development of world science: VII International scientific and practical conference*, Vancouver (Canada), March 18–20, 2020: 157–162.
43. Ruban S, Danshin V. Perspectives for the use of genomic selection for genetic improvement of dairy cattle in Ukraine. *Ukr Black Sea Reg Agr Sci*. 2023; 27 (1): 20–29. DOI: 10.56407/bs.agrarian/1.2023.20.
44. Salleh SM, Mazzoni G, Løvendahl P, Kadarmideen HN. Gene co-expression networks from RNA sequencing of dairy cattle identifies genes and pathways affecting feed efficiency. *BMC Bioinform*. 2018; 19: 513. DOI: 10.1186/s12859-018-2553-z.
45. Seymour DJ, Cánovas A, Baes CF, Chud TCS, Osborne VR, Cant JP, Brito LF, Gredler-Grandl B, Finocchiaro R, Veerkamp RF, de Haas Y, Miglior F. Invited review: Determination of large-scale individual dry matter intake phenotypes in dairy cattle. *J Anim Sci*. 2019; 102 (9): 7655–7663. DOI: 10.3168/jds.2019-16454.
46. Thomasen JR, Lassen J, Nielsen GGB, Borggard C, Stentebjerg PRB, Hansen RH, Hansen NW, Borchersen S. Individual cow identification in a commercial herd using 3D camera technology. *Proc. World Congress on Genetics Applied to Livestock Production*. Auckland (New Zealand), 2018: 613.
47. VanRaden PM, Cole J, Neupane M, Toghiani S, Parker Gaddis KL, Tempelman RJ. Net merit as a Measure of Lifetime Profit: 2021 Revision. *AIP RESEARCH REPORT NM$8 (05-21)*. 2021: 20 p. Available at: https://www.ars.usda.gov/ARSUserFiles/80420530/Publications/ARR/nmcalc-2021_ARR-NM8.pdf
48. Wallace RJ, Sasson G, Garnsworthy PC, Tapio I, Gregson E, Bani P, Huhtanen P, Bayat AR, Strozzi F, Biscarini F, Snelling TJ, Saunders N, Potterton SL, Craigon J, Minuti A, Trevisi E, Callegari ML, Piccioli Cappelli F, Cabezas-Garcia EH, Vilkki J, Pinares-Patino C, Fliegerová KO, Mrázek J, Sechovcová H, Kopečný J, Bonin A, Boyer F, Taberlet P, Kokou F, Halperin E, Williams JL, Shingfield KJ, Mizrahi I. A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. *Sci Adv*. 2019; 5 (7): eaav8391. DOI: 10.1126/sciadv.aav8391.
49. Zhang L, Gengler N, Dehareng F, Colinet F, Froidmont E, Soyeurt H. Can we observe expected behaviors at large and individual scales for feed efficiency-related traits predicted partly from milk mid-infrared spectra? *Animals*. 2020; 10 (5): 873. DOI: 10.3390/ani10050873.

Ефективність використання корму молочної худоби як генетична ознака

С. Ю. Рубан, В. О. Даншин
rubansy@gmail.com

Національний університет біоресурсів і природокористування України, вул. Героїв Оборони, 15, м. Київ, 03041, Україна

Цю оглядову статтю присвячено визначенню показників ефективності використання корму в розведенні молочної худоби. Ефективною вважають корову, яка дає однакову кількість молока та його сухих компонентів, споживаючи менше корму і залишаючись здоровою та плідною, що дозволяє скоротити витрати без зниження об'єму виробництва. Підвищення ефективності використання корму є економічно важливим через зростання вартості кормів. Ефективність використання корму — генетично складна ознака, яку можна описати в одиницях виходу продукту (наприклад, надій) на одиницю спожитого корму. На сьогодні генетичну оцінку ефективності використання корму молочної худоби регулярно проводять у кількох країнах, серед яких — Австралія, США, Канада, Нідерланди, Данія, Швеція, Фінляндія, Норвегія та Велика Британія. У різних країнах використовують різні показники ефективності використання корму молочних корів. Основними ознаками ефективності використання корму є споживання сухої речовини, валова ефективність використання корму, залишкове споживання корму, енергетичний баланс і економія корму. Повногеномні дослідження зв'язків показали, що ефективність використання корму є полігенною ознакою. Тим не менш, було виявлено кілька генів, які значно впливають на ефективність використання корму. Оцінки успадковуваності цих ознак коливаються від 0,07 до 0,49, показують наявність значної генетичної мінливості цих ознак і, отже, можливість їх генетичного покращення за умов введення до селекційних програм. Зміни в раціоні та мікробіом рубця суттєво впливають на ефективність використання корму молочних корів. Ефективність використання корму пов'язана з емісією метану і надлишковим виділенням азоту. Генетичне покращення ефективності використання корму потребує обліку індивідуальних даних про споживання корму коровами. Такі дані обмежені. Існує два варіанти вирішення цієї проблеми: використання непрямих предикторів і геномне передбачення. Точність геномного передбачення в різних країнах коливається від 0,21 до 0,61. Міжнародні спільні проекти (такі, як *Efficient Dairy Genome* Project в Канаді) були запроваджені з метою створення великих баз даних і підвищення точності геномного передбачення ознак ефективності використання корму. Майбутніми напрямками досліджень є використання новітніх технологій — спектроскопії середнього інфрачервоного діапазону, штучного інтелектк, голо-оміки.

Ключові слова: споживання сухої речовини, енергетичний баланс, залишкове споживання корму, економія корму, успадковуваність, геномна селекція, голо-оміка

Ruban SY, Danshyn VO. Feed efficiency of dairy cattle as genetic trait. *Bìol Tvarin*. 2024; 26 (1): 3–10. DOI: 10.15407/animbiol26.01.003.