
Morkuniene, K., Kerziene, S., Miceikiene, A. (2018), „Economic Evaluation of Genomic Selection in Lithuanian Dairy Cattle”, *Transformations in Business & Economics*, Vol. 17, No 2 (44), pp.21-32.

-----TRANSFORMATIONS IN -----
BUSINESS & ECONOMICS

© Vilnius University, 2002-2018
© Brno University of Technology, 2002-2018
© University of Latvia, 2002-2018

ECONOMIC EVALUATION OF GENOMIC SELECTION IN LITHUANIAN DAIRY CATTLE

¹Kristina Morkuniene

*Institute of Biology Systems and Genetics
Lithuanian University of Health Sciences
Tilzes 18, Kaunas, LT -47181
Lithuania
Tel.: +37065633177
E-mail: kristina.morkuniene@lsmuni.lt*

²Sigita Kerziene

*Department of Physics,
Mathematics and Biophysics
Lithuanian University of Health Sciences
Tilzes 18, Kaunas, LT -47181
Lithuania
Tel.: 837363722
E-mail: sigita.kerziene@lsmuni.lt*

³Astrida Miceikiene

*Institute of Economics,
Accounting and Finance
Aleksandras Stulginskis
university
Universiteto str. 10, LT-53361
Akademija, Kaunas distr.
Lithuania
Tel. +370 37 752257
E-mail: astrida.miceikiene@asu.lt*

¹Kristina Morkuniene, Lecturer in the University of Health Sciences, Institute of Biology Systems and Genetics, Lithuania. Research interests include genomic selection in dairy and beef cattle, genetic analysis of the milk proteins that are responsible for the quantity and quality of production, identification of cattle genetic diseases, which could determine economic losses.

²Sigita Kerziene is Assoc. Professor of Lithuanian University of Health Sciences Department of Physics, Mathematics and Biophysics, where she delivers courses on Informatics, Mathematics and Statistics. Her current research includes projects in Biomedical data analysis and modeling by statistical methods. Articles have been published in various international journals, such as “Journal of Food Safety”, “Medycyna Weterynaryjna”, “Acta veterinaria Scandinavica”, “Health Sciences in Eastern Europe” and others.

³Astrida Miceikiene is a professor of Aleksandras Stulginskis University Institute of Economics, Accounting and Finance. Research interests include: public finance, optimal taxation, insurance.

*Received: January, 2017
1st Revision: May, 2017
2nd Revision: July, 2017
Accepted: October, 2017*

ABSTRACT. *The pilot study was conducted to evaluate economic benefit of application of genomic selection in Lithuanian dairy cattle. Igenity dairy cattle genomic profile was determined for each cow, including traits of productive life, somatic cell count, milk yield, fat amount, fat %, protein amount, protein %, dairy form.*

Application of genomic selection in dairy cattle has enabled the authors to evaluate dairy cattle genomic potential, increase accuracy of selection, choose different selection models and increase selection intensity, all together resulting in the new selection tool taking into account economic benefit of usage. Genomic selection method is recommended to be applied not only to separate cattle herds, but also whole dairy breed (Lithuanian Black and White, Lithuanian Red, Holstein) selection programs, as the genomic information of each animal is ranked on the basis of international data enabling international breeding value evaluation and participation in cross-country international dairy cattle breeding programs.

KEYWORDS: economic benefit, genomic selection, cattle, identity dairy profile, Lithuania.

JEL classification: Q1, Q12, Q14.

Introduction

The use of genomic information in genetic evaluation has brought about revolutionary change in dairy cattle selection (Schaeffer, 2006; Mackay *et al.*, 2009; Pryce *et al.*, 2010; Buch *et al.*, 2012). In genomic selection, breeding values are estimated based on thousands of molecular markers, instead of own performance and family information. Application of molecular markers enables generation of accurate breeding values for animals of both sexes early in life, which can be used to shorten the generation interval for dairy cattle by omitting the progeny test (Schaeffer, 2006; Garcia-Ruiz *et al.*, 2016). Thus, selection decisions in dairy cattle breeding can now be made on young animals with higher accuracy than using a parent average breeding value. This has substantial implications on the design of breeding schemes, because, instead waiting until a bull has daughters with phenotypic records, the process that typically takes 5–6 years, young bulls with no progeny can rather be used as sires. The use of genomic selection gives tremendous economic effect. Costs for genotyping are negligible when focusing on a population wide perspective and considering additional costs for herd book registration, milk recording, keeping of bulls and heifers till mature age (König *et al.*, 2009). In practice, genomic selection refers to selection decisions based on genomic estimated breeding values (GEBV). GEBVs are calculated by estimating SNP effects from prediction equations, which are derived from a subset of animals in the population (i.e. reference population) with SNP genotypes and phenotypes for traits of interest. The accuracy of GEBV depends on the size of reference population used to derive prediction equations, heritability of the trait, and the extent of relationships between selection candidates and reference population (Scheffers *et al.*, 2012).

Genomic testing helps to make the best decisions for future by providing estimates of true genetic potential of animals as soon as they are born. Genomic testing increases herd profitability through increased genetic gain, parentage verification, management of inbreeding, confident mating decisions. Expected gains in net merit add tremendous economic value to dairy herds. With production and type traits identified early on, a breeder can match genomic profiles of heifers with those of bulls to improve the herd. Breeding with the use of heifers, which are genetically inferior to bulls, provides value for the heifers and keeps

inferior genetics from entering the herd gene pool, also enabling identification of the best replacement females by using genomics and breeding them to sexed semen sires. The use of genomic tested heifers allows to identify, cull or reprioritize, poor performing animals. Tested calf genomic data are compared to the information of thousands of other cattle known production traits. Genomic profiles can provide from 15 up to 45 key traits important for dairy production. Profiles include content for coat colour, milk components and genetic conditions. The cost of the development of high-throughput genotyping methods and reduced genotyping has made the application of genomic selection feasible (Pryce *et al.*, 2012; Meuwissen, 2009). Genomic selection could contribute to higher genetic gain without increased inbreeding, and particularly important for traits with low heritability, such as fertility and productive age. (Daetwyler *et al.*, 2009; Calus *et al.*, 2013). Genome wide selection in dairy cattle is used in many countries with highly developed animal husbandry, such as New Zealand, USA, Netherlands, Germany, France (Harris, Johnson, 2010; Wiggans *et al.*, 2011; Boichard *et al.*, 2012; Taylor *et al.*, 2016).

Aim of the study: The pilot study was conducted with the aim to apply genomic selection in Lithuanian dairy cattle and to evaluate economic benefit of the application.

1. Material and Methods

The study involved the collection of blood samples from 200 dairy cows and heifers. DNA was extracted by chloroform salt method (Sambrook *et al.*, 1989). Genotyping was performed by Igenity SNP panel identifying the genetic potential for dairy cattle traits - productive life, somatic cell count, milk yield, fat amount, fat %, protein amount, protein, dairy form. For each animal 360 single nucleotide polymorphisms (SNPs) covering the entire genome and related to dairy cattle phenotypic traits were tested by DNA technology. 72 000 SNP were investigated in total. Dairy cattle Igenity DNA profile was determined for every tested animal. DNA information was transformed into genomic scores showing genetic potential of each cow or heifer. The Igenity dairy cattle profile calculates genomic scores for traits using multiple DNA markers. The largest score indicates the best genomic value for productive life, milk yield, fat amount, fat %, protein amount, protein %, the lowest score indicates the best genomic value for somatic cell count. Combined results provide more complete picture of an animal's production potential. Genotypes were rated under the Igenity dairy cattle reference group (www.igenity.com).

Igenity custom sort software (www.igenity.com) was used to sort and rank animals according to DNA information based on the traits that are most important to dairy cattle breeders. This software allows to apply the priority filter for traits expressed by genomic scores. Weights or percentages of importance were applied to the traits. In the first model, we have applied 100 percent priority to milk yield, without any account of other traits. In the second model, 25% importance was applied for milk kg, 15% for fat %, 15% for protein %, 15% for productive life, 15% for somatic cell score and 15% for dairy form. The cattle were ranked on the basis of all entered criteria by means of the custom sort software. The result was customized, overall genomic index score on the familiar 1-to-10 scale from Igenity was generated. This allowed evaluating cattle based on the traits that are the most important in view of the selection goals. All rankings and calculation had been made separately for cows and heifers. As part of the model of application of genomic selection, 30% of poor performing cows that received the lowest genomic scores were replaced with 30% of best heifers that received the highest genomic scores.

Genomic scores were translated to actual figures for each trait using Igenity custom sort software allowing to evaluate genomic potential of the animal and additive genomic value effect. Genomic potential of the animal and additive genomic value effect expressed in net merit was recalculated to economic effect expressed in euros for extra milk, expressed in kilograms, and extra prolonged productive life, expressed in months. Productive life expressed in months was recalculated into production values – i.e. the kilograms of extra milk that can be produced by the cow with longer productive life and the potential economic benefit.

Prognostic economical effect of replacing 30% of poor performing cows with well performing heifers in 100 cow herd was evaluated.

2. Results and Discussion

Powerful DNA technology provides a wealth of valuable breeding, management and marketing information. Genomic selection offers many advantages in terms of improvement of the rate of genetic gain in dairy cattle breeding programs. The most important factors that contribute to faster genetic gain include: greater accuracy of predicted genetic merit for young animals; shorter generation interval as a result of heavier use of young, genetically superior males and females; increased intensity of selection, as breeders can use genomic testing to screen a larger group of potentially elite animals. By increasing the accuracy and intensity of selection and shortening the generation interval, the rate of genetic progress for economically important dairy traits can be approximately doubled. The introduction of genomic selection in the U.S. in 2008 reduced the generation intervals by six years. This change contributed significantly to the growth of all other developments. When the genomic selection was introduced the analysis showed that genetic enhancements contributed to increase in milk, fat and protein yield. When data was directly compared between 2008 and 2014, the improvement was 71%, 111% and 81%, of milk, fat and protein, respectively (Garcia-Ruiz *et al.*, 2016).

Igenity uses the power of DNA to help understand and manage the potential of animals to perform and transmit traits that are economically important. The Igenity dairy cattle profile shows animal genetic potential tested by DNA SNP multiple markers and transformed into genetic scores for dairy form, milk yield, fat amount, fat percent, protein amount and protein percent, somatic cell score, dairy form. The correlation between the genomic profile and phenotypic features was tested in four cattle populations for different breeds of cattle kept under different conditions, diversifying the population from 4000 to 6000 cattle, using the multivariate statistical model. The genomic profile was confirmed in 250,000 animals' population. Milk, fat and protein yields have routinely been collected for as long as a century. The yield traits have had varying economic weights in total merit indices (Miglior *et al.* (2005), but progress would be anticipated based on their moderate heritability (~0.30) (Van Tassell *et al.*, 1999). Different selection methods have been used starting from simple phenotypic evaluation up to the best linear unbiased prediction (BLUP). The revolution in selection occurred with the application of genomic selection method. SNP markers used by Igenity identify genetic variations that help to regulate milk yield, protein and fat content, without decreasing fertility. Dairy form research has shown that cows, high in dairy form, are more susceptible to metabolic, reproductive and foot and legs problems. Dairy form is closely related to productive life, especially through its effect on reproductive traits. Animals received 10 score for dairy form as a part of the Igenity profile, will have low dairy form – a good

indicator of longevity. The value of each extra month of productive life translates into additional profit per cow. Productive life (PL) (VanRaden, Wiggans, 1995) is a measure of animal longevity based on the amount of time a cow spends producing milk in its life. Longer lived animals typically are more profitable than shorter lived animals, particularly when the cost of raising an animal from birth to the start of lactation is high. The heritability of PL is relatively low ($h^2 = 0.08$), and selection accuracy is typically low for young animals that have few offspring with direct culling information (Weigel *et al.*, 1998). Despite these challenges, the trait has substantial economic value and currently receives 22% of the total emphasis in the combined economic index. PL has strong correlations with fertility and other fitness traits. Somatic Cell Score (SCS) is a profit driver for many producers as well as an indicator of potential for mastitis. It is a measure of udder health derived from somatic cell count that is associated with intramammary infection, mastitis. The SCS trait is important because it has strong relationship with the presence of clinical and subclinical mastitis and is much easier to measure than mastitis in dairy cattle (Shook, Schutz, 1994; Miller *et al.*, 2009). Sensitiveness to mastitis has great economic importance in the dairy industry because of losses associated with reduced milk production; discarded milk; premature culling; and increased costs for therapeutics, veterinary care and replacement animals (Hogeveen *et al.*, 2011). As Igenity profiles can be used at any age, the Igenity analysis for SCS can be used to identify calves and heifers with potential for high SCS and susceptibility to mastitis before they enter the parlour. An animal which scores a 10 for SCS has the potential for higher Somatic Cell Scores and may be more susceptible to mastitis than an animal with a 1 genomic score.

Table 1. Summarized results of Igenity profile genomic scores for Lithuanian dairy cattle

Genomic scores	Percent of animals in tested population, which have certain genomic score by traits							
	Productive Life, months	Somatic Cell Score	Milk, kg	Fat, kg	Fat, %	Protein, kg	Protein, %	Dairy form
10	2.5*	1.5	0	8.0*	6.0*	2.0*	3.5*	0
9	4.5	3.0	3.0*	3.5	5.5	7.0	14.0	4.0*
8	16.0	9.0	10.0	14.0	5.5	18.0	24.0	4.5
7	22.5	17.0	22.0	17.5	16.5	17.0	30.5	12.0
6	24.0	18.0	27.0	19.5	18.5	22.0	22.5	21.5
5	17.0	16.0	17.5	14.5	10.5	14.0	5.0	21.0
4	8.5	19.0	14.5	10.5	19.5	12.5	0.5	18.0
3	4.5	9.0	4.5	9.0	10.0	3.0	0	11.5
2	0.5	3.0	1.5	3.5	5.0	4.0	0	5.5
1	0	4.0*	0	0	3.0	0.5	0	2

Notes: *indicates percent of animals that have the best genomic score by the respective trait.

Source: calculated by the authors.

High genomic scores varying from 8 to 10 points in productive life were received by 23% of tested cows, in milk yield 13%, in fat kg 25.5%, in fat percent 17%, in protein kg 27%, in protein percent 41.5%. Low genomic scores ranging from 1 to 3 which are desirable in somatic cell count were demonstrated by 13% of tested animals. 35% of all tested dairy cattle had middle genomic scores: 5 or 6. (Table 1)

Table 2. Comparison of average genomic values between the Lithuanian dairy cattle with Igenity reference group animals

Traits	Average genomic values of tested dairy animals	Average genomic values of Igenity reference animal group
Fat kg	6.19	5.02
Fat %	5.80	4.96
Milk kg	6.01	5.93
Productive Life	6.26	5.99
Protein kg	6.18	6.36
Protein %	7.26	6.67
Somatic Cell Score	5.38	5.55

Source: calculated by the authors.

Average genomic values of tested dairy animals were higher than average genomic values of Igenity reference animal group especially for fat kg and fat %, approximately 1 genomic point, for milk kg - nearly the same, for protein kg - less than in the Igenity reference animal group. Somatic Cell Score genomic value was better in our tested dairy animals than in reference animal group (*Table 2*).

Table 3. Additive genomic value effect to dairy cattle phenotypic traits

Genomic scores	Additive genomic value effect					
	Milk, kg	Fat, kg	Protein, kg	Productive Life months	Somatic Cell Score (0-9)	Dairy form
10	-	33	18	5.5	0.35	-3.4
9	970	28	16	4.6	0.31	-2.9
8	853	24	14	4.1	0.27	-2.6
7	731	21	12	3.5	0.23	-2.2
6	617	18	10	3.0	0.20	-1.9
5	504	14	8	2.4	0.16	-1.5
4	387	11	6	1.9	0.12	-1.2
3	263	7	4	1.7	0.09	-0.8
2	150	4	3	1.3	0.05	-0.5
1	0	0	0	0	0	0.0

Source: calculated by the authors.

In the Igenity animal reference group, animals are rated by genomic scores according to the SNP information and correlations with phenotypic traits. The genomic scores are related to the expression of additive phenotype traits. Following the comparison between the SNP data of each tested animal and the SNP data of animal reference group, genomic scores were input for tested animals. The best cows that got genomic score 9, had the genetic potential to give 970 kg more milk per lactation than cows that had genomic score 1. There were 3 percent of such animals in the tested group of 200 animals (*Table 3*) and they could give extra 5,820 kg per lactation in comparison to animals with genomic score 1. Consequently, if there are 13% of cows in the herd that got high genomic scores ranging from 8 to 9 in milk yield, 22,880 extra milk kg per lactation can be drawn. If there are 25.5% of cows in the herd that got genomic scores ranging from 8 to 10 in fat kg and 27% in protein kg, extra 1,396 kg of milk fat and 800 kg of protein per lactation in tested herd can be drawn. Prolonged productive life can give extra 200.1 months of milking the best cows that can be

converted in 96,656 kg of extra milk kg in 200 cow herd, while the average milk yield per cow is 5,600 kg.

Table 4. Additive genomic value effect, where the increase in milk yield is the priority (100 % for milk kg)

Average genomic score for all traits	Additive genomic value effect								
	Milk, kg	Fat, kg	Fat, %	Protein, kg	Protein, %	Productive Life Months	Somatic Cell Score (0-9)	Dairy form	Dairy cattle
5.5	548 ±189 ^{1*}	24 ±11	0.29±0.12 ^{1***}	10 ±4 ^{1***}	0.13±0.02 ^{1***}	2.95±0.91	0.19±0.08 ^{1***, 2**}	1.7±0.7 ^{1***}	Cows the entire herd
6.01	641 ±128	17±8	0.24±0.09	11±3	0.12±0.02	2.96±0.84	0.19±0.09	1.7±0.7	Cows - 70 % of the best selected according to the genomic scores
6.06	527±130 ^{1*}	21±7	0.26±0.08	9±4	0.13±0.02	3.41±0.96	0.24±0.08 ^{1***}	1.2±0.5 ^{1***}	Heifers – the entire herd
8.28	876±58	19±5	0.17±0.06	14±2	0.10±0.01	3.18±0.68	0.27±0.08	1.6±0.8	Heifers - 30 % of the best selected according to the genomic scores
6.41	696±163	17±8	0.22±0.09 ^{1***}	12±3 ^{1***}	0.11±0.02 ^{1***}	3.02±0.82	0.21±0.09 ^{2**}	1.61±0.69	Herd with 30% of cows replaced with 30% of heifers

Notes: 1, 2, 3 – the difference is statistically significant. * - indicates value of significance (*P<0.05 ** P<0.01 ***P<0.001).

Source: calculated by the authors.

In the first selection model, cows and heifers were sorted and ranked with the Igenity custom sort software by applying 100 % priority to milk yield, without any account of other traits. 70 % of cows with the highest genomic scores were selected to remain in the herd and 30 % of heifers with the best genomic scores for milk yield were selected for replacement. Average additive effect to milk yield per cow per lactation in 100 cows herd was 548 kg, following selection of 70 % of the best cows - 641 kg per cow per lactation, in herd with 30% of cows replaced with 30% of the best heifers - 696 kg per cow per lactation. Consequently, the increase can amount to 148 kg per cow per lactation or 14,800 kg per lactation per 100 cows herd. The average genomic score of the herd after replacement of cows with the genomically evaluated best heifers increased from 5.50 to 6.41. Nonetheless, where only milk yield is accounted for, other important dairy cattle traits became worse – lower genomic potential of the milk fat percent, milk protein percent, increased somatic cell score (*Table 4*).

In the second selection model, cows and heifers were sorted and ranked with Igenity custom sort software by balanced accounting of all traits - 25% for milk kg, 15% for fat %, 15% for protein %, 15% for productive life, 15% for somatic cell score, 15% for dairy form. 70 percent of cows with the highest genomic scores were selected to remain in the herd and 30 percent of heifers with the best genomic scores were selected for replacement. Average additive effect to milk yield per cow per lactation in 100 cows herd was 548 kg, while following selection of 70 % of best cows - 553 kg per cow per lactation, in herd with 30% of

cows replaced with 30% of the best heifers - 524 kg per cow per lactation, meaning the decrease of 24 kg per cow per lactation or 2400 kg per lactation per 100 cow herd. But the additive effect of all other traits increases considerably: milk fat percent - from 0.28 to 0.32, resulting in 4 kg of fat per cow or 400 kg per 100 herd, productive life increased from 2.95 month to 3.45 month, resulting in 0.5 month extra productive life per cow, 50 extra milking month per herd, decreased somatic cell score and dairy form showing cows being less susceptible to mastitis, metabolic, reproductive and foot and leg problems (*Table 5*).

Table 5. Additive genomic value effect with equal priority to all important dairy traits in selection (25 % for milk kg, 15 % for fat %, 15 % for protein %, 15 % for productive life, 15 % for somatic cell score, 15 % for dairy form)

Average genomic scores	Additive genomic value effect when attention in selection is 25 % for milk kg, 15 % for fat %, 15 % for protein %, 15 % for productive life, 15 % for somatic cell score, 15 % for dairy form								
	Milk, kg	Fat, kg	Fat, %	Protein, kg	Protein, %	Productive Life, months	Somatic Cell Score (0-9)	Dairy form	Dairy cattle
6.08	548±190 ^{1*}	16±6 ^{1*}	0.28±0.13 ^{1**}	10±4 ^{2**}	0.13±0.02 ^{1*}	2.95±0.91 ^{1**}	0.20±0.09 ^{1***}	1.71±0.65 ^{1***}	Cows – the entire herd
6.31	553±167	20±9	0.29±0.12	9±3	0.13±0.02	3.32±0.76	0.16±0.05	1.64±0.71	Cows - 70 % of the best selected according to the genomic scores
7.21	611±172 ^{1*}	18±7	0.26±0.11	10±4 ^{1**}	0.13±0.02	3.13±0.91	0.24±0.08 ^{1***}	1.38±0.60 ^{1***}	Heifers – the entire herd
6.85	665±158	24±7 ^{1*}	0.38±0.10 ^{1**}	6±4 ^{2**}	0.15±0.02 ^{1*}	4.24±0.66	0.21±0.08	1.52±0.48	Heifers – 30 % of the best selected according to the genomic scores
6.45	524±174	21.00±9	0.32±0.12	8±2 ^{1**}	0.13±0.02	3.45±0.92 ^{1**}	0.17±0.06	1.61±0.66	Herd with 30 % of cows replaced with 30 % of heifers

Notes: 1, 2 – the difference is statistically significant. * - indicates value of significance (*P<0.05 ** P<0.01 ***P<0.001).

Source: calculated by the authors.

Table 6. Economical evaluation of additive genomic value effect with the increase of milk as the selection priority (100 % for milk kg)

Dairy cattle	For milk per lactation per cow, EUR/ per 100 cow herd, EUR	For prolonged productive life, where average milk yield per cow is 5600 kg per cow, EUR/ per 100 cow herd, EUR
Cows – 100 %	148/14,800	446/4,460
Cows - 70 % of the best selected according to the genomic points.	173/17,300	448/4,480
Heifers - 100 %	142/14,200	516/5,160
Heifers - 30 % of the best selected according to the genomic points.	237/23,700	481/4,810
Herd with 30% of the cows replaced with 30% of the best heifers.	188/18,800	457/4,570

Source: calculated by the authors.

Converting additive genomic value of traits into Euro in the first model, when milk yield was the only selection priority, extra milk yield resulted in 148 EUR (0.27 EUR per milk kg) per cow in the preselected herd, 173 EUR per cow in 70% of the best selected cow herd, 237 EUR in 30% of the best selected heifers herd and 188 EUR in herd with 30% of the cows replaced with 30% of the best heifers. Consequently, increase in EUR per cow per lactation using first genomic selection model was 40 EUR or 4,000 EUR for 100 cow herd annually. Given that the best selected heifers provide 237 EUR per animal, replacement of all cows with the best heifers leads to potential increase in money to 9,800 EUR per herd (*Table 6*).

Table 7. Economical evaluation of additive genomic value effect in EUR with all important dairy traits characterised by equal selection priority (25 % for milk kg, 15 % for fat %, 15 % for protein %, 15 % for productive life, 15 % for somatic cell score, 15 % for dairy form)

Dairy cattle	For milk during lactation per cow, EUR/ per 100 cow herd, EUR	For prolonged productive life, where average milk yield per cow is 5600 kg per cow, EUR/ per 100 cow herd, EUR
Cows – 100 %	148/14,800	446/4,460
Cows - 70 % of the best selected according to the genomic points	149/14,900	448/4,480
Heifers - 100 %	128/12,800	516/5,160
Heifers - 30 % of the best selected according to the genomic points	126/12,600	481/4,810
Herd with replaced 30 % of cows replaced by 30 % of best heifers	141/14,100	457/4,570

Source: calculated by the authors.

Converting additive genomic value of traits into Euro in the second selection model with all important dairy traits having equal selection priority resulted in 148 EUR (0.27 EUR per milk kg) per cow in the preselected herd, 149 EUR per cow in 70 % of the best selected cow herd, 126 EUR in 30 % of the best selected heifer herd and 141 EUR in the herd with 30% of the cows replaced with 30% of the best heifers. Consequently, under the second genomic selection model, the decrease in EUR per cow per lactation using was only 4 EUR, or 400 EUR per 100 cow herd 400 EUR annually (*Table 7*). Nonetheless, the increase in other important production and health traits, such as milk fat, milk proteins, decrease in somatic cell count showing better udder condition as well as better dairy form gives more value than insignificant decrease in milk yield.

The genomic selection effect depends on genomic value of heifers chosen by the authors for replacement. Following the evaluation of heifers' herd, if the genomic value of heifers is too low, the farmer may make the decision to purchase heifers with certain genomic value for separate traits from outside, in view of the selection trend chosen by a farmer. The one-to-ten scoring system provides a more definitive and focused profile. The results can be used to make more accurate breeding decisions, assist in heifer selection, whether buying, selling or keeping replacements, improve voluntary culling decisions, select superior dams or donor animals, adjust management practices, take inventory of herd and establish a baseline for improvement, calculate the economic effect of genetic progress of the herd, by using genomic selection.

Comprehensiveness of the Igenity profile allows to monitor the traits that are the most important for future profitability. This convenient scoring system used in combination with

published genetic evaluations enables benchmarking and monitoring of the genetic progress in herd. Testing animals early in their lives provides a powerful genetic basis for the many breeding, selection and management decisions. Bovine cattle rating according to genomic profiles makes it possible to select cattle with the best variants of the genomic profile in all dairy cattle characteristics, i.e. animals with the highest breeding genomic values (Hayes *et al.*, 2009).

Directions in herd improvement can be taken and economic effect can be calculated by determining the genomic profile for each bovine, ranking animals in herds according to the genomic profile results for individual traits, genomic profile results for various combinations of traits and upon selection of the highest genomic value cattle according to the genomic profiles and based on the obtained results.

Genomic profiles of dairy cattle can be input into the international database of dairy cattle genomic profiles and a farmer can then identify location of the herd by genetic potential in comparison to other herds in a separate breed, place of the herd or individual animal in the international database of almost 500,000 individuals in accordance with genomic profiles. Genomic selection already plays an important role in dairy cattle breeding programs, and this will be the case for the foreseeable future. Genomic selection is attractive for dairy cattle breeding, because it relaxes the need to perform phenotypic measurements of close relatives of all selection candidates. In dairy cattle breeding programs, genomic selection allows breeders to identify genetically superior animals at a much earlier age. In fact, animals that have been DNA tested can receive an accurate genomic estimated breeding value (GEBV) before they reach sexual maturity. This leads to decrease in generation intervals and increases genetic gain per year for all breeding goal traits. Introduction genomic selection is revolutionising breeding programs worldwide. This new selection tool is particularly beneficial for dairy cattle breeding programs because it allows to significantly reduce generation intervals and increase selection intensity at low cost, and the accuracy of selection is only marginally lower compared with progeny testing schemes. Genomic selection employs reference population to estimate effects for genome-wide single nucleotide polymorphism (SNP) that are used subsequently to predict breeding values for selection candidates. (Scheffers *et al.*, 2012; Wiggans *et al.*, 2016)

Conclusions

Following the pilot study of application of genomic selection in dairy cattle, it can be concluded that it provides the possibility to evaluate dairy cattle genomic potential, increases accuracy of selection when choosing different selection models and increases selection intensity, all of this resulting into economic benefit of application of the new selection tool. The genomic selection method is recommended for application not only to separate cattle herds but in the overall dairy breeds (Lithuanian Black and White, Lithuanian Red, Holstein) selection programs, as the genomic information of each animal is ranked in the international database, enabling international breeding value evaluation and participation in cross-country international dairy cattle breeding programs.

References

- Boichard, D., Guillaume, F., Baur, A., Croiseau, P., Rossignol, M.N., Boscher, M.Y., Druet, T., Genestout, L., Colleau, J.J., Journaux, L., Ducrocq, V.A., Fritz, S. (2012), "Genomic selection in French dairy cattle", *Animal Production Science*, Vol. 52, No 3, pp.115-120.

- Buch, L.H., Sorensen, M.K., Berg, P., Pedersen, L.D., Sorensen, A.C. (2012.), „Genomic selection strategies in dairy cattle: strong positive interaction between use of genotypic information and intensive use of young bulls on genetic gain“, *Journal of Animal Breeding and Genetics*, Vol. 129, No 2, pp.138-151.
- Calus, M.P.L., de Haas, Y., Pszczola, M., Veerkamp, R.F. (2013), „Predicted accuracy of and response to genomic selection for new traits in dairy cattle“, *Animal*, Vol. 7, No 2, pp.183-191.
- Daetwyler, H.D., Villanueva B., Bijma P., Woolliams, J.A. (2009), „Inbreeding in genome-wide selection“, *J. Anim. Breed. Genet.*, Vol. 124, No 6, pp.369-376.
- Garcia-Ruiz, A., Cole, J.B., VanRaden, P.M., Wiggans, G.R., Ruiz-Lopez, F.J., Van Tassell, C.P. (2016), „Changes in genetic selection differentials and generation intervals in US Holstein dairy cattle as a result of genomic selection“, *Proc Natl Acad Sci.*, Vol. 113, No 28, pp.3995-4004.
- Hayes, B.J., Bowman, P.J., Chamberlain, A.J., Goddard, M.E. (2009), „Invited review: Genomic selection in dairy cattle: progress and challenges“, *Dairy Sci.*, Vol. 92, No 3, pp.1313.
- Harris, B.L., Johnson, D.L. (2010), „The Impact of High Density SNP chips on Genomic Evaluation in Dairy Cattle“, *Interbull Bulletin*, No 42, pp.40-43.
- Hogeveen, H., Huijps, K., Lam, T.J. (2011), „Economic aspects of mastitis: New developments“, *N Z Vet J.*, Vol. 59, No 1, pp.16-23.
- König, S., Simianer, H., Willam, A. (2009), „Economic evaluation of genomic breeding programs“, *J. Dairy Sci.*, Vol. 92, No 1, pp.382-391.
- Mackay, T.F., Stone, E.A., Ayroles, J.F. (2009), „The genetics of quantitative traits: Challenges and prospects“, *Nat. Rev. Genet.* Vol. 10, No 8, pp.565-577.
- Meuwissen, T. (2009), „Accuracy of breeding values of ‘unrelated’ individuals predicted by dense SNP genotyping“, *Genetics Selection Evolution*, Vol. 41, No 1, pp.1-9.
- Miglior, F., Muir, B.L., Van Doormaal, B.J. (2005), „Selection indices in Holstein cattle of various countries“, *J Dairy Sci.*, Vol. 88, No 3, pp.1255-1263.
- Miller, R.H., Norman, H.D., Wright, J.R., Cole, J.B. (2009), „Impact of genetic merit for milk somatic cell score of sires and maternal grandsires on herd life of their daughters“, *J Dairy Sci.*, Vol. 92, No 5, pp.2224-2228.
- Pryce, J.E., Daetwyler, H.D. (2012), „Designing dairy cattle breeding schemes under genomic selection: a review of international research“, *Animal Production Science*, Vol. 52, No 3, pp.107-114.
- Pryce, J.E., Goddard, M.E., Raadsma, H.W., Hayes, B.J. (2010), „Deterministic models of breeding scheme designs that incorporate genomic selection“, *Journal of Dairy Science*, Vol. 93, No 11, pp.5455-5466.
- Sambrook, J., Fritsh, E.F., Maniatis, T. (1989), *Molecular Cloning. A laboratory manual*, 2nd Edition, New York: Cold Spring Harbor Lab. Soller.
- Schaeffer, L.R. (2006), „Strategy for applying genome-wide selection in dairy cattle“, *J. Anim. Breed. Genet.*, Vol. 123, No 4, pp.218-223.
- Schefers, J.M., Weigel, K.A. (2012), „Genomic selection in dairy cattle: Integration of DNA testing into breeding programs“, *Animal Frontiers*, Vol. 2, No 1, pp.4-9.
- Shook, G.E., Schutz, M.M. (1994), „Selection on somatic cell score to improve resistance to mastitis in the United States“, *J Dairy Sci.*, Vol. 77, No 2, pp.648-658.
- Taylor, J.F., Taylor, K.H., Decker, J.E. (2016), „Holsteins are the genomic selection poster cows“, *PNAS*, Vol. 113, No 28, pp.7690-7692.
- VanRaden, P.M., Wiggans, G.R. (1995), „Productive life evaluations: Calculation, accuracy and economic value“, *J Dairy Sci.*, Vol. 78, No 3, pp.631-638.
- Van Tassell, C.P., Wiggans, G.R., Norman, H.D. (1999), „Method R estimates of heritability for milk, fat, and protein yields of United States dairy cattle“, *J Dairy Sci.*, Vol. 82, No 10, pp.2231-2237.
- Weigel, K.A., Lawlor, T.J., Vanraden, P.M., Wiggans, G.R. (1998), „Use of linear type and production data to supplement early predicted transmitting abilities for productive life“, *J Dairy Sci.*, Vol. 81, No 7, pp.2040-2044.
- Wiggans, G.R., Cooper, T.A., VanRaden, P.M., Van Tassell, C.P., Bickhart, D.M., Sonstegard, T.S. (2016), „Increasing the number of single nucleotide polymorphisms used in genomic evaluation of dairy cattle“, *J Dairy Sci.*, Vol. 99, No 6, pp.4504-4511.
- Wiggans, G.R., VanRaden, P.M., Cooper, T.A. (2011), „The genomic evaluation system in the United States: Past, present, future“, *J Dairy Sci.*, Vol. 94, No 6, pp.3202-3211.
- Igenity Dairy Dashboard (2016), available at, <https://www.igenity.com>, referred on 23/12/2017.

LIETUVOS PIENINIŲ GALVIJŲ GENOMINĖS SELEKCIJOS EKONOMINIS ĮVERTINIMAS

SANTRAUKA

Kristina Morkūnienė, Sigita Kerzienė, Astrida Miceikienė

Siekiant įvertinti ekonominę genomines selekcijos panaudojimo naudą Lietuvos pieniniams galvijams, buvo atliktas bandomasis tyrimas. Kiekvienai karvei buvo nustatytas genomis pieninių galvijų „Igenity“ profilis pagal produktyvaus amžiaus požymį, somatinių ląstelių skaičių, primilžį, riebalų ir baltymų kiekį bei procentą, ir pieninę formą. Didelis, nuo 8 iki 10 siekiantis produktyvaus amžiaus požymio, genomis potencialas buvo nustatytas 23 % ištirtų karvių, primilžyje – 13 %, riebalų kg – 25,5 %, riebalų procentais – 17 %, baltymų kg – 27 %, baltymų procentais – 41,5 %. Nuo 1 iki 3 svyruojanti bei somatinių ląstelių skaičiui pageidautina žema genetinė vertė buvo nustatyta pagal 13 % ištirtų gyvūnų. Pieninių galvijų genomines selekcijos taikymas leido autoriams įvertinti pieninių genčių potencialą, padidinti selekcijos tikslumą, pasirinkti skirtingus atrankos modelius ir taikant naują selekcijos priemonę, didinti jos intensyvumą. Genominės selekcijos metodą rekomenduojama taikyti ne tik atskiroms galvijų bandoms, bet ir visose pieninių galvijų veislių (Lietuvos juodmargiams, Lietuvos žaliesiems, Holšteinams) selekcijos programose, nes kiekvieno gyvūno genomine informacija yra vertinama remiantis tarptautiniais duomenimis, suteikiant galimybę įvertinti veislinę vertę tarptautiniu mastu ir dalyvauti tarpvalstybinėse tarptautinėse pieninių galvijų veisimo programose.

REIKŠMINIAI ŽODŽIAI: ekonominė nauda, genomine atranka, galvijai, pieninių galvijų profilis, Lietuva.