Upgrading Dairy Cattle Evaluation System in Russian Federation

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Abstract

Russian Federation has a strong initiative to increase milk production and to meet increasing demand for dairy products. Typically dairy farms in the Leningrad region are large, e.g. have from 500 up to 2 100 cows. The average 305d production in 2015 was 8 331 kg milk, but the top herd had an average milk yield over 12 000 kg. Accurate selection of the next generation parents is a prerequisite for genetic improvement. Currently the prediction of breeding values of dairy cattle in Russian Federation is based on contemporary comparison following the instructions by the Ministry of Agriculture of USSR published in 1980. The contemporary comparison approach estimates breeding values for bulls only. Animal model BLUP can be expected to give less biased and more accurate estimates of breeding values.

Implementation of the animal model and genomic selection in the future requires farmers support. In order to demonstrate to the farmers the benefits of using cow EBVs in within herd selection and mating plans, a new animal model evaluation utilizing already collected phenotypic data from Russian Black and White and Holstein cattle in the Leningrad region was developed. The pedigree had 452 622 animals and the data had 356 907 repeated records from 320 798 cows. Breeding values were predicted for milk, fat and protein productions using repeatability animal model with variance components estimated by REML. The results were compared to EBVs from the old evaluation system. Until now 450 bulls and 1 100 cows have been genotyped using Illumina 50Kv2 and IDBv3 chips to enhance the development of the genomic prediction.

Keywords: genomic selection, BLUP AM, Russian dairy industry, evaluation methods

Introduction

During the last three decades, world milk production has increased by more than 50 percent, from 500 million tons in 1983 to 769 million tons in 2013 (FAO, 2016). According to Ministry of Agriculture (Yearbook 2016) report, Russian dairy sector produced around 30.7 million tons of milk in 2016, which is 4% of world dairy production. Most of the 8.2 million cows milking in Russia are Russian Black and White (54%) and Holstein (13%) and their crosses. Russian Black and White breed resembles the old Friesian breed and was developed by crossing local cows with Ost-Friesian bulls over 100 years ago. Modern dairy farmers are actively moving from the old dual-purpose Russian Black and White breed towards more dairy-type cows by using Holstein bulls as sires of the next generation. The rest of the dairy cows are Simmental (7%), Kholmogor (7%) and other breeds (33%). Farms in Russia are divided into three groups: commercial, family and smallholders, usually differing in the number of cows, legal status and recording systems. Smallholders and family farms are producing the same amount of milk as commercial farms, despite of the higher number of milking cows, 4.98 vs 3.22 million cows.

Commercial farms are a diverse group including breeding herds, breeding reproducers and commodity farms. Breeding herds and reproducers are farms with obligatory performance and pedigree recording, and are keeping only pure breed animals. Both breeding herds and reproducers are involved in breeding, multiplication and selling animals to commodity farms and smallholders, but only farms with the breeding herd status can sell young bulls to AI stations.

At least 60 Russian regions are keeping dairy herds with varied number of animals and production levels. Some regions, like Bashkirkostan and Tatarstan, produce a lot of milk but the production level per cow is low. In contrast, some regions like Leningrad and Kirov have less cows but the production level per cow is higher. Possibility to transmit genetics from the best regions to the regions with abundant feed and land resources, may increase the level of national milk production. In order to produce more milk, farms with good management usually use imported semen because genetic level of local bulls is not high enough to keep herd in progress. The results of this is an intensive use of imported genetic material from USA, Canada or Europe as parents of the next generation.

The current official evaluation method used for breeding value estimation in Russia is Contemporary Comparison (CC), according to the official published legislation (Instruction, 1979). Evaluations by CC have not been used in many countries since 1980s to 1990s (Schaeffer, 2013) because it allows breeding value estimation only for bulls with daughters, and do not work properly in herds with different environment conditions. Development and modernization of Russian dairy cattle breeding can be achieved through updating the breeding value evaluation and educating farmers. An opportunity to get accurate EBVs and GEBVs for young animals, cows and bulls, can also motivate farmers to invest in more accurate milk recording systems. The goal for Russia is also to become a member of the Interbull community and to get MACE and GMACE predictions for bulls.

For the purpose of introducing a modern genomic evaluation system to Russian farmers, Russian Research Institute of Farm Animal Genetics and Breeding (Russia), University of Helsinki (Finland) and Natural Recourses Institute of Finland (LUKE) have established a research project (RUGE), using Leningrad region as a model to genomic evaluation. The purpose of this study was to develop a BLUP animal model for Holstein and B&W herds in Leningrad region as a first step to genomic evaluation.

Material and Methods

Milk Recording in Leningrad region

Leningrad region, laying on Baltic Sea and bordering with Finland, Estonia and Karelia, is one of the most developed dairy regions in Russia with high level of integration of modern technologies in agriculture sector. For many years the region has had the highest average milk production per cow in Russia. Most popular and common breeds are Holstein or B&W (48 herds) and Ayrshire (12 herds). Herd sizes vary from 500 to 2 100 milking cows with herd average production level up to 13 000 kg.

Breeding herds and reproducers provide data to the regional recording centers or to the local departments of the Ministry of Agriculture. A single recording center is serving one region at the time by collecting data from farms, making data quality control and providing data to the central database. For herd management and performance recording the breeding herds and reproducers are usually using Russian software Selex® (http://plinor.spb.ru/index.php?l=0&p=3). Milk recording is based on monthly recording of milk volume and milk composition by farmers. Milk composition is analyzed using on-farm equipment or milk laboratory services. Due to variability in milking and milk analysis systems the data recording centers allow farmers to make manually updates into the database. The Selex® software accepts direct data flow from laboratory and on-farm equipment to the database. Equipment used by farmers for milking and milk composition analyses are not always ICAR certified.

Contemporary comparison

According to the Instruction (1979), bulls are ranked to quality categories depending on the level (superiority) of their daughters over contemporaries based on milk and fat yields. Quality categories are shown in Tables 1 and 2 for milk yield and fat content, respectively.

Bulls beyond A, B and N grades are defined as negative, and cannot be used for breeding purposes in commercial farms. For accurate category definition, bull's superiority in kg should be corrected for the number of daughters using a correction coefficient table (Table 3), e.g., if 50 daughters produced 100 kg more milk than their contemporaries in one herd, according to Table 3, the 100 kg should be corrected by multiplying it by 0.81. Thus, the corrected superiority of the daughters is 81 kg. This value is compared to Table 1 to find the appropriate category for the bull.

In addition to above described relative production compared to contemporaries, the Instruction (1979) determine that bulls having daughters with 180% higher yield than phenotypic base of their breed can be assigned at least into category Neutral. Phenotypic bases for the selected breeds are shown in Table 4. Phenotypic base is very low today as it was defined already in the 1980s (. Modern imported and local bulls with negative value in relative CC production categories are using this loophole to reach Neutral category as their daughters' production level is surely higher than the defined base.

BLUP Animal model

Data was provided by Leningrad local recording center - Plinor. Data from 2000 to 2016 included 552 000 phenotypic records of milk, fat and protein yields from 206 000 cows. The pedigree data included 452 662 animals starting from 1962. As Russian animals are not obligatory identified according to the ICAR standards, internal Selex® numbers were used to link the pedigree and phenotypic data. Pedigree renumbering and pruning was done using RelaX2 program (Strandén & Vuori, 2006). Because the number of imported animals in the region is quite high, phantom parent groups were used to account for different genetic level of imported sires during the years. Single trait repeatability animal model was used to estimate variance components and breeding values (EBV):

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_1a} + \mathbf{Z_2p} + \mathbf{e} \qquad [1]$$

where **y** is a vector of yield records (either 305-day milk, fat or protein yield), **b** is the vector of fixed effects, $\mathbf{a}\sim N(0,\mathbf{A}\sigma^2_a)$ and $\mathbf{p}\sim N(0,\mathbf{I}\sigma^2_p)$ are vectors of random animal and permanent environmental effects, respectively, **X** is the design matrix, which relates records to appropriate fixed effects, and $\mathbf{Z_1}$ and $\mathbf{Z_2}$ are the design matrices relating records to random effects, and $\mathbf{e}\sim N(0,\mathbf{I}\sigma^2_e)$ is the vector of residual effects. Matrix **A** is a relationship matrix, **I** is a identity matrix, and σ^2_a, σ^2_p, and σ^2_e correspond to additive genetic, permanent environmental and residual variances, respectively.

Model [1] was run twice per trait, using records only from the first or all the available lactations up to five. The model included two fixed effects: herd –year –season (HYS) and days open – age of calving (DOAC). The HYS effect included 2603 levels and the DOAC effect had 255 levels.

Variance components were estimated using the AI - REML method of the DMU program package (Per Madsen & Just Jensen, 2013). Breeding value evaluation was done using MiX99 software (MiX99, http://www.luke.fi/mix99).

Results

About 40% of the data was excluded during data editing. The final data included 356 907 records. Average phenotypic values for the three traits by lactation in the final dataset are presented in Tables 5 to 7.

The variance components of milk, fat and protein yields are given in Table 8. Milk yield genetic trend (kg) using first and multiple lactation records for cows born in 2003-2016 are shown in Figure 1. Base population for the trend was defined as the mean of cows born in 2009-2011. Average genetic trends for both models were quite similar, 57 and 53 kg/year for first and multiple lactation models, respectively. Trend validation was done using the Interbull test criteria I. The difference between the first lactation and the multiple lactation model trends was smaller than the Interbull test criteria I threshold of $0.02*\sigma_a$ (11.5 kg).

Fat and protein trends are presented in Figures 2 and 3. Average trends for the first and multiple lactation models were 1.77 kg/year and 1.81 kg/year for fat yield and 1.58 kg/year and 1.63 kg/year for protein yield.

Discussion

The estimated variance components suggested relatively low heritabilities and even repatabilities, which was expected given the data collection pitfalls. Data preparation and validation took the main part of the time when developing the evaluations. Farmers' chance to enter data manually leads to random mistakes or introduces some bias, which makes it challenging to get reliable predictions. However, the low heritability can be mostly explained by possible excessive environmental variation that is difficult to model. Including phantom parents groups in the pedigree improved heritability by several percent.

While genomic evaluation stands as the main goal for the RUGE project, the main sub-goal was to show farmers and industry the benefits of using modern genetic evaluation system. An important outcome was to show farmers, why it is vital to record reliable data, as poor quality data reduces the opportunity for future predictions. The correlation of BLUP EBVs with the CC values was only 0.37, which highlights the need for fast implementation of routine BLUP evaluation to increase the accuracy of selection. New breeding values for cows and heifers confuse farmers at first, but increase their interest to use BLUP EBVs in mating process. In the same time, current political pressure and poor Ruble exchange rate make imported semen twice as expensive, and increases the demand of local bulls. During the three project years, a positive change in the data recording and appreciation of EBVs has been noticed, which pinpoints the need for research and development in this area

Despite many pitfalls in Russian dairy sector today, utilization of modern evaluation methods with certain level of bias can be a good start for industry to change working strategy. Future changes can reduce and eliminate bias in prediction through high quality data collection according to the ICAR guidelines.

Until now 500 cows and 270 bulls are genotyped using Illumina 50Kv2 chip, and 600 cows and 201 bulls were genotyped by Illumina IDBv3 chip. The project will continue genotyping more animals and developing a genomic model for prediction of breeding values.

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Appendix

Table 1. Bull's categories according to daughter's superiority in milk yield.

Contemporary group Production level (kg)		Difference from contemporary group in %			
		A1	A2	A3	Neutral
I	>4501	>3	2.9-2.0	1.9-1.0	+0.9 – (3.5)
II	4001-4500	>4	3.9-3.0	2.9-2.0	+1.9 – (-3.0)
III	3401-4000	>6	5.9-4.0	3.9-2.5	+2.4 – (-2.5)
IV	2800-3400	*	>9	8.9-3.0	+2.9 - (-2.0)

Table 2. Bull's categories according to daughter's superiority in fat %.

Contemporary group	Production level (fat %)	Difference from contemporary group in %			
		B1	B2	B3	Neutral
I	>4.4	>0.05	0.04-0.03	0.02-0.01	+0.0 – (-0.10)
II	4.2-4.39	>0.10	0.09-0.07	0.06-0.04	+0.01 – (-0.09)
III	4.0-4.19	>0.15	0.14-0.10	0.09-0.06	+0.05 – (-0.07)
IV	3.8-3.99	>0.20	>0.19-0.15	0.14-0.08	+0.07 - (-0.05)

Table 3. Daughters number correction coefficient.

Number of daughters	Correction coefficient	Number if daughters	Correction coefficient
15-19	0.58	50-59	0.81
20-24	0.64	60-69	0.83
25-29	0.70	70-79	0.85
30-34	0.73	80-89	0.87
35-39	0.75	90-99	0.88
40-44	0.77	100-199	0.90
45-49	0.79	200-299	0.95
		>300	0.99

Table 4. Phenotypic basis in milk yield and fat content for selected breeds.

Breed	Milk yield, kg	Fat %
Ayrshire	2550	4.2
Jersey	2300	5.6
Simmental	2300	3.5
Kholmogor	2500	3.7
Black and White (Fritz)	2700	3.6
Yaroslav	2400	4.0
Red steppe	2550	3.7

Table 5. Average phenotypic value for milk yield in final data set.

Lactation number	Mean (kg)	Standard deviation	Min value	Max value
1	7758	1682	2712	12804
2	8165	2037	2054	14276
3	8160	2109	1833	14487
4	7961	2116	1613	14309
5	7644	2078	1410	13878

Table 6. Average phenotypic value for fat yield in final data set.

Lactation number	Mean (kg)	Standard deviation	Min value	Max value
1	296	63.2	106.4	485.6
2	314	75.9	87.2	542.6
3	317	79	80	554
4	311	80	71	551
5	300	77	69	531

Table 7. Average phenotypic value for protein yield in final data set.

Lactation number	**Mean (kg)**	**Standard deviation**	**Min value**	**Max value**
1	256	49	108	402
2	271	59.5	92	449
3	270	62	84	456
4	263	62	77	449
5	252	60	72	432

Table 8. Variance components and genetic parameters**.**

Traits	**Variances**			**Parameters**	
	σ^2_a	σ^2_{pe}	σ^2_e	h^2	**r**
Milk yield	330956	270116	1244178	0.18	0.33
Fat yield	420	308	1718	0.17	0.29
Protein yield	242	149	972	0.18	0.28

Figure 1. Cows genetic trend in milk yield.

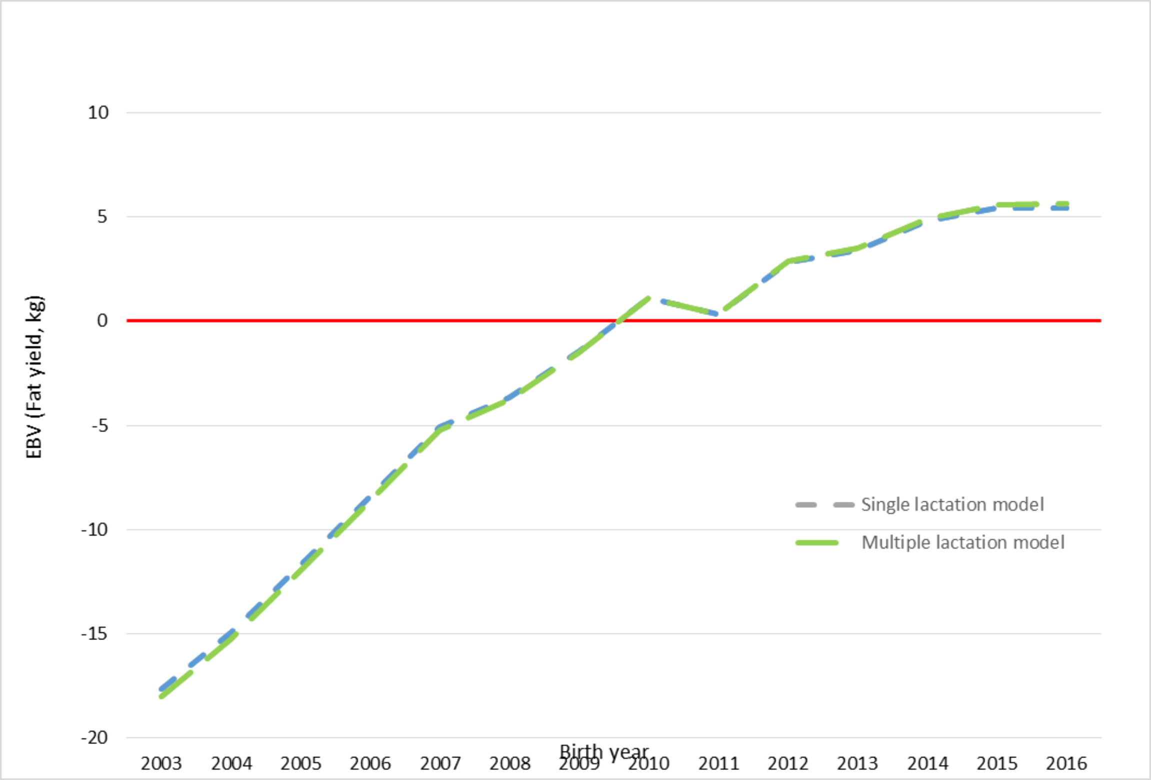

Figure 2. Cows genetic trend in fat yield.

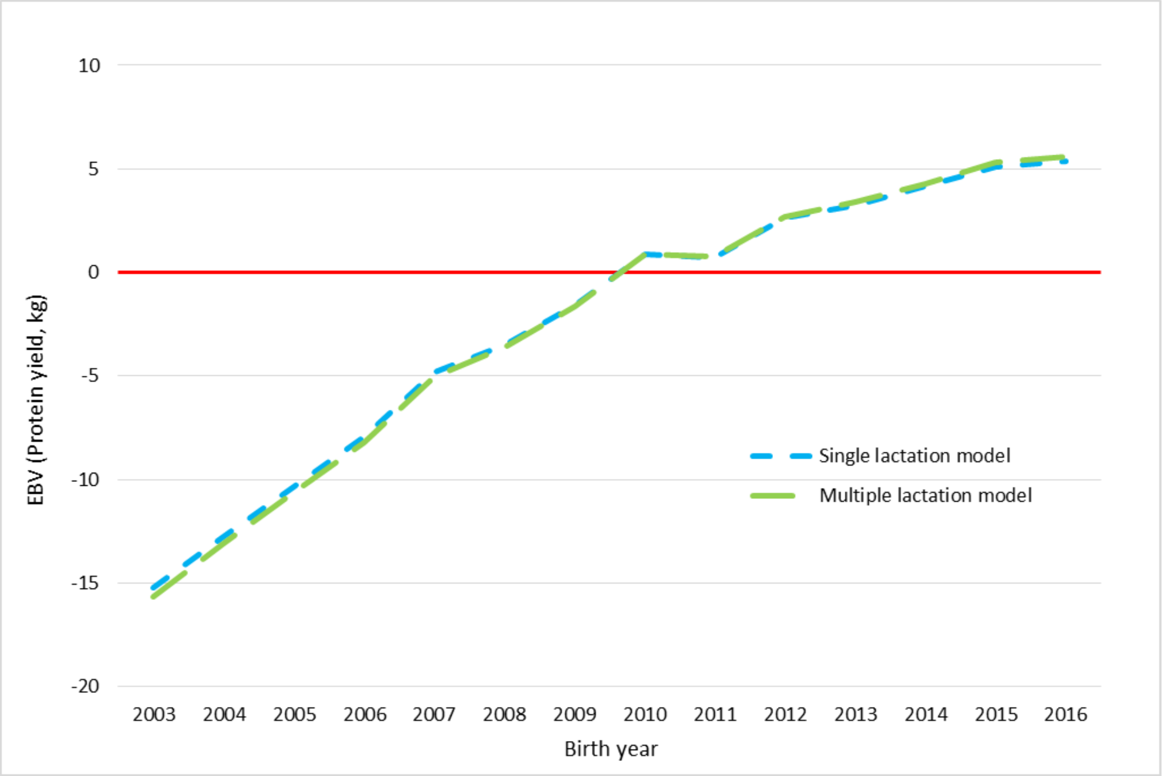

Figure 3. Cows genetic trend in protein yield.