



## Data Article

# Assessment of the variability of reproductive abilities of a black and white cattle using genealogical data and paratypical factors



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## ABSTRACT

The purpose of this study was to assess the role of paratypical and genetic factors in the variation of the complex of traits associated with the reproductive quality of livestock in the conditions of the CJSC breed livestock factory farm “Irmenev” in a retrospective aspect. Black-and-White Irmenskiy interbreeds type breed was officially registered in 2000 by the Ministry of Agriculture of the Russian Federation as a breeding achievement and is a unique cattle subpopulation, bred only at the Irmenev breed livestock factory farm, in Western Siberia, (Russia). This type is the best in all of Western Siberia in terms of milk yield and appearance among annual competitions and official state assessments. Therefore, the authors chose this breed as a material of research. Over 19 years, the authors studied the variability of traits such as milk yield, fat and protein content in milk, productive life, insemination rate, calving interval, open days, dry period, calving ease, and body weight. These traits are closely associated with the reproductive characteristics of the Black-and-White breed of the Irmenskiy subpopulation. The authors assessed the variability of these traits, which is influenced by the factors by “Year”, “Lactation number” and “Sire’s genotype”. The

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data obtained showed a close genotype-environment interaction. Also, the conditions of feeding and keeping at the breed livestock factory farm have a significant impact on these traits.

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## Specifications Table

Subject	Agriculture, Animal Science, Animal Breeding, Livestock, Dairy Cattle
Specific subject area	Animal Breeding and Genetics, Reproduction of cattle
Type of data	Text and tables
How the authors got the data	The authors collected the materials of this research for the period from 2000 to 2019 at the breed livestock factory farm "Irmen". The authors of this research, collected data, recorded and analysed it.
Data format	Raw and analysed
Parameters for data collection	The parameters for data collection were the main traits of the White - and - Black cattle: milk yield, fat and protein content in milk, productive live, insemination frequency, calving interval, open days, dry period, calving ease and body weight.
Description of data collection	The research materials were individuals' cattle, which at the "Irmenskiy" breed livestock factory farm (Novosibirsk region, Russia) from 2000 to 2019. The authors collected material for research based on individuals' data with open days no more than 150 days, lactation - from 290 to 320 days, intercalving period - from 300 to 600 days. The authors did not include all other animals of the Irmenskiy breed livestock factory farm in the statistical data processing. Data obtained from the SELEX Dairy Cattle program. PLINOR production (St. Petersburg, Russia). This software is the de facto standard of the Russian Federation in the field of selection and breeding work with cattle. Link to the program SELEX Dairy Cattle <a href="https://plinor.spb.ru/index.php?l=0&amp;p=3">https://plinor.spb.ru/index.php?l=0&amp;p=3</a>
Data source location	The authors carried out the statistical analysis of the source data and the construction of the mathematical model using the statistical programming language R and free spreadsheet software like OpenOffice Calc. Novosibirsk State Agrarian University, Novosibirsk, Russian Federation
Data accessibility	The authors provided the raw data files and additional table in the Data in Brief (Harvard Dataverse), <a href="https://doi.org/10.7910/DVN/FDWVQL">https://doi.org/10.7910/DVN/FDWVQL</a> . The tables show a matrix of correlation coefficients with an assessment of significance. All significant correlations in the matrix are marked with asterisks (divided into three levels of value).

## Value of the Data

- The results obtained have a pronounced practical value. And they are associated with the need to improve the reproductive qualities of animals against the background of an increase in milk production. It is known that highly productive animals, as a rule, have reduced reproductive abilities; therefore, it is necessary to search for the required tools to improve reproduction;
- These data are useful for animal breeders and geneticists, specialists in the field of cattle reproduction, researchers in the field of veterinary genetics. Primarily, this article will be helpful to farmers who are engaged in the reproduction of Black-and-White cattle as well as veterinarians and livestock specialists who are interested in increasing the reproductive traits of cows;
- Other specialists can repeat similar studies, but in other environmental conditions and other cattle populations, the results may be different. The same studies will clarify the possible

role of genetic factors in the variability of traits associated with animal reproduction, as well as for compiling a list of factors that have a permanent effect on the parameters under study.

## 1. Data Description

**Table 1.** Variability of some economically useful traits in 2019. This table presents the most essential economically useful traits used on dairy farms. And also, some traits associated with reproductive abilities are given. The authors have selected such characters that can be found in any farm in Russia. Any researcher in this way can conduct similar research.

**Table 1**

Variability of some economically useful traits in 2019.

Indicator	n	Mean	S.E.	Me	IQR	Cv
Milk yield for 305 days of lactation, kg	693	11,127	71.1	11,207	2395	16.8
Fat content in milk*, %	693	3.75	0.012	3.72	0.293	8.2
Protein content in milk*, %	688	3.23	0.003	3.23	0.08	2.4
Productive life, years	704	6.86	0.085	6.49	2.47	33
Number of semen doses per a pregnant dairy cow	703	1.5	0.026	1	1	45.3
Inter calving period, days	704	421.4	2.97	396	98.6	18.7
Open days, days	704	98	0.94	92	41	25.4
Dry period, days	704	65.5	0.512	64	8	20.7
Calving ease, points	704	3.05	0.018	3	0	15.6
Body weight, kg	704	626.7	2.35	615	79.6	10

**Table 2.** The influence of sire genotype, lactation and the year on traits related to livestock reproductive abilities. This table shows the influence of independent factors on the variability of dependent variables, which were studied using multivariate analysis of variance.

**Table 2**

The influence of the sire genotype, lactation and the year on indicators related to livestock reproductive ability.

Factors	Pillay criterion	F	%	Df	num Df	den Df	$\alpha$
Lactation	0.95401	243.6	79.5	8	56	86,450	< 0.001
Year	0.50159	52.96	17.3	18	126	86,450	< 0.001
Father genotype	0.79363	8.97	3.2	176	1232	86,450	< 0.001

**Table 3.** Contribution of studied factors to discrimination between traits related to livestock reproductive abilities. This table shows the results of discriminant analysis, which made it possible to establish those traits for which the differences were the most significant, depending on the influence of a different factor. The standardized coefficients of the discriminant function make it possible to judge the magnitude of such a contribution. The structural coefficients indicate the correlation of individual variables with the discriminant function.

## 2. Experimental Design, Materials and Methods

Productive longevity of cows, as one of the indicators taken into account in the selection and compilation, is a complex trait. The variability of this trait depends not only on features associated with the reproductive health of animals but also on susceptibility to other diseases. Thus, several authors have put forward a theory and demonstrated the role of tumor necrosis factor- $\alpha$  (TNF- $\alpha$ ) in the resistance of livestock to mastitis, which, in turn, leads to the culling of cows. The active participation of pro-inflammatory cytokines TNF- $\alpha$  in the functioning of the body's immune system explains this process [1,8,11]. Therefore, when assessing the role of genetic and

**Table 3**

Contribution of studied factors to discrimination between traits related to livestock reproductive abilities.

Indicators	Standardised coefficients		Structural coefficients	
	function 1	function 2	function 1	function 2
<b>Lactation</b>				
Open days	-0.003	0.051	0.001	0.015
Dry period	0.056	0.111	0.057	0.143
Calving ease	<b>0.939</b>	-0.340	<b>0.952</b>	-0.125
Body weight	0.292	<b>0.790</b>	0.418	<b>0.698</b>
Inter calving period	-0.070	-0.106	-0.054	-0.039
Productive life	0.148	<b>0.569</b>	0.327	<b>0.738</b>
Insemination frequency	-0.0002	0.008	-0.0002	0.015
% of variability	72.8	25.7	-	-
R <sup>2</sup>	0.589	0.335	-	-
<b>Year</b>				
Open days	0.053	-0.261	-0.033	-0.032
Dry period	0.005	0.039	0.053	-0.035
Calving ease	-0.025	-0.096	0.128	-0.282
Body weight	0.161	<b>-0.786</b>	0.272	<b>-0.830</b>
Intercalving period	0.065	0.062	-0.004	0.004
Productive life	<b>0.996</b>	0.037	<b>0.992</b>	-0.099
Insemination frequency	0.040	<b>0.678</b>	0.013	-0.430
% of variability	96.1	2.1	-	-
R <sup>2</sup>	0.466	0.019	-	-
<b>Sire genotype</b>				
Open days	-0.0004	-0.078	-0.079	-0.132
Dry period	0.004	-0.006	0.035	-0.123
Calving ease	0.016	-0.127	0.147	-0.323
Body weight	0.025	<b>-0.977</b>	0.184	<b>-0.982</b>
Intercalving period	0.014	-0.085	-0.042	-0.118
Productive life	<b>1.000</b>	-0.048	<b>0.999</b>	-0.231
Insemination frequency	-0.008	-0.026	-0.026	-0.115
% of variability	85.5	6.3	-	-
R <sup>2</sup>	0.576	0.09	-	-

paratypic factors in the variability of reproduction rates, it is essential to take this feature into account.

The indicators of milk productivity in animals need to be improved, while production should be at a low cost. The breeders are continually improving technologies in this direction. Therefore, genetic-breeders pay great attention to the indicators of the reproductive capacity of livestock in the selection process, taking into account the influence of environmental and genetic factors.

The authors of this study also understood that any object is in a multidimensional space. There are a vast number of interacting random and fixed factors that affect the traits of interest [2–4,7]. Without understanding these things, it would be impossible to do this research.

In this regard, we aimed to assess the role of paratypical and genetic factors in changing the complex of traits associated with the reproductive qualities of livestock in a retrospective aspect. Achieving this goal will improve the performance of livestock breeders and other livestock specialists dealing with reproduction problems. Today, the unique Black-and-White cattle of the Irmensky type is the best in the whole of Western Siberia among annual competitions and according to official government estimates. These criteria formed the basis for the choice of the object and material of this study.

## 2.1. Research methods

The authors performed statistical analysis of the raw data and building mathematical models using the statistical programming language R and free spreadsheet software such as OpenOffice Calc.

Testing the degree of compliance of empirical distributions concerning the Gaussian distribution was carried out using the Anderson-Darling and Shapiro-Wilk criteria. The authors also assessed the variability of the list of dependent traits using multivariate linear regression and analysis of variance (MANOVA) model. They also transformed the original digital material before evaluating the correlation between components by extracting decimal logarithms. The construction of a linear regression model was accompanied by testing the levels of contributions of independent factors to the variability of indicators associated with the reproductive abilities of livestock. The authors also used canonical discriminant analysis to rank the contribution of fixed and random effects on the variability of dependent signs [5,6].

When evaluating the source material, the researchers selected only individuals with an open day of no more than 150 days, lactation from 290 to 320 days, and the inter calving period from 300 to 600 days. The authors did not take into account the rest of the animals of the Irmen breed livestock factory farm in the statistical data processing.

Previously, the authors have already explored the possible role of the TNF- $\alpha$ -824 A/G and TNF-R1 - 1703 T/C SNP genotypes in various measures related to livestock's reproductive qualities milk production. The bovine TNF- $\alpha$  gene fragment was studied using PCR-RFLP, 5'-CCGAGAAATGGGACAACCT-3' forward primer, and 5'-GCCATGATCCCCAAAGAAT-3' reverse primer. They determined SNP TNF-R1 - 1703 C/T by staging allele-specific PCR in S.E. buffer G using primers 5'-1872-GGCTGCCAGATCGTGCCTGC-3'-common, on the lower chain 5'-1686-TCCGAGCCCCGCCTTCTGT-3'-for the wild type on the upper chain and 5'-1686-TCCGAGCCCCGCCTTCTAC-3'- for the mutant species. The authors carried out allele-specific PCR for 35 cycles at an annealing temperature of 60 °C. The PCR product was evaluated by vertical electrophoresis at 4% PAGE (polyacrylamide gel).

At the Irmen breed livestock factory farm (Novosibirsk region), breeders raised cattle with economically useful traits. They studied these traits from 2003 to 2019. As of January 1, 2020, the total livestock population was 7867 heads, including 2900 cows (as of January 1, 2019, there were 2730 animals). Since the beginning of 2019, bulls have inseminated 2696 cows and 1480 heifers with an average consumption of 2.2 and 1.5 insemination per fetus, respectively. The insemination efficiency during this period was 43.4%, and live calves born from 100 cows was 78%.

In 2019, the milk yield of cows for 305 days of lactation according to the outcomes of the appraisal was 9953 kg, MFF (mass fraction of fat) - 3.74% and MFP (mass fraction of protein) - 3.24%; 11.5% of the cows from the whole herd (314 cows) have milk yield of more than 12,000 kg of milk per 305 days of lactation. Thus, the level of livestock productivity is comparable to the best herds in the U.S.A., Canada, and Western Europe.

## 2.2. Stages of research

The first stage of research was to assess the average subpopulation variability levels of some economically useful traits. The traits associated with the reproductive traits of animals, those that can be obtained by a specialist breeder from the SELEX program are selected (Table 1). The authors calculated the statistical indicators after choosing the option by the previously indicated limitations. Noteworthy is the low level of phenotypic variability of milk yield, body weight, and calving ease. This result is of many years of targeted selection. It indicates a high consolidation of the "Irmenskiy" intrabreed type and was made possible thanks to many years of improvement of the local broodstock by the gene pool of Holstein cattle, mainly of Canadian and American origination. The authors also note a higher variability in the rate of insemination. Also, they suggest that this is due to the peculiarities of the genotype-environment interaction under conditions when the increase in milk production, as noted earlier, is often negatively associated with reproductive qualities.

The second stage of the research consisted of assessing the levels and directions of relations between the studied traits for all years and lactations. The authors explain this approach that

with an increase in the value of the correlation coefficient in absolute terms, the proportion of conjugate variability attributable to unaccounted genetic and paratypical factors decreases.

The data obtained generally indicated the existence of a dependence of the studied traits on each other. Nevertheless, it is worth highlighting the correlations between the insemination frequency and the duration of the open days ( $0.406 \pm 0.080$ ;  $p < 0.001$ ;  $n = 12,606$ ), calving ease and lactation number ( $0.275 \pm 0.008$ ;  $p < 0.001$ ;  $n = 14,156$ ), intercalving and dry periods ( $0.275 \pm 0.008$ ;  $p < 0.001$ ;  $n = 14,155$ ), body weight and calving ease ( $0.197 \pm 0.008$ ;  $p < 0.001$ ;  $n = 14,044$ ). The correlation between the productive life of cows and such traits as calving ease ( $0.158 \pm 0.008$ ;  $p < 0.001$ ;  $n = 14,156$ ) and the open days ( $-0.089 \pm 0.008$ ;  $p < 0.001$ ;  $n = 14,156$ ) was less pronounced. The authors did not take into account significant correlations with absolute values less than 0.100 due to the little slope of the regression line. The values of the correlation coefficients were comparable. The authors calculated ones separately for each lactation (from the first to the fifth and higher lactation). The directions of the correlations did not differ from each other.

The next step was to assess the role of the father's genotype, the year, and the number of lactations in the variability of the list of dependent variables. The factor "Year" (from 2003 to 2019) incorporated the influence of feeding, keeping, and the impact of natural and climatic conditions. The independent factor "Lactation" (10 lactations) made it possible to take into account the biological characteristics of lactating cows that manifest themselves at different periods of ontogenetic development. The authors assessed the contribution of the sire genotype ( $n = 140$ ) to the variation of the dependent variables using the "Father's genotype" effect, which also made it possible to find bulls with the maximum differences in the variability of traits associated with reproductive abilities.

The influence of a set of factors ("Year", "Lactation" and "Sire genotype") on the traits related to reproductive qualities was the result of this step revealed. These indicators can be ranked in descending order of coefficient of determination of the multivariate regression model and the Fisher criterion: productive life ( $R^2 = 0.682$ ;  $F = 142.0^{***}$ ), calving ease ( $R^2 = 0.621$ ,  $F = 108.5^{***}$ ), body weight ( $R^2 = 0.382$ ;  $F = 41.0^{***}$ ), insemination rate ( $R^2 = 0.073$ ;  $F = 5.24^{***}$ ), open days ( $R^2 = 0.071$ ;  $F = 5.037^{***}$ ), intercalving period ( $R^2 = 0.062$ ;  $F = 4.37^{***}$ ) and dry period ( $R^2 = 0.044$ ;  $F = 3.08^{***}$ ).

The resulting model using multiple regression was assessed. The authors calculated the frequency of occurrence of gradation in the list of predictors for all possible combinations of dependent variables (total possible combinations:  $6 + 5 + 4 + 3 + 2 + 1 = 21$ ). Thus, a high-frequency value characterizes the greater contribution of factor level to the variability of the dependent variable as a whole. The genotypes of the following bulls used in the breed livestock factory farm over the past 20 years (number of combinations  $\geq 10$ ) had the greatest impact on indicators related to the reproductive qualities of daughters: Roger 18 (15), Jordan 48 (14), Watchout 7,816,504 (12), Irwin 4901 (11), Comstar 162 (11), Moscow 132,582,764 (11), Flint 1223 (11), Frank 1223 (11), Frank 937 (11) and Mathys 103,439,288 (10). Similar processing was carried out for the years (2012 (19), 2013 (19), 2018 (19), 2010 (15), 2016 (15), 2017 (15) and 2009 (12)) and lactation (lactation 6 (15), lactation 4 (12) and lactation 3 (10)).

The authors explained the obtained data by the multivariate nature of the variability of the studied dependent variables, the study of which they carried out using multivariate analysis of variance (Table 2).

The high values of the Pillai's test criteria testified to the significant contribution of all effects to the model. Taking into account the tabular value of the measure for the factor "Lactation", the significance of its influence, the authors additionally checked according to the Wilk criterion ( $\Lambda = 0.265$ ,  $F = 243.6^{***}$ ). The data obtained allowed us to conclude that the number of lactations was the most significant factor in the variability of reproductive traits. Feeding and housing conditions also played a role. But at the same time, the factor "Sire genotype" at the population level showed a low share of influence that can be neglected. Nevertheless, for a small number of sires listed above, it would be wrong to ignore the variability of the list of dependent variables.

Under conditions of the breed livestock factory farm, the number of lactations turned out to be the most significant factor in the variability of several reproductive traits, mainly the calving

ease. The authors noted that the conditions of housing, feeding of animals and the sire's genotype played a significantly smaller role in the study. They also followed the conclusion that the genotypes of some bulls, the conditions of feeding and housing, play a significant role in the variability of body weight and animal's productive life.

The final stage of research led to estimates of the canonical discriminant analysis (Table 3). The discriminant analysis made it possible to establish those traits by which the differences were most significant, depending on the influence of a single factor. The standardised coefficients of the discriminant function made it possible to judge the value of such a contribution. Structural coefficients indicated the mutual relationship of individual variables with the discriminant function. A high value of the structural coefficient told that the information about the discriminant function is to a greater extent contained in the corresponding variable.

The authors found that the coefficient of determination has a relatively high value compared to variables. The influence of the factor under consideration extended to a greater extent to the calving ease, body weight, and productive life.

The values of "sire's genotype" and "year" were reflected in life expectancy and animal body weight changes. The authors explain the appearance of high structural coefficients value for the body weight of these two factors because in the process of ontogenetic development, the number of lactation increases. Since this is a natural process, it means that the body weight also increases. In other words, in 2019, the body weight of cows risen from 540 kg per one lactation to 646 kg by three and more.

The productive life span of a cow is not only a physiological indicator but an economically and complex indicator. Since the healthier the animal, the higher its milk production. Accordingly, a cow with a large number of lactations is used by farmers for a longer time. Thus, with the increase in the number of lactations in the cow, better reproductive health is observed. The productive life of a cow can replace on the duration of economic use indicator because they are correlated with each other. All estimates obtained were confirmed by the high expression of the corresponding structural coefficients.

The validity of the previously made conclusions regarding the role of some bulls in the degree of variation of dependent traits was significant. The authors confirmed by the coefficient of determination of the first discriminant function and the value of the Pillay criterion mentioned above. The low percentage of variability, which the authors explain by the effect of the factor "year", is a consequence of the "capacity" of this indicator. That is, the conditions for feeding and keeping animals were improved continuously, which affected the change in a massive number of traits and accounted for factors associated with the response. Therefore, these results the authors reflected in a relatively higher intergroup variance.

Other researchers detected single nucleotide polymorphism  $\text{TNF-}\alpha$ -824 A/G SNP detected in a population of "Irmen" type cattle [9,10]. Cows with the G/G genotype showed a higher milk yield compared to heterozygous A/G organisms for 305 days of lactation. The authors did not observe this tendency for the  $\text{TNF-R1}$  genotypes. did not find a statistically significant relationship with the reproductive quality of the livestock. Within the framework of this observation, this factor we can ignore in the previously constructed models. Nevertheless, it is advisable to research other  $\text{TNF-}\alpha$  SNP variants and their possible participation in the variability of such a complex quantitative trait as the duration of productive life. In other words,  $\text{TNF-}\alpha$ -824 A / G SNP and  $\text{TNF-R1}$  -1703T / C SNP - these genotypes had not significantly affected the variability of traits associated with the reproductive abilities of animals.

Thus, it seems appropriate to carry out the selection by productive longevity (bulls evaluated by daughters; bulls, cows and heifers evaluated by fathers and mothers) and take into account the number of lactation when assessing the calving ease. For other traits, such a selection seems less significant. The outcomes obtained reflect the characteristics of the "Irmenskiy" Black-and-White subpopulation of the Siberian cattle gene pool under the conditions of CJSC "Irmen" breed livestock factory farm and are a consequence of the "genotype-environment" interaction.

## Ethics Statement

Our research relates to population genetics using multivariate statistical methods. No animals in the study were exposed to or discarded due to the results obtained. The authors point out that the study is only statistical and analytical, so no animals were harmed. In the breed livestock factory farm "Irmen", farmers keep all animals in the conditions necessary for their well-being and functioning. The authors followed all animal welfare guidelines regarding their research topic. All animal experiments were by ARRIVE guidelines and were conducted by the UK Animal (Scientific Procedures) Act 1986 and EU Directive 2010/63 / EU for animal experiments.

## CRedit Author Statement

**Evgeniy Varisovich Kamaldinov:** Methodology, Software, Formal analysis, Investigation, Writing - Original Draft, Project administration; Supervision; **Olga Dmitrievna Panferova:** Software, Validation, Data Curation, Writing - Original Draft; **Olga Viktorovna Efremova:** Validation, Formal analysis, Resources, Funding acquisition; **Vladimir Grigorievich Marenkov:** Investigation, Formal analysis; **Inga Nikolaevna Ryumkina:** Writing - Review & Editing, Visualization; **Alexey Fedorovich Petrov:** Investigation, Formal analysis.

## Declaration of Competing Interest

Authors declare that they have no known competing financial interests or personal relationships which have, or could be perceived to have, influenced the work reported in this article.

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## Supplementary Materials

Supplementary material associated with this article can be found in the online version at doi:[10.1016/j.dib.2021.106842](https://doi.org/10.1016/j.dib.2021.106842).

## References

- [1] G. Banos, et al., Identification of immune traits correlated with dairy cow health, reproduction and productivity, *PLoS ONE* (2013), doi:[10.1371/journal.pone.0065766](https://doi.org/10.1371/journal.pone.0065766). Accessed January 10, 2020
- [2] H. Ben Zaabza, et al., Genetic parameters of reproductive traits in Tunisian holsteins, *Arch. Anim. Breed.* 59 (2) (2016) 209–213.
- [3] C.P. Ferris, et al., Calving traits, milk production, body condition, fertility, and survival of Holstein-Friesian and Norwegian Red dairy cattle on commercial dairy farms over five lactations, *J. Dairy Sci.* 97 (8) (2014) 5206–5218.
- [4] M.J. Groot, K.E. van Hooft, The hidden effects of dairy farming on public and environmental health in the Netherlands, India, Ethiopia, and Uganda, considering the use of antibiotics and other agrochemicals, *Front. Public Health* 4 (2016) 1–9.
- [5] E.V. Kamaldinov, O.S. Korotkevich, Canonical discriminant model differentiation between the breeds of pigs on biochemical parameters, *Agric. Russia* (5) (2011) 8–12.
- [6] E.V. Kamaldinov, The canonical discriminant model of the influence of the father's genotype on some interior indicators of his descendants in pigs, *Bull. Krasnoyarsk. State Agrar. Univ.* (1) (2012) 117–122.
- [7] M.D. Royal, et al., The genetic relationship between commencement of luteal activity and calving Interval, body condition score, production, and linear type traits in Holstein-Friesian dairy cattle, *J. Dairy Sci.* 85 (11) (2002) 3071–3080.



- [8] Website of the Ministry of Agriculture of the Russian Federation [Electronic Resource] <http://mcx.ru/news/news/show/58342.355.htm>. Accessed January 10, 2020.
- [9] V.A. Safonov, et al., Free radical oxidation of lipids and the reproductive health of cows, *Agric. Biol.* (6) (2014) 107–115.
- [10] K. Wojdak-Maksymiec, J. Szyda, T. Strabel, Parity-dependent association between TNF- $\alpha$  and L.T.F. gene polymorphisms and clinical mastitis in dairy cattle, *BMC Vet. Res.* 9 (2013) 114.
- [11] N.A. Zinovieva, Fertility haplotypes of the Holstein cattle, *Agric. Biol.* 51 (4) (2016) 432–435.