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ABSTRACT

Increasing the genetic potential of productive traits and creating highly productive dairy herds requires systematic evaluation of genotypes and phenotypes. Our research aimed to develop a digital method for studying animal conformation, objectively assess cow and replacement heifer traits, and analyze phenotypic patterns in realizing dairy cows' genetic potential. Studies were conducted on Holstein cows and daughters of the Reflection Sovereign and Wis Back Ideal lines at LLP "Turar" (Fedorovsky District) and LLP "Sadchikovskoye" (Kostanay District), Kostanay Region. The sample included 450 first-lactation cows and 200 heifers. Least variable traits were height at withers (4.6–5.6%), straight body length (4.8–5.9%), pelvic length (5.7–6.3%), and body conformation index (4.0–4.2%), while rump width showed the greatest variability (11.2–12.7%), offering higher selection potential. Pelvic index variability ranged 6.8–7.6%. Moderate positive correlations were observed between key parameters: height at withers with body length (0.58 in cows, 0.47 in heifers), chest depth (0.52, 0.44), and pelvic length (0.55, 0.41). The "dam" factor significantly influenced heifer traits (24.4–34.7%), especially chest depth (34.7%), body length (33.9%), height at withers (33.4%), and pelvic length (31.6%).

Keywords: Body conformation type, Dairy productivity, Cow conformation index, 3D imaging, Programmable controller.

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INTRODUCTION

The preservation of the gene pool, improvement of existing breeds and efficient utilization of elite genetic resources are fundamental goals in modern animal breeding science. Sustainable breeding progress is achievable only if there is sufficient genetic diversity within the population. It allows the selection of outstanding genotypes that are adaptable to specific environmental conditions. The initial stage of livestock breeding involves evaluating breeding value. The assessment is a complex process that requires comparison and analysis of selection characteristics not only in the individual animals but also in their relatives, progeny, and ancestors.

Throughout the twentieth century, breeding value in dairy cattle was assessed based on phenotypic indicators such as milk production and external appearance (Kuznetsov, 2012; Lukyanov et al., 2015). In recent decades, more efficient methods have been developed. The novel methods rely primarily on use of molecular genetic markers. A significant breakthrough was the decoding of the genomes of principal livestock species and the introduction of statistical approaches such as the Best Linear Unbiased Prediction (BLUP) method (Hayes et al., 2009; Berry et al., 2013; Kalashnikova et al., 2013). The BLUP method allows breeders to eliminate the influence of non-genetic factors on the variability of selected traits in a population. It further allows the isolation and accurate evaluation of the genetic

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component. The use of molecular genetic markers increases the precision of breeding value estimation, shortens generation intervals, and enhances the efficiency of selection (Radko et al., 2007; VanRaden et al., 2010; Baschenko et al., 2020; Nazar et al., 2022; Wang et al., 2022; Papusha et al., 2023; Erdoğan et al., 2024).

The central objective of breeders is to ensure the stable inheritance of economically valuable traits from elite ("model") animals to their offspring. At a specific stage lines, families, or entire herds, it becomes necessary to achieve minimal phenotypic and genetic variability (Brade, 2011; Konstandoglo et al., 2017; Conte et al., 2017; Baimukanov et al., 2022). The accurate evaluation of conformation and constitutional traits is therefore crucial, as it provides comprehension into biological foundations of productivity, structural soundness and early signs of constitutional weakening (Prozherin et al., 2008; Kharitonov et al., 2011; Khmelnychy et al., 2023b).

The study of animal conformation is based on three main principles: 1) the direction and level of productivity are reflected in specific body conformation features; 2) external conformation traits are correlated with each other and with the development of internal organs, and 3) conformation features are determined by the genetic characteristics of the animal (Brade, 2017; Xue et al., 2022).

Currently, in countries with developed dairy farming, conformation assessment is integrated with genomic evaluation. In the early 1980s, a completely new system for assessing dairy cow conformation was developed in the USA, Canada, and Western European countries. This system established standardized visual scoring methods, minimized subjective bias, and defined the model dairy cow type. This enabled the evaluation of sire based on the conformation of their daughters (Mantysaari, 2011; Nazar et al., 2022; Shamshedin et al., 2024). In all countries like USA, Canada, Japan, and European countries, body conformation type (along with milk productivity) is a primary selection criterion for improvement of dairy breeds (Weller et al., 2012; Khmelnychy et al., 2023c; Wolfe et al., 2023; Cattaneo et al., 2023; Dong et al., 2023).

The model Holstein cow developed by American breeders is a major example of an animal capable of sustaining high milk productivity while maintaining good health under intensive management conditions. This model can be effectively adopted in Kazakhstan and other regions to enhance herd performance. Because conformation traits are closely linked to economic efficiency and breeding potential. Thus, precise evaluation is indispensable for improvement of the genetic merit of dairy cattle (Kuznetsov, 2002; Nusupov et al., 2021; Khmelnychy et al., 2023a; Khamzina et al., 2024; Khamzina et al., 2025).

The production type of an animal represents an integrative trait shaped by both hereditary and environmental factors. Animals with optimal production type are best adapted to their environment. They express their genetic potential most effectively. The use of scientific methods and digital technologies in determination of production type provides a more objective and accurate assessment. Worldwide, more than 500 million cattle are evaluated annually for breeding value, conformation, health, and production potential. However, most current

methods remain labor-intensive and subjective. Therefore, the development of a comprehensive, digitally based conformation assessment system is both timely and practically significant (Mussayeva et al., 2023; Uskenov et al., 2024; Merkelytė et al., 2025).

In this context, our research aimed to develop a method for studying animal conformation using digital technologies. Our study further aimed to assess the traits of cows and replacement heifers objectively, and to analyze phenotypic patterns in the expression of dairy cows' genetic potential.

MATERIALS & METHODS

The experimental studies were conducted in two stages on Holstein cows and heifers of different lineages i.e. Reflection Sovereign and Wis Back Ideal, under the production conditions of LLP "Turar" (Fedorovsky District) and LLP "Sadchikovskoye" (Kostanay District) in the Kostanay Region of the Republic of Kazakhstan (Include map of the area). The sample size included 450 first-lactation cows and 200 replacement heifers. Basic data on animal pedigree and milk productivity were obtained from production and breeding records and from the electronic database of the Republican Information and Analytical System (IAS).

Conformation Assessment

Conformation evaluation of animals was done between the 90th and 150th days of lactation by measuring and calculating the Body Conformation Index (BCI) and Pelvic Index (PI). The selected measurements reflect heritable body-type characteristics that remain relatively stable with age and are minimally influenced by environmental factors (Kuznetsov, 2002; Abugaliev et al., 2021). The study was divided into two main stages: Stage 1. Conformation assessment of cows between the 90th and 150th days of lactation. Stage 2. Conformation assessment of heifers before insemination (breeding period), at 11–12 months of age. The following measurements were measured for each animal: height at withers, straight body length, chest depth, chest width, loin depth, hook width, rump width at ischial tuberosities, straight pelvic length, sacrum length, and cannon bone circumference. These parameters accurately characterize the overall animal's frame.

For a more comprehensive assessment of body type, the conformation index 1) and pelvic index and 2) were calculated using formulas developed by Batanov et al. (2023): (1) where the formula for a truncated pyramid determined body volume:

$$BCI = \frac{{}^4\sqrt{V_{body} \cdot CC}}{HW} \quad (1)$$

Where pelvic volume was determined by the formula for a truncated pyramid:

$$V_{body} = \frac{1}{3} \cdot SBL \cdot \left((HWk \cdot PL) + \sqrt{CD \cdot CW \cdot HWk \cdot PL} + (CW \cdot CD) \right)$$

where: SBL – straight body length (cm); HWk – hook width (cm); PL – pelvic length (cm); CD – chest depth (cm); CW – chest width (cm).

$$PI = \frac{\sqrt[3]{V_{pelvis}}}{SBL}$$

(2), the pelvic volume of the animal was determined using the formula for a truncated pyramid:

$$V_{pelvis} = \frac{1}{3} \cdot SL \cdot \left((HW \cdot LD) + \sqrt{RW \cdot PL \cdot HW \cdot LD} + (RW \cdot PL) \right) \quad (2)$$

Where: SL – sacrum length, cm; HW – hook width (ШМ), cm; LD – loin depth (ГП), cm; RW – rump width at ischial tuberosities (ШЗ), cm; PL – pelvic length, cm.

3D Imaging and Digital Measurement

Conformation parameters were obtained from 3D imaging of animals (Fig. 1). For 3D imaging, Intel RealSense D456 depth cameras with an extended

operating range were used. The depth camera consists of two infrared sensors and an infrared projector to calculate the depth of objects within the field of view. Infrared sensors register the emitted pattern—object distances—are processed using triangulation methods. The calibrated camera, along with known positions of the projector and sensors, analyzed the displacement of each point in the pattern, calculated the reflection angle, and determined the distance to the object's surface, and generated a 3D model (Fig. 2). The cameras were connected to a Raspberry Pi 5 programmable board equipped with a quad-core Broadcom BCM2712 Arm Cortex-A76 @ 2.4 GHz processor and up to 16 GB of RAM. The Raspberry Pi 5 processed input from the stereo cameras and recorded measurement data from the images into a separate file (Fig. 3).

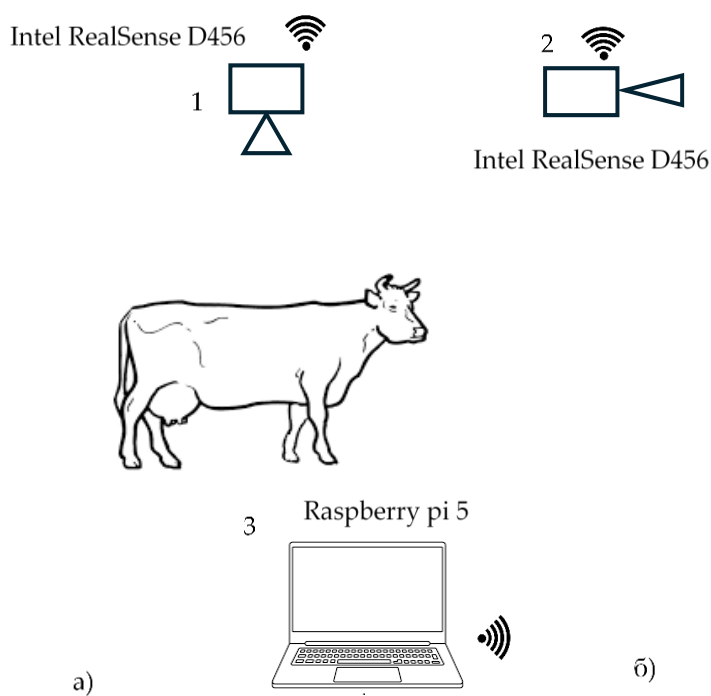


Fig. 1: Contactless measurement of cattle: (a) side view, (b) top view; 1, 2 – positions of Intel RealSense stereo depth cameras; 3 – Raspberry Pi 5 programmable board and laptop.

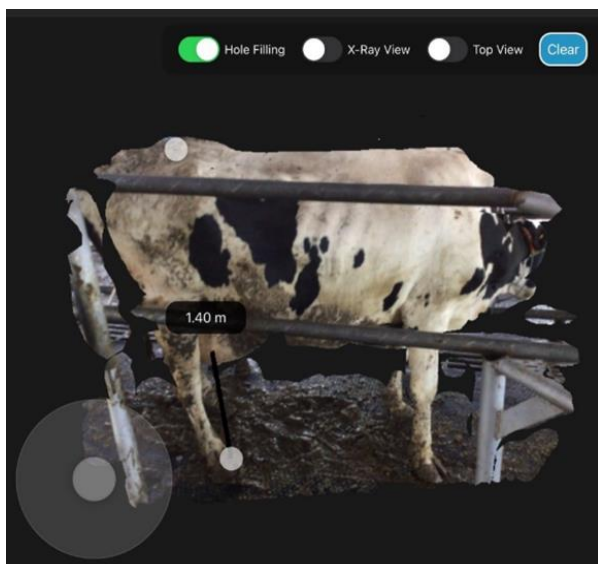


Fig. 2: Three-dimensional image of a cow.



Fig. 3: Measurement: hook width.

Milk Productivity Evaluation

Stage 3. Milk productivity was evaluated using the following parameters: milk yield over 305 days of first lactation (MY), fat content (%), and protein content (%), according to the Instruction for Livestock Appraisal (Minister of Agriculture of the Republic of Kazakhstan, 2014). Based on these indicators, the productive index was calculated using formula (3):

$$PI = \frac{Ud \cdot (fat_mass_f + Protein_mass_f)}{Fat_mass_b + Protein_mass_b} \quad (3)$$

Where Fat_mass_f — Fat mass in milk at the final (current) period (%); Protein_mass_f — Protein mass in milk at the final (current) period (%); Fat_mass_b — Fat mass in milk at the baseline (initial) period (3.6%); Protein_mass_b — Protein mass in milk at the baseline (initial) period (3.2%).

Statistical Analysis

Based on the obtained data, selection and genetic parameters of conformation and productivity traits were calculated for the studied population of replacement heifers (daughters). The relationships between conformation parameters, body type, and milk productivity were determined through correlation analysis. A multivariate analysis of variance was performed in MATLAB to assess the influence of genotypic factors (dam) on biological traits (conformation parameters) in dam–daughter pairs. The numerical data were processed using the method of variation statistics proposed by Nurbaev (2013), with the assessment of differences between mean values and determination of the Student's t-test (td) for the difference between group means, calculated using the formula:

$$t_d = \frac{\bar{X}_1 - \bar{X}_2}{\sqrt{m_{\bar{X}_1}^2 + m_{\bar{X}_2}^2}} \quad (4)$$

Where \bar{X}_1 – mean value of the experimental group indicators; \bar{X}_2 – mean value of the control group indicators; $m_{\bar{X}_1}^2$ – standard error of the mean of the experimental group; $m_{\bar{X}_2}^2$ – standard error of the mean of the control group.

The degrees of freedom was also determined using the formula: $v = n_1 + n_2 - 1$ and significance of the results was determined using the Student's t-distribution table.

RESULTS

The Holstein cows and heifers in this study generally exhibited a strong, elongated, and deep-bodied conformation. They were found with correctly set limbs, which indicated good adaptation to intensive dairy management conditions. Phenotypic development was relatively uniform across the conformation traits. The coefficients of variation (CV) for individual traits mainly were low, ranging from approximately 4.6% up to 11.7% in first-lactation cows and 3.3 to 12.7% in heifers (Table 1 and 2). Stature (height at withers), straight body length, straight pelvic length, and the composite Body Conformation Index (BCI) were the least variable traits (CV on the order of 4–6%). Whereas, rump width at the ischial tuberosities showed greatest variability (about 11–13%

CV). The pelvic index (PI) also had a moderate variability (approximately 6.8–7.6%). These results suggest that most body dimensions in the herd are relatively homogeneous, with rump width being a notable outlier, offering greater potential for selection response due to its higher phenotypic variance.

Table 1: Selection and genetic parameters of the conformation of first-lactation cows (n=450)

Indicators	$\bar{X} \pm m_{\bar{X}}$	Lim	Cv, %
Height at withers, cm	139.3±0.41	(124.5–149.1)	4.6
Straight body length, cm	151.8±0.47	(139.3–167.7)	4.8
Chest width, cm	45.9±0.25	(40.1–51.3)	6.7
Chest depth, cm	74.9±0.39	(67.3–85.2)	7.6
Hook width, cm	61.6±0.47	(49.1–70.4)	8.7
Rump width at ischial tuberosities, cm	46.33±0.59	(38.5–57.1)	11.2
Pelvic length, cm	105.4±0.45	(95.7–113.9)	9.3
Loin depth, cm	71.2±0.43	(63.2–79.7)	4.5
Sacrum length, cm	54.43±0.50	(48.7–61.5)	11.7
Cannon bone circumference, cm	22.1±0.12	(18.9–24.8)	6.2
Body Conformation Index (BCI)	0.457±0.002	(0.447–0.471)	3.9
Pelvic Index (PI)	0.481±0.003	(0.465–0.594)	6.8

Table 2: Selection and genetic parameters of conformation of replacement heifers (11–12 months)

Indicators	$\bar{X} \pm m_{\bar{X}}$	Lim	Cv, %
Height at withers, cm	122.6±0.31	(118.3–126.5)	5.6
Straight body length, cm	136.3±0.25	(132.4–141.2)	5.9
Chest width, cm	35.8±0.25	(31.3–42.3)	7.2
Chest depth, cm	64.9±0.22	(61.4–69.9)	3.3
Hook width, cm	45.8±0.25	(40.3–51.1)	5.5
Rump width at ischial tuberosities, cm	30.9±0.41	(26.6–37.2)	12.7
Pelvic length, cm	76.8±0.26	(70.5–81.3)	3.4
Loin depth, cm	54.8±0.24	(50.0–59.1)	4.4
Sacrum length, cm	34.7±0.24	(3.2–38.3)	4.5
Cannon bone circumference, cm	15.7±0.13	(13.7–18.1)	8.7
Body Conformation Index (BCI)	0.407±0.003	(0.395–0.419)	4.2
Pelvic Index (PI)	0.301±0.004	(0.289–0.316)	7.6

Present some data (3–4 parameters) in graphs by comparing first-lactation cows vs heifers.

Conformation traits were intercorrelated in ways that reflect a consistent dairy type. Table 3 presents the correlation matrix among the measurements. We observed numerous significant positive correlations between key linear body measurements. Height at withers was moderately correlated with straight body length (phenotypic $r=0.58$ in cows, 0.47 in heifers) and with chest depth ($r=0.52$ in cows, 0.44 in heifers). Height at withers also showed a similar correlation with pelvic length ($r=0.55$ in cows, 0.41 in heifers). These relationships indicate that taller animals tended to be longer and deeper-bodied, with greater overall body volume. Likewise, straight body length was moderately associated with chest depth ($r = 0.44$ in cows) and pelvic length ($r \sim 0.45$ in cows). Many of these correlations, were in the moderate range (roughly 0.3–0.6), and reflected that no single trait completely determines another but that there is a coordinated growth of the frame in well-bred Holsteins. In contrast, only weak correlations were found among certain traits that reflect different body dimensions. Like, withers height and chest width showed little association ($r \approx 0.15$ –0.17), as did straight body length and chest width ($r<0.22$). Such low correlations suggest that width of front body (chest) varies somewhat independently of linear dimensions like height and length. Overall, the correlation structure highlights an expected harmony among stature, length, and depth traits, with more independence for width measures.

Table 3: Correlations between conformation parameters in cows and replacement heifers

	1*	2*	3*	4*	5*	6*	7*	8*	9*	10*	11*	12*
Cows												
1*	1.00	0.58	0.15	0.52	0.31	0.11	0.55	-0.28	0.21	0.37	-0.28	0.41
2*	0.58	1.00	0.21	0.44	0.45	0.15	0.45	0.13	0.45	0.19	0.32	0.37
3*	0.15	0.21	1.00	0.08	0.13	0.33	0.29	0.14	0.07	0.24	0.21	0.25
4*	0.52	0.44	0.08	1.00	0.05	0.11	-0.06	0.29	0.15	0.21	0.17	0.05
5*	0.31	0.45	0.13	0.05	1.00	0.33	0.21	0.13	0.35	0.10	0.52	0.17
6*	0.11	0.15	0.33	0.11	0.33	1.00	0.19	0.12	0.27	0.25	0.45	0.24
7*	0.55	0.45	0.29	-0.06	0.21	0.19	1.00	0.38	0.25	0.18	0.16	0.54
8*	-0.28	0.13	0.14	0.29	0.13	0.12	0.38	1.00	0.03	0.28	0.21	0.31
9*	0.21	0.45	0.07	0.15	0.35	0.27	0.25	0.03	1.00	-0.09	0.27	0.42
10*	0.37	0.19	0.24	0.21	0.10	0.25	0.18	0.28	-0.09	1.00	0.34	0.006
11*	-0.28	0.32	0.21	0.17	0.52	0.45	0.16	0.21	0.27	0.34	1.00	0.39
12*	0.41	0.37	0.25	0.05	0.17	0.24	0.54	0.31	0.42	0.06	0.39	1.00
Replacement Heifers												
1*	1.00	0.47	0.17	0.44	0.33	0.09	0.41	-0.32	0.19	0.42	-0.22	0.33
2*	0.47	1.00	0.18	0.31	0.41	0.12	0.38	0.16	0.41	0.11	0.21	0.27
3*	0.17	0.18	1.00	-0.05	0.09	0.25	0.22	0.11	-0.05	0.18	0.11	0.19
4*	0.44	0.31	-0.05	1.00	0.07	0.14	0.35	0.25	0.09	0.24	0.09	-0.07
5*	0.33	0.41	0.09	0.07	1.00	0.29	0.37	0.18	0.37	0.08	0.34	0.08
6*	0.09	0.12	0.25	0.14	0.29	1.00	0.17	0.15	0.21	0.05	0.31	0.13
7*	0.41	0.38	0.22	0.35	0.37	0.17	1.00	0.35	0.28	0.21	0.21	0.48
8*	-0.32	0.16	0.11	0.25	0.18	0.15	0.35	1.00	-0.04	0.19	0.12	0.33
9*	0.19	0.41	-0.05	0.09	0.37	0.21	0.28	-0.04	1.00	0.31	0.31	0.44
10*	0.42	0.11	0.18	0.24	0.08	0.05	0.21	0.19	0.31	1.00	0.25	0.11
11*	-0.22	0.21	0.11	0.09	0.34	0.31	0.21	0.12	0.31	0.25	1.00	0.31
12*	0.33	0.27	0.19	-0.07	0.08	0.13	0.48	0.33	0.44	0.11	0.31	1.00

Consistent with the moderate correlations observed among phenotypic traits, we found evidence of appreciable genetic influence on conformation. In a dam–daughter analysis (Table 4), the conformation measurements in heifers were positively correlated with the same traits in their dams, which indicated genetic component to their inheritance. Notably, the highest mother–offspring correlation was for height at withers ($r=0.45$), followed by straight pelvic length ($r=0.38$), chest depth ($r=0.37$), and cannon bone circumference ($r=0.36$). A somewhat lower correlation was observed for body length ($r=0.22$). These results imply that a moderate proportion of the phenotypic variation in key conformation traits is transmissible from one generation to the next under the given management conditions. In other words, cows with superior size and body development tended to produce daughters that were also above-average in those traits. We quantified the influence of genetic factors more formally using analysis of variance: the “dam” factor (i.e., maternal genetic and perhaps maternal common environmental effects) explained a significant share of the variance in daughter conformation, ranging from about 24.4% to 34.7% across traits. For chest depth, straight body length, height, and pelvic length of heifers, the maternal influence was exceptionally high (around 32–35%, $P<0.01$). Even the composite indices were markedly affected by the dam: the Body Conformation Index of heifers showed ~30.2% of variance attributable to the dam, and the Pelvic Index ~35.1%. These findings demonstrate a substantial genetic contribution (broadly reflecting heritability) to conformation traits in our Holsteins. By contrast, the effect of lineage or sire line was relatively minor. The two predominant paternal lines (Reflection Sovereign vs. Wis Back Ideal) did not diverge strongly in conformation: the “line” factor accounted for only 4.4–27.3% of trait variance and was not statistically significant for most individual traits. An exception was that line background had a significant effect on the composite indices – specifically, line explained

about 21.3% of variation in BCI and 22.5% in PI (Table 4). This suggests that while basic linear dimensions are relatively uniform across these international Holstein lines, specific aggregate shape characteristics might differ subtly by lineage. Overall, the genetic analyses confirm that improvement of conformation through selection is feasible, as substantial additive genetic variance is present despite a long history of intensive breeding.

Table 4: Results of one-way analysis of variance

Indicators	Influence factor “Line”, $\eta^2 \pm SE$	P	Influence factor “Dam”, $\eta^2 \pm SE$	P
Height at withers	0.044±0.008	0.01	0.334±0.004	0.01
Straight body length	0.120±0.008	0.01	0.339±0.006	0.01
Chest width	0.163±0.007	0.01	0.298±0.007	0.01
Chest depth	0.063±0.008	0.01	0.347±0.004	0.01
Hook width	0.273±0.004	0.01	0.244±0.005	0.01
Rump width at ischial tuberosities	0.254±0.005	0.01	0.285±0.005	0.01
Straight pelvic length	0.115±0.006	0.01	0.316±0.008	0.01
Loin depth	0.087±0.005	0.01	0.323±0.004	0.01
Sacrum length	0.144±0.007	0.01	0.327±0.005	0.01
Cannon bone circumference	0.166±0.006	0.01	0.306±0.007	0.01
Body Conformation Index (BCI)	0.213±0.008	>0.05	0.302±0.004	0.01
Pelvic Index (PI)	0.225±0.005	>0.05	0.351±0.005	0.01

It will be better if you present this table in comparison between first-lactation cows and heifers.

Milk production data (Table 5) showed that the cows were high-producing and relatively consistent in output between the two herds studied. The average 305-day milk yield for first-lactation cows was ~9360kg (with 3.82% fat and 3.22% protein) in herd “Tutar”. Similarly, herd Sadchikovskoye, had about 9017kg (3.83% fat, 3.23% protein). We further stratified the cows by the level of milk production, i.e., low producers (less than 7000kg in 305 days), average (7000–9000kg), and high producers (greater than 9000kg) in order to explain the relationship between body conformation and productivity. These groups had clear and statistically significant differences in body structure. Generally, the more productive cows were larger and more angular, conforming to the traditional dairy type, which was more concerned with milk production, whereas the low-yielding group was rather compact and robust.

High-yield cows (yielding over 9000kg) were found to be much taller at the withers and longer in the body compared to those with lower yields. Their mean height was higher than the mean of the low-yield group by 0.9% and the mid-yield group by 0.6%. In the same way, high-yield cows were found to be longer in the straight body length-Trimmed by approximately 1.8% in comparison to cows in the low category and 1.3% in comparison to cows in the average category (differences are highly significant, $P<0.001$). These high-producing cows also tended to have well-developed chests (deep and capacious), indicative of a strong constitution and high feed intake capacity to support lactation. By contrast, low-yield cows (< 7000 kg) were on average shorter and exhibited a broader, heavier body type. They had a notably more massive skeletal frame: for instance, low-yield cows surpassed the high-yield cows in chest width by ~1.8% ($P<0.05$), in hook (hip) width by ~6.8% ($P<0.001$), and in rump width at the ischial tuberosities by ~7.3% ($P<0.01$). They also showed thicker leg bones, with cannon bone circumference about 2.3% greater than in the high-yield group. These differences paint a picture of the

Table 5: Selection and genetic parameters of conformation and productivity of cows with different levels of milk yield

Indicators	$\bar{X} \pm m_s$	Lim	Cv, %	$\bar{X} \pm m_s$	Lim	Cv, %	$\bar{X} \pm m_s$	Lim	Cv, %
	Low milk yield (up to 7000 kg), n=155			Average milk yield 7000–9000 kg, n=187			High milk yield (over 9000 kg) n=108		
Lactation milk yield, kg	6524.4±74.4	(6070–6991)	9.5	8082.7±63.0	(7012–8994)	8.9	10111.7±85.0	(9029–11850)	5.7
Fat content, %	4.04±0.04	(3.72–4.95)	9.9	3.91±0.02	(3.51–4.78)	9.1	3.83±0.03	(3.42–4.59)	7.5
Protein content, %	3.31±0.03	(2.95–3.42)	2.5	3.24±0.03	(2.97–3.35)	2.7	3.18±0.04 **	(2.95–3.32)	2.8
Productivity index, kg	7042.5±78.3	(6436.8–7281.6)	15.3	8498.7±42.0	(7103–9041)	8.7	10429.0±91.8	(9049.1–11018.2)	8.1
Height at withers, cm	138.5±0.52	(125.6–149.5)	4.8	138.9±0.39	(127–152)	4.5	139.8±0.81	(128.2–153.8)	4.1
Straight body length, cm	149.9±0.65	(137.4–158.5)	4.9	150.7±0.47	(139–161)	5.7	152.6±1.29 ***	(140.1–162.5)	6.4
Chest width, cm	46.2±0.28	(40.0–51.8)	6.9	45.8±0.21	(40–52)	6.6	45.4±0.44 *	(40.1–52.2)	6.8
Chest depth, cm	74.6±0.51	(64.1–85.2)	7.5	75.1±0.36	(62–84)	7.6	75.5±0.47 *	(65.9–82.7)	7.0
Hook width, cm	64.2±0.52	(53.7–75.2)	8.9	62.3±0.47 ***	(51–75)	12.2	60.1±0.32 ***	(53.4–68.5)	7.2
Rump width at ischial tuberosities, cm	48.7±0.73	(37.5–62.1)	15.3	46.9±0.57	(34.1–57.5)	13.3	45.4±0.76 **	(42.8–56.3)	16.5
Pelvic length, cm	103.4±0.61	(91.2–115.7)	6.2	105.6±0.39	(95.4–112.9)	5.9	107.4±0.81 **	(95.3–116.8)	8.9
Loin depth, cm	70.3±0.61	(59.5–77.8)	9.5	71.0±0.58	(65.1–79.4)	8.7	73.1±0.46	(64.5–81.2)	7.7
Sacrum length, cm	55.0±0.75	(49.1–61.2)	15.1	54.4±0.47	(46.8–61.5)	13.7	54.1±0.42	(45.4–60.9)	13.0
Cannon bone circumference, cm	22.7±0.15	(19.3–24.9)	7.4	22.4±0.12	(17.7–24.8)	8.6	22.2±0.23	(18.1–24.5)	7.5
Body Conformation Index (BCI)	0.462±0.004	(0.445–0.475)	5.1	0.460±0.003	(0.44–0.47)	4.5	0.456±0.002	(0.445–0.467)	4.1
Pelvic Index (PI)	0.498±0.003	(0.481–0.519)	6.8	0.488±0.002	(0.37–0.50)	6.7	0.477±0.002	(0.462–0.495)	6.1

Note: Values are presented as mean \pm standard error ($\bar{X} \pm m_s$). Cv – coefficient of variation (%); Differences between means are statistically significant at: * $P<0.05$; ** $P<0.01$; *** $P<0.001$.

lower-yielding animals being stouter or coarser – with wider hindquarters and heavier bone –. In contrast, the top yielders were leaner, taller, and more refined in build. The medium-yield group (7000–9000kg) tended to be intermediate for most measurements, generally falling between the other groups as expected; when significant differences existed between mid- and extreme groups, they are noted below.

The development of the posterior body (pelvic region) was exciting across productivity levels. High-yielding cows had a more elongated pelvis and well-muscled loin compared to lower-producing cows. Specifically, cows giving >9000kg had a straight pelvic length on average 3.9% greater than low producers ($P<0.01$) and 1.7% greater than the mid producers ($P<0.05$). Loin depth (an indicator of muscling and support over the topline) was also significantly greater in the high group – by about 4.0% compared to low yielders ($P<0.001$) and 3.0% compared to the mid group (the latter difference not reaching significance). There were no significant differences among groups in sacrum length (the length of the rump from hook to pin), suggesting that the basic pelvic skeletal frame was similar. However, the high-yield cows had more extension in the pelvic region (perhaps reflecting larger abdominal capacity and better body condition in the loin). Taken together, these results indicate that superior producers combine greater body size with a particular development of the rear third of the body, which may facilitate higher feed intake and endurance in milk production.

While individual linear measurements provide insight, composite indices allow a more holistic assessment of body proportionality in relation to function. We calculated two such indices – the Body Conformation Index (BCI) and Pelvic Index (PI) – to integrate multiple traits. The high-yielding cows (group 3) had the lowest values for both indices, which suggested a more proportionate and harmonious build concomitant with high milk output. The mean percentage of BCI of the high-producing group was approximately 1.03 less than that of the high-yield cow group 1. Essentially, the high-yield cows were more inclined to be slightly trimmer (not bulky) in relation to height. The trend of the pelvic index was even more evident: group 3 had a pelvic index that was 4.2% lower than that of group 1 ($P<0.001$) and 2.0%

lower than that of the mid-producing group ($P<0.01$). A smaller PI indicates that the pelvic volume was smaller relative to body length; in high-yield cows, this probably reflects a more streamlined body shape with a sufficient (but not excessively large) pelvic volume relative to body size. It is noteworthy that the group 1 vs 2 was also significant (difference between low and intermediate producers) (2.0, $P<0.01$). It meant that gradual increases in conformation index are consistent with increased production. These observations confirm the notion that cows that are more harmonious and balanced in their physiques, neither too thick-set, and whose pelvis is ideally shaped, are the ones that can produce the highest milk yields.

DISCUSSION

Findings from the present research indicate clear trends in the relationship between conformation characteristics and dairy performance in Holstein cows in the Kazakh climate. First, the phenotypic variability of the important linear traits (e.g., approximately 5% coefficient of variation in withers height and body length) is relatively low, indicating a fairly homogeneous herd in dimensions. This is consistent with the idea that intensive selection can make some body traits homogenous in superior Holstein lines. When an optimum range is obtained in breeding programs, reducing variability in economically important traits is a common objective. The increased variability observed in rump width (approximately 12% CV in our herd) suggests that more can be achieved through selection improvement in the same trait. Interestingly, others, such as Brade (2011) reported similar trends in mature Holstein populations in which stature and length were found to stabilize whilst traits such as width are more variable. This variability implies that the herd can be further refined with specific selection (e.g. wider rumps) since the pelvic structure is one of the factors that are important in calving and productivity.

The positive average level phenotypic relationships that we observed between frame properties (e.g. withers height and body length $r=0.58$ in cows) indicate coordinated skeletal frame development. There are strong genetic correlations between stature and depth, as well as other size characteristics, in Holsteins worldwide (Xue et al., 2022).

Chinese Holsteins show genetic correlations up to 0.76 between chest width and loin strength. Our finding that dams significantly influenced 24–35% of the variation in heifer measurements (especially for chest depth, body length, withers height, and pelvic length) underscores that these conformation traits are moderately heritable. This is consistent with a large body of literature that has provided heritability (h^2) estimates of linear type traits in dairy cattle of about 0.2–0.4. For example, studies in various Holstein populations have estimated h^2 for stature from about 0.25 up to 0.69, and around 0.17–0.47 for pelvic width and related measures. Zink et al. (2014) reported heritabilities of 0.39 for height and 0.22 for rump width in Czech Holsteins, whereas an Italian study reported even lower h^2 estimates for rump traits (~ 0.10). Our implicit heritability estimates (with dam-offspring similarities) are in this middle zone, indicating that such selection on these conformation parameters would be useful in Kazakh Holsteins.

One of the key results of our research was that high-milking cows possessed a characteristic body profile as opposed to low-producing cows. The high-yielding Holsteins were much taller, longer, and deeper in the chest, but were more refined, e.g. with narrower chests and rumps, and less heavy, i.e. less bone (less cannon circumference) than their lower-yielding counterparts. This dichotomy is the familiar one, the opposition between dairy type and beefy or coarse type. We found that cows weighing >9000kg at weaning weighed some 2–4 percent more in body length and pelvic length than those weighing less than 7000kg ($P < 0.01$), but the high producers were approximately 6–7% thinner across the hooks and pins ($P < 0.001$). Bone circumference was smaller by about 2 percent of the normal range (signifies a leaner frame). These findings strongly support the hypothesis that an angular, capacious, but not excessively massive body shape correlates with high milk production. On the same note, Baimukanov et al. (2022) found that Holsteins with a yield above 8000kg had 2% longer and much lower conformation indices (34% lower) than their modest-production counterparts. A more petite body conformation index there indicates a less stocky more proportional build, which confirms that the high-producing cows are large but more of a harmonious build. The Body Conformation Index (a ratio of trunk volume to height) of the high-yield group was the lowest in our study, which also aligns with these results. High producers thus combined greater skeletal size with a more streamlined shape – presumably to accommodate larger feed intake capacity and mammary development without excess fat or muscle load. This kind of dairy build has been deliberately emphasized in modern Holstein breeding: for decades, conformation assessment systems worldwide have sought cows that are tall, deep-bodied, and angular to support high milk output. Our results validate that under Kazakh farm conditions, the imported Holstein genotypes express the same phenotypic pattern seen in intensive dairy industries of North America and Europe – the “model” dairy cow type characterized by height, dairy form, and an optimal balance of capacity vs. fleshiness.

It is insightful to compare the magnitude of conformation-production relationships in our herd with

those reported globally. We did not estimate genetic correlations directly, but the phenotypic differences and dam effects imply moderate underlying genetic correlations between specific traits and milk yield. Numerous studies have quantified such genetic links. Classic U.S. analyses by Short and Lawlor (1992) found that “dairy form” (an index of angularity) had a strongly positive genetic correlation (~ 0.5) with milk yield. In contrast, a trait like udder depth was negatively correlated with yield ($r_g \approx -0.48$). This means cows genetically inclined to produce more milk tend to have more angular bodies and deeper udders – exactly the phenotype we observed. Indeed, our low-yield cows had shallower udders and thicker bodies, whereas top yielders were more angular and deep-uddered. In the literature, genetic correlations between milk yield and linear conformation traits range from near zero to moderate or high, depending on the trait. Many recent studies report only weak positive correlations for frame traits: for example, Samoré et al. (2010) found correlations of only 0.09–0.10 between milk yield and stature in Italian Holsteins; Kruszyński et al. (2013) likewise reported essentially negligible genetic correlations (~ 0.01 –0.04) between milk yield and height, depth, or rump width in Polish Holsteins. In our population, the association was stronger – high producers clearly were larger-framed – suggesting that within this herd, there is a meaningful genetic coupling of size and production. Consistent with this, other studies in developing dairy industries have found moderate correlations: Khmelnychi and Karpenko (2021) reported genetic correlations of 0.21–0.34 between first-lactation milk yield and stature in Ukrainian Black-and-White cows. Zink et al. (2014) found that Holstein milk yield was genetically correlated with stature at ~ 0.19 and with body depth at ~ 0.19 , values that are quite comparable to those implied by our phenotypic data. Meanwhile, some environments or breeds show even stronger relationships: De Haas et al. (2007) documented higher genetic correlations (0.39–0.48) between milk yield and frame traits like height and body depth in Swiss cattle, and a Turkish study likewise noted relatively strong correlations of stature with production. Our findings thus tend to support the moderate viewpoint: larger cows produce more milk, but the correlation is far from perfect. Selection solely for increased size would not proportionally increase milk yield, and indeed huge cows can have diminishing returns in specific management systems. It is also noteworthy that the milk yield is also complicated with the body condition and health traits. The cost of high milk production is usually paid with body reserves, which is observed in such characteristics as angularity or thinness. As an example, a recent Chinese study reported a weak negative genetic relationship between milk yield and overall conformation score, fuelled by the fact that high-yielding cows scored lower in certain body traits (such as foot angle and heel depth) (Xue et al., 2022).

One of the most impressive conformations in our case is the pelvic structure. Cows with high yield were very long in the length of the pelvis (strait pelvic length) but very narrow in the pins thus, causing them to have a low Pelvic Index. Baimukanov et al. (2022) also found that the

maximum-yielding cows among them were the most harmonious (with a pelvic index that was approximately 3.8% lower than it was in low-yielding cows). The abdominal area, being long and capacious, is able to accommodate bigger digestive organs and may have a bigger uterus that facilitates the production of milk as well as the capacity to have a child. A skinny pelvic width may however become a problem in calving ease. Our positive phenotypic relationship between our composite pelvic index and productivity (observed by Baimukanov et al. 2022) as well, $r=0.38$) indicates that an optimal pelvic shape is a factor that leads to performance. However, breeders must take care not to go too far with the type of dairy (e.g. too angular or too narrow a rumps) that could adversely impact fertility or calving. The comparison of two prominent Holstein lineages in our herd (Reflection Sovereign vs. Wis Burke Ideal) revealed that genetic background also plays a role in performance under the local environment. Although both lines are elite Holstein, cows of the Wis Burke Ideal line tended to outperform those of the Reflection Sovereign line in 305-day milk yield (in our data, by roughly 10%, similar to trends noted at the farms). This result is in agreement with regional studies in Kazakhstan: Baimukanov et al. (2022) found that daughters of the Wis Back Ideal line produced about 700–830 kg more milk per lactation than Reflection Sovereign line contemporaries. The lack of difference we noted in milk fat and protein percentages between lines is also consistent with their report, suggesting that while overall yield differed, milk composition remained comparable. These lineage effects underscore that certain imported Holstein genetics may be better suited to Kazakhstan's management and feeding conditions. It could be that the Wis Burke Ideal line has greater adaptability or genetic potential that expresses under the local diet and climate. Identifying such line or family differences is valuable for breeding decisions – it indicates an opportunity to selectively propagate the better-performing lineage in Kazakh herds. Similar line comparisons in other countries (e.g. China) also emphasize genotype-by-environment interactions: recent work in Ningxia, China noted that despite overall high genetic merit, performance can vary by herd and lineage, reaffirming the need to choose bull lines that match the regional conditions (Xue et al., 2022).

Overall, our findings reinforce global conclusions that conformation traits are important correlates of productivity and should be actively managed in breeding strategies. Importantly, they provide region-specific evidence that high-yielding Holsteins can thrive in Kazakhstan given appropriate selection and management, and that careful attention to body structure will help sustain the genetic gains in milk production over the long term.

Conclusion

This study showed that Holstein cows in Kazakhstan exhibit strong genetic and phenotypic links between body conformation and milk productivity. High-yielding cows were taller, longer, and more proportionate, with lower body and pelvic indices indicating functional efficiency. Moderate heritability of key traits confirms the potential for genetic improvement. The integration of digital 3D imaging

provides an objective tool for conformation assessment, supporting more accurate selection and sustainable breeding of high-performing dairy herds under local production conditions.

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REFERENCES

- Abugaliev, S., Bupebayeva, L., Kulbayev, R., & Baisabyrova, A. (2021a). Introduction of the modern methods of assessing the breeding value of cows in the selection of dairy cattle in the Republic of Kazakhstan.

- Archives of Razi Institute, 76(6), 1715. <https://doi.org/10.22092/ari.2021.356236.1810>
- Baimukanov, D.A., Bissembayev, A.T., Batanov, S.D., Baranova, I.A., & Kuzmina, N.N. (2022). Exterior and body types of cows with different levels of dairy productivity. *American Journal of Animal and Veterinary Sciences*, 17(2), 154-164. <https://doi.org/10.3844/ajavsp.2022.154.164>
- Baschenko, M., Bojko, O., Gonchar, O., & Sotnichenko, J. (2020). Influence of genotypical and paratypical factors on the productivity of dairy cattle. *Agrovisnyk*, 2020(3): UDC 636.082: 22 / 28.034.061. <https://doi.org/10.31073/agrovisnyk202003-08>
- Batanov, S.D., Baranova, I.A., & Starostina, O.S. (2023). Development of methods for determining the composite body conformation index for early prediction of milk productivity and live weight in cattle. *Bulletin of the Orenburg State Agrarian University*, 1(99), 299-307. <https://doi.org/10.37670/2073-0853-2023-99-1-299-307>
- Berry, D.P., Coffey, M.P., Pryce, J.E., de Haas, Y., Lovendahl, P., Krattenmacher, N., Crowley, J.J., Wang, Z., Spurlock, D., Weigel, K., Macdonald, K., & Veerkamp, R.F. (2013). International genetic evaluations for feed intake in dairy cattle. *Proceedings of the Interbull Technical Workshop*, 47, 52.
- Brade, V. (2011). Genomic selection: A revolution in breeding. *New Agriculture: Journal of Agro Manager*, 4, 66-67.
- Brade, W. (2017). Body size of Holstein cows – A critical analysis from the point of view of breeding and animal welfare. *Berichte Ueber Landwirtschaft*, 95(3), 21-27.
- Cattaneo, L., Piccioli-Cappelli, F., Minuti, A., & Trevisi, E. (2023). Metabolic and physiological adaptations to first and second lactation in Holstein dairy cows. *Journal of Dairy Science*, 106(5), 3559-3575. <https://doi.org/10.3168/jds.2022-22684>
- Conte, A.F., Kharitonov, S.N., Sermyagin, A.A., Ermilov, A.N., Yanchukov, I.N., & Zinovieva, N.A. (2017). Variability of genetic parameters for linear type traits in Russian Black-and-White cattle population. *Journal of Dairy and Beef Cattle Breeding*, 8, 3-9.
- De Haas, Y., Janss, L.L.G., & Kadarmideen, H.N. (2007). Genetic and phenotypic parameters for conformation and yield traits in three Swiss dairy cattle breeds. *Journal of Animal Breeding and Genetics*, 124(1), 12-19.
- Dong, J., Liu, Y., Li, S., Sun, Z., Chen, X., Wang, D., Qin, G., & Zhen, Y. (2023). The physiological dissimilarities of Holstein dairy cows with different milk yields. *Veterinary Medicine and Science*, 9(1), 429-442. <https://doi.org/10.1002/vms3.966>
- Erdoğan, M., Çinkaya, S., Brenig, B., Çelikeloğlu, K., Demirtaş, M., Saribrahimoglu, S., & Tekerli, M. (2024). Genome-wide association studies for milk production traits and persistency of first calving Holstein cattle in Türkiye. *Frontiers in Veterinary Science*, 11, 1461075. <https://doi.org/10.3389/fvets.2024.1461075>
- Hayes, B.J., Bowman, P.J., Chamberlain, A.J., & Goddard, M.E. (2009). Genomic selection in dairy cattle. *Journal of Dairy Science*, 92(2), 433-443.
- Kalashnikova, L.A., & Khabibrakhmanova, Ya.A. (2013). Genomic assessment of cattle. *Lesnye Polyany*, 32 p.
- Khamzina, A.K., Igoshin, A.V., Muslimova, Z.U., Turgumbekov, A.A., Khussainov, D.M., Yudin, N.S., Ussenbekov, Y.S., & Larkin, D.M. (2025). Resequencing Composite Kazakh Whiteheaded Cattle: Insights into Ancestral Breed Contributions, Selection Signatures, and Candidate Genetic Variants. *Animals*, 15(3), 385. <https://doi.org/10.3390/ani15030385>
- Khamzina, A.K., Yurchenko, A.A., Yudin, N.S., Ibragimov, R., Ussenbekov, Y., & Larkin, D.M. (2024). History, status and genetic characteristics of native cattle breeds from the Republic of Kazakhstan. *Vavilov Journal of Genetics and Breeding*, 28(4), 416-423. <https://doi.org/10.18699/vjgb-24-47>
- Kharitonov, S.N., Yanchukov, I.N., & Ermilov, A.N. (2011). Improvement of the evaluation system for dairy cattle based on a complex of conformation traits. *Izvestiya of TSHA*, 4, 103-113.
- Khmelnichyi, L., & Karpenko, B. (2021). Evaluation and variability of linear classification indicators in their relationship with milk yield of cows of Holstein breed of regional selection. *Scientific Papers Series: Management, Economic Engineering in Agriculture and Rural Development*, 21(1), 423-430. https://managementjournal.usamv.ro/pdf/vol.21_1/Art48.pdf
- Khmelnichyi, L., Khmelnychi, S., Karpenko, B., Samokhina, Y., & Cherniavska, T. (2023b). Measurements of the udder of firstborn cows of Black-and-White cattle of Ukrainian breeding, the level of their heritability and correlative variability with milk yield. *Scientific Papers Series: Management, Economic Engineering in Agriculture and Rural Development*, 23(1), 319-324.
- Khmelnichyi, L., Samokhina, E., Khmelnychi, S., & Karpenko, B. (2023c). The heritability and correlative variability of linear traits with milk yield of Holstein firstborn cows. In *Gestionarea fondului genetic animalier – probleme, solutii, perspective* (pp. 149-155).
- Khmelnichyi, L.M., Samokhina, E., Khmelnychi, S.L., & Karpenko, B. (2023a). The heritability and correlative variability of linear traits with milk yield of Holstein firstborn cows. *Management of the Genetic Fund of Animals – Problems, Solutions, Outlooks*, 149-155. <https://doi.org/10.61562/mgfa2023.19>
- Konstandoglo, A., Foksha, V., Stratan, G., & Stratan, D. (2017). Evaluation of the exterior of Holstein and Simmental primiparous cows. *Scientific Papers. Series D. Animal Science*, 60, 35-39.
- Kruszyński, W., Pawlina, E., & Szewczuk, M. (2013). Genetic analysis of values, trends and relations between conformation and milk traits in Polish Holstein-Friesian cows. *Archives Animal Breeding*, 56(1), 536-546.
- Kuznetsov, V. (2012). Problems of biology of productive animals. *Problems of Biology of Productive Animals*, 4, 18-57.
- Kuznetsov, V.M. (2002). Strategy of the development of genetic assessment of animals in the 21st century. In *Health-Nutrition-Biological Resources: Materials of the International Scientific and Practical Conference dedicated to the 125th anniversary of the birth of N.V. Rudnitskiy* (Vol. 2, pp. 299-310). Kirov: ARI of North-East.
- Lukyanov, K., Soloshenko, V.A., Klimenok, I.I., & Yudin, N.S. (2015). Genetics and breeding of animals. *Genetics and Breeding of Animals*, 3, 63-69.
- Mantysaari, E. (2011). Use of MACE results as input for genomic models. *Proceedings of the Interbull Technical Workshop*, 43, 27.
- Merkelytė, I., Šiuškėius, A., & Nainienė, R. (2025). The Role of Sensor Technologies in Estrus Detection in Beef Cattle: A Review of Current Applications. *Animals*, 15(15), 2313. <https://doi.org/10.3390/ani15152313>
- Minister of Agriculture of the Republic of Kazakhstan (2014). On approval of the instructions for grading farm animals and breed standards (Order No. 3-3/517, October 10, 2014). <https://adilet.zan.kz/rus/docs/V14F0009818>
- Mussayeva, G.K., Meldebekov, A.M., Meldebekova, N.A., Shaykamal, G.I., Buralkhiyev, B.A., Rametov, N.M., & Zhumanov, K. (2023). Dairy productivity of Holstein cows of different genetic lines in the conditions of Kostanay region of Kazakhstan. *Pakistan Journal of Zoology*, 55(3), 1257-1265. <https://dx.doi.org/10.17582/journal.pjz/20210818080851>
- Nazar, M., Abdalla, I.M., Chen, Z., Ullah, N., Liang, Y., Chu, S., Xu, T., Mao, Y., & Lu, X. (2022). Genome-wide association study for udder conformation traits in Chinese Holstein cattle. *Animals*, 12(19), 2542. <https://doi.org/10.3390/ani12192542>
- Nurbaev, S.D. (2013). Elementary biometrics (fundamentals, concepts, methods) (Vol. 1). Germany: Palmarium Academic Publishing, 207 p.
- Nusupov, A., Sambetbaev, A.A., Kozhebaev, B.Z., Nurzhanova, K.H., & Gorelik, O.V. (2021). A comparison of the milk yield and morphometrics of Irtysh type Simmental cows and their Holstein and Simmental crosses in East Kazakhstan. *Biodiversitas: Journal of Biological Diversity*, 22(9), 3663-3670. <https://doi.org/10.13057/biodiv/d220908>
- Papusha, N.V., & Smailova, M.N. (2023). Modern methods of rearing replacement young cattle during the dairy period: A textbook. Kostanay: NAO "KRU named after A. Baitursynov", 90 p.
- Prozherin, V.P., Zavertyaev, B.P., Yaluga, V.L., & Mohnatkina, Y.M. (2008). Linear evaluation of the exterior of Kholmogory cows. *Zootechniya Journal*, 12, 3-4.
- Radko, A., & Slota, E. (2007). Polymorphism of microsatellite DNA sequences used for parentage control in Holstein-Friesian bulls of the Black-and-White variety in Poland. *Annals of Animal Science*, 7(2), 189-196.
- Samoré, A.B., Rizzi, R., Rossoni, A., & Bagnato, A. (2010). Genetic parameters for functional longevity, type traits, somatic cell scores, milk flow and production in the Italian Brown Swiss. *Italian Journal of Animal Science*, 9(2), e28.
- Shamshedin, A.S., Khazhau, A., Bissembayev, A.T., & Abylgazinova, A.T. (2024). Evaluation of Holstein bulls by the exterior type of their daughters. *Science and Education*, 2-2(75), 179-189. <https://doi.org/10.52578/2305-9397-2024-2-2-178-189>
- Short, T.H., & Lawlor, T.J. (1992). Genetic parameters of conformation traits, milk yield, and herd life in Holsteins. *Journal of Dairy Science*, 75(7), 1987-1998.
- Uskenov, R., Issabekova, S., Mukhanbetkaliyeva, A., Akibekov, O., & Zhagipar, F. (2024). Digital technologies in dairy cattle breeding to improve the reproductive function of cows and heifers: A case study in Northern Kazakhstan. *Veterinary World*, 17(10), 2385.
- VanRaden, P.M., & Sullivan, P.G. (2010). International genomic evaluation methods for dairy cattle. *Genetics Selection Evolution*, 23(1), 319-324.
- Wang, P., Li, X., Zhu, Y., Wei, J., Zhang, C., Kong, Q., Nie, X., & Wang, Z. (2022). Genome-wide association analysis of milk production, somatic cell score, and body conformation traits in Holstein cows. *Frontiers in Veterinary Science*, 9, 932034. <https://doi.org/10.3389/fvets.2022.932034>
- Weller, J.I., Glick, G., Shirak, A., Ezra, E., Zeron, Y., & Ron, M. (2012). Predictive

- ability of selected subsets of single nucleotide polymorphisms (SNPs) for moderately sized dairy cattle populations. *Proceedings of the Interbull Meeting*, 46, 28.
- Wolfe, A.R., Rezamand, P., Agostinho, B.C., Konetchy, D.E., & Laarman, A.H. (2023). Effects of weaning strategies on health, hematology, and productivity in Holstein dairy calves. *Journal of Dairy Science*, 106(10), 7008–7019. <https://doi.org/10.3168/jds.2022-22738>
- Xue, X., Hu, H., Zhang, J., Ma, Y., Han, L., Hao, F., Jiang, Y., & Ma, Y. (2022). Estimation of genetic parameters for conformation traits and milk production traits in Chinese Holsteins. *Animals*, 13(1), 100. <https://doi.org/10.3390/ani13010100>
- Xue, X., Hu, H., Zhang, J., Ma, Y., Han, L., Hao, F., Jiang, Y., & Ma, Y. (2022). Estimation of genetic parameters for conformation traits and milk production traits in Chinese Holsteins. *Animals*, 13(1), 100. <https://doi.org/10.3390/ani13010100>
- Zink, V., Zavadilová, L., Lassen, J., Štípková, M., Vacek, M., & Štolc, L. (2014). Analyses of genetic relationships between linear type traits, fat-to-protein ratio, milk production traits, and somatic cell count in first-parity Czech Holstein cows. *Czech Journal of Animal Science*, 59(12), 539–547. <https://doi.org/10.17221/7793-CJAS>