Russian Journal of Veterinary Pathology. 2026;25(1):41-49. eISSN 2949-4826

ANIMAL BREEDING, SELECTION, GENETICS, AND BIOTECHNOLOGY

РАЗВЕДЕНИЕ, СЕЛЕКЦИЯ, ГЕНЕТИКА И БИОТЕХНОЛОГИЯ ЖИВОТНЫХ

Original Empirical Research

UDC:619:636.2:575.174.4
https://doi.org/10.23947/2949-4826-2026-25-1-41-49

EDN: TSFAPY

Finding Associations of Single Nucleotide Polymorphisms with Exterior Traits (Pelvic Parameters) in Holstein Cows

Maksim V. Bytov ✉, **Vladlena D. Zubareva**, **Alexander S. Krasnoperov**, **Natalia A. Bezborodova**, **Marina A. Pechenkina**, **Olga V. Sokolova**
Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences, Ekaterinburg, Russian Federation
✉ bytovmaks@mail.ru

Abstract

Introduction. Exterior traits of a cow can have crucial effect on development of pathological conditions, for example, sacrum anatomy features can be related to the risk of dystocia (pathological or difficult parturition). In dairy farming, pelvic parameters are one of the key factors enabling control of easy calving. However, modern breeding focuses on selection of the herd individuals with the highest milk yield and long-term economic productivity, whereas the exterior traits, unfortunately, are taken into account to a lesser extent. The aim of the present research is to identify associations of single-nucleotide polymorphisms with cow pelvic exterior parameters that are important prerequisites of susceptibility to easy or difficult calving. As a result, it will be possible to determine the genetic markers to be included into the selection-breeding programs.

Materials and Methods. The study was conducted at Ural Research Veterinary Institute — a structural division of Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences in the period from 2023 to 2025. The exterior trait inheritance patterns were studied in Holstein cows (n=155) across three pelvic dimensions: sacrum height, hip width, and ischial tuberosity width. Association tests were conducted using SNPassoc R package.

Results. The mean values and standard deviations for pelvic height at sacrum in cows were found to be 161.7±5.3 cm; for width at hips — 41.1±3.9 cm; for width at ischial tuberosities — 22.4±2.1 cm. For each individual, genotyping with 13 polymorphisms was performed. Rs109452259 polymorphism in C* allele was revealed to have negative effect on hip width in Holstein cows. Rs134055603 and rs43038601 polymorphisms in G/G and C/A genotypes respectively, were established to have putative epistatic interaction with positive effect on the sacrum height. Also, rs134055603 and rs137396952 polymorphisms in C/A and C/C genotypes respectively were found to have possibly synergistic effect.

Discussion and Conclusion. The data obtained in the frame of the study are reliable for the observed-level statistical interaction. Potential limitations of the study include possible influence of the unaccounted confounding factors, such as variability of animals within the studied groups by age, live body weight, lactation number, etc. For confirmation of the biological mechanisms, further functional studies are required.

Keywords: cows, Holstein breed, exterior traits, sacrum height, hip width, ischial tuberosity width, polymorphisms, genetic associations, selection-breeding

Funding. The research was conducted in the frame of the State Assignment of the Ministry of Science and Higher Education of the Russian Federation No. 0532-2025-0003 “Development of High-Precision Methods for Identifying Genetic Determinants of Disease Resistance for Use in Cattle Breeding”.

For Citation. Bytov MV, Zubareva VD, Krasnoperov AS, Bezborodova NA, Pechenkina MA, Sokolova OV. Finding Associations of Single Nucleotide Polymorphisms with Exterior Traits (Pelvic Parameters) in Holstein Cows. *Russian Journal of Veterinary Pathology*. 2026;25(1):41–49. https://doi.org/10.23947/2949-4826-2026-25-1-41-49

Оригинальное эмпирическое исследование

Поиск ассоциаций однонуклеотидных полиморфизмов с показателями экстерьера (тазовые параметры) коров голштинской породы

М.В. Бытов ✉, В.Д. Зубарева, А.С. Краснопёров, Н.А. Безбородова, М.А. Печёнкина, О.В. Соколова

Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук, г. Екатеринбург, Российская Федерация

✉ bytovmaks@mail.ru

Аннотация

Введение. Экстерьерные параметры коровы могут иметь решающее значение в развитии патологического состояния, например, особенности строения крестца могут быть связаны с риском дистоции (патологические или трудные роды). Параметры таза являются одним из ключевых факторов управления легкостью отела в молочном скотоводстве, однако современная селекция направлена на закрепление в стаде особей с наибольшей молочной продуктивностью и длительным хозяйственным использованием, и экстерьерные параметры, к сожалению, учитываются в меньшей степени. Цель исследования — выявить ассоциации однонуклеотидных полиморфизмов с экстерьерными показателями таза коров, играющими важную роль в предрасположенности к легкому или трудному отелу, что позволит определить генетические маркеры для использования в селекционных программах.

Материалы и методы. Исследование проведено в Уральском НИВИ — структурном подразделении ФГБНУ УрФАНИЦ УрО РАН в период с 2023 по 2025 гг. Исследованы модели наследования экстерьерных параметров по трем проекциям таза коров голштинской породы (n=155): высота в крестце, ширина в маклоках, ширина в седалищных буграх. Ассоциативные тесты проведены с использованием SNPassoc для программной среды R.

Результаты исследования. Установлено, что средние значения и стандартные отклонения для высоты таза коров в крестце равны 161,7±5,3 см; для ширины в маклоках — 41,1±3,9 см; для ширины в седалищных буграх — 22,4±2,1 см. Проведено генотипирование каждой особи по 13 полиморфизмам. Для коров голштинской породы по rs109452259 выявлен отрицательный эффект аллеля *C** на ширину в маклоках. Обнаружено предположительно эпистатическое взаимодействие для rs134055603 и rs43038601 для генотипов *G/G* и *C/A*, соответственно, с положительным эффектом на высоту в крестце. Также обнаружено эпистатическое взаимодействие для rs134055603 и rs137396952, вероятно, с синергическим характером для генотипа *C/A* и *C/C* соответственно.

Обсуждение и заключение. Полученные в ходе исследования данные статистически достоверны для наблюдаемого взаимодействия. К потенциальным ограничениям исследования следует отнести возможное влияние неучтённых смешивающих факторов, таких как вариабельность внутри исследуемых групп по возрасту животных, живой массе, номеру лактации и т. д. Подтверждение биологических механизмов требует дополнительных функциональных исследований.

Ключевые слова: коровы, голштинская порода, экстерьерные показатели, высота в крестце, ширина в маклоках, ширина в седалищных буграх, полиморфизмы, генетические ассоциации, селекция

Финансирование. Работа выполнена в рамках Государственного задания Министерства науки и высшего образования Российской Федерации по теме № 0532-2025-0003 «Разработка высокоточных методов идентификации генетических детерминант устойчивости к заболеваниям для использования в селекции крупного рогатого скота».

Для цитирования. Бытов М.В., Зубарева В.Д., Краснопёров А.С., Безбородова Н.А., Печёнкина М.А., Соколова О.В. Поиск ассоциаций однонуклеотидных полиморфизмов с показателями экстерьера (тазовые параметры) коров голштинской породы. *Ветеринарная патология*. 2026;25(1):41–49. https://doi.org/10.23947/2949-4826-2026-25-1-41-49

Introduction. In modern animal husbandry, the exterior of cattle is an important production indicator directly affecting health, productivity, and reproductive function [1]. Body constitution indices are taken into account in dairy cow breeding among the primal indicators to assess the non-productive traits [2]. Gibson et al. believe that height of a calf is related to the lactation efficiency of an adult cow: taller calves will produce more milk in the future through several lactations compared to the shorter calves, live weight considered [3]. The results of the study conducted by Schmidtmann et al. show that larger animals with visibly protruding bones and a low BCS (Body Condition Score) are more susceptible to metabolic disorders [4].

Exterior traits can be decisive for the development of pathological conditions in animals. For example, sacrum anatomy features can be related to the risk of dystocia (pathological or difficult parturition) [5]. Significantly higher incidence of dystocia has been found in cows with the sacrum size both narrower and, on the contrary, wider than optimal for calving [6]. The influence of a breed on the incidence of dystocia is explained by the differences in a relative body weight at birth, pelvis anatomy, and significant variations in dimensions of pelvis in some breeds [5]. Due to modern breeding focusing on selection of the herd specimens with the highest milk yield and long-term economic productivity, dystocia remains a serious problem with incidence rate estimated at 10 to 50% [7].

The aim of the study is to identify associations of single-nucleotide polymorphisms with pelvic exterior parameters in Holstein cows that are important prerequisites for forming susceptibility to easy or difficult calving. The data obtained will make it possible to determine the genetic markers to be included into the herd improvement breeding programs.

Materials and Methods. The study was carried out at the Department of Genomic Research and Animal Breeding of Ural Research Veterinary Institute, structural division of Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences, in the period from 2023 to 2025. PCR tests of DNA samples from Holstein cows (n=155) from two cattle breeding agricultural enterprises (AEs) (AE No. 1, n=70; AE No. 2, n=85) were performed. The research sample included animals with one or more lactations. The research was held in compliance with the ethical standards, the studies (e.g., blood sampling from the caudal veins of animals) were approved by the Bioethics Committee of Ural Federal Agrarian Research Center, Ural Branch of the Russian Academy of Sciences (Protocol No. 136 of October 13, 2025).

Exterior traits of the animals were assessed across three dimensions: sacrum height, hip width, and ischial tuberosity width. Statistical data for a phenotype —mean values and standard deviations—were calculated using STATISTICA 12 software (StatSoft Inc, USA).

13 Single Nucleotide Polymorphisms (SNPs) were genotyped across entire sample of cows. To perform association tests, the following polymorphic markers were studied: rs134055603, rs137396952, rs109452259, rs110347054, rs110352004, rs133674837, rs109529386, rs109279094, rs109611915, rs134668940, rs41567027, rs43038601, rs41255693, which had previously shown significant associations with a number of physiologically valuable parameters in cattle during GWAS studies:

– productive longevity [8];
– easy calving [9, 10];
– body weight [11];
– carcass length after cutting [12];
– and other parameters of productivity [10, 13].

The article presents both authors' own findings based on TaqMan genotyping technology and earlier described test systems (Table 1).

Based on the genetic data obtained, the relationship of each polymorphic locus with a phenotype was assessed in separate. Five patterns of trait inheritance were assessed using the SNPStats web tool (Institut Català d'Oncologia, Spain) [19] and the SNPassoc package [20] in R programming environment (Autonomous University of Barcelona, Spain): codominant, dominant, recessive, overdominant, and log-additive; the effect size was interpreted as the odds ratio (the differences in the values of the exterior traits) with a 95% confidence interval compared to alternative allele homozygote.

To conduct association studies using the SNPassoc package in the R programming environment, the WGassociation function was used. To test for the presence of "gene-gene" interactions, the interactionPval (Phen, data=data, model='co') function was used. Association tests were performed across three pelvic dimensions: sacrum height, hip width, and ischial tuberosity width; the presence of "gene-gene" interactions was also assessed for each of the exterior traits. For a more detailed study of allele combinations contributing to the formation of a trait, taking into account "gene-gene" interactions, a linear model was created: lm("Phen ~", "SNP1", "*", "SNP2", data=data). With regard to epistatic interactions, this model envisaged sorting through each combination of genotypes and determining mean value of each of these combinations for a phenotype. A post-hoc Bonferroni correction was performed for each analysis

Results. The mean values and standard deviations for sacrum height in Holstein cows were determined to be 161.7±5.3 cm; for hip width — 41.1±3.9 cm; and for ischial tuberosity width — 22.4±2.1 cm.

Larger values of pelvic width proved to ensure sufficient space for successful development of a fetus and easy calving, and necessary space between hindlimbs to ensure a more voluminous cup-shaped udder [21]. Thus, higher values of each of the three exterior traits are considered a favourable phenotype.

Significant effects of rs109452259 SNP on hip width in Holstein cows were acknowledged in codominant, dominant, and log-additive inheritance patterns. The lowest AIC value for rs109452259 was found in the dominant inheritance pattern, with the C/A and A/A genotypes having 2.17 cm difference from C/C; p-value=0.0006.

When studying a phenotype inheritance mechanism, an interesting feature was revealed, i.e. the presence of "gene-gene" interactions among polymorphisms. In the present study, the epistatic interactions for the pairs of rs134055603–rs43038601 and rs134055603–rs137396952 polymorphisms were identified according to the codominant inheritance pattern (Fig. 1). The significance level for these pairs was corrected to $\alpha<0.00032$.

Table 1

Oligonucleotides used in the present study for genotyping in cattle

SNP, localization and genomic context	Oligonucleotides	Amplicon, bp	Source
rs133674837 6:21766662 *BDH2*	F,AAAGAAGGTGCCAAAGT	91	This study
	R,TCAAGCTATGGAGGTGCT		
	P1,[R6G]ATCAATGACTCCAAACT[BHQ1]		
	P2,[ROX]ATATCAATGAATCCAAACT[BHQ2]		
rs41567027 6:43657946 *PPARGC1A*	F, CACTAGAAAGCACACTTCA	197	This study
	R, ATACTTGGCTGTGTGGAA		
	P1, [R6G]AGAAGCCGCAAGGTCA[BHQ1]		
	P2, [ROX]CAGAAGCTGCAAGGTCA[BHQ2]		
rs109279094 6:45175137 *PPARGC1A*	F, ACTAAACCTCTCTGTCTT	338	This study
	R, GATTTGTGTCAGCTCCT		
	P1, [R6G]TCCCCCAGACTCATAA[BHQ1]		
	P2, [ROX]CTCCCCTAGACTCATAAC[BHQ2]		
rs109611915 6:88739941 *GC – NPFFR2*	F, CCTTGTAAATGCAGAATCCAC	132	This study
	R, GAACCAAACGTTGACCTGAT		
	P1, [R6G]TCATTTTGCAGATAACAGAAC[BHQ1]		
	P2, [ROX]TTCATTTTGAAGATAACAGAACTA[BHQ2]		
rs110347054 6:88751491 *GC – NPFFR2*	F, GGAGCTGGGATTGATGCCTAC	226	[14]
	R, AAGAAAATCA+CA+CTTCAAAAGGATA		
	P1, [ROX]CCTACTCCCTC+C+A+CTGGGTG[BHQ2]		
	P2, [Cy5]CCTACTCCCTCC+G+CTGGGTG[BHQ2]		
rs109452259 6:88800322 *GC – NPFFR2*	F, GCAAAAACACAATATGCTGGAT	415	[16, 15]
	R, AGGTCAAACAACTAAACAGTGG		
	P1, [ROX]CTTGTC+A+A+CTT+C+CA[BHQ2]		
	P2, [FAM]CTTGTC+A+C+CTTCCA[BHQ1]		
rs137396952 6:88817457 *GC – NPFFR2*	F, ATGCAGCAGAAACAAGGGTTAAA	225	[17]
	R, GTACAGCCACTGTGCAACAAC		
	P1, [HEX]GA+TT+CAGCATG+G+T+G+TCAG[BHQ2]		
	P2, [Cy5]GATT+CAGCATG+G+C+G+TCAG[BHQ3]		
rs134055603 6:88832335 *GC – NPFFR2*	F, GACAAGGCTTTTGATAGGTGAAA	316	[17]
	R, CAAAGCAACCACACAATGTTG		
	P1, [HEX]CAT+TT+TCT+T+A+GA+CT+T+CTG[BHQ1]		
	P2, [Cy5]CATTTTCT+T+G+GA+CT+T+CTG[BHQ3]		
rs134668940 6:88838658 *GC – NPFFR2*	F, GGCAGAGAACTTGACT	276	This study
	R, AGTATCTTG+GCCTCTT		
	P1, [R6G]AGAATAGCACATGGCACA[BHQ1]		
	P2, [ROX]TAGAATAGCAAATGGCACATA[BHQ2]		
rs110352004 6:88948552 *GC – NPFFR2*	F, GTAGGGATT+GAT+GC+CCTTGAA	232	[14]
	R, TACAATA+CA+C+CATAT+CTTTTTCATCC		
	P1, [HEX]AA+TA+C+GTAC+AA+CACT+CT+T[BHQ1]		
	P2, [ROX]TA+C+GTAC+GA+CACTCTGT[BHQ2]		
rs109529386 25:26982725 *LOC100847190 – ZNF688*	F, ACTAAAGATCCCACGTGCTA	500	This study
	R, GTCTTACTACTGTCCCCACA		
	P1, [R6G]AAGGTGCCACAGCCAGA[BHQ1]		
	P2, [ROX]AGGTGCCGCAGCCA[BHQ2]		
rs43038601 18:57032285 *TRNAG-UCC – TRNAG-UCC*	F, TGATAACACGTACA+GAGT	180	This study
	R, CAATAAGGCGATTCGTGG		
	P1, [R6G]TGGTGTCTCGGTTGC[BHQ1]		
	P2, [ROX]TGTCTAGGTTGCTTTTACTG[BHQ2]		
rs41255693 26:21272422 *SCD1*	F, CCCTTATGACAAGACCATCAACC	90	[18]
	R, GACGTGGTCTTGCTGTGGACT		
	P1, [FAM]CTTACCCACAGCTCCCA[BHQ1]		
	P2, [HEX]TACCCGCAGCTCCC[BHQ1]		

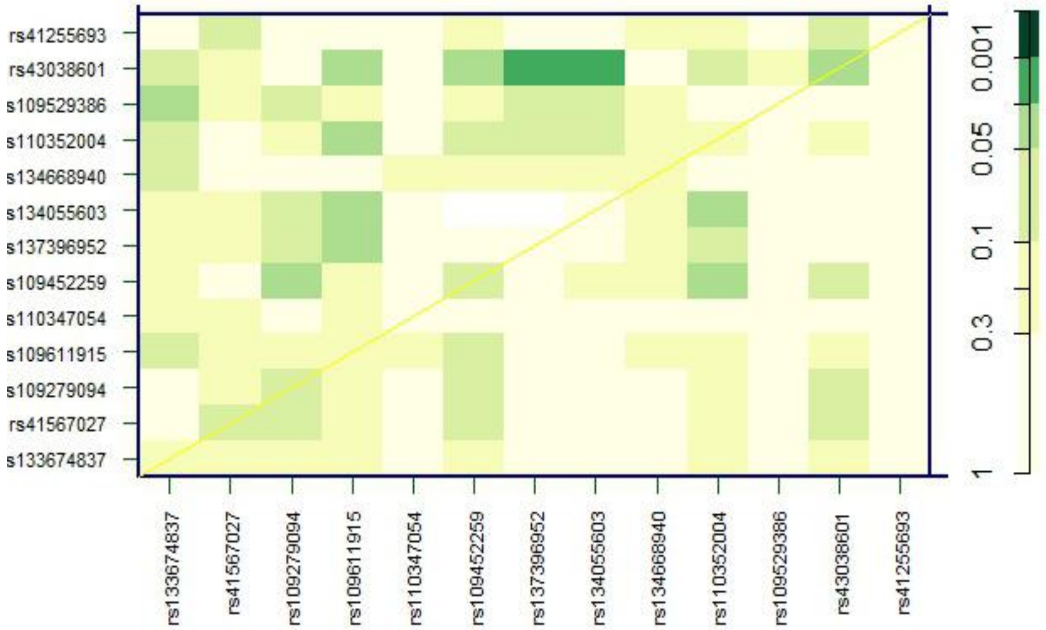

Fig. 1. Screening for the presence of epistatic and additive interactions among polymorphisms in relation to sacrum height parameter inheritance in Holstein cows

A statistically significant epistatic interaction was found for rs134055603 polymorphism. This SNP has a significantly positive contribution to sacrum height only in the presence of A* allele in a genotype identified by rs43038601 polymorphism, while its absence (the combination of G/G and C/C genotypes identified by rs134055603 and rs43038601, respectively) has a negative effect on the phenotype (Fig. 2). It is worth noting that the number of specimens of A/A genotype identified by rs43038601 polymorphism for each of the three combinations was ≤ 3. Therefore, interpretation of these genotype combinations is impossible. For each of the other six combinations, the sample size was ≥ 10.

Epistatic interactions of opposite nature for 134055603 with rs137396952 polymorphism were found. The combination of A* allele in genotype of rs134055603 and the C* allele in genotype of rs137396952 had a positive effect on sacrum height (Fig. 3). It is worth emphasising that the number of specimens with A/A genotype identified by rs43038601 polymorphism for each of the three combinations was ≤ 3.

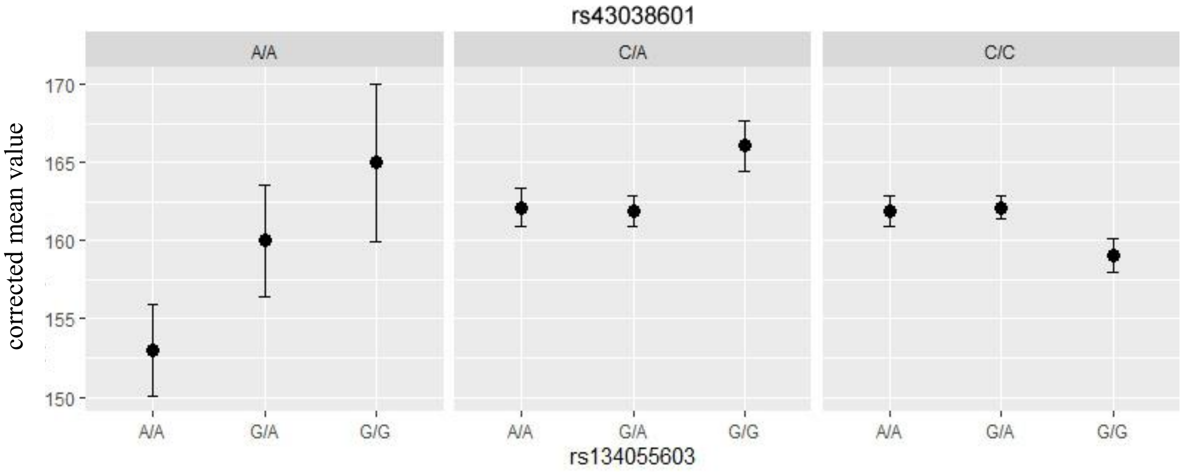

Fig. 2. Facet matrix for the pooled samples of Holstein cows in relation to sacrum height for rs134055603 and rs43038601 epistatic interaction. Corrected $R^2 = 0.0923$. F-test = 2.957. p-value < 0.0043

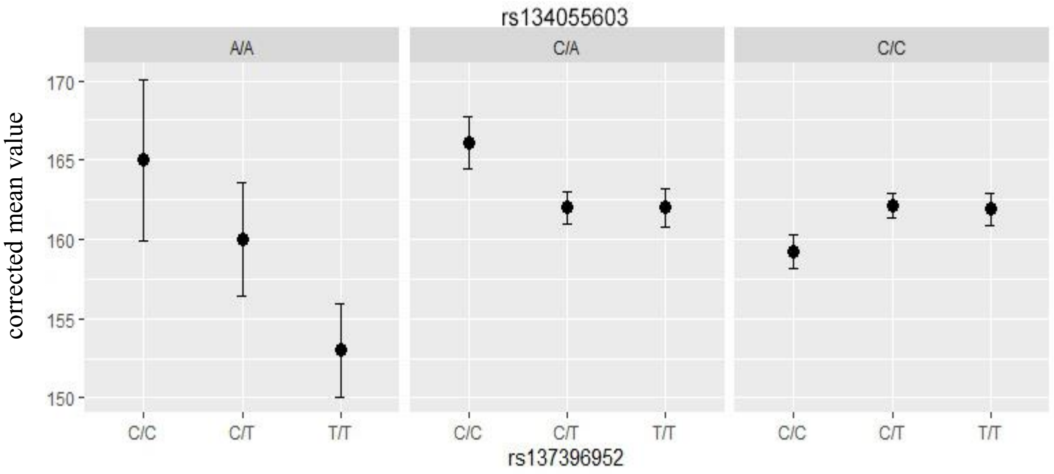

Fig. 3. Facet matrix for the pooled samples of Holstein cows in relation to sacrum height for rs134055603 and rs137396952 epistatic interaction. Adjusted $R^2 = 0.0902$. F-test = 2.909. p-value < 0.0049

Discussion and Conclusion. During the study conducted in 155 Holstein cows, the mean values and standard deviations for sacrum height (161.7±5.3 cm), hip width (41.1±3.9 cm), and ischial tuberosity width (22.4±2.1 cm) were determined. Genotyping of 13 polymorphisms was conducted for each specimen. It was revealed that in Holstein cows, genotyping of rs109452259 requires negative selection by C* allele to increase the hip width. Epistatic interaction of rs134055603 and rs43038601, probably of synergistic nature for G/G and C/A genotypes respectively, was identified. Epistatic interaction of rs134055603 and rs137396952, probably of synergistic nature for the C/A and C/C genotypes respectively, was identified. The data obtained during the study are significant for the observed-level statistical interaction; for confirmation of the biological mechanisms, further functional studies are required.

The potential limitations of the study include possible influence of the unaccounted confounding factors, such as, variability of the studied groups of animals by age, live body weight, lactation number, and origin (of an agricultural enterprise). The above mentioned limitations could have influenced the results obtained and their subsequent interpretation.

References

1. Peng Ch, Cao Sh, Li Sh, Bai T, Zhao Z, Sun W. Automated Measurement of Cattle Dimensions Using Improved Keypoint Detection Combined with Unilateral Depth Imaging. *Animals*. 2024;14(17):2453. https://doi.org/10.3390/ani14172453

2. Zhang Zh, Yang J, Yao Y, Wang D, Lu X, Yang Zh. Body Conformation Traits in Early-Lactation Associated with Clinical Mastitis and Lameness in Lactating Chinese Holstein Cows. *BMC Veterinary Research*. 2024;20(1):85. https://doi.org/10.1186/s12917-024-03931-1

3. Gibson MJ, Adams BR, Back PJ, Hickson RE, Dittmer KE, Rogers CW. Live Weight and Bone Growth from Birth to 23 Months of Age in Holstein–Friesian, Jersey and Crossbred Heifers. *Dairy*. 2022;3(2):333–344. https://doi.org/10.3390/dairy3020026

4. Schmidtmann C, Segelke D, Bennewitz J, Tetens J, Thaller G. Genetic Analysis of Production Traits and Body Size Measurements and Their Relationships with Metabolic Diseases in German Holstein Cattle. *Journal of Dairy Science*. 2023;106(1):421–438. https://doi.org/10.3168/jds.2022-22363

5. Bila L, Tyasi TL, Fourie P, Katikati A. Classification and Regression Tree Analysis to Predict Calving Ease in Sussex Heifers Using Pelvic Area Dimensions and Morphological Traits. *Journal of Advanced Veterinary and Animal Research*. 2021;8(1):164–172. https://doi.org/10.5455/javar.2021.h499

6. Sawa A, Bogucki M, Krężel-Czopek S, Neja W. Association between Rump Score and Course of Parturition in Cows. *Archiv Tierzuch (Archives Animal Breeding)*. 2013;56(81):816–822. https://doi.org/10.7482/0003-9438-56-081

7. Crociati M, Sylla L, De Vincenzi A, Stradaioli G, Monaci M. How to Predict Parturition in Cattle? A Literature Review of Automatic Devices and Technologies for Remote Monitoring and Calving Prediction. *Animals*. 2022;12(3):405. https://doi.org/10.3390/ani12030405

8. Nayeri S, Sargolzaei M, Abo-Ismail MK, Miller S, Schenkel F, Moore SS, Stothard P. Genome-Wide Association Study for Lactation Persistency, Female Fertility, Longevity, and Lifetime Profit Index Traits in Holstein Dairy Cattle. *Journal of Dairy Science*. 2017;100(2):1246–1258. https://doi.org/10.3168/jds.2016-11770

9. Abo-Ismail MK, Brito LF, Miller SP, Sargolzaei M, Grossi DA, Moore SS, et al. Genome-Wide Association Studies and Genomic Prediction of Breeding Values for Calving Performance and Body Conformation Traits in Holstein Cattle. *Genetics, Selection, Evolution*. 2017;49:82. https://doi.org/10.1186/s12711-017-0356-8

10. Jiang J, Li M, Prakapenka D, VanRaden PM, Cole JB, Da Y. A Large-Scale Genome-Wide Association Study in U.S. Holstein Cattle. *Frontiers in Genetics*. 2019;10:412. https://doi.org/10.3389/fgene.2019.00412

11. Snelling WM, Allan MF, Keele JW, Kuehn LA, McDaneld T, Smith TP, et al. Genome-Wide Association Study of Growth in Crossbred Beef Cattle. *Journal of Animal Science*. 2010;88(3):837–848. https://doi.org/10.2527/jas.2009-2257

12. Liu R, Fang X, Lu X, Liu Y, Li Y, Bai X, et al. Polymorphisms of the SCD1 Gene and Its Association Analysis with Carcass, Meat Quality, Adipogenic Traits, Fatty Acid Composition, and Milk Production Traits in Cattle. *Animals*. 2024;14(12):1759. https://doi.org/10.3390/ani14121759

13. Pozovnikova MV, Serdyuk GN, Tulinova OV, Terletskiy VP, Dementeva NV, Mitrofanova OV. Association of Polymorphic Types of Stearoyl-Coa Desaturase Gene (*SCD1*) with Economically Valuable Traits in Russian Population of Ayrshire Cows. *Agricultural Biology*. 2017;52(6):1139–1147. (In Russ.) https://doi.org/10.15389/agrobiology.2017.6.1139eng

14. Bytov MV, Nokhrin DYu, Zubareva VD, Isaeva AG, Sokolova OV. Post-GWAS Study of the Predisposition of Cows of Different Breeds to Mastitis. *Agrarian Bulletin of the Urals*. 2024;24(12):1648–1672. (In Russ.) https://doi.org/10.32417/1997-4868-2024-24-12-1648-1672

15. Bytov MV, Zubareva VD, Volskaya SV, Isaeva AG, Nokhrin DY, Osipova YA, et al. Assessing the Genetic Diversity of Five Cattle Breeds Using SNP Markers Associated with Health. *Russian Journal of Genetics*. 2024;60(6):55–61. (In Russ.) https://doi.org/10.31857/S0016675824060056

16. Bytov MV, Zubareva VD, Volskaya SV, Isaeva AG, Nokhrin DY, Osipova YA, et al. Assessing the Genetic Diversity of Five Cattle Breeds Using SNP Markers Associated with Health. *Russian Journal of Genetics*. 2024;60:747–753. https://doi.org/10.1134/S1022795424700182

17. Bytov MV, Sokolova OV, Bezborodova NA, Krasnoperov AS, Isaeva AG. Cattle Genotyping Methods for Post-GWAS Annotation of SNPs. *Agrarian Bulletin of the Urals*. 2023;235(6):67–75. (In Russ.) https://doi.org/10.32417/1997-4868-2023-235-06-67-75

18. Kovalchuk SN, Arkhipova AL, Klimov EA, Skachkova OA. *Method for Cattle Genotyping by Alleles 878 of scd1 (rs41255693) Gene by PCR in Real Time.* Patent of the Russian Federation No 2744174. 2021. (In Russ.)

19. Solé X, Guinó E, Valls J, Iniesta R, Moreno V. SNPStats: A Web Tool for the Analysis of Association Studies. *Bioinformatics*. 2006;22(15):1928–1929. https://doi.org/10.1093/bioinformatics/btl268

20. González JR, Armengol L, Solé X, Guinó E, Mercader JM, Estivill X, et al. SNPassoc: an R Package to Perform Whole Genome Association Studies. *Bioinformatics*. 2007;23(5):644–645. https://doi.org/10.1093/bioinformatics/btm025

21. Boyarina OA. Linear Assessment of the Exterior of Holstein Cows According To The Canadian System. *Bulletin of KSAU*. 2025;(221):156–165. (In Russ.) https://doi.org/10.36718/1819-4036-2025-8-156-165

About the Authors:

Maksim V. Bytov, Postgraduate Student, Junior Research Associate of the Genomic Research and Animal Breeding Department, Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences (112a, Belinsky Str, P.O. Box 269, Ekaterinburg, 620142, Russian Federation), SPIN-код, ORCID, Researcher ID, Scopus ID, bytovmaks@mail.ru

Vladlena D. Zubareva, Junior Research Associate of the Genomic Research and Animal Breeding Department, Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences (112a, Belinsky Str., P.O. Box 269, Ekaterinburg, 620142, Russian Federation), SPIN-код, ORCID, Researcher ID, Scopus ID, zzub97@mail.ru

Alexander S. Krasnoperov, Cand.Sci. (Veterinary), Head of the Laboratory of Immunology and Pathobiochemistry, Ural Research Veterinary Institute, Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences (112a, Belinsky Str., P.O. Box 269, Ekaterinburg, 620142, Russian Federation), SPIN-код, ORCID, Researcher ID, Scopus ID, marafon.86@list.ru

Natalia A. Bezborodova, Cand.Sci. (Veterinary), Head of the Genomic Research and Animal Breeding Department, Ural Research Veterinary Institute, Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences (112a, Belinsky Str., P.O. Box 269, Ekaterinburg, 620142, Russian Federation), SPIN-код, ORCID, Scopus ID, n-bezborodova@mail.ru

Marina A. Pechenkina, Laboratory Assistant of the Genomic Research and Animal Breeding Department, Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences (112a, Belinsky Str., P.O. Box 269, Ekaterinburg, 620142, Russian Federation), SPIN-код, ORCID, Researcher ID, Scopus ID, pn190503@mail.ru pn190503@mail.ru

Olga V. Sokolova, Dr.Sci. (Veterinary), Director of the Ural Research Veterinary Institute, Ural Federal Agrarian Research Center of the Ural Branch of the Russian Academy of Sciences (112a, Belinsky Str., P.O. Box 269, Ekaterinburg, 620142, Russian Federation), SPIN-код, Researcher ID, Scopus ID, nauka_sokolova@mail.ru

Claimed Contributorship:

MV Bytov: development of methodology, formal analysis, preparing the draft of the manuscript.

VD Zubareva: conducting experiments and data collection, preparing the draft of the manuscript.

AS Krasnoperov: conducting experiments and data collection.

NA Bezborodova: conducting experiments and data collection.

MA Pechenkina: manuscript editing and refining.

Sokolova OV: manuscript editing and refining.

Conflict of Interest Statement: **the authors declare no conflict of interest.**

All authors have read and approved the final manuscript.

Об авторах:

Максим Владимирович Бытов, аспирант, младший научный сотрудник отдела геномных исследований и селекции животных Уральского научно-исследовательского ветеринарного института, Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук (620142, Российская Федерация, г. Екатеринбург, а/я 269, ул. Белинского, 112а), SPIN-код, ORCID, Researcher ID, Scopus ID, bytovmaks@mail.ru

Владлена Дмитриевна Зубарева, младший научный сотрудник отдела геномных исследований и селекции животных Уральского научно-исследовательского ветеринарного института, Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук (620142, Российская Федерация, г. Екатеринбург, а/я 269, ул. Белинского, 112а), SPIN-код, ORCID, Researcher ID, Scopus ID, zzub97@mail.ru

Александр Сергеевич Красноперов, кандидат ветеринарных наук, заведующий лабораторией иммунологии и патобиохимии Уральского научно-исследовательского ветеринарного института, Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук (620142, Российская Федерация, г. Екатеринбург, а/я 269, ул. Белинского, 112а), SPIN-код, ORCID, Researcher ID, Scopus ID, marafon.86@list.ru

Наталья Александровна Безбородова, кандидат ветеринарных наук, заведующий отделом геномных исследований и селекции животных Уральского научно-исследовательского ветеринарного института, Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук (620142, Российская Федерация, г. Екатеринбург, а/я 269, ул. Белинского, 112а), SPIN-код, ORCID, Scopus ID, n-bezborodova@mail.ru

Марина Андреевна Печёнкина, лаборант отдела геномных исследований и селекции животных Уральского научно-исследовательского ветеринарного института, Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук (620142, Российская Федерация, г. Екатеринбург, а/я 269, ул. Белинского, 112а),

Ольга Васильевна Соколова, доктор ветеринарных наук, руководитель Уральского научно-исследовательского ветеринарного института, Уральский федеральный аграрный научно-исследовательский центр Уральского отделения Российской академии наук (620142, Российская Федерация, г. Екатеринбург, а/я 269, ул. Белинского, 112а), nauka_sokolova@mail.ru

Заявленный вклад авторов:
М.В. Бытов: разработка методологии, формальный анализ; подготовка первоначального варианта рукописи.
В.Д. Зубарева: проведение экспериментов и сбор данных; подготовка первоначального варианта рукописи.
А.С. Красноперов: проведение экспериментов и сбор данных.
Н.А. Безбородова: проведение экспериментов и сбор данных.
М.А. Печёнкина: редактирование и доработка рукописи.
О.В. Соколова: редактирование и доработка рукописи.

Конфликт интересов: **авторы заявляют об отсутствии конфликта интересов.**

Все авторы прочитали и одобрили окончательный вариант рукописи.

Received / Поступила в редакцию 12.01.2026
Reviewed / Поступила после рецензирования 06.02.2026
Accepted / Принята к публикации 09.02.2026