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Preliminary evidence of a possible hereditary predisposition to rear udder underdevelopment in Holstein and Jersey dairy cattle

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Abstract

This study reports the results of a long-term investigation of udder morphology in dairy cattle conducted within routine breeding evaluation programs. The aim was to describe a previously underreported developmental abnormality manifested by reduced development of the rear portion of the udder and to evaluate evidence suggestive of a possible hereditary predisposition.

A total of 3,061 Holstein and 700 Jersey lactating cows from commercial dairy herds in the Republic of Kazakhstan were included in the study. Additional comparative observations were obtained from a large Holstein population in the Russian Federation. Morphological assessment of the udder was combined with pedigree evaluation to investigate possible patterns associated with the occurrence of the condition.

Animals exhibiting a similar structural alteration were detected in several independent herds, including cattle bred in Kazakhstan and Russia as well as imported animals originating from Germany. Comparable manifestations were recorded in both Holstein and Jersey populations. The recurrence of this abnormality among descendants of certain sire lineages and its presence in geographically distant herds may suggest an inherited predisposition. Nevertheless, the underlying biological mechanisms and genetic determinants remain unclear and require further investigation.

The results suggest that rear udder underdevelopment may represent an insufficiently recognized morphological abnormality of potential relevance to dairy cattle breeding and herd management. The repeated detection of this condition in different populations, production systems, and geographical regions highlights the need for comprehensive studies incorporating pedigree analysis, genomic approaches, and large-scale population screening to clarify its prevalence, biological significance, and possible hereditary background.

Introduction

Udder morphology is one of the most important functional traits in dairy cattle because it directly affects milk production efficiency, milking performance, udder health, productive longevity, and overall economic efficiency of dairy herds (Goonewardene et al. 2003; Bhutto et al. 2010; Poppe et al. 2019; Perez-Cabal et al. 2024). Consequently, mammary gland conformation traits are routinely included in breeding programs and breeding value assessment systems in many countries.

Characteristics such as udder depth, teat placement, symmetry of udder quarters, and fore and rear udder development are widely recognized as important indicators of functional suitability and breeding value. Similar relationships between conformation traits and milk productivity have also been reported in Holstein cattle populations of Kazakhstan (Abugaliev et al. 2026).

The increasing implementation of machine milking and automated milking systems has further enhanced the importance of functional udder traits in dairy cattle breeding. Proper development of

mammary gland structures is essential for efficient milk removal, stable milking performance, and successful adaptation of cows to modern production technologies (Meyer et al. 2020; Wieland et al. 2022; Wieland and Sipka 2023). As a result, technological selection increasingly favors animals with balanced udder morphology and teat characteristics suitable for machine milking.

Numerous studies have demonstrated that many udder-related traits exhibit moderate to high heritability and therefore respond effectively to genetic selection (Jardim et al. 2018). Recent advances in genomic evaluation and genomic selection have improved the identification of genetic factors associated with mammary gland morphology and related functional traits, further strengthening the role of udder conformation in modern dairy cattle breeding programs.

In parallel with the improvement of economically important traits, increasing attention has been devoted to inherited defects and developmental abnormalities affecting dairy cattle populations. Numerous hereditary disorders and recessive haplotypes have been described in Holstein cattle, including bovine leukocyte adhesion deficiency (BLAD), complex vertebral malformation (CVM), brachyspina syndrome, cholesterol deficiency, and other genetic defects that negatively affect fertility, viability, productivity, and herd profitability (Pausch et al. 2015; Cole et al. 2016; Schutz et al. 2016; Segelke et al. 2016; Zhang et al. 2020; Martynov et al. 2023). Importantly, many of these conditions were initially recognized through repeated phenotypic observations before their molecular and genomic mechanisms were elucidated.

Despite extensive research devoted to udder conformation, milkability, and udder health, information concerning developmental abnormalities affecting the rear portion of the udder remains extremely limited. Most available studies focus on conventional linear type traits, mastitis resistance, and milking performance, whereas abnormalities associated with impaired development of mammary tissue have received considerably less scientific attention. Consequently, the prevalence, biological significance, and possible hereditary background of such conditions remain poorly understood.

Therefore, the objective of the present study was to document and characterize this previously underreported developmental abnormality and to evaluate observational evidence suggesting a possible hereditary predisposition to rear udder underdevelopment in dairy cattle.

Materials and methods

Study population

The study was conducted between 2014 and 2025 and included 3,761 lactating dairy cows, comprising 3,061 Holstein and 700 Jersey animals maintained in commercial dairy herds in different regions the Republic of Kazakhstan. The investigated herds were located in Kostanay, Almaty, Aktobe, Atyrau and West Kazakhstan regions. Additional comparative observations were obtained during a research visit to a Holstein dairy herd in the Udmurt Republic of the Russian Federation.

Phenotypic assessment

The research was based on the analysis of routine breeding records, livestock classification data, linear type evaluation results, and visual assessment of udder morphology. Annual livestock evaluation of dairy cattle in Kazakhstan is performed according to the official Instructions for the Bonitation approved by the Ministry of Agriculture (Order 3-3/517, 2014).

The methodology includes assessment of productive performance, conformation characteristics, and breeding value of individual animals. Particular attention was paid to mammary gland morphology during routine conformation evaluation. Animals exhibiting pronounced reduction in the development of the rear portion of the udder compared with normal breed-specific morphology were identified and documented. Phenotypic observations were recorded throughout the study period and compared across herds, years, and breeds.

Animals with evident traumatic injuries, severe mastitis-related deformation, or clearly acquired unilateral udder damage were considered separately and were not included in the main phenotype group.

Visual assessment remains one of the most widely used approaches for evaluating conformation traits in dairy cattle and continues to be applied alongside modern digital phenotyping technologies (Batanov et al. 2026).

Pedigree analysis

For animals exhibiting the described abnormality, available pedigree information was examined to identify potential recurrence of the condition within sire lineages and related families. Particular attention was given to the occurrence of similar phenotypes among descendants of common ancestors. The pedigree analysis was used exclusively as an observational tool for evaluating possible hereditary patterns and was not intended to establish causality or a definitive mode of inheritance.

Ethical statement

The study was based exclusively on routine breeding evaluations and visual observations conducted under standard herd management conditions. No experimental procedures, invasive sampling, collection of biological material, or interventions affecting animal welfare were performed. Therefore, according to institutional and national regulations, specific ethical approval was not required.

Results

3.1 Occurrence of rear udder underdevelopment in the studied population

During routine breeding value assessment conducted between 2014 and 2025, a distinctive morphological abnormality characterized by underdevelopment of the rear portion of the udder was identified in dairy cattle populations maintained in several regions of the Republic of Kazakhstan and in the Russian Federation.

A total of 3,761 lactating cows were evaluated, including 3,061 Holstein and 700 Jersey animals. Rear udder underdevelopment was detected in 507 cows, representing 13.48% of the examined population. The abnormality was predominantly observed in Holstein cattle, whereas only a single case was recorded in Jersey cattle (Table 1).

Table 1. Occurrence of rear udder underdevelopment in the studied dairy cattle population

Breed	**Examined cows**	**Revealed with an underdeveloped back of the udder**	**%**
Holstein	3 061	506	16.53
Jersey	700	1	0.14
Total	3 761	507	13.48

3.2 Morphological characteristics of normal udder development

The bovine mammary gland normally consists of four anatomically distinct quarters, including two fore and two rear quarters. Under normal conditions, all quarters are well developed and functionally active (Figure 1).

During the last month of pregnancy, milk formation begins in the udders of pregnant heifers. In young cows, the udder can develop rapidly, creating favorable conditions for increasing their milk yield and achieving high productivity. Growth and development of the udder glandular tissue occur until the sixth to eighth calving. Subsequently, as the organism ages, glandular tissue is gradually replaced by connective tissue, leading to a reduction in udder capacity and decreased milk yields.

The uniformity of development of individual udder quarters is determined by the udder index (percentage ratio of milk quantity in the rear quarters to the total daily milk volume) and corresponds to the following proportion: 47-49% of milk quantity in the fore quarters and 51-53% in the rear quarters, which indicates a better development of the rear udder quarters (Jardim at al., 2018). In normally developed udders, the rear quarters generally contribute a slightly larger proportion of total milk yield than the fore quarters, which was used as one of the reference points for visual assessment of rear udder development.

A cow's udder is divided into four quarters – two fore and two rear. Each udder quarter has its own teat with an independent excretory duct.

The udder consists of glandular tissue, which plays the primary role in milk formation, as well as adipose and connective tissues. The cavities of alveoli, milk ducts, canals, and cisterns form the udder capacity.

Connective tissue performs a supportive function and also protects the udder from adverse environmental influences.

The udder is divided into left and right halves, each consisting of a fore and a rear quarter (Figure 2).

Each udder half contains two independent glandular quarters with separate teat canals and secretory tissue (Figure 3).

These anatomical characteristics served as the basis for identifying deviations associated with impaired development of the rear portion of the udder.

Evaluation and selection of cows for machine milking suitability are carried out considering udder morphological features, milk flow rate and milking time, completeness of milk-out, and animal reaction to the milking machine (Toledo at al. 2020).

3.3 Distribution of the phenotype among herds

Cases of rear udder underdevelopment were identified in several independent dairy herds located in different regions of Kazakhstan and in one dairy herd in the Russian Federation. The phenotype was observed in animals of local origin, imported cattle, and descendants of internationally used artificial insemination sires.

The distribution of affected animals among farms is presented in Table 2.

Table 2. Distribution of cows with rear udder underdevelopment among investigated dairy herds

Farms	Breed	Examined cows	Number of cases
“Medeu Commerce” LLP	Holstein	572	116
“Pervomaisky” LLP	Holstein	516	90
“Ays” LLP	Holstein	870	14
“Ringo milk” LLP	Holstein	323	226
“Aidarbayev E.S.” LLP	Holstein	339	58
	Jersey	700	1
“Kolos” LLC	Holstein	441	2
Total		3 761	507

3.4 Environmentally associated udder abnormality

During the investigation, an individual Holstein cow from “Saryagash” LLP exhibited severe unilateral underdevelopment of the left side of the udder (Figure 4).

Figure 4 shows that the left udder half of the Holstein cow is completely atrophied. Most likely, the atrophy of the cow's left udder half was influenced by a non-hereditary factor – unsatisfactory housing conditions for this cow during its period of growth and development. This cattle stock was purchased in the USA and imported to the farm in the physiological state of pregnant heifers at 5-7 months of gestation. It is possible that these heifers were kept from birth until artificial insemination using loose-housing technology during winter under a shelter without bedding.

A feature of dairy cattle, both adult and young, is that they mostly lie on their left side when resting. Due to the systematic absence of bedding under the animals, ice formed (this is a layer of ice formed on the surface of the animal's resting place, when liquids freeze: urine, melted snow, etc.), which led to irreversible processes (atrophy of the left udder lobe occurred). This anomaly in the udder structure is due, as noted above, to technological and environmental factors. According to herd history and management observations, this case differed from the phenotype investigated in the present study. The unilateral character of the lesion and available management information suggested a possible acquired or environmental origin. Therefore, this animal was considered separately and was not included in the main group of cows with rear udder underdevelopment.

3.5 Rear udder underdevelopment in Holstein cattle

The first cases of rear udder underdevelopment corresponding to the investigated phenotype were identified in Holstein cattle from “Medeu Commerce” LLP. Affected animals demonstrated pronounced reduction in the development of the rear udder quarters while maintaining relatively normal development of the fore quarters.

Similar cases were subsequently recorded in several other dairy herds, including “Pervomaisky” LLP, “Ays” LLP, “Ringomilk” LLP, “Arystanov” farm and “Kolos” LLC in the Udmurt Republic of the Russian Federation.

Representative examples of the phenotype observed in Holstein cattle are shown in Figures 5-7.

Despite differences in herd management systems and geographical location, affected animals exhibited similar morphological characteristics, including reduced development of the rear udder quarters and altered udder symmetry.

3.6 Rear udder underdevelopment in Jersey cattle

A similar phenotype was identified in Jersey cattle maintained at “Aidarbayev E.S.” farm. The affected animal demonstrated marked reduction in the development of the rear udder quarters while preserving the general anatomical structure of the mammary gland (Figure 8).

The occurrence of a comparable phenotype in both Holstein and Jersey cattle indicates that the abnormality is not restricted to a single dairy breed.

3.7 Pedigree observations

Pedigree analysis of affected animals revealed repeated occurrence of the phenotype among descendants of several common sire lineages. Similar observations were recorded in independent dairy herds located in different regions of Kazakhstan, as well as in imported cattle of German origin and animals maintained in the Russian Federation.

The first cases of rear udder underdevelopment potentially associated with hereditary factors were identified at “Medeu Commerce” LLP, a farm specializing in Holstein cattle of Hungarian origin. During routine conformation assessment, three cows with abnormal udder morphology were identified: HO Can F 108393309 (sire: Ralma Altachairman-ET Housam 53774748), HO Can F 11741087 (sire: DE-SU Altacamrose-ET Housam 69473993) and HO Can F 11741062 (sire: DA-SO-Burn Altasonic-ET Housam 68972296). In all cases, pronounced underdevelopment of the rear udder quarters was observed. Pedigree examination showed that the sires of these animals carried the breeding prefix “Alta”.

Similar structural changes were subsequently identified at “Pervomaisky” LLP in cows 840003013484512 (sire: Regel Altarenegade-ET), 840003013484637 (sire: Regel Altarenegade-ET), 840003013484617 (sire: DE-SU Altafluid-ET), 840003011844412 (sire: WA-Del Altafelix), 840003011844574 (sire: NO-Fla Altaunesco-ET), 840003130940220 (sire: Synergy Altajenkins 64410464), and 840003130940142 (sire: Synergy Altajenkins 64410464). The average udder evaluation score of these cows was 3.0±0.01 points on a five-point scale.

At “Ays” LLP, rear udder underdevelopment was recorded in cows KZD157606060, KZD157606040, KZD157605087, KZD157605145, and KZD157605093. All affected animals originated from the same sire, AltaPrince 011HO08801. The average udder evaluation score in this group was 3.4±0.02 points.

A comparable phenotype was also observed at “Ringomilk” LLP, a farm established using imported Holstein cattle from Germany. During the evaluation of 323 cows, rear udder underdevelopment was identified in animals 26156 (sire: Match P DK02371403055), 80480 (sire: Garfield DE1603891597), 71670 (sire: Beatclub NL734691569), 57875 (sire: Minosch DE0121814244), and 47432 (sire: Alta Lime US 72145256).

Particular attention was drawn to the repeated occurrence of the phenotype among descendants of sires carrying the “Alta” breeding prefix, including Altachairman, Altacamrose, Altasonic, Altarenegade, Altafluid, Altafelix, Altaunesco, Altajenkins, AltaPrince, and Alta Lime. However, in the interest of objectivity, it should be emphasized that the observed phenotype was not restricted exclusively to descendants of sires carrying this prefix. Comparable udder morphology was also identified in animals descending from sires of German and other breeding origins. Therefore, the observed pedigree pattern should be interpreted as evidence of recurrence within several paternal lineages rather than as proof of involvement of any particular sire, breeding company, or breeding program.

The repeated detection of comparable morphological abnormalities among descendants of common paternal lineages in geographically distant herds suggests a possible hereditary component underlying the observed phenotype. Nevertheless, the available pedigree information remains insufficient to determine the mode of inheritance or identify specific genetic factors responsible for rear udder underdevelopment. Further studies involving genomic analyses and large-scale population screening are required to clarify the biological basis of this condition.

Discussion

The present study documented a morphological abnormality characterized by reduced development of the rear portion of the udder in dairy cattle. The condition was recorded in several independent herds, different geographical regions, and two dairy breeds. These observations indicate that the phenotype is not an isolated finding associated with a single herd, farm, or production system.

From a practical breeding perspective, rear udder underdevelopment may be important because the udder is not only an exterior trait but also a functional structure associated with technological suitability. Modern dairy production requires animals with balanced mammary gland development, appropriate udder attachment, suitable teat position, and uniform milk removal. Previous studies have demonstrated that conformation traits are associated with functional longevity and productive performance in dairy cattle (Sewalem et al. 2004). Therefore, impaired development of the rear udder may potentially affect machine milking efficiency, udder balance, and the overall technological adaptability of cows. However, the present study did not directly evaluate milk yield, milk flow, somatic cell count, mastitis incidence, or milking duration in affected animals.

A central finding of this study was the repeated occurrence of a similar phenotype among animals originating from certain paternal lines. This does not prove a genetic cause, but it provides a reasonable basis for considering a possible hereditary predisposition. In dairy cattle breeding, intensive use of a limited number of elite sires can increase the contribution of particular ancestors to the population and may contribute to the accumulation of homozygosity. Inbreeding depression and the expression of deleterious recessive variation are well-recognized biological consequences of increased relatedness in animal populations (Hedrick and Garcia-Dorado 2016).

The possible hereditary background of the observed phenotype should therefore be interpreted cautiously. The available data demonstrate recurrence by pedigree, but they do not allow identification of a specific gene, mutation, haplotype, or mode of inheritance. Similar caution is necessary because complex traits in dairy cattle are often influenced by both genetic and environmental factors. Genomic selection has substantially improved breeding efficiency in dairy cattle, but its successful application requires accurate phenotyping and careful interpretation of genetic associations (Boichard et al. 2016). For this reason, the phenotype described in this study should be considered a candidate condition for further genomic investigation rather than a confirmed genetic defect.

The importance of such caution is supported by the broader experience of dairy cattle genetics. Several fertility-associated haplotypes and recessive variants in Holstein cattle were recognized because of their negative effects on reproduction, embryonic survival, or calf viability, and only later became subjects of targeted genomic control (Zinovieva 2016; Yakovlev 2019). Studies on the genetics and genomic improvement of fertility traits have shown that reproductive and developmental outcomes in dairy cattle may have complex genetic architectures involving multiple loci and biological pathways (Ma et al. 2019). Therefore, it would be premature to classify rear udder underdevelopment as a genetic anomaly without molecular confirmation.

Modern genomic studies have demonstrated that numerous conformation traits in dairy cattle possess a detectable genetic architecture and may be associated with specific genomic regions (Cole et al. 2011). Genome-wide association studies have further identified genomic regions associated with udder conformation traits in Holstein cattle, highlighting the importance of genetic factors in mammary gland development (Nazar et al. 2022).

At the same time, the results of the present study justify further research. The relatively high frequency of the phenotype, its repeated detection in different herds, and its occurrence among animals with common paternal ancestry indicate that this abnormality should not be ignored in breeding practice. The phenotype may represent either a hereditary condition, a multifactorial developmental abnormality, or the result of interaction between genetic predisposition and environmental factors.

The study has several limitations. First, it was based on visual assessment and available pedigree records obtained during routine breeding evaluation. Second, no genotyping, whole-genome sequencing, haplotype analysis, or genome-wide association study was performed. Third, the study did not include quantitative morphometric measurements of udder structures, histological examination of mammary tissue, or direct comparison of production and milking traits between affected and unaffected cows. These limitations prevent definitive conclusions about the biological mechanism of the abnormality.

Future studies should include standardized phenotypic scoring of the rear udder, digital morphometric measurements, detailed pedigree analysis, and genomic testing of affected and unaffected animals from the same sire families. The use of whole-genome approaches, including genome-wide association studies and haplotype analysis, would be particularly important. Modern reproductive and genomic technologies already allow genetic evaluation from limited biological material and may be useful for early identification of undesirable variants in breeding populations.

Overall, the findings suggest that rear udder underdevelopment is a distinct and insufficiently studied morphological phenotype in dairy cattle. The present results do not prove its hereditary nature, but they provide preliminary evidence that warrants coordinated investigation using phenotypic, pedigree-based, genomic, and production-level data.

The pedigree observations presented in this study should not be interpreted as evidence that any specific sire, breeding company, or breeding program is responsible for the occurrence of the observed

phenotype.

The available data are observational and only indicate the need for further investigation. Should future genomic and population-based studies confirm that the observed phenotype represents a distinct biological condition, the term "Cow Udder Anomaly" (CUA) may be considered as a provisional working designation for this abnormality.

Conclusion

The present study documented a previously underreported morphological abnormality characterized by underdevelopment of the rear portion of the udder in dairy cattle. The phenotype was identified in several independent dairy herds, in geographically distant regions, and in animals of different origin, including imported cattle.

The repeated occurrence of the phenotype among descendants of several common sire lineages suggests the possibility of a hereditary predisposition. However, the available evidence is based on phenotypic observations and pedigree analysis and does not permit definitive conclusions regarding the genetic basis or mode of inheritance of the condition.

The findings indicate that rear udder underdevelopment represents a distinct morphological phenotype that warrants further investigation. Comprehensive studies combining detailed morphological assessment, pedigree analysis, and modern genomic approaches are required to clarify its biological nature, prevalence, and possible hereditary background.

The results also emphasize the continuing importance of systematic conformation assessment in dairy cattle breeding. In addition to genomic evaluation, regular linear classification and visual examination of udder morphology may facilitate the early detection of undesirable phenotypes and contribute to more informed breeding decisions.

Declarations

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Author Contributions

Serimbek Abugaliyev performed the field investigations, analyzed the data, and drafted the manuscript. Darkhan Smagulov supervised the project and provided scientific guidance throughout the study. Stepan Batanov and Aleidar Alentayev assisted in data interpretation and critically revised the intellectual content of the paper. Lyaila Bupebayeva, Ainur Davletova, and Kamilya Beis were responsible for data

collection, participated in on-farm research activities, and assisted with data processing. All authors reviewed and approved the final version of the manuscript.

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Data Availability

The datasets generated and analyzed during the current study are available from the corresponding author upon reasonable request, subject to the permission of the participating dairy farms.

Ethical Approval

The study was based on routine breeding evaluation, pedigree analysis, and visual assessment of dairy cattle and did not involve invasive procedures, biological sampling, or experimental manipulation of animals. Therefore, specific ethical approval was not required under the applicable institutional regulations.

Conflict of Interest

The authors declare that they have no competing interests.

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Figures

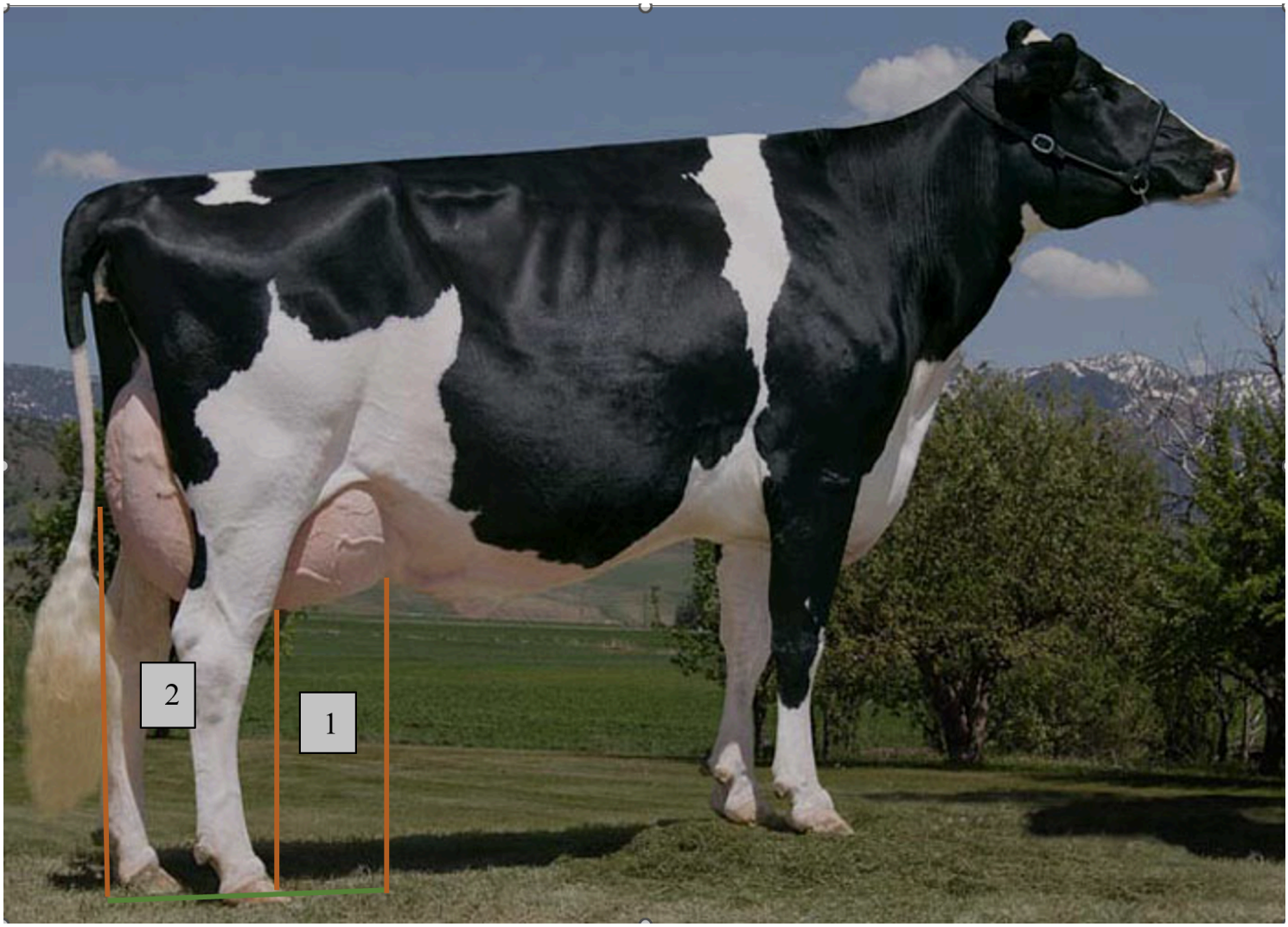


Figure 1

Normal udder morphology in dairy cow:

1 – fore udder quarters; 2 – rear udder quarters

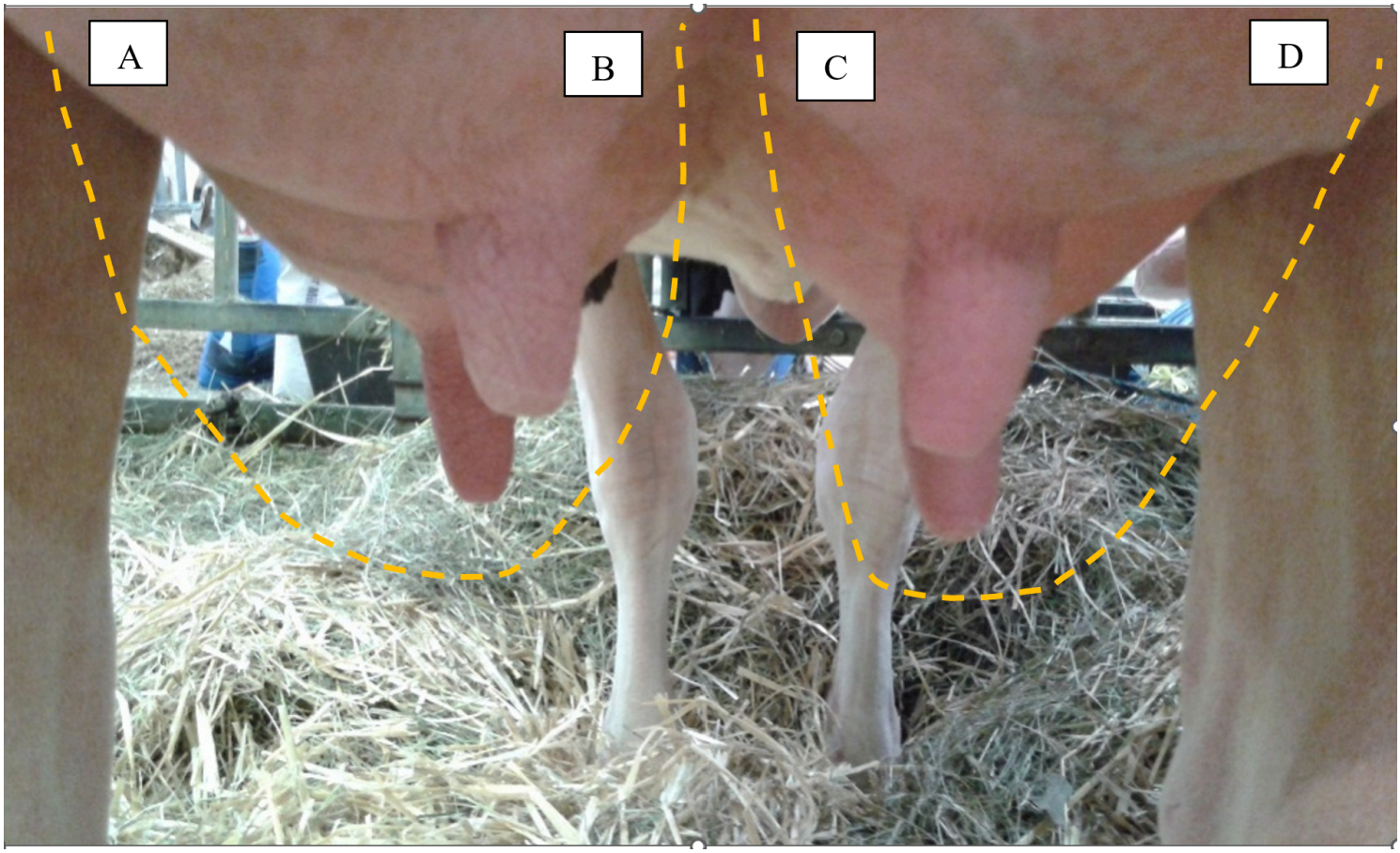


Figure 2

Anatomical division of the bovine udder into left and right halves:

Line A-B – left half; Line C-D – right half

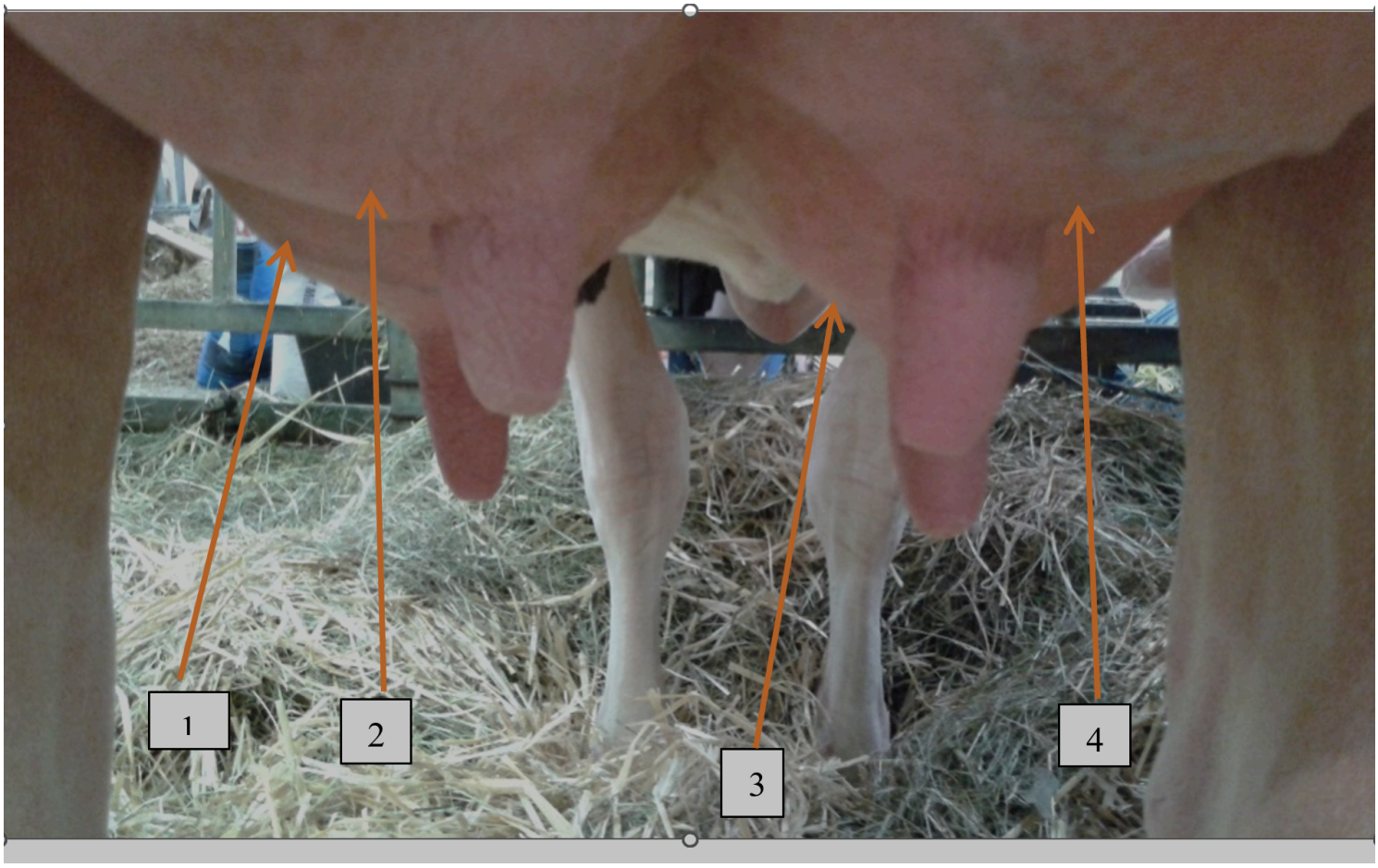


Figure 3

Arrangement of udder quarters of a dairy cow:

1 – left fore (LF); 2 – left rear (LR);

3 – right fore (RF); 4 – right rear (RR)

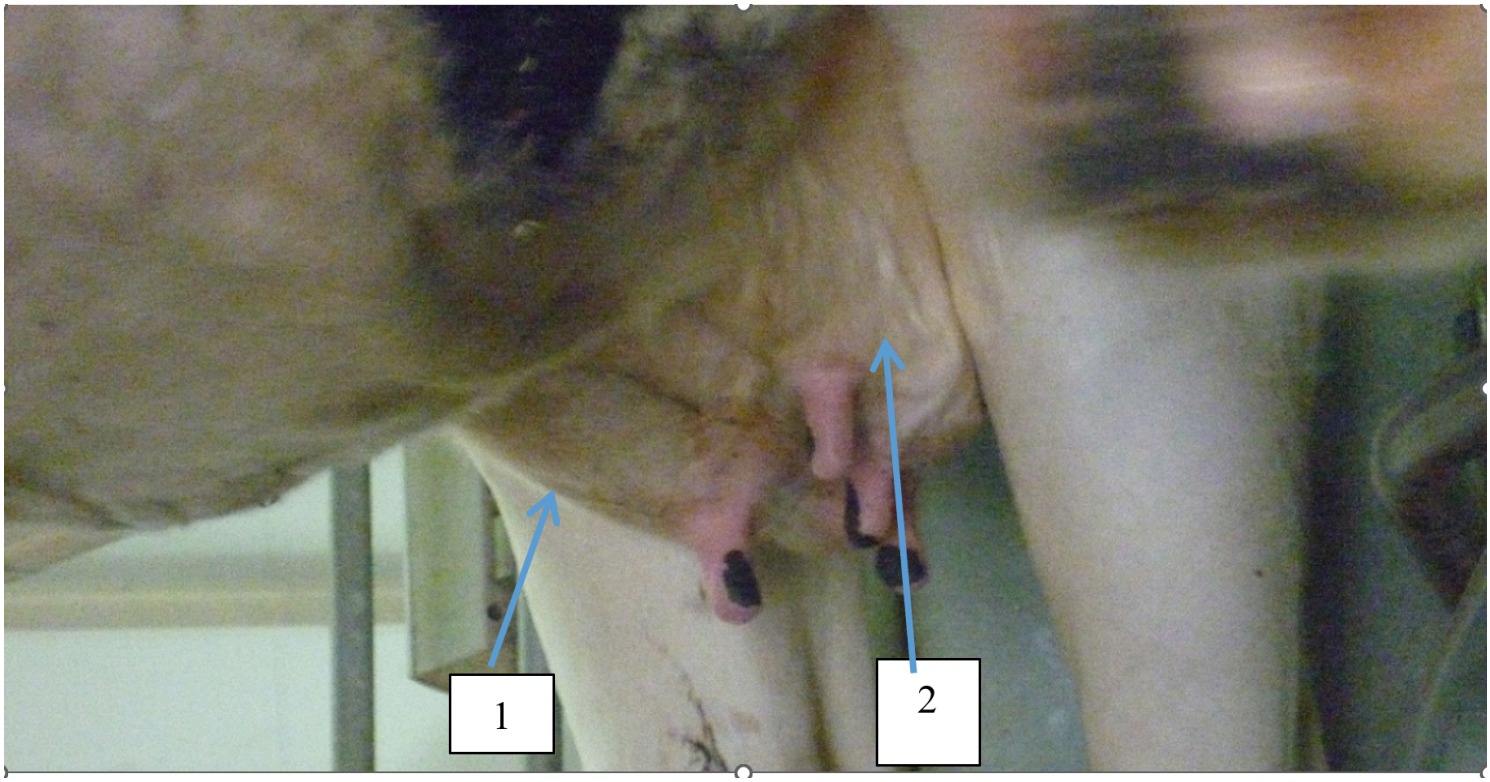


Figure 4

Udder morphology of cow No.8664:

1 – right half; 2 – left half

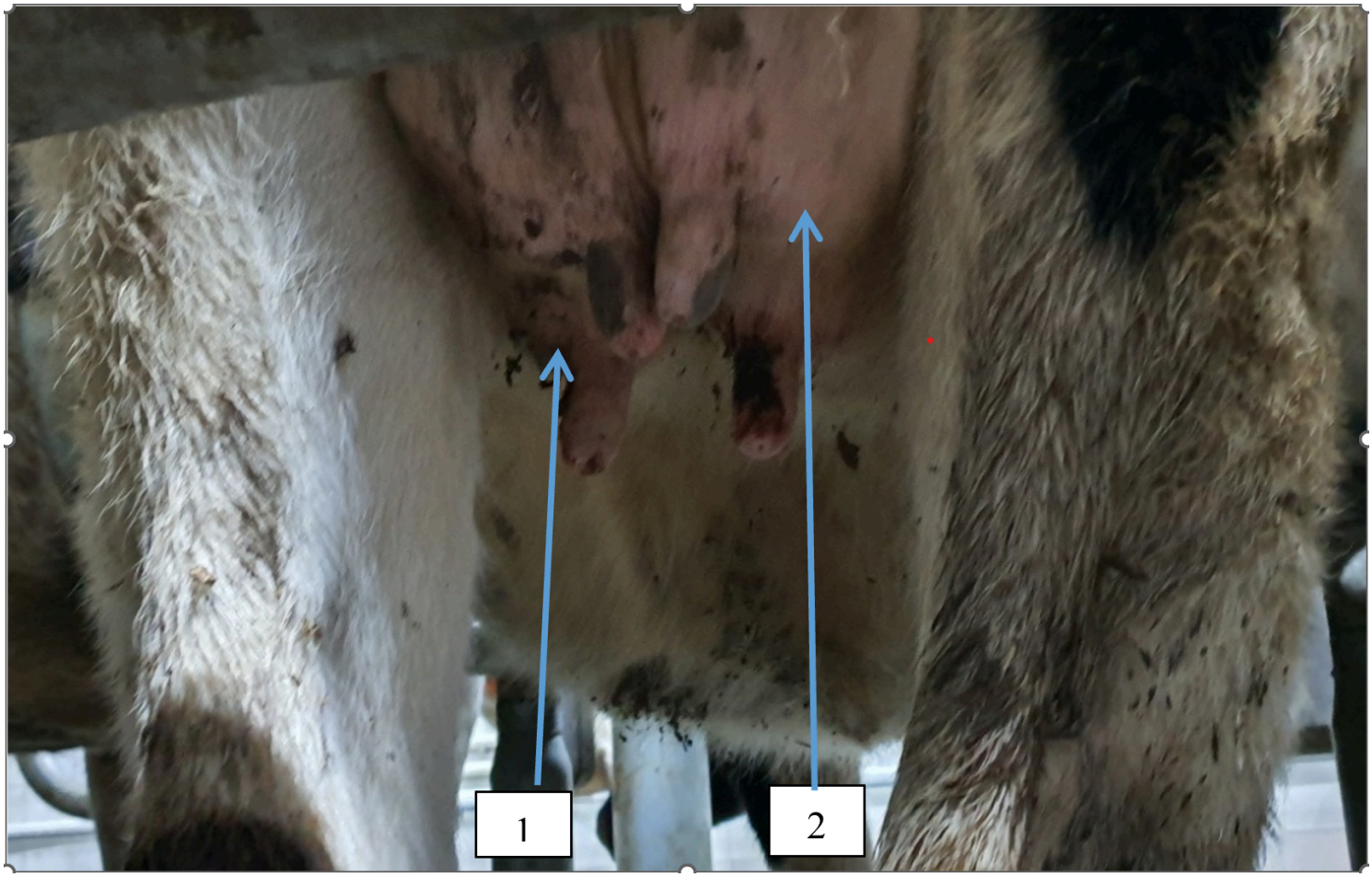


Figure 5

Underdevelopment of the udder quarters of the cow at “Ringomilk” LLP:

1 – fore quarters; 2 – rear quarters

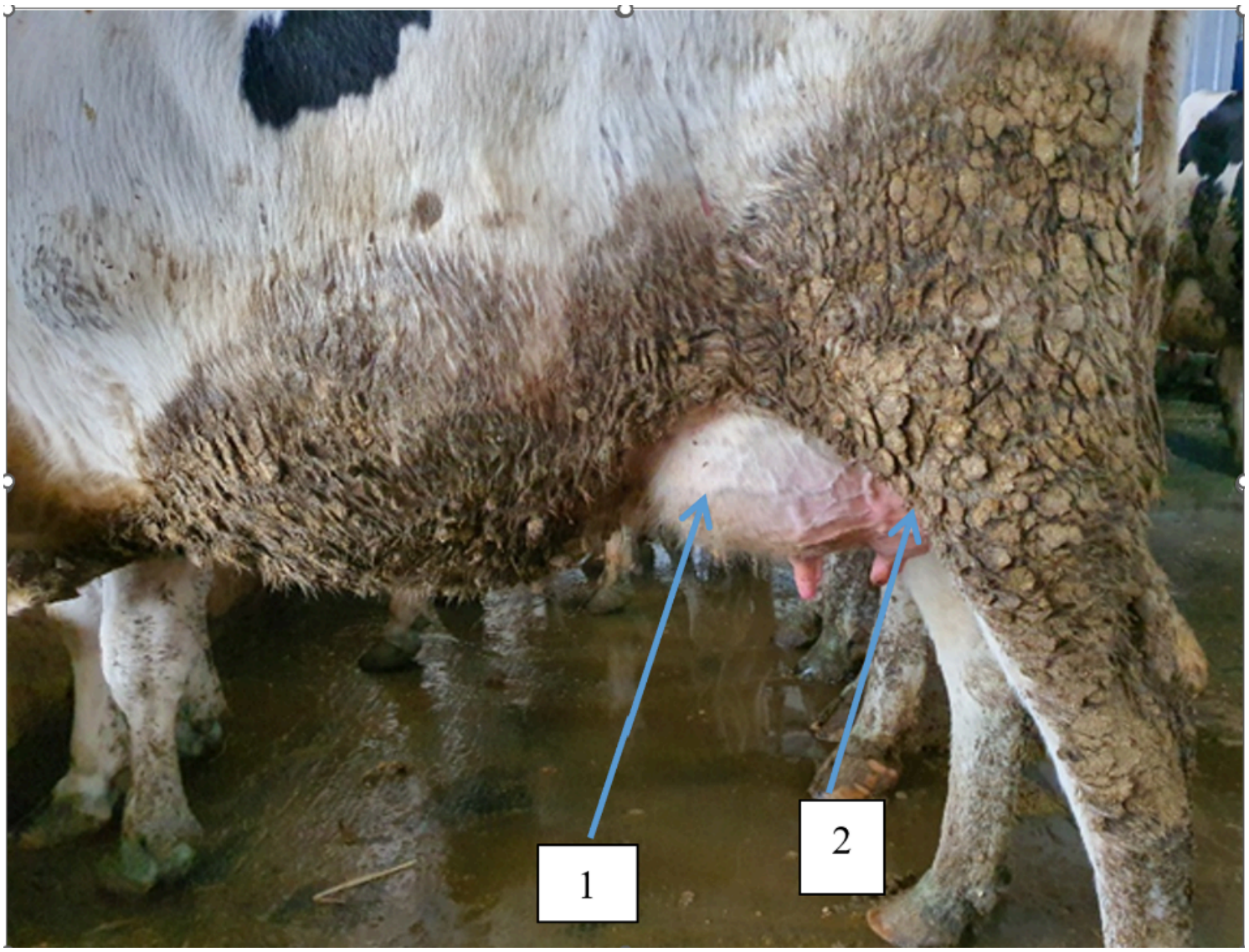


Figure 6

Underdevelopment of the udder quarters of the cow at “Arystanov” farm:

1 – fore quarters; 2 – rear quarters

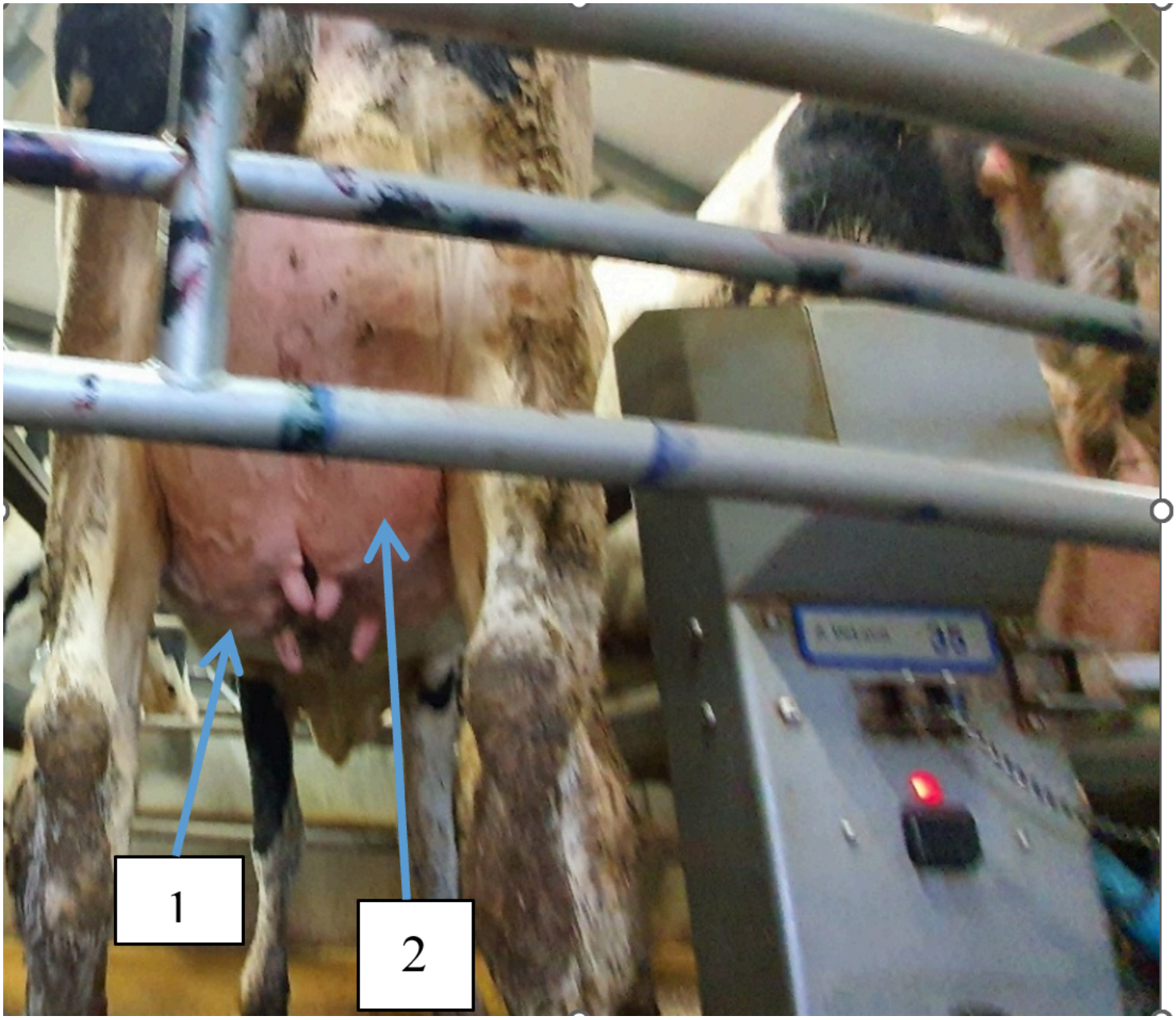


Figure 7

Underdevelopment of the udder quarters of the cow at “Kolos” LLC:

1 – fore quarters; 2 – rear quarters

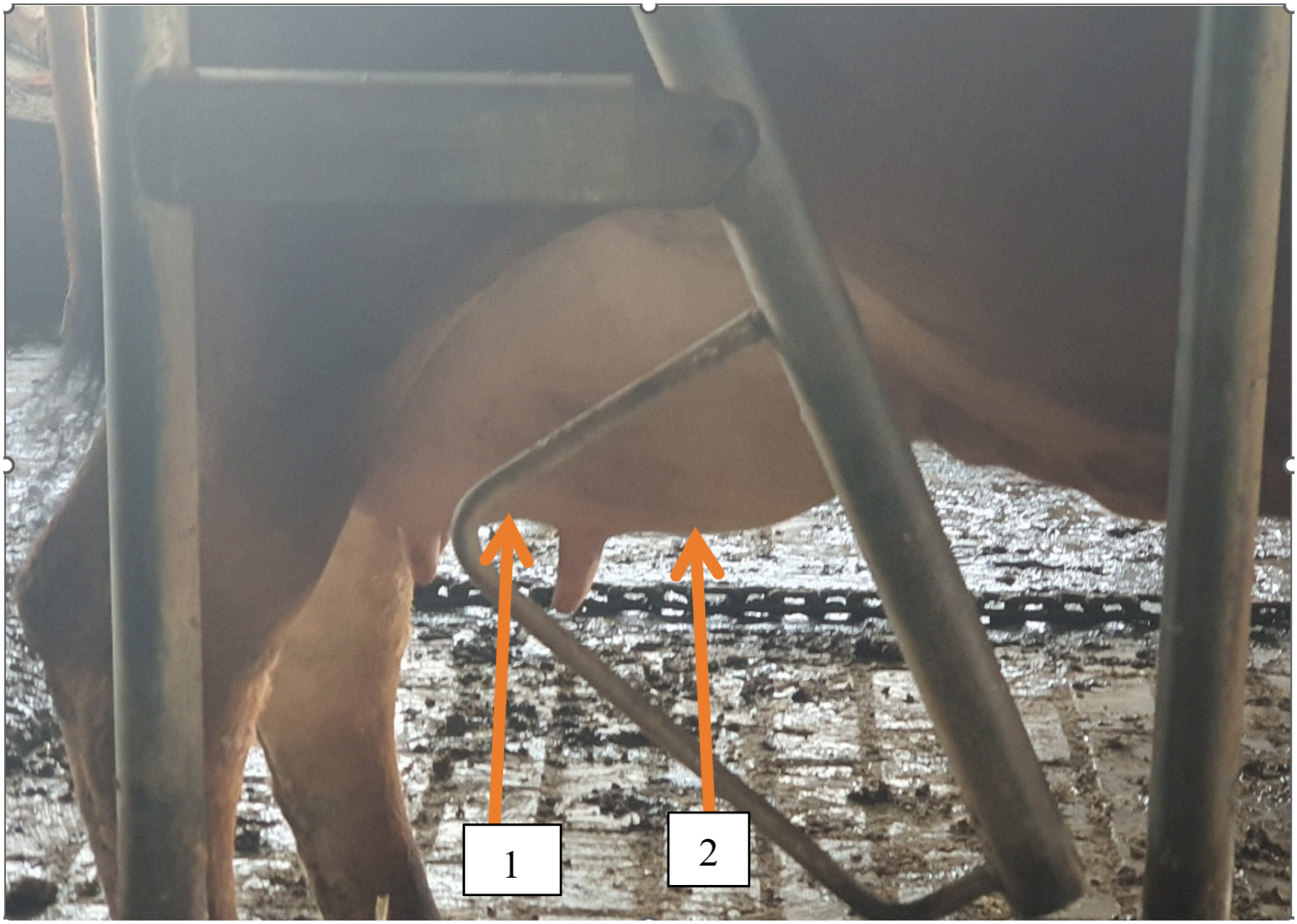


Figure 8

Underdevelopment of the udder quarters of cow DK066008-04661

(sire's number and name: Solbakken Haley Hirts 304552) at “Aidarbayev E.S.” farm:

1 – fore quarters; 2 – rear quarters