

Heritabilities, genetic and phenotypic correlations between body conformation and milking traits of Holstein-Friesian cows milked by milking robots

Research Article

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Abstract: This study estimated heritabilities and genetic correlation (r_G) and phenotypic correlation (r_P) between body conformation traits and milking parameters in 796 primiparous Polish Holstein-Friesian cows milked using Lely Astronaut A4 robotic systems across 7 herds. The objective was to identify genetic relationships affecting milk yield (MY, kg/day), milking efficiency (ME, kg/min), average number of teat cup attachments (AN, n/milking), and attachment time (AT, s/milking) in relation to udder-related (e.g., udder depth, UD; teat length, TL) and non-udder-related traits (e.g., body depth, BD; height at sacrum, HS). A two-trait animal model with Gibbs sampling was applied to 60 days averaged data centered on the time of conformation scoring. Heritability estimates ranged from low to high, spanning from 0.140 (rear teat placement) to 0.598 (HS) for conformation traits and from 0.145 (AT) to 0.390 (ME) for milking parameters. Strong genetic correlations were observed between MY and BD ($r_G = 0.973$) as well as angularity ($r_G = 0.568$), whereas a negative relationship was found with UD ($r_G = -0.281$). ME showed favorable genetic associations with rump width ($r_G = 0.662$) and unfavorable ones with rear legs set ($r_G = -0.382$). Attachment-related traits were strongly genetically associated with rear udder width ($r_G = 0.977$ with AT) and fore udder attachment ($r_G = -0.607$ with attachment number). Phenotypic correlations were generally weak ($|r_P| < 0.310$). Overall, the results highlight two main findings: (i) key traits such as ME and HS exhibit moderate-to-high heritability, and (ii) several conformation traits show strong genetic relationships with milking performance and robot-related parameters. These findings suggest the potential usefulness of these traits in selection for improved adaptability to automatic milking systems, emphasizing the importance of balanced udder morphology and overall body structure for enhanced production efficiency and robotic compatibility.

Keywords: Conformation traits • Dairy cows • Genetic correlations • Heritability • Milking efficiency • Milk yield • Robotic milking

1. Introduction

Functional traits, including body conformation traits, constitute an important component of selection indices used in dairy cattle breeding programs in countries with advanced genetic evaluation systems. In Poland, for example, conformation traits account for approximately 25% of the total selection index value (PFHBiPM, 2025). Their inclusion is justified by their documented influence

on milk production, health, fertility, and longevity in dairy cows (Stefani et al., 2018; Zink et al., 2011; Gibson & Dechow, 2018; Török et al., 2021).

Numerous studies have demonstrated that body conformation traits, particularly those related to udder morphology, are genetically and phenotypically associated with milk production and functional performance. Favorable udder characteristics, such as shallow udders and strong attachment, are generally linked with higher milk yield (MY), improved udder health, and lower somatic cell score (Dadpasand et al., 2012;

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Morek-Kopeć & Zarnecki, 2012). Reported genetic correlations (r_G) between conformation and MY, however, vary in magnitude and direction, indicating a complex relationship between these traits (Sartori et al., 2018; Kelm & Freeman, 2000; Short & Lawlor, 1992). In addition, specific conformation traits, such as pelvic structure, may influence other functional traits, including calving ease (Nogalski et al., 2024).

Traditionally, cattle breeding programs have prioritized milk production traits; however, numerous studies have identified genetic correlations between conformation features and MY (De Haas et al., 2007; Ptak et al., 2011; Loker et al., 2012; Bohlouli et al., 2015). Greater stature has frequently been associated with increased MY. Body conformation, particularly udder morphology, strongly affects udder health and somatic cell score (SCS). Cows with shallower, well-attached udders and balanced body conformation tend to have lower SCS and reduced susceptibility to mastitis, making conformation traits useful indirect indicators of udder health (Dadpa-sand et al., 2012).

Recent studies have confirmed a strong connection between conformation and both milk production and reproduction (Battagin et al., 2013; Bobbo et al., 2019; Carthy et al., 2016; Eaglen et al., 2013). These relationships underline the importance of conformation traits as functional indicators that influence overall reproductive efficiency in dairy cattle.

Despite this well-established role of conformation traits in conventional production systems, relatively little is known about their relationship with traits specific to automatic milking systems (AMSs). Since their introduction in the early 1990s, AMSs have been increasingly adopted, particularly in Europe, due to their potential to reduce labor requirements and improve herd management efficiency (Jacobs & Siegford, 2012; Nixon et al., 2009). In addition to these operational benefits, AMSs provide detailed, high-frequency data on milking processes, including traits such as number of attachments (AN), attachment time (AT), and milking efficiency (ME), which may serve as novel indicators of cow adaptability and performance in automated environments (Aerts et al., 2022). While AMS have been associated with increased milking frequency and, in many cases, higher MY, the genetic relationships between AMS-derived traits and traditional conformation characteristics remain insufficiently explored. Understanding these relationships is essential for optimizing breeding strategies in herds utilizing automated technologies. Therefore, the aim of this study was to estimate heritabilities and genetic and phenotypic correlations (r_P) between MY, ME, AN, AT, and selected udder- and non-

udder-related conformation traits in Holstein-Friesian cows milked using automated milking systems.

2. Material and methods

The research material consisted of data from 796 primiparous Polish Holstein-Friesian cows kept in 7 herds equipped with Lely Astronaut A4 milking robots (Lely Holding B.V., Maassluis, the Netherlands). The pedigree database was compiled up to three generations and included a total of 3,690 animals. The cows included in the analysis ($n = 796$), evaluated for conformation and AMS-related milking traits, were daughters of 320 sires, resulting in an average of 2.5 daughters per sire. The studied cows first calved in 2012–2014 to ensure data consistency and comparability across herds and recording conditions. The cows were housed in free-stall barns and fed a partial mixed ration feed. The cows received a variable dose of the concentrate, either from the milking robot or the feeding station, depending on their MY.

Data on the assessment of conformation came from the IT resources of the Polish Federation of Cattle Breeders and Dairy Producers. The linear conformation traits, collected in accordance with the International Committee for Animal Recording (ICAR, 2018) standards, included:

- udder depth (UD, pts),
- teat length (TL, pts),
- rear udder width (RUW, pts),
- rear udder height (RUH, pts),
- rear teat placement (RTP, pts),
- front teat placement (FTP, pts),
- fore udder attachment (FA, pts),
- central ligament (CL, pts),
- angularity (AY, pts),
- foot angle (FTA, pts),
- rear legs rear view (RLRV, pts),
- height at sacrum (HS, cm),
- body depth (BD, pts),
- chest width (CW, pts),
- rump angle (RA, pts),
- rump width (RW, pts),
- rear legs set (RLS, pts).

Primiparous cows were monitored for the following features characterizing the course of automatic milking:

- Daily MY (kg/day) – daily MY of the cow summed during 1 day in milk,
- ME (kg/min) – MY per day divided by box time (total time spent by a cow per day in the robot milking box),
- AN (n/milking) – the average number of attempted connections of the milking device to the teat,

- AT (s/milking) – the average time of attempted connections of the milking device to the teat.

Data on milk performance characteristics of primiparous cows milked in AMS were obtained from the T4C management and data registration system (Lely East). The amount of recorded information from the AMS database for each cow was limited to the 30 days period preceding and the 30 days period following the day of conformation assessment. These data included daily MY and milking parameters. For each animal, the values recorded within this 60 days interval were averaged, and the arithmetic mean values were used for subsequent exploratory and genetic analyses. Records showing milk-performance traits beyond three standard deviations were discarded prior to analysis. The use of 60 days averaged AMS data was necessary due to the structure of the dataset, where conformation traits were recorded as a single observation per cow, while milking parameters were available as repeated daily measurements. Without aggregation, this would result in pseudo-replication. However, this approach may reduce phenotypic variance and lead to partial loss of temporal information, particularly for highly variable traits such as AT and AN.

A preliminary multivariate analysis using General Linear Model (GLM) procedure (SAS Institute Inc., 2014) was performed to identify fixed factors significantly affecting the variability of milking and conformation traits. Interaction effects identified in the preliminary GLM analysis were not explicitly included in the final animal model but were accounted for within combined fixed effects (contemporary groups). The fixed effects included in the linear model were: herd (7 levels), year of calving (2012, 2013, 2014), calving season (summer: March–August; winter: September–February), and stage of lactation at the time of conformation scoring (5–60, 61–90, > 90 days). First-order interactions among these factors were also considered:

$$y_{ijklm} = \mu + h_i + yc_j + sc_k + lp_l + (h \times yc)_{ij} + (h \times sc)_{ik} + (yc \times sc)_{jk} + e_{ijklm}, \quad (1)$$

where, y_{ijklm} – the phenotype value of the trait, μ – the overall mean value, h_i – the fixed effect of the i th herd, yc_j – the fixed effect of the j th year of calving, sc_k – the fixed effect of the k th season of calving, lp_l – the fixed effect of the l th stage of lactation, $(h \times yc)_{ij} + (h \times sc)_{ik} + (yc \times sc)_{jk}$ – the first-order interactions among herd, year of calving, and season of calving, and e_{ijklm} – random error.

Because all these factors were found to be statistically significant, they were included in the linear model used to estimate heritability, as well as the genetic (r_G) and phenotypic (r_P) correlations. In order to estimate the variance and covariance components, the two-trait animal model was given as follows:

$$\begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \end{pmatrix} + \begin{pmatrix} Z_1 & 0 \\ 0 & Z_2 \end{pmatrix} \begin{pmatrix} a_1 \\ a_2 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \end{pmatrix},$$

$$E \begin{pmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{pmatrix} = 0, \text{ var} \begin{pmatrix} a_1 \\ a_2 \\ e_1 \\ e_2 \end{pmatrix} = \begin{pmatrix} A\sigma_{a1}^2 & A\sigma_{a12} & 0 & 0 \\ A\sigma_{a21} & A\sigma_{a2}^2 & 0 & 0 \\ 0 & 0 & I\sigma_{e1}^2 & I\sigma_{e12} \\ 0 & 0 & I\sigma_{e21} & I\sigma_{e2}^2 \end{pmatrix},$$

where y is the vector of phenotypic records; b is the vector of fixed effects (combined effect of herd (7), year (2012, 2013, 2014), and calving season (summer: March–August; winter: September–February, stage of lactation); a is the vector of breeding values; e is the vector of random error terms; X and Z are incidence matrices relating records to fixed effects and additive genetic effects, respectively; σ_a^2 , and σ_e^2 are the additive genetic variance, and error variance; A is an additive genetic relationship matrix and I is an identity matrix. Fixed effects were the combined effects of herd–calving year–calving season, and lactation stage (three levels).

The GIBBS1F90 program (Misztal *et al.*, 1992) and a linear two-trait animal model were used. In each analysis, 100,000 samples were generated, of which the first 30,000 were discarded, treating them as the so-called burn-in period. The number of “burn-in period” samples was determined using the POSTGIBBS1F90 program (Misztal *et al.*, 1992).

The genetic parameters of the controlled traits were calculated using the following formulas:

1. Heritability: $h^2 = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_e^2}$,
2. Genetic correlations: $r_G = \frac{\sigma_{a12}}{\sqrt{\sigma_{a1}^2 + \sigma_{a2}^2}}$,
3. Phenotypic correlations: $r_P = \frac{\sigma_{p12}}{\sqrt{\sigma_{p1}^2 + \sigma_{p2}^2}}$,

where, σ_a^2 – additive genetic variance, σ_e^2 – residual variance, σ_p^2 – phenotypic variance, σ_{a12} – additive covariance between traits x and y , σ_{a1}^2 , σ_{a2}^2 – additive genetic variance of traits $x(1)$ and $y(2)$, respectively, σ_{p1}^2 , σ_{p2}^2 – phenotypic variance of traits $x(1)$ and $y(2)$, respectively, and σ_{p12} – phenotypic covariance between traits x and y .

3. Results

3.1 Descriptive statistics of body conformation traits and milking parameters

The results of the linear conformation classification of the cows under study ranged within a narrow numerical

interval, from 4.7 for TL to 6.6 for RTP (Table 1). The average height at the sacrum of these cows was 145.3 cm. All conformation traits exhibited low variability (coefficient of variation ranging from 2.81% to 25.59%). The examined cows produced on average 31.03 kg of milk per day; their ME was 1.56 kg/min; the average number of teat cup attachment attempts required for effective connection was 1.40; and the mean duration of this procedure (AT) was 11.52 s. The variability of milking traits – daily MY, ME, and number of teat cup attachment attempts – was also limited, with

coefficients of variation ranging from 22.14 to 24.87%, except for AT, which showed high variability (CV = 53.38%).

3.2 Heritabilities of body conformation traits and milking parameters

The estimated heritabilities for body conformation traits ranged from low to high, spanning 0.140 for RTP to 0.598 for HS (Table 2). Traits such as RTP, RLRV, and RLS were

Table 1. Descriptive statistics of studied body conformation traits and milking parameters

Trait	Mean value	SD	CV (%)
Body conformation traits			
UD	6.0	1.2	20.00
TL	4.7	1.1	23.65
RUW	5.3	1.0	18.24
RUH	5.9	0.9	14.73
RTP	6.6	1.1	17.26
FTP	5.2	1.0	18.72
FA	5.5	1.0	18.44
CL	5.9	1.3	22.42
AY	6.2	1.0	16.18
FTA	5.1	1.3	25.59
RLRV	5.6	1.3	23.28
HS	145.3	4.1	2.81
BD	6.2	1.2	18.39
CW	5.2	1.3	25.26
RA	5.3	1.1	21.12
RW	5.4	1.0	19.46
RLS	5.6	1.0	18.04
Milking parameters			
MY	31.03	7.17	23.09
ME	1.56	0.39	24.87
AN	1.40	0.31	22.14
AT	11.52	6.15	53.38

Abbreviations: UD: udder depth [pts]; TL: teat length [pts]; RUW: rear udder width [pts]; RUH: rear udder height [pts]; RTP: rear teat placement [pts]; FTP: front teat placement [pts]; FA: fore udder attachment [pts]; CL: central ligament [pts]; AY: angularity [pts]; FTA: foot angle [pts]; RLRV: rear legs rear view [pts]; HS: height at sacrum [cm]; BD: body depth [pts]; CW: chest width [pts]; RA: rump angle [pts]; RW: rump width [pts]; RLS: rear legs set [pts]; MY: milk yield [kg/day]; ME: milking efficiency [kg/min]; AN: attachment number [n/milking]; AT: attachment time [s/milking].

Table 2. Heritabilities of studied body conformation traits and milking parameters

Trait	σ_a^2	SE (σ_a^2)	σ_e^2	SE (σ_e^2)	h^2	SE (h^2)
Body conformation traits						
UD	0.5142	0.1542	0.6505	0.1370	0.442	0.122
TL	0.4584	0.1207	0.7077	0.1007	0.393	0.096
RUW	0.2627	0.0892	0.5419	0.0831	0.327	0.105
RUH	0.1362	0.0636	0.5345	0.0639	0.203	0.092
RTP	0.1521	0.0842	0.9379	0.0913	0.140	0.075
FTP	0.1801	0.0978	0.7180	0.0962	0.201	0.106
FA	0.4089	0.1530	0.6148	0.1368	0.399	0.140
CL	0.4194	0.1880	1.1767	0.1788	0.263	0.113
AY	0.3188	0.1034	0.5064	0.0921	0.386	0.116
FTA	0.6578	0.2250	0.8459	0.1977	0.438	0.138
RLRV	0.1747	0.0813	1.0686	0.0937	0.141	0.064
HS	5.5741	1.1989	3.7518	0.9898	0.598	0.112
BD	0.2586	0.1113	0.7926	0.1076	0.246	0.102
CW	0.2753	0.1239	0.9090	0.1207	0.233	0.101
RA	0.2556	0.1159	0.8704	0.1143	0.227	0.099
RW	0.2527	0.1092	0.7832	0.1063	0.244	0.101
RLS	0.1689	0.0922	0.7942	0.0937	0.175	0.093
Milking parameters						
MY	10.1183	3.8609	24.9099	3.6026	0.289	0.104
ME	0.0557	0.0177	0.0871	0.0254	0.390	0.115
AN	0.0191	0.0099	0.0737	0.0095	0.205	0.104
AT	4.9859	2.8380	29.3218	2.9548	0.145	0.080

σ_a^2 = additive genetic variance, σ_e^2 = residual variance.

Abbreviations: UD: udder depth [pts]; TL: teat length [pts]; RUW: rear udder width [pts]; RUH: rear udder height [pts]; RTP: rear teat placement [pts]; FTP: front teat placement [pts]; FA: fore udder attachment [pts]; CL: central ligament [pts]; AY: angularity [pts]; FTA: foot angle [pts]; RLRV: rear legs rear view [pts]; HS: height at sacrum [cm]; BD: body depth [pts]; CW: chest width [pts]; RA: rump angle [pts]; RW: rump width [pts]; RLS: rear legs set [pts]; MY: milk yield [kg/day]; ME: milking efficiency [kg/min]; AN: attachment number [n/milking]; AT: attachment time [s/milking].

categorized as lowly heritable ($0 < h^2 \leq 0.2$). Conversely, traits including TL, RUW, RUH, FTP, FA, CL, AY, BD, CW, RA, and RW demonstrated moderate heritability ($0.2 < h^2 \leq 0.4$). UD, FTA, and HS were classified as highly heritable ($h^2 > 0.4$), with the highest value obtained for HS ($h^2 = 0.598$). Milking parameters also exhibited varying heritabilities, with daily MY at 0.289, ME at 0.390, and AT at 0.145 being moderate, while the average number of teat cup attachment attempts was lowly heritable (0.205).

3.3 Genetic and phenotypic correlations between traits

Genetic correlations between daily MY and body conformation traits were predominantly positive, with AY ($r_G = 0.568$) and BD ($r_G = 0.973$) showing strong associations (Table 3). Other traits, such as RUW ($r_G = 0.162$) and FA ($r_G = 0.102$), demonstrated weaker but still positive correlations. Interestingly, UD exhibited a moderate negative

genetic correlation with MY ($r_G = -0.281$). Phenotypic correlations were generally weaker, with RUW ($r_P = 0.291$) and BD ($r_P = 0.308$) showing the highest positive values.

Genetic correlations between ME and body conformation traits ranged widely, from -0.382 for RLS to 0.662 for RW (Table 3). In addition to the RLS, moderate negative correlations with ME were also observed for RLRV ($r_G = -0.339$) and TL ($r_G = -0.251$). By contrast, a strong positive correlation was found for BD ($r_G = 0.646$), and a moderate positive correlation for AY ($r_G = 0.354$). Genetic correlations between ME and the remaining conformation traits, whether negative or positive, were generally low. Phenotypically, the correlations were negligible, with values close to zero across most traits; only TL exceeded $|0.1|$ ($r_P = -0.139$).

Genetic correlations between the average number of teat cup attachment attempts and body conformation traits ranged from -0.607 to 0.962 (Table 3). Strong positive correlations were observed for RLRV ($r_G = 0.962$), RUW ($r_G = 0.844$), RTP ($r_G = 0.593$), RUH ($r_G = 0.494$), and FTA

Table 3. Genetic (r_G) and phenotypic correlations (r_P) between the body conformation traits and milk yield, ME, AN, and AT

Traits	r_G	r_P	r_G	r_P	r_G	r_P	r_G	r_P
	MY		ME		AN		AT	
UD	-0.281	-0.096	0.174	-0.001	-0.185	-0.043	-0.456	-0.060
TL	0.099	0.102	-0.251	-0.139	0.254	-0.045	0.798	-0.070
RUW	0.162	0.291	-0.105	0.087	0.844	-0.003	0.977	-0.012
RUH	0.162	0.199	-0.121	0.100	0.494	-0.035	0.939	-0.025
RTP	-0.053	0.006	-0.159	-0.024	0.593	0.035	0.884	0.070
FTP	0.144	0.024	0.142	-0.020	-0.038	-0.005	-0.381	0.026
FA	0.102	0.191	0.198	-0.017	-0.607	-0.099	-0.567	-0.128
CL	-0.356	0.091	-0.146	0.019	0.293	-0.007	0.397	0.023
AY	0.568	0.287	0.354	0.108	0.198	-0.020	0.782	-0.021
FTA	0.338	0.138	0.051	-0.035	0.466	0.022	0.799	-0.014
RLRV	-0.523	0.103	-0.339	-0.010	0.962	0.077	0.970	0.072
HS	-0.020	0.127	0.058	0.032	0.062	-0.072	-0.215	-0.100
BD	0.973	0.308	0.646	0.048	-0.150	-0.034	0.231	-0.046
CW	-0.041	0.122	0.389	0.009	-0.379	-0.100	-0.575	-0.129
RA	0.483	0.026	-0.139	-0.024	-0.196	0.061	-0.468	0.046
RW	-0.025	0.125	0.662	-0.024	-0.223	-0.075	-0.227	-0.080
RLS	-0.124	-0.116	-0.382	0.085	0.074	-0.015	0.024	-0.021

Abbreviations: UD: udder depth [pts]; TL: teat length [pts]; RUW: rear udder width [pts]; RUH: rear udder height [pts]; RTP: rear teat placement [pts]; FTP: front teat placement [pts]; FA: fore udder attachment [pts]; CL: central ligament [pts]; AY: angularity [pts]; FTA: foot angle [pts]; RLRV: rear legs rear view [pts]; HS: height at sacrum [cm]; BD: body depth [pts]; CW: chest width [pts]; RA: rump angle [pts]; RW: rump width [pts]; RLS: rear legs set [pts]; MY: milk yield [kg/day]; ME: milking efficiency [kg/min]; AN: attachment number [n/milking]; AT: attachment time [s/milking].

($r_G = 0.466$). A strong negative correlation was found for FA ($r_G = -0.607$). Moderate positive values were noted for CL ($r_G = 0.293$) and TL ($r_G = 0.254$), whereas AY ($r_G = 0.198$) showed a weaker positive association. Moderate negative correlations were obtained for CW ($r_G = -0.379$) and RW ($r_G = -0.223$). BD, HS, RLS, and RA exhibited weak genetic associations with the average number of attachment attempts. Phenotypic correlations were generally close to zero for most traits. The highest positive values were recorded for RLRV ($r_P = 0.077$) and RA ($r_P = 0.061$), whereas the strongest negative correlations were observed for CW ($r_P = -0.100$), RW ($r_P = -0.075$), and height at the sacrum ($r_P = -0.072$).

Genetic correlations between AT and body conformation traits ranged from -0.575 to 0.977 (Table 3). The strongest positive correlations were found for RUW ($r_G = 0.977$), RLRV ($r_G = 0.970$), RUH ($r_G = 0.939$), and RTP ($r_G = 0.884$). The extremely high genetic correlations observed in this study should be interpreted with caution. Such values may reflect strong biological relationships but may also be influenced by methodological factors, including the use of bivariate models, limited effective sample size for certain trait combinations, and reduced phenotypic variance resulting from averaging AMS-derived data. Therefore, these correlations should be interpreted primarily in terms of their direction rather than their absolute magnitude. TL ($r_G = 0.798$), FTA ($r_G = 0.799$), and AY ($r_G = 0.782$) also showed high positive correlations with AT. Negative correlations of considerable magnitude were recorded for FA ($r_G = -0.567$), CW ($r_G = -0.575$), and RA ($r_G = -0.468$). Other traits displayed only weak or moderate genetic associations with AT, including CL ($r_G = 0.397$), BD ($r_G = 0.231$), HS ($r_G = -0.215$), RW ($r_G = -0.227$), and RLS ($r_G = 0.024$). Phenotypic correlations were generally low, with values close to zero. The highest positive values were observed for RLRV ($r_P = 0.072$) and RTP ($r_P = 0.070$), while the strongest negative phenotypic correlations were noted for CW ($r_P = -0.129$) and FA ($r_P = -0.128$).

4. Discussion

4.1 Conformation and milking traits

The dairy sector is facing an increasing shortage of skilled labor, driven by an aging rural workforce and rising labor costs. At the same time, growing demands for flexibility in farm management have further intensified these challenges. In response, the adoption of AMS has accelerated, as these systems reduce labor requirements and improve

the allocation of time and financial resources. The rapid pace of automation is particularly evident in Poland, where the proportion of cows milked using AMS increased from 4.88% (707 robots in 406 herds) in 2022 to 7.7% (1,120 robots in 626 herds) in 2024 (PFHBiPM, 2025).

The primiparous cows analyzed in this study were Polish Holstein-Friesians (PHF), which constitute approximately 86% of the national dairy population (PFHBiPM, 2025). Their average 305 days MY (9,464 kg) was close to the national average reported for 2024 (9,930 kg), confirming that the study population was representative of contemporary PHF performance. The mean daily MY observed in the present study was comparable to values reported by Piwczyński et al. (2020, 2021) for Holsteins milked by Lely Astronaut robots (27.3–30.0 kg/day).

ME, defined as MY per minute of box time, is considered a key indicator of a cow's suitability for AMS (Aerts et al., 2022). The ME observed in this study (1.56 kg/min) was similar to values reported for PHF cows managed under AMS conditions (Aerts et al., 2022; Piwczyński et al., 2021). The mean AT (11.52 s) was approximately twice as high as that reported by Piwczyński et al. (2021), although the number of attachment attempts (1.4) was nearly identical. This may suggest differences in AMS model configuration, system calibration, or cow training procedures.

4.2 Heritability of conformation and milking traits

4.2.1 Body conformation traits

The heritability estimates for conformation traits ranged from 0.140 (RTP) to 0.598 (HS), indicating moderate to high genetic determination and substantial potential for effective selection. These findings are broadly consistent with results reported in previous studies (Dal Zotto et al., 2007; Oliveira et al., 2021; Poppe et al., 2019; Xue et al., 2023).

Traits such as UD, TL, RUH, CL, BD, and RW exhibited moderate heritability, suggesting that selection directed toward these characteristics could effectively improve both functional and structural suitability for AMS. The highest heritability observed for HS (0.598) further supports the conclusion that stature is strongly genetically determined, consistent with earlier studies.

4.2.2 Milking characteristics

The heritability estimates obtained for MY were within the range previously reported in the literature (0.17–0.46)

(Gäde *et al.*, 2006; Nixon *et al.*, 2009; Berry *et al.*, 2013; Aerts *et al.*, 2021). The heritability of ME estimated in this study (0.390) was similar to the value reported by Sitkowska *et al.* (2024) for Polish Holsteins (0.349), but lower than that reported by Wethal and Heringstad (2019) for Norwegian Red cattle. These moderate estimates suggest that selection for ME may be more effective than selection for MY alone, particularly in herds operating under AMS conditions. The heritability estimates for AN (0.205) and AT (0.145) were low, indicating a substantial environmental influence on these traits. Similar findings were reported by Piwczyński *et al.* (2021) and Sitkowska *et al.* (2024), who noted that AMS attachment-related traits are characterized by high variability and relatively low genetic determination influenced by management practices, cow behavior, and robot-specific technical factors.

In summary, traits such as HS, TL, RUW, RUH, CL, and ME, which are characterized by moderate to high heritability, may represent effective selection targets for improving both milk productivity and functional adaptation to AMS environments.

4.3 Genetic and phenotypic correlations between conformation and milking traits

4.3.1 Genetic correlations

The genetic correlations observed in this study revealed meaningful associations between udder structure and AMS milking performance. Udder traits such as UD, TL, RUW, RTP, and CL were moderately to strongly correlated with AN and AT, indicating their influence on the robot's ability to locate teats and attach the milking cluster effectively. Deeper udders were associated with longer ATs and lower ME, which is consistent with findings by Carlström *et al.* (2016) and Xue *et al.* (2023). These results suggest that cows with shallower udders and stronger suspensory ligaments are better suited to robotic milking. Similarly, longer teats and wider udders were associated with a greater number of attachment attempts, reducing ME. RUH and RTP also showed positive correlations with AN and AT, confirming that teat spacing and udder geometry influence AMS performance. Conversely, a stronger FA facilitated easier cup attachment and shorter AT, whereas a pronounced CL was associated with increased AN and AT and slightly lower MY.

Beyond udder conformation, general body traits also influenced milking performance. Cows characterized by

AY and moderate BD exhibited higher MY and ME, although they also required longer ATs. This suggests that highly dairy-type cows tend to produce more milk but may present greater challenges for robot attachment. Correct hind leg posture was also found to be important, as excessively straight or sickle-shaped legs negatively affected ME by altering udder accessibility and teat alignment (Xue *et al.*, 2023). Height at the sacrum showed a moderate negative correlation with AT, suggesting that moderately taller cows may achieve faster teat attachment. However, extreme stature may impair robot alignment, as also reported by Aerts *et al.* (2022), who found that cows measuring 145–152 cm in height were most compatible with AMS design parameters.

Overall, these findings suggest that selection for balanced conformation, moderate stature, well-attached and moderately shallow udders, appropriate TL and spacing, and correct hind leg posture may improve cow suitability for robotic milking systems.

4.3.2 Phenotypic correlations

Most phenotypic correlations were low ($|r| < 0.1$), indicating that observable body conformation traits have limited predictive value for milking performance under AMS conditions. Only a few traits, including RUW, AY, and BD, showed moderate positive associations with MY, confirming that cows with wider udders, greater AY, and deeper bodies tend to achieve higher milk output. Phenotypic correlations between conformation traits and AN or AT were generally weak and inconsistent, reflecting substantial environmental influences from management practices, robot design, and system calibration. Similar patterns were reported by Oliveira *et al.* (2021) and Ismael *et al.* (2021).

4.4 Practical implications

The genetic and phenotypic relationships identified in this study highlight the potential to improve cow compatibility with AMS through targeted breeding strategies. Selection for moderately to highly heritable traits such as ME, HS, RUW, TL, FA, AY, and FTA may improve both production and functional efficiency in robotic milking systems. In contrast, excessive UD, extreme teat positions, or suboptimal leg posture may reduce adaptability to AMS.

From a practical perspective, traits such as ME, HS, and selected udder conformation traits appear to be the most promising candidates for inclusion in breeding programs. However, caution is warranted due to the potential

antagonistic relationships between MY and traits related to ME. These findings are consistent with the growing need to adapt dairy cattle breeding programs to the technological realities of precision dairy farming. By integrating genomic selection tools with data automatically recorded by AMS, it may be possible to develop new selection indices that combine MY, ME, and conformation traits directly relevant to robotic milking systems.

5. Conclusion

Traits with moderate to high heritability, such as HS, TL, RUW, RUH, CL, and ME, represent effective selection targets for improving cow adaptability to AMS. Udder conformation significantly influences AMS attachment success, with shallower, well-attached udders and optimal teat placement contributing to improved ME. In addition, balanced body conformation, including appropriate BD, body width, and correct leg posture, enhances both MY and performance in robotic milking systems. Most phenotypic correlations were weak, indicating that selection decisions should rely primarily on genetic evaluation rather than visual assessment alone. The integration of AMS-derived data into dairy cattle breeding programs may accelerate genetic progress toward cows that are optimally suited for robotic milking environments.

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Author contributions

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Conflict of interest statement

Authors state no conflict of interest.

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