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Genetic parameters estimation and relationships between image-derived morphometric and sensor-based behavioral traits in Holstein cows

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Introduction

Conformation traits (CT), also known as type traits, are essential for improving productivity, fertility, health, and herd longevity (Miglior *et al*., 2017). However, conventional measurement of CT is costly, labor-intensive, and subject to scorer variation, which limits recording frequency and scalability. Digital phenotyping based on computer vision offers a promising alternative by enabling non-invasive, continuous, and remote assessment of body morphology without disrupting routine management (Billah *et al*., 2025). Rumination and activity time are valuable indicators of animal health and behavior and can be automatically recorded using neck-mounted sensors (Hooker *et al.,* 2025). Previous studies have reported moderate heritability for these behavioral traits, indicating their potential relevance for genetic improvement (Byskov *et al*., 2017).

As these technologies become more available in dairy systems, they create an opportunity to generate objective phenotypes that could complement existing traits used in genetic evaluation and improve selection for health, efficiency, and longevity. However, their use in breeding programs depends on reliable estimates of heritability and genetic correlations. Despite this, genetic parameters for image derived morphometric traits and their genetic relationships with sensor based behavioral traits remain largely unknown. We hypothesized that image derived morphometric traits are genetically correlated with sensor-based behavioral traits, such that cows with larger body size tend to exhibit higher rumination time and lower activity levels. Therefore, the objective of this study was to estimate genetic parameters for image derived morphometric traits, daily rumination time, and daily activity time in Holstein cows.

Materials & Methods

Data collection. Data was collected from automatic milking systems (AMS) on 1,312 lactating Holstein cows, between September and November 2024 on a commercial dairy farm in Chowchilla, California. Intel RealSense D435 cameras were mounted approximately 2.5 meters above the floor on the smart access gates to the VMS units to capture top-view near-infrared grayscale and depth images. Image acquisition was automated using a custom C++ program. Cow identity in each image was retrieved by linking their timestamps with the RFID information collected at smart access gates. Rumination and activity were recorded using SCR heatime collars, with vendor daily summaries used to derive daily rumination time (DRT) and daily activity time (DAT).

Image pre-processing and pose model training. Images were filtered to include only those capturing the body from neck to tail, without major occlusion or severe blur. A random subset of 2,500 images recorded in September was labeled using the CVAT platform, with keypoints annotated on the hip bones, pin bones, shoulder blades, and the midsagittal line of the back. Annotations were exported in COCO JSON format and converted to the Ultralytics pose format. A YOLOv8n pose model was trained for 150 epochs using the Ultralytics framework (v8.3.179) with a 70:30 train–test split, using an image size of 640 × 640, a batch size of 16, and two data loader workers. Data augmentation during training included horizontal flipping, scaling, rotation, and translation. The trained model was then used to predict keypoint coordinates for the images from October and November across the entire dataset.

Image-derived morphometric traits. Predicted keypoint pixel coordinates were used to compute six image-derived morphometric traits as Euclidean distances (in pixels): rump width (RW), the distance between left and right pin bone points; body length (BL), the straight-line distance from tail to neck; hip width (HW), the distance between left and right hip bone points; shoulder width (SW), the distance between left and right shoulder blade points; right rump length (RL_R), the distance between the right hip point and the right pin bone point; and left rump length (RL_L), the distance between the left hip point and the left pin bone point. Body landmark distances were averaged per cow and day to compute individual daily observations for each image-derived trait.

Data editing and statistical analyses. Daily image and sensor records were merged by cow ID and date. Records with missing information for both image and sensor traits, inconsistent dates, or implausible values were removed. After data cleaning, 918 cows were retained, comprising 22,193 daily averages for image-derived traits and 71,887 observations for sensor-based traits. Cows were genotyped using one of four SNP chip densities from Zoetis, and lower-density genotypes were imputed into a 50k panel using FImpute v2 software, based on linkage disequilibrium and a reference population of ~13,000 genotyped animals. Variance components for all traits were estimated using the BLUPF90+ (Misztal *et al.*, 2002) based on the AI-REML algorithm and a multi-trait GBLUP repeatability model. The general model can be described as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wp} + \mathbf{e} \quad (1)$$

where $\mathbf{y}$ is the vector of observations across traits, $\mathbf{b}$ is the vector of fixed effects, $\mathbf{a}$ is the vector of random additive genetic effects, $\mathbf{p}$ is the vector of random permanent environmental effects of the cow, and $\mathbf{e}$ is the vector of random residual values. Fixed effects included contemporary groups, lactation number, days in milk (linear and quadratic covariate), age, reproductive status, and number of images per day. Additive genetic, permanent environmental, and residual effects were assumed to follow a multivariate normal distribution, with $\mathbf{a} \sim N(\mathbf{0}, \mathbf{G} \otimes \mathbf{\Sigma}_a)$, $\mathbf{p} \sim N(\mathbf{0}, \mathbf{I}_n \otimes \mathbf{\Sigma}_p)$, and $\mathbf{e} \sim N(\mathbf{0}, \mathbf{I}_n \otimes \mathbf{\Sigma}_e)$, where $\mathbf{G}$ is the genomic relationship matrix (VanRaden 2008; method 1), $\mathbf{I}_n$ is an identity matrix, and $\mathbf{\Sigma}_a$, $\mathbf{\Sigma}_p$ and $\mathbf{\Sigma}_e$ are the respective (co)variance matrices. Narrow-sense heritability (h^2) and repeatability (t^2) were estimated as described in Falconer & Mackay (1996), based on variance components obtained from converged models. Genetic correlations among image- and sensor-based traits were estimated as $r_{a_{i,j}} = \frac{\sigma_{a_{i,j}}}{\sqrt{\sigma^2_{a_i} \times \sigma^2_{a_j}}}$, where $\sigma_{a_{i,j}}$ is the genetic covariance between traits i and j, and $\sigma^2_{a_i}$ and $\sigma^2_{a_j}$ are the corresponding additive genetic variances. Genetic covariances among image-based traits were estimated using pairwise combinations, whereas covariances combining one image-based trait with both DRT and DAT were estimated simultaneously.

Results & Discussion

The final YOLOv8-Pose model achieved a mean squared error of 36.7 px², a normalized mean error of 0.01, and a Percentage of Correct Keypoints (PCK) of 98.83%, indicating highly accurate keypoint localization across validation images.

Heritability estimates for digital morphometric traits were moderate to high, ranging from 0.32 ± 0.04 (BL) to 0.53 ± 0.07 (HW), while t^2 values ranged from 0.51 ± 0.01 to 0.90 ± 0.01 (Table 1). Heritability estimates for image-based rump traits and body length were within the 0.40–0.48 and 0.29–0.42 range, respectively, for manual measurements reported by Nemcova *et al.* (2011), Kumar *et al.* (2025), and Sheidi *et al.* (2025). Although no manual morphometric measurements were collected in this study, these results support the idea that pixel-based distances can capture additive genetic differences related to different body dimensions when the imaging setup is consistent. Except for BL, t^2 estimates were greater than 0.74 for all morphometric traits, indicating strong within-animal consistency in image-derived measurements across days. The lower t^2 value for BL was likely due to greater measurement error at the cow endpoints caused by variations in posture, stride phase, and occlusion by the smart access gates. For sensor-based traits, DAT showed higher heritability and repeatability than DRT (Table 1), indicating more consistent differences between cows for daily activity than for daily rumination. Heritability estimates for DRT in this study were lower than those reported by Byskov *et al.* (2017).

Table 1. Heritability (h^2) and repeatability (t^2) and their respective standard error (se) estimate of image-derived morphometric and sensor-based behavioral traits.

Trait	$h^2 \pm se$	$t^2 \pm se$
RW	0.43 ± 0.06	0.83 ± 0.01
BL	0.32 ± 0.04	0.51 ± 0.01
HW	0.53 ± 0.07	0.90 ± 0.01
SW	0.38 ± 0.06	0.74 ± 0.01
DRT	0.09 ± 0.02	0.15 ± 0.01
DAT	0.20 ± 0.05	0.44 ± 0.02
RL_R	0.45 ± 0.06	0.74 ± 0.01
RL_L	0.46 ± 0.06	0.76 ± 0.01

BL: body length; HW: hip width; SW: shoulder width; RW: rump width; RL_L: rump length left side; RL_R: rump length right side; DRT: daily rumination time; DAT: daily activity time.

Genetic correlations (Figure 1) showed that the image-derived morphometric traits were positively correlated (0.77 to 0.99), with the highest observed value between RW and HW (0.99) and between RL_R and RL_L (0.99). Body length (BL) also showed strong positive correlations with RW, HW, SW, RL_R, and RL_L (0.91–0.97), suggesting that most additive genetic variation is shared across body size and pelvic frame dimensions. Consequently, selection on one morphometric trait is likely to produce correlated responses in others. In contrast, genetic correlations between the image- and sensor-based traits were much smaller, ranging from 0.17 (RW) to 0.32 (RL_R) for DRT, and from -0.16 (RW) to -0.09 (SW) for DAT (Figure 1). Larger body frame sizes are associated with higher feed intake, which in turn may influence rumination time (Byskov *et al.*, 2017), providing a physiological explanation for the modest but consistent positive genetic correlations observed between morphometric and DRT. Conversely, genetic correlations between image-based traits and DAT suggest largely independent genetic control of body structure and activity behavior, limiting correlated responses (Falconer & Mackay, 1996). Finally, DRT and DAT exhibited a moderate

negative genetic correlation (-0.36), indicating a genetic trade-off consistent with daily time budgets, in which cows genetically inclined to spend more time ruminating tend to spend less time on activity.

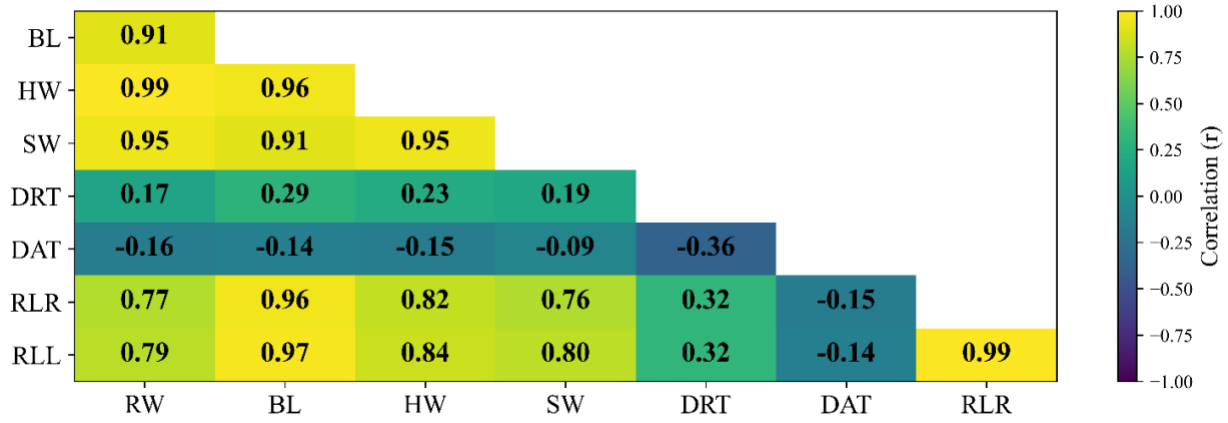

Figure 1. Genetic correlations among image-derived morphometric traits in cattle
BL: body length; HW: hip width; SW: shoulder width; RW: rump width; RL_L: rump length left side; RL_R: rump length right side) and behavioral traits (DRT: daily rumination time; DAT: daily activity time

Conclusions

Image-derived morphometric traits are heritable and repeatable, supporting their use as complementary conformation traits in genetic selection. The strong positive genetic correlations among morphometric traits indicate that selection on one trait will produce correlated responses in others. In contrast, behavioral traits showed weaker genetic associations with morphometric traits. The negative genetic correlation between rumination time and activity time likely reflects an expected biological tradeoff in daily time allocation, as cows are usually less active while ruminating. This relationship should not be viewed as inherently unfavorable, since higher activity may reflect either normal or adverse conditions depending on context.

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