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Genetic parameters for sensor-based behavior traits and their relationship with milk production in Holstein-Friesian dairy cattle

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Introduction

Rumination is a key physiological process in ruminants that enables the efficient utilization of fibrous feeds by regurgitating, remasticating, resalivating, and reswallowing ingesta from the reticulorumen. This process contributes to ruminal homeostasis by buffering ruminal pH and enhancing microbial fermentation by reducing feed particle size. Rumination time (RT; min/day) is influenced by nutritional, management, and environmental factors, including diet composition, dry matter intake, feed access, and feeding competition (Welch, 1982; Souza *et al*., 2022). However, substantial variation in RT has been observed among cows under similar dietary and physiological conditions, suggesting that a portion of this variation is due to a genetic component. Sensor-based technologies now enable automated RT recording for health monitoring, estrus detection, and feeding management (Byskov *et al*., 2017). While rumination physiology is well documented, its genetic basis is less well characterized than that of milk production traits. Heritability estimates for RT indicate moderate genetic contribution (0.14–0.49), while genetic correlations with milk yield (MY) vary from −0.38 to 0.51 (Byskov *et al*., 2017; Moretti *et al*., 2017; Atashi *et al*., 2023; Lopes *et al*., 2024), emphasizing the need for population-specific estimates. Genetic parameters of RT and its association with MY and daily activity (DA) in Mexican dairy cattle are scarce. Therefore, the objectives of this study were to estimate the heritability and repeatability of RT, MY, and DA; to quantify genetic, permanent environmental, and phenotypic correlations among these traits; and to evaluate their genetic trends over time.

Material & Methods

Rumination time, daily activity, and milk yield data were obtained from three commercial dairy herds with rotary milking systems, located in the central and central-eastern region of México; the sampled herds had their own feeding management and diet formulation. Pedigree records, including sire and dam identification, were available for the sampled animals and used to construct the additive genetic relationship matrix. Data from 6,514 lactations corresponding to 4,599 cows collected between 2019 and 2023 were included in the analysis. Data were collected using the Allflex DataFlow™ II system, a sensor-based platform, in combination with validated SCR Hi-Tag collars positioned on the left side of the neck for real-time recording of RT and DA. Device operation has been previously described (Iqbal *et al*., 2021). RT was identified based on characteristic regurgitation and chewing sounds, whereas DA was derived from analysis of head and neck movement signals associated with cow activity. The associated software generated standardized data records for each cow at 2-h intervals. Twelve consecutive intervals were arithmetically averaged to obtain daily values for RT and DA (Reith *et al*., 2014; Paudyal, 2021). MY was defined as the average daily milk yield per lactation for each cow, whereas RT and DA were expressed as average daily minutes per lactation per animal. Extreme or biologically implausible values (mean ± 3 SD) and records with missing data were excluded. Contemporary groups were defined by herd, year, and calving season (HYS), and groups with

fewer than five animals were removed. Data editing and descriptive statistics were performed using SAS 9.4.

Statistical Analysis. Genetic analyses for RT, DA, and MY were conducted using a single-trait animal model and multi-trait models for RT–MY, RT–DA, and DA–MY. The models included fixed effects for herd–year–season (HYS) and parity, and random effects foradditive genetic, permanent environmental, and residual effects. The convergence criterion used was –2Log likelihood with a value equal to or less than 10^{-12}. Variance components were estimated using restricted maximum likelihood (REML) with the average information algorithm implemented in BLUPF90+ software. Heritabilities (h^2), repeatabilities (t), and genetic ($\hat{r}_a$) and phenotypic correlations ($\hat{r}_f$) were derived from the estimated variance and covariance components. Phenotypic trends were estimated by linear regression on cow birth year (2016–2019). Similarly, genetic trends were estimated by regressing the means of estimated breeding values from sires with daughters born in the evaluated years and on birth year, whereas environmental trends were calculated as the difference between phenotypic and genetic trends.

Results & Discussion

Mean (± SD) RT and MY across all cows were 543.1 ± 43.3 min/day and 39.7 ± 18.7 kg/day, respectively, while mean DA was 506.7 ± 43.3 min/day. Differences between the values estimated in the present study and values reported in the literature for RT (e.g., 527 ± 73 min/day with MY = 38.3 ± 10.3 kg/day (Andreen *et al*., 2021)) may reflect variation and/or interaction among herd management (milking sessions, diet composition, and feed ration administration), the physiological state of the cow (including parity and chewing capacity) and environmental factors such as feed availability, competition, ambient temperature, and distance to the milking parlor. Similarly, variations in DA likely arise from management and environmental factors, including feeding behavior, social interactions, and movement across the farm (Moulder *et al*., 2024; Nascimento *et al*., 2024).

RT exhibited moderate heritability ($h^2 = 0.47 \pm 0.06$), higher than estimates reported in Holstein cattle from different geographical regions ($h^2 = 0.14$–0.49) (Lopes *et al*., 2024; Weller and Erza, 2024). These results suggest that RT could serve as an early lactation selection indicator, given its consistent genetic expression throughout lactation. The moderate repeatability ($t = 0.54 \pm 0.01$) observed in our population suggests RT variation is influenced by both cow-intrinsic factors (digestive capacity, feed retention time, ruminal passage rate) and environmental factors (distance to feed/water, availability of resting space). The estimated h^2 for DA was 0.11 ± 0.03, with $t = 0.58 \pm 0.01$, consistent with literature values (Moulder *et al*., 2024). Limited research exists on DA genetic parameters, as previous studies focused on health and reproductive applications (Bewley *et al.,* 2010). From a practical perspective, high DA values may indicate energy allocation away from production, although high-producing cows can exhibit low resting times. The h^2 for MY was 0.18 ± 0.02, consistent with values reported for Mexican Holstein populations (Martínez-Marín et al., 2021), whereas the t value (0.18 ± 0.02) was lower than the ones reported in the literature, indicating that additional records are needed for accurate future performance prediction.

The genetic correlation between RT and MY was low ($\hat{r}_a = 0.19 \pm 0.06$), consistent with reports across various regions, which range from -0.04 to 0.51. The phenotypic correlation ($\hat{r}_f = 0.11 \pm 0.02$) was positive, with literature values ranging from -0.14 to 0.40, suggesting cows with longer RT may have greater MY (Byskov *et al*., 2017; Weller and Ezra,2024). For RT-DA, values of $\hat{r}_a = -0.05 \pm 0.15$ and $\hat{r}_f = -0.06 \pm 0.03$ were estimated. No previous $\hat{r}_a$ estimates were found in literature, while reported $\hat{r}_f$ values showed negative associations of varying magnitude (Krpálková *et al*., 2022). For DA-MY, $\hat{r}_a = 0.43 \pm 0.14$ and $\hat{r}_f = 0.21 \pm 0.02$ were estimated. Previous studies reported lower phenotypic associations (Krpálková *et al*., 2022). Increased

DA in high-producing cows may reflect greater displacement to meet feed intake requirements. This study provides the first genetic association estimate between MY and DA, though one crossbred study reported no phenotypic association (Moulder *et al*., 2024).

Genetic (Tg), phenotypic (Tf), and environmental (Ta) trends were estimated for each trait across sire birth years from 2016 to 2019 (Figure 1). For RT, variable increasing trends were observed, although none were statistically significant (Tg = 1.65 min day^{-1} year^{-1}, p = 0.18; Tf = 1.89 min day^{-1} year^{-1}, p = 0.43; and Ta = 0.23 min day^{-1} year^{-1}, p = 0.86). For DA, a nearly flat Tg trend was observed (0.02 min day^{-1} year^{-1}, p = 0.97), while both Tf and Ta showed strongly significant increasing patterns (Tf = 9.16 min day^{-1} year^{-1}, p = 0.004; Ta = 9.14 min day^{-1} year^{-1}, p = 0.003). For MY, trends were not statistically significant, with positive Tg (0.24 kg day^{-1} year^{-1}, p = 0.32) and negative Tf (-0.25 kg day^{-1} year^{-1}, p = 0.75) and Ta (-0.49 kg day^{-1} year^{-1}, p = 0.44). Currently, RT and DA are not included in national genetic evaluation programs in Mexico. For RT, despite the apparent phenotypic increase, the lack of significant genetic contribution indicates substantial environmental influence on the observed changes. For DA, the significant phenotypic and environmental increases ($p < 0.01$) with negligible genetic change demonstrate that improvements in this trait are entirely driven by environmental factors rather than genetic selection. Regarding MY, although evidence exists of genetic gain in sire breeding values for milk production in other populations, no significant trends were observed in our population for any component, which may be attributed to the limited temporal scope of the data (2016-2019) and relatively small sample size within this timeframe.

Technological advances now provide cost-effective phenotyping alternatives through sensors and automated systems, offering numerous traits for selection but creating challenges in trait selection. Traits should ideally meet criteria such as economic value, high heritability, consistent, low-cost measurement, and strong genetic correlation with economically important traits. Interest in RT and DA stems from sensor portability, cost-effectiveness, and practicality for health monitoring, estrus detection, and feeding evaluation (Weller and Ezra, 2024).

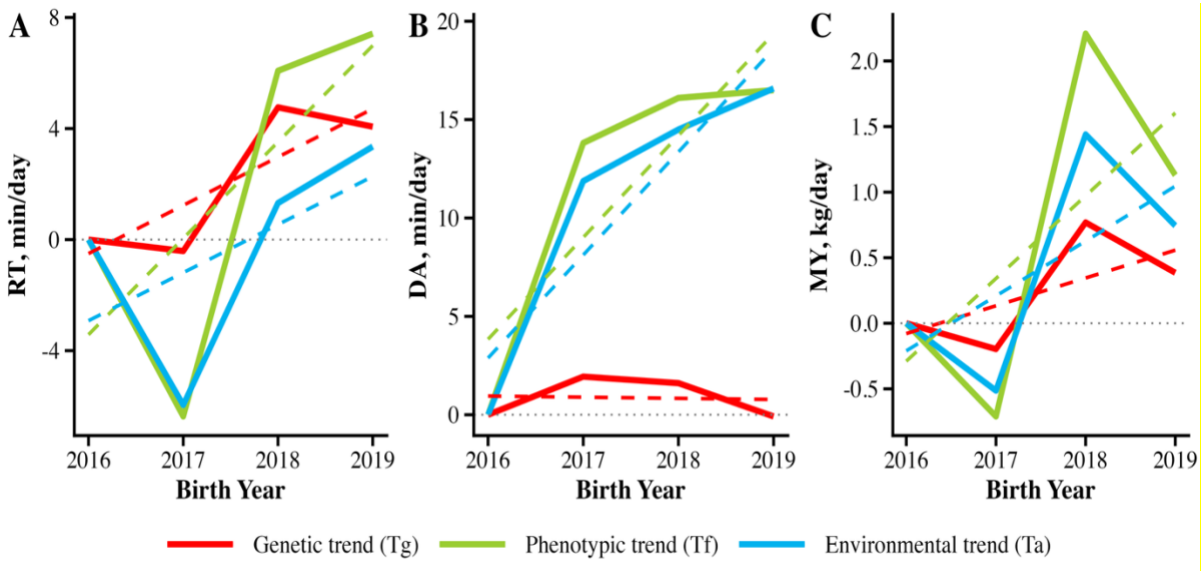

Figure 1. Genetic, phenotypic, and environmental trends for behavioral and production traits in dairy cattle across sire birth years from 2016 to 2019. Solid lines represent observed trends for sire breeding values with phenotyped daughters (Tg, red), phenotypic values (Tf, green), and environmental effects (Ta, blue). Dashed lines represent linear regression of annual change. The dotted horizontal line at zero represents the reference line. Panels show: (A) rumination time (RT, min/day), (B) daily activity (DA, min/day), and (C) milk yield (MY, kg/day). Values are expressed as deviations from the 2016 baseline (centered at zero), with the dotted horizontal line indicating zero deviation.

Conclusions

In conclusion, RT showed moderate heritability without significant genetic variation over the evaluated period, and a low genetic association was observed between RT and MY. Understanding phenotypic variability in behavioral traits is crucial for identifying new selection criteria in dairy cattle breeding programs. The availability of automatically, continuously, and accurately recorded phenotypes for RT and DA could enable the use of complex analytical models throughout lactation, facilitating the identification of genetic variation in different lactation periods and genetic associations with MY. Furthermore, DA showed low heritability, null genetic and environmental association with RT, but moderate-to-low association with MY, suggesting that increased productive performance may be related to more efficient resource use per unit of milk—a distinction in energy allocation between productive and metabolic processes. A key limitation of this study was the small dataset size; increasing the number of herds and incorporating genomic information would enhance prediction accuracy and broaden the applicability of these behavioral traits as selection tools for MY in Holstein cattle.

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