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Evaluating dairy cattle resilience through proxies and alternative approaches to lactation curve modeling

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Introduction

Resilient cows sustain performance and welfare under pathogens, environmental stressors, and management hurdles, leading to lower treatment costs, longer productive life, and greater farm profitability (Krupová *et al.*, 2025). Although genetic enhancement of resilience is valuable, direct selection is difficult because resilience is latent and cannot be observed outright. The prevalent strategy for general resilience contrasts observed lactation curves against "unperturbed" baselines; deviations are condensed into per-animal resilience indicators that act as phenotypic proxies (Kašná *et al.*, 2022). Computing deviation-based indicators entails two methodological choices: selecting a model to define the unperturbed lactation curve and picking a metric to measure deviations (Berghof *et al.*, 2018; Poppe *et al.*, 2020). Yet, evidence on how the lactation curve model influences resilience estimates and animal rankings remains scarce. This study had two aims: (i) to quantify phenotypic consistency of resilience rankings across eighteen lactation curve models and nine deviation-based indicators using daily milk yield from Italian Holsteins; and (ii) to build a simulation framework to test the genetic validity of model–indicator pairs by correlating resulting resilience phenotypes with breeding values generated under a known genetic architecture.

Materials & Methods

Animals and data processing

Daily milk yield data were collected from a family-run Italian Holstein dairy farm (n ≈ 500 cows) during 2022–2024 using automatic milking systems. Quality control included: exclusion of missing/zero values and outliers (>3 SD from mean); lactations were included if they started ≤15 days in milk (DIM) and lasted ≥280 DIM (maximum 305 DIM); removal of lactations with gaps >20 consecutive DIM; and exclusion of the first 10 DIM from resilience analyses. The final dataset comprised 514,131 daily observations from 819 cows across 1,423 lactations.

Lactation curve models and resilience indicators. Eighteen lactation curve models were evaluated across three categories: classical parametric functions (Ali-Schaeffer, Wilmink, Wood, Nelder), iterative refinements of these models (IAli, IWilmink, IWood, INelder), polynomial models (3rd and 4th order; Poly3 and Poly4), quantile regression (0.50, 0.70, 0.80 quantiles; Q05, Q07, Q08), and smoothing approaches (moving median with 5, 11, 21-day windows – MM5, MM11, MM21; adaptive and penalized splines – ASpline, WSpline). Nine resilience indicators were calculated: five variance-based metrics (log variance, log mean square, relative log variance, RMSE, mean absolute deviation, the relative milk loss), one temporal metric (lag-1 autocorrelation), and two distribution-based metrics (area under curve, skewness).

Ranking consistency. To assess model influence on cow rankings, we compared the top 50 and bottom 50 ranked cows across all pairwise model combinations for each resilience indicator. Results are reported as mean percentage (±SD) of cows consistently ranking in the top or bottom 50.

Simulation study. A simulation study validated resilience indicators against known breeding values using 140 health-cleared cows as a resilient benchmark. Environmental and genetic perturbations were applied to lactation curves, with intensity, duration, and recovery modulated by pre-generated resilience breeding value components. These components were calculated by multivariate normal distributions reflecting negative correlation with milk production BV. Correlations between resilience indicators and simulated breeding values of resilience intensity, duration and recovery were calculated to assess genetic validity. The simulation workflow is shown in Figure 1.

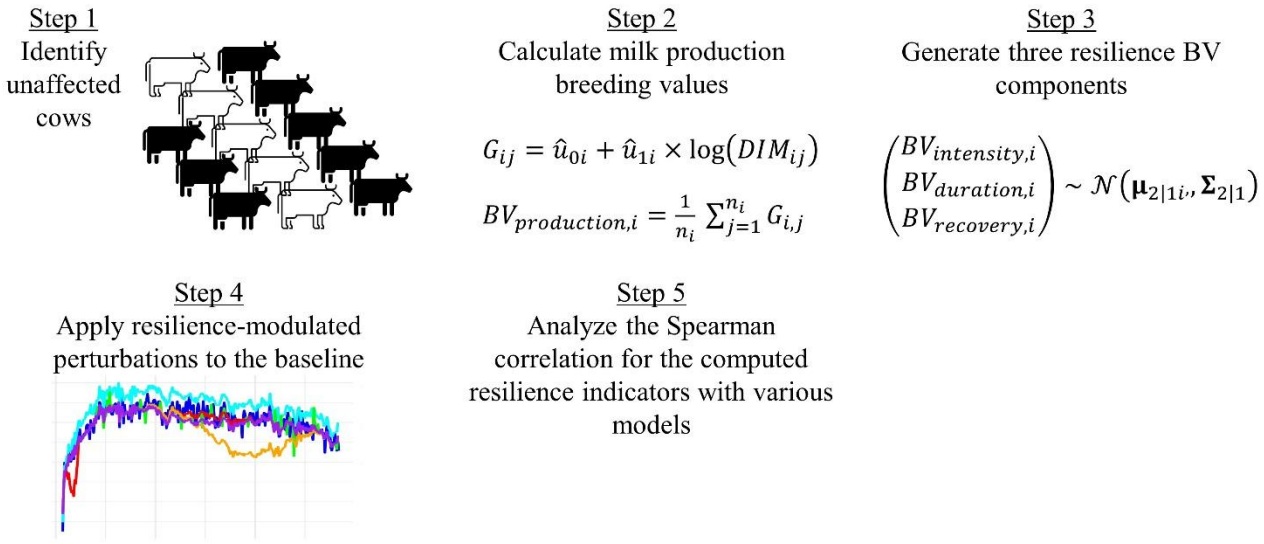

Figure 1. Simulation's workflow: Step 1 involved selecting the 200 cows with the lowest LnVar values, calculated from Ali & Schaeffer deviations. Cows affected by diseases or health issues were excluded by removing those that received medical treatments and had somatic cell counts above 250,000/mL. In Step 2, naïve breeding values for milk production were calculated using a random regression model, where *i* represents the *i-th* DIM of each *j-th* cow-lactation. Step 3 involved creating three resilience breeding values (BVs)—intensity, duration, and recovery—which exhibited a strong positive correlation with each other (0.90) and a negative correlation with milk production BV (-0.30). Step 4 consisted of the random application of perturbation events, with cows' responses modulated by the pre-generated resilience components. Specifically, for each perturbation, its intensity, duration, and recovery were regulated by the three resilience components through genetic quantitative models, where genetic variance was controlled by a heritability set at 0.15. Step 4 was replicated 150 times, with environmental autocorrelation randomly adjusted to ensure variation. Perturbation and environmental events were randomly assigned per replicate.

Results

Lactation curve models produced divergent cow rankings with respect to resilience indicators, with similarity across indicators ranging from 11% to 86%. Closely related models (e.g., quantile fourth-degree polynomials) yielded more concordant rankings (Q07-Q08, 86% ± 8%), whereas dissimilar models (e.g., spline interpolation versus Wilmink) showed the poorest agreement (12% ± 5%). Classical parametric models and their iteratively refined counterparts showed moderate to good concordance (e.g., IWilmink-Wilmink, 65% ± 28%). Data-driven smoothing methods, particularly splines, diverged substantially from parametric approaches.

Simulations indicated that resilience indicators capture only a portion of the genetic variance for resilience. As shown in Figure 2, the correlation between resilience indicators and simulated resilience breeding values components ranged from 0.04 to 0.24, far below the theoretical upper bound of 0.38 (square root of heritability). Patterns of correlation are very similar among resilience BV components, but slightly different for the milk production BV, which shows high correlation with

resilience indicators, far above the theoretical bound of -0.09 (square root of heritability multiplied by the superimposed genetic correlations). The best-performing combination was WSpline with AUC (LSM = least squares means = 0.22–0.25 across resilience BV components; LSM = 0.24 for production BV). Variance-based indicators showed similar performance across models but varied slightly across resilience BV components. Among resilience indicators, the area under the curve (AUC), the relative logarithm of the variance (LnVaRel; Keßler *et al*. (2024)), skewness (Skew), and the relative milk loss (ΔAvg; Guinan *et al*., 2025) were least effective at capturing genetic signal; while among the models, third-degree polynomials (Poly3) and moving-median with 5-days window (MM5) were the least effective ones; model performance varied more across resilience BV components than indicator performance. However, indicator effectiveness should be evaluated in combination with specific models, as shown in Figure 2.

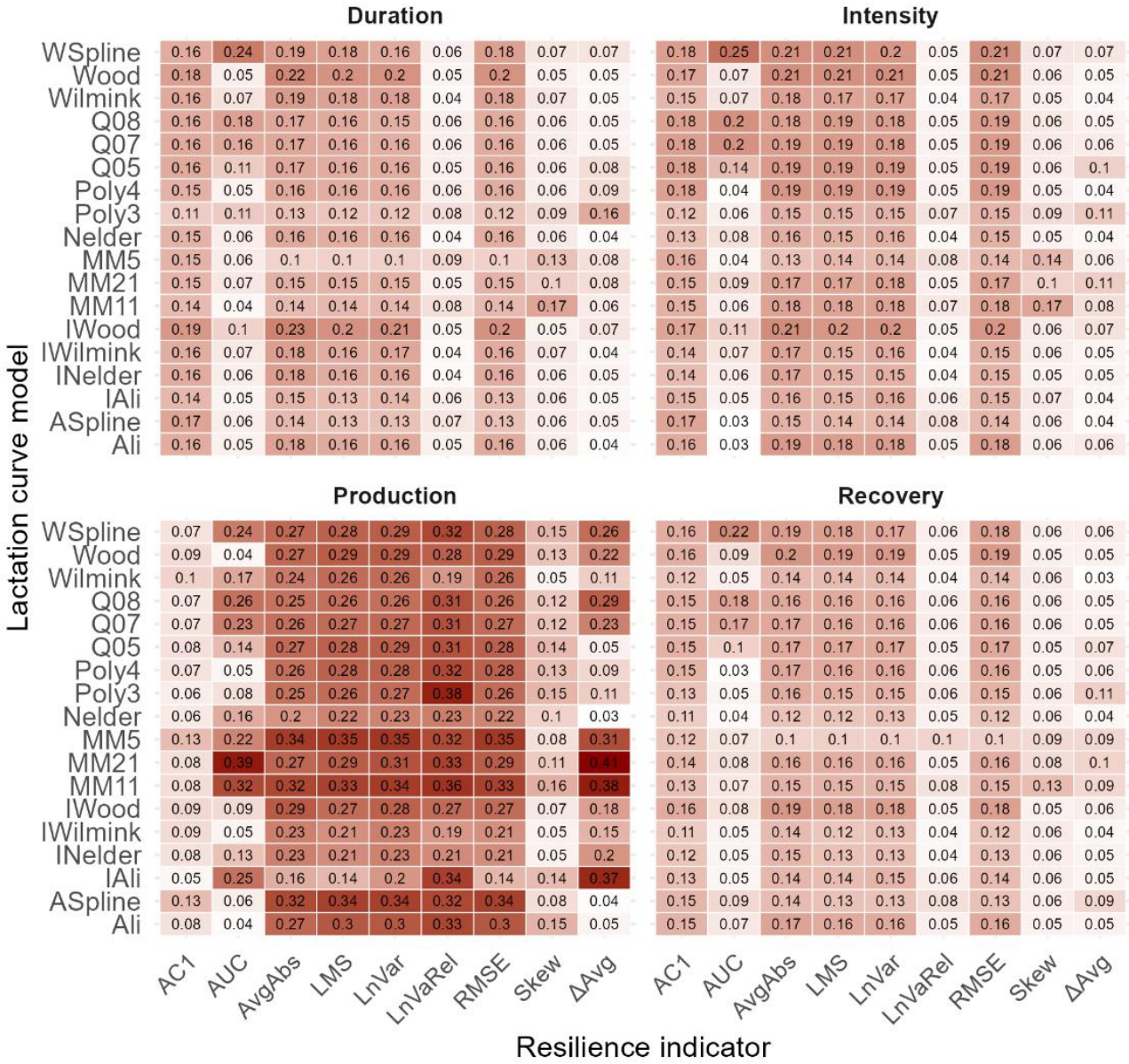

Figure 2. Spearman correlation was analyzed using a linear model in which proxies of resilience were evaluated as the sum of the main effects of the indicator and model, plus their interaction. The figure shows a heatmap displaying the least squares means (LSM) of the interaction effect for each model-indicator combination. Thus, each panel represents LSM of the model-indicator interaction effects for absolute Spearman correlation between resilience proxies and a different BV, those related to resilience —namely the intensity, duration and recovery components—as well as production.

Discussion

The substantial ranking inconsistencies observed across lactation curve models highlight a critical concern for standardized resilience assessment. Our findings indicate that methodological choices profoundly influence which animals are identified as resilient, with direct implications for breeding value estimates and genetic evaluations. Variance-based indicators, particularly logarithm of variance with heritability estimates of 0.13–0.23 (Chen *et al.*, 2023; Poppe *et al.*, 2020), demonstrate superior capacity to capture genetic resilience compared to temporal or distribution-based metrics. However, the suboptimal correlation with simulated breeding values (0.15–0.22) suggests that current resilience proxies capture incomplete genetic information.

Standardization of lactation curve modeling approaches is essential for developing comparable resilience phenotypes across herds and breeding programs. Future work should focus on hybrid approaches incorporating elements from multiple methodologies and enhanced indicator construction to maximize genetic signal detection.

Conclusions

Resilience indicators derived from milk-yield deviations show potential for genetic selection, but accuracy is constrained by lactation-curve model choice and limited correlation with true resilience. Substantial ranking inconsistencies exist between fundamentally different modeling approaches, with particular divergence between parametric and data-driven methods. Improvements in curve-fitting strategies and indicator construction are required to enhance their effectiveness for breeding robust, sustainable dairy cattle.

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