Estimation of Genetic Parameters for Lactation Persistency and Productive Maturity in the Italian Brown Swiss Breed

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Abstract

Modern dairy cattle breeding increasingly emphasizes functional efficiency and lifetime productivity to enhance herd sustainability. The Italian Brown Swiss breed, characterized by relatively flat lactation curves, represents a suitable population for selection on lactation persistency and productive maturity. This study aimed to estimate genetic parameters for protein yield (kg) across four lactation phases using a multi-trait repeatability animal model. Traits were defined as early (0–150 days) and late (150–300 days) production in first and subsequent lactations. After stringent data editing procedures, approximately 500,000 test-day derived records were included in the analysis. Heritability estimates ranged from 0.11 to 0.25 across phases, in agreement with values commonly reported for protein yield in Brown Swiss populations. Genetic correlations between phases were high (0.75–0.88), indicating substantial shared genetic background across lactation stages and parities. Correlations with the official protein index were above 0.90, supporting the consistency of the proposed model with the current evaluation system. Model validation, based on residual diagnostics and sire ranking comparisons, confirmed its ability to discriminate animals according to differences in lactation curve shape. Based on these results, synthetic indices for persistency and productive maturity are under evaluation to provide new selection tools aimed at reducing metabolic stress and improving lifetime efficiency.

Key words: Brown Swiss, Persistency, Maturity, Genetic parameters, Repeatability model.

Introduction

In modern dairy cattle breeding, moving beyond peak yield toward balanced production cycles is fundamental for establishing functional and long-lived herds. Lactation persistency and productive maturity play central roles in three major domains: animal welfare, biological efficiency, and economic sustainability.

Post-peak stability drastically reduces metabolic stress, particularly during early lactation when energy demands outpace dry matter intake (Collard et al., 2000; Pryce et al., 2004).

Flat lactation curves align with the natural genetic propensity of the Brown Swiss breed, optimizing roughage utilization.

Growth across lactations (maturity) maximizes lifetime profitability, lowers replacement costs, and extends herd longevity (Van Arendonk, 1985).

While random regression (RR) models are widely used to generate continuous genetic lactation curves (Schaeffer and Dekkers, 1994; Jamrozik and Schaeffer, 1997), they present significant limitations when applied to highly stratified datasets with small cohort sizes (e.g., Italian mountain herds), leading to statistical instability and biased early genomic evaluations (Vicario and Degano, 2005).

To overcome these challenges, a multi-trait repeatability approach was developed to deliver stable, unbiased genetic proofs tailored to the Italian population structure.

Materials and Methods

The dataset comprised approximately 500,000 test-day protein yield (kg) records from Italian Brown Swiss cows. The productive career was partitioned into a 4-phase matrix defined by parity and stage of lactation:

- F_early: First lactation, initial phase (0–150 Days in Milk, DIM).
- F_late: First lactation, final phase (150–300 DIM).
- S_early: Second and following lactations, initial phase (0–150 DIM).
- S_late: Second and following lactations, final phase (150–300 DIM).

Genetic parameters were estimated using a linear multi-trait repeatability animal model:

$$y = htd + Ye \times L \times nlat \times age \times dim \times prg + pe + a + e$$

where:

- htd: Herd-Test-Day fixed effect.
- Ye: Year fixed effect (grouped by quinquennium).
- L: Herd production level effect (representing the gap between primiparous and multiparous cows).
- $nlat$: Lactation number.
- age: Calving age effect.
- dim: Days in milk effect.
- prg: Days pregnant effect.
- pe: Permanent environmental random effect.
- a: Additive genetic random effect.
- e: Random residual error.

To condense complex multi-trait genetic evaluations into practical selection tools for breeders, synthetic indices and evaluation traits were formulated to capture lactation curve shape (persistency) and career trajectory (productive maturity) in descriptive functional terms:

- Persistency Ratio (Per÷): Evaluates persistency as the average proportional ratio of protein yield produced in the late phase (150–300 DIM) relative to the early phase (0–150 DIM), averaged across first and following lactations. Higher values identify cows that retain a higher proportion of peak production into late lactation.
- Persistency Percentage (Per%): Expresses early-lactation protein production (0–150 DIM) as a percentage of total 300-day combined output across both early and late phases in all lactations. Lower percentage values correspond to flatter, more persistent lactation curves.
- Persistency Difference (Per-): Quantifies persistency as the average absolute physical difference (in kilograms of protein) between late-phase and early-phase yields across lactations.
- Maturity Ratio Index (Mat÷): Measures productive maturity as the average proportional ratio of first-lactation yield relative to subsequent lactation yields, evaluated across both early and late lactation stages
- Maturity Percentage (Mat%): Expresses total first-lactation protein yield as a percentage of total combined output produced across lactations.
- Maturity Difference (Mat-): Quantifies maturity as the average difference (in kilograms of protein) between first-lactation production and following lactation production.

Results & Discussion

Heritability (h^2) and repeatability (R) estimates across the four lactation phases are presented in Table 1.

Table 1: Estimates of heritability (h^2) and repeatability (R) for protein yield across lactation phases

Lactation	Days in Milk	h^2	R
1	0–150	0.107	0.264
1	150–300	0.253	0.611
>1	0–150	0.149	0.360
>1	150–300	0.198	0.465

Across all phases, heritability estimates ranged from 0.11 to 0.25. Peak heritability occurred during the late phase of first lactation (25.3%). While subsequent lactations exhibited a similar pattern (14.9% early vs. 19.8% late), the differential between early and late phases was substantially more pronounced in first lactation. These estimates are consistent with those of the official evaluation performed by ANARB (0.18) (Interbull Centre, 2026).

Genetic correlations between the four lactation phases are structured as a symmetric correlation matrix in Table 2.

Table 2. Genetic correlation matrix between protein yield traits in the four lactation phases.

Trait	F_late	S_early	S_late
F_early	0.85	0.83	0.75
F_late		0.80	0.86
S_early		—	0.88

Genetic correlations between phases were high overall, ranging from 0.75 to 0.88, confirming substantial shared genetic background and high model stability. Crucially, the lowest correlation observed (0.75 between F_early and S_late) demonstrates that the initial phase of the first lactation possesses a degree of genetic independence from late-career maturity, validating the necessity of a 4-phase matrix architecture.

Correlations between sire estimated breeding values (EBVs) for total protein yield (P.Kg.), individual phase EBVs, and the synthetic persistency and maturity indices are reported in Table 3.

Table 3. Sire EBV correlations between synthetic persistency/maturity indices, total protein yield (P.Kg.), and individual phase traits.

Index	P.Kg.	F_early	F_late	S_early	S_late
Pers÷	0.18	0.02	0.20	0.07	0.25
Pers%	0.08	0.24	0.26	0.13	0.30
Pers−	0.49	0.63	0.67	0.54	0.72
Matu÷	-0.30	-0.22	-0.26	-0.32	-0.34
Matu%	-0.25	-0.38	-0.30	-0.41	-0.44
Matu−	-0.83	-0.75	-0.81	-0.88	-0.90

Daughter average lactation curves for the top and bottom 10% sires confirmed that the persistency indices effectively discriminate animals based on post-peak curve slope.

However, productive maturity indices showed strong negative genetic correlations with overall protein yield (-0.25 to -0.83). This marked antagonism indicates that direct selection for higher maturity under current index formulations would result in a substantial penalty on overall protein production, restricting its direct application in selection programs.

Conclusions

The multi-trait repeatability model developed in this study provides a robust and statistically stable methodology for evaluating lactation persistency and productive maturity in the Italian Brown Swiss breed.

High genetic correlations across the four lactation phases (0.75 to 0.88) confirm the structural consistency of the evaluation system, while the relative genetic independence observed during the initial phase of the first lactation underscores that distinct career stages are governed by partially independent biological drivers.

The synthetic persistency indices successfully discriminate animals according to lactation curve geometry, providing practical tools to select cows capable of sustained post-peak output and reduced metabolic stress. Conversely, the marked genetic antagonism observed between productive maturity indices and overall protein yield restricts the immediate, direct application of current maturity formulas in commercial selection programs.

To overcome these constraints, ongoing research is focused on evaluating direct phenotypic ratios and simple yield differences between phases, analyzing individual residuals from single-trait evaluation models to capture curve deviations, and identifying the most stable and heritable alternative traits for

integration into the national single-step genomic evaluation pipeline.

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