Improving the Stability of the Test-Day Repeatability Model for Production Traits in Italian Brown Swiss

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Abstract

The genetic evaluation of Brown Swiss cattle has undergone a significant methodological improvement with the introduction of a new algorithm designed to enhance the accuracy and stability of genetic indices for productive traits. This innovation addresses issues observed in previous models, particularly the significant variability in early evaluations of genomic bulls. The updated model incorporates a classification system for herds based on productivity differences between primiparous and multiparous cows, ensuring more precise genetic assessments. The new approach has resulted in greater stability in genetic indices and reduced the impact of initial data distribution biases. This advancement strengthens the reliability of genetic evaluations, supporting breeders in achieving their productivity goals.

Key words: Brown Swiss, Test days, Stability, primiparous, production traits, genomic

Introduction

Genetic evaluations in Italian Brown Swiss have been based on a test-day repeatability model since the early 2000s. This system was designed to support evaluations in a diverse environment with many small and mountain herds (Dal Zotto 2000). Genomic selection was introduced in 2011 (Rossoni 2009), and since 2019, the single-step genomic evaluation based on deregressed EBVs has been adopted (Vicario 2016).

However, over time, several issues related to index instability have emerged, particularly for widely used young genomic bulls. This instability undermines breeder confidence and complicates selection decisions.

This study investigates potential sources of instability and proposes a revised model incorporating a herd-level classification to better account for structural differences in herd productivity.

Materials and Methods

Data from routine national evaluations were analyzed to identify patterns and potential biases affecting the stability of early genetic indices.

We investigated several potential sources of instability, including:

- A high proportion of short lactations
- Predominantly first-parity records
- Cows calving at very young ages

However, none of these factors were found to be the actual source of the observed instability. In addition, we considered the non-random distribution of daughters across herds with varying management levels as a possible source of bias. As a first step, we tested whether heterogeneity of variance across herds could be responsible for the observed instability. However, this hypothesis was ruled out, as the observed pattern was exactly the opposite of what would be expected under variance heterogeneity. Typically, such heterogeneity leads to an overestimation of bulls whose daughters are mostly in high-producing herds. In contrast, in our case, bulls with daughters in high-producing herds appeared underestimated.

This led us to focus more closely on the average production difference between first- and later-parity cows within herds, which could interact with the distribution of daughters and contribute to the observed instability. To address these, a new herd-level classification was introduced based on the average milk yield gap between primiparous and multiparous cows in the previous three years period. Three levels were defined:

- High: Top 25% herds with the largest production differences
- Medium: Middle 50% of herds
- Low: Bottom 25% with smallest differences

This level was included in interaction with year, lactation number, age at calving, days in milk, and pregnancy status in the linear model:

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

Where:

htd = herd test day

Ye = quinquennium of production

L = herd level based on production gap

nlat = number of lactations

age = age of calving

dim = days in milk

prg = days of pregnancy

pe =permanent environmental

a = additive effect

e = error.

As shown in Figure 1, the thresholds used to classify herds into Low, Medium, and High groups remained relatively stable until around 2010. After that point, particularly for the upper threshold separating Medium and High herds, a marked upward trend can be observed. This indicates an increasing divergence over time, with High-level herds showing a progressively larger milk yield gap between primiparous and multiparous cows compared to the others.

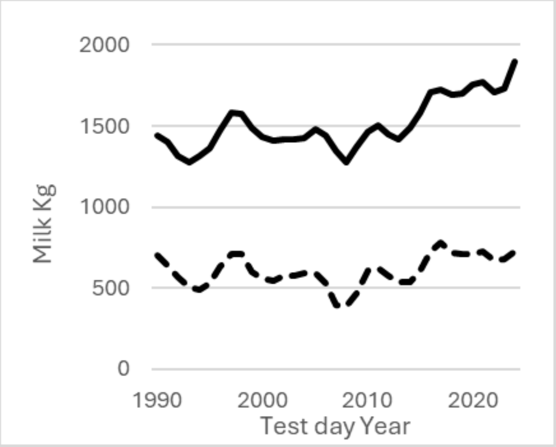

Figure 1. Herd average milk yield gap (kg) between primiparous and multiparous cows across herds classified Low (below the dashed line), Medium (between the dashed and solid lines) and High (above the solid line)

Results & Discussion

The updated model improved the stability of EBVs by reducing the influence of biased early data distributions. As shown in Figure 2, correlations between subsequent evaluations increased, and the advantage of the new model becomes more evident as the time interval between evaluations grows, reaching a difference of up to 0.03 when comparing evaluations four years apart.

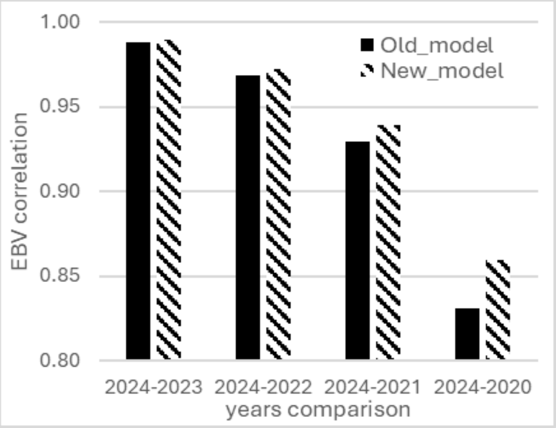

Figure 2. Correlations between estimated breeding values (EBVs) for sires across consecutive years, comparing the new model (white bars with diagonal hatching) and the previous model (solid black bars).

The updated model shows its greatest advantages in improving the stability of genetic evaluations for young bulls. As illustrated in Figure 4, which highlights the bulls with the largest changes in EBV between their first publication and the most recent one, the new model consistently produces smaller variations compared to the previous approach.

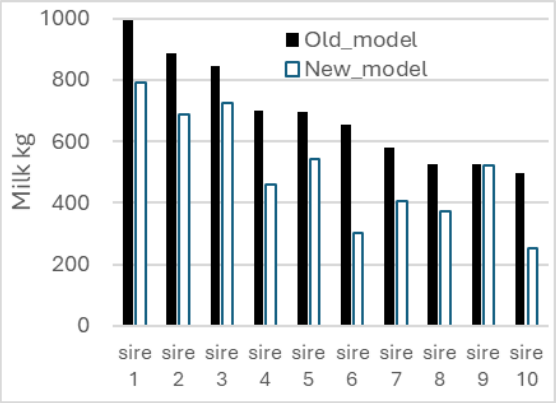

Figure 4. Difference between the first daughter-based evaluation and the most recent available evaluation for the 10 sires with the largest changes. Solid bars refer to the previous model, while white bars indicate the new model.

This increased stability is largely due to the model's improved handling of non-random herd distribution, a common issue when genomic bulls are initially used intensively in high-performing herds. By classifying herds according to the productivity gap between primiparous and multiparous cows, the new model incorporates both management level and its interaction with parity, thereby reducing bias and enhancing the reliability of early predictions.

Conclusions

Incorporating farm classification based on production differences between primiparous and multiparous cows into the genetic evaluation model substantially improves the reliability of early evaluations in the Italian Brown Swiss breed. This helps breeders make more confident decisions when selecting genomic bulls and enhances the credibility of the national genetic evaluation system.

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