

## International evaluations for clinical mastitis in Brown Swiss

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### Abstract

The SNP training for clinical mastitis (STCM) trait was introduced by the Interbull Centre in April 2021. Previously, the mastitis trait within the udder trait group allowed for a wide range of trait definitions: direct clinical mastitis, somatic cell score, or a combination of clinical and subclinical mastitis. Since the introduction of STCM, the Council on Dairy Cattle Breeding (CDCB) has participated with data for Holsteins and Jerseys, aiming to enhance the domestic SNP reference population with foreign evaluations. As expected, for Holstein and Jersey the inclusion of Multiple Across Country Evaluation (MACE) evaluations had a minor impact on the US evaluation due to the dominance of US animals in the reference population. In the August 2022 evaluation, Brown Swiss (BSW) animals began receiving domestic health evaluations in the US, which were also incorporated into the Net Merit Index. During the January 2023 test run, the BSW STCM successfully completed Trend Methods I and III validation at Interbull. Effective as of the April 2023 evaluation and going forward, BSW foreign evaluations are included in the United States of America (US) clinical mastitis evaluations. The initial expectation was that the impact of this inclusion would be limited, as only two other foreign countries (France and Switzerland) contribute to the Interbull clinical mastitis evaluation. However, the observed impact on the evaluations was noticeable. Correlations between April 2023 and March 2023, triannual genomic evaluations were as low as 0.73 for reference animals and 0.56 for young animals. Along with the significant variation in Genomic Estimated Breeding Values (GEBV), the mean genomic reliabilities (GREL) for young animals increased from 24% in March 2023 to 30% in April 2023. These results can be explained by two main factors: i) the contribution of foreign bulls from France and Switzerland in the SNP reference population for US BSW made the inclusion of MACE evaluations more relevant; ii) a large number of US BSW clinical mastitis records became available prior to the April 2023 evaluation and were added to the national cooperator database. Large changes in GEBV and GREL resulting from the initial inclusion of foreign data are not expected in subsequent evaluations unless more countries participate.

**Key words:** foreign information, participating countries, PTA variation, reliability, gain, young bulls

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### Introduction

The United States of America (US) has ongoing health trait evaluations for three breeds: Holsteins (HOL; Parker Gaddis et al., 2017), Jerseys (JER; Parker Gaddis et al., 2020), and Brown Swiss (BSW; CDCB Connection, 2022), commencing in 2018, 2020, and 2022, respectively. Health traits evaluations consists of six disease resistance traits: milk fever, displaced abomasum, ketosis, mastitis, metritis and retained placenta. All six traits are

incorporated into Net merit index (NMS) with a sub-index Health dollars, accounting for a total weight of 2%. (VanRaden et al., 2021). The same pipeline for all three breeds (HOL, JER and BSW), and the predicted transmitting abilities (PTA) are presented as percentage points of event resistance above or below breeds average (Mota et al, 2021).

As the most common and costly trait among the six traits, mastitis has a significant impact on the dairy cattle sector. Mota et al. (2021) noted the rapid increase in mastitis phenotypes,

with an increase from 1.8 to 5.1 million records in three years. Two years later, the national cooperator database managed by the Council on Dairy Cattle Breeding (CDCB) accounts for 7.1 million records, including 5.7 million HOL, 840k JER, 19k BSW, and half a million from other breeds where health trait evaluations have not yet been implemented.

The SNP training for clinical mastitis (STCM) trait was introduced by the Interbull Centre in April 2021. Previously, the mastitis trait within the udder trait group allowed for a wide range of trait definitions: direct clinical mastitis, somatic cell score, or a combination of clinical and subclinical mastitis. Since the introduction of Multiple Across Country Evaluation (MACE) evaluations for STCM, CDCB has participated with data for HOL and JER, aiming to enhance the domestic SNP reference population with foreign evaluations. In the case of BSW, this is even more crucial since over 50% of the reference population originates from Switzerland (CHE) and France (FRA). The percentage of bulls with MACE in more than 10 herds are 31% from FRA and 27% from CHE. The US has only 22% of its reference population consisting of domestic animals.

To assess the impact of adding foreign information to the clinical mastitis evaluation for BSW, during the January 2023 test run, the BSW STCM successfully completed Trend Methods I and III validation at Interbull (Interbull Centre, 2018). Effective as of April 2023, BSW foreign evaluations are included in the US clinical mastitis evaluations. As expected, for HOL and JER, the inclusion of MACE evaluations had a minor impact on the US evaluation due to the dominance of US animals in the reference population. However, even though the initial expectation is that the impact of this inclusion will be limited, as only two other foreign countries (FRA and CHE) contribute to the CDCB clinical mastitis evaluation, the non-US dominating reference population may suggest otherwise.

## Materials and Methods

The data used in this study were BSW MACE values provided by the Interbull Centre, Uppsala, Sweden (Interbull Centre, 2020).

To assess the impact of including clinical mastitis MACE information in BSW, PTA means and standard deviations were calculated, as well as correlations among three different scenarios: i) 2303<sub>D</sub>, the previous March run with domestic information only; ii) 2304<sub>D</sub>, the current April run with domestic information only; iii) 2304<sub>F</sub>, the current April run including MACE information.

The Pearson correlations were calculated as follows:

$$rg = \frac{\sigma_{ab}}{\sqrt{\sigma_a^2 * \sigma_b^2}}$$

where  $r_g$  is the genetic correlation, and  $a$  and  $b$  can be either of the investigated runs (2303<sub>D</sub>, 2304<sub>D</sub> or 2304<sub>F</sub>).

The statistical analyses were done by using SAS software (Statistical Analysis System, Version 9.4, 2023).

Finally, the investigation was conducted for the reference population and prediction animals divided in five different groups: i) all animals; ii) all bulls; iii) all cows; iv) bulls with REL > 50%; v) cows with REL > 50%.

## Results and Discussion

The total number of animals within each group is presented in Table 1. Please note that the GEBV and GREL means, and standard deviations may vary for the same evaluation. This variation is due to the different number of animals whose GEBV is affected by MACE when compared to a specific evaluation.

**Table 1.** Number of bulls in common between evaluation scenarios.

Group	Reference Population		
	2303 <sub>F</sub> vs. 2304 <sub>D</sub>	2303 <sub>F</sub> vs. 2304 <sub>F</sub>	2304 <sub>D</sub> vs. 2304 <sub>F</sub>
All	1,165	1,354	1,354
Bulls	561	902	902
Cows	604	452	452
Bulls GREL >50%	168	164	168
Cows GREL >50%	21	20	21
Group	Prediction Population		
	2303 <sub>F</sub> vs. 2304 <sub>D</sub>	2303 <sub>F</sub> vs. 2304 <sub>F</sub>	2304 <sub>D</sub> vs. 2304 <sub>F</sub>
All	62,168	61,979	62,301
Bulls	45,361	45,020	45,066
Cows	16,807	16,959	17,235
Bulls GREL >50%	-	-	-
Cows GREL >50%	-	-	-

2303<sub>F</sub>: foreign March 2023 run; 2304<sub>D</sub>: domestic April 2023 run; 2304<sub>F</sub>: foreign April 2023 run

The GEBV and GREL means, standard deviations, as well as correlations among three evaluation scenarios (2303<sub>D</sub>, 2304<sub>D</sub>, or 2304<sub>F</sub>) are presented in Table 2 for the reference population and in Table 3 for the prediction population.

In Table 2, which represents the reference population, GEBV means and standard deviations were very similar when domestic data was the sole source of information. However, when MACE information was included, there was a notable increase in GEBV variability. This had a pronounced impact on the correlations, particularly for non-reliable animals. The GEBV correlations exhibited a

slight drop, ranging from 0.01 to 0.03 for bulls or cows with REL > 50%, but a drastic drop occurred in the group of all bulls, decreasing to 0.69 when compared to the March run and to 0.68 within the same April run.

Despite this substantial GEBV variability, a significant increase in GREL was observed for the reference population, with an increase of approximately 38% for all animals and 47% for bulls. It is worth noting that both groups exhibited noticeable drops in correlations for both GEBV and GREL. As expected, the effects on bulls were much more pronounced than on cows.

Table 3 reveals an even greater GEBV variability in the prediction population, amounting to approximately 52% increase in GEBV variability between the April evaluations with (2304<sub>F</sub>) and without (2304<sub>D</sub>) MACE information. Regarding GEBV correlations, the observed decrease was more significant compared to the reference population, plummeting from 0.95 (all groups) to a range of 0.55-0.56 for all animals and 0.45-0.49 for the group of all bulls.

Conversely, the increase in GREL was also quite notable, with a 25% increase for all animals and a 30% increase for the group of all bulls. These results highlight a substantial impact on both traditional and genomic evaluations in the US. Despite the substantial GEBV variability, the gain in GREL suggests that it is worthwhile to incorporate foreign information into the US mastitis evaluation. In general, these initially unexpected results, which have a noticeable impact on US evaluations, can be explained by several factors. First, the US BSW population is relatively small, with approximately 50% of the reference population originating from either CHE or FRA. Furthermore, all foreign BSW bulls in the reference population have genotypes in the national cooperator database, a situation different from that of HOL and JER breeds, where the impact was less pronounced due to the predominance of US animals in the reference population.

**Table 2.** GEBV and GREL means (standard deviations), and correlations between evaluations for five groups of reference population animals.

BSW Reference Population						
2303 <sub>F</sub> vs. 2304 <sub>D</sub>						
Group	GEBV Mean (SD)		r	GREL Mean (SD)		r
All	0.56 (2.14)	0.50 (2.23)	0.97	41 (11)	41 (11)	0.99
Bulls	0.55 (2.33)	0.49 (2.40)	0.98	46 (13)	46 (13)	0.99
Cows	0.57 (1.95)	0.51 (2.07)	0.97	36 (6)	36 (6)	0.99
Bulls GREL >50%	0.61 (2.92)	0.57 (3.00)	0.99	63 (10)	63 (10)	0.99
Cows GREL >50%	0.53 (2.33)	0.54 (2.39)	0.99	55 (5)	55 (5)	0.99
2303 <sub>F</sub> vs. 2304 <sub>F</sub>						
All	0.73 (2.00)	-0.09 (2.96)	0.73	37 (13)	51 (14)	0.33
Bulls	0.76 (2.00)	-0.14 (3.20)	0.69	38 (15)	56 (15)	0.29
Cows	0.65 (2.00)	-0.01 (2.42)	0.86	36 (7)	41 (7)	0.93
Bulls GREL >50%	0.61 (2.92)	-0.06 (3.29)	0.92	63 (10)	69 (12)	0.78
Cows GREL >50%	0.53 (2.33)	0.26 (2.53)	0.93	55 (5)	58 (5)	0.93
2304 <sub>D</sub> vs. 2304 <sub>F</sub>						
All	0.62 (2.07)	-0.09 (2.96)	0.73	37 (13)	51 (14)	0.33
Bulls	0.66 (2.05)	-0.14 (3.20)	0.68	38 (15)	56 (15)	0.29
Cows	0.54 (2.12)	-0.01 (2.42)	0.88	36 (7)	41 (7)	0.93
Bulls GREL >50%	0.53 (2.99)	-0.11 (3.30)	0.92	63 (10)	68 (12)	0.79
Cows GREL >50%	0.46 (2.36)	0.16 (2.50)	0.94	55 (5)	59 (5)	0.94

GEBV: genomic estimated breeding value; GREL: genomic reliability; 2303<sub>F</sub>: foreign March 2023 run; 2304<sub>D</sub>: domestic April 2023 run; 2304<sub>F</sub>: foreign April 2023 run

**Table 3.** GEBV and GREL means (standard deviations), and correlations between evaluations for five groups of prediction population animals\*.

BSW Prediction Population						
2303 <sub>F</sub> vs. 2304 <sub>D</sub>						
Group	GEBV Mean (SD)		r	GREL Mean (SD)		r
All	0.81 (1.24)	0.61 (1.31)	0.95	24 (5)	24 (5)	0.99
Bulls	1.00 (1.08)	0.77 (1.14)	0.95	23 (5)	23 (5)	0.99
Cows	0.32 (1.49)	0.18 (1.61)	0.95	27 (6)	27 (6)	0.99
2303 <sub>F</sub> vs. 2304 <sub>F</sub>						
All	0.81 (1.24)	0.15 (1.99)	0.56	24 (6)	30 (6)	0.64
Bulls	1.00 (1.08)	0.30 (1.97)	0.49	23 (5)	30 (6)	0.62
Cows	0.32 (1.49)	-0.24 (1.99)	0.70	27 (6)	31 (6)	0.77
2304 <sub>D</sub> vs. 2304 <sub>F</sub>						
All	0.61 (1.31)	0.15 (1.99)	0.55	24 (6)	30 (6)	0.64
Bulls	0.77 (1.14)	0.30 (1.97)	0.45	23 (5)	30 (6)	0.62
Cows	0.18 (1.61)	-0.24 (1.99)	0.72	27 (6)	31 (6)	0.77

GEBV: genomic estimated breeding value; GREL: genomic reliability; 2303<sub>F</sub>: foreign March 2023 run; 2304<sub>D</sub>: domestic April 2023 run; 2304<sub>F</sub>: foreign April 2023 run; \*No young animals with GREL >50%

Additionally, the clinical mastitis data for BSW only has three contributors: CHE, FRA, and the US (<https://interbull.org/ib/geforms>). The volume of BSW information provided by the US is relatively small compared to the other two countries. In the most recent April 2023 evaluation, the US submitted only 82 estimated breeding values (EBV), while FRA and CHE combined contributed a total of 1,167 EBV. Finally, the impact on evaluations can also be attributed to the fact that the CDCB received a substantial number of US records that became available after the December 2022 evaluation

and were incorporated into the system for the April 2023 evaluation.

In summary, while these results were initially unexpected, they can be reasonably explained by the factors mentioned above. With data stability, we do not anticipate such a significant impact in future runs, unless substantial changes occur in terms of data availability and the participation of countries.

## Conclusions

The use of foreign information has enabled an increase in the reference population, but the US still has a long way to go to build a strong reference population for BSW. There has been a noticeable impact in both traditional and genomic evaluations, with a 52% increase in GEBV standard deviations, which is more than expected from the prediction GREL gain (30% vs. 24%). No impact is expected in subsequent evaluations unless more countries participate. The authors hope that these results serve as inspiration to facilitate the exchange of such traits, particularly to assist small population countries like the US.

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The mention of trade names or commercial products is solely for the purpose of providing specific information and does not imply recommendation or endorsement by CDCB. CDCB is an equal opportunity provider and employer.

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