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Within herd genetic relationships between bulls and active females in Canadian dairy breeds as a metric for controlling inbreeding

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Introduction

Genomic selection has now been implemented in Canadian dairy breeding for nearly two decades (Sweett, 2024), offering substantial gains in the reliability of estimated breeding values relative to traditional pedigree-based evaluations (Schenkel *et al.,* 2009). Despite these benefits, a more rapid increase in the annual rate of inbreeding has been observed (Makanjuola *et al.,* 2020; Van Doormaal, 2025). Elevated inbreeding reduces genetic diversity and may constrain long-term genetic progress. Inbreeding primarily arises from the mating of closely related animals. Therefore, effective inbreeding management at the herd level should rely on mate allocation strategies that minimize genetic relatedness between mating pairs. One practical strategy is the identification and use of outcross sires that are less genetically related to a predefined population of active females. To implement this strategy, the average genetic relationship between available sires and a predefined population of active females within a herd can be estimated using pedigree data (R-values) and genomic information (GR-values). This metric, developed in Canada by Van Doormaal *et al.* (2003), represents the proportion of DNA shared between an animal and the predefined active female population.

The objective of this study was to estimate within-herd R-values and GR-values between bulls and active Canadian Ayrshire, Brown Swiss, and Jersey females.

Materials & Methods

Herdbook records for currently active females in Canada and available sires across three breeds, Ayrshire, Brown Swiss, and Jersey, along with genotype data were provided by Lactanet Canada (Guelph, Ontario).

Bull and female data. The herdbook records across the three breeds included a total of 50,127 females from 1,406 herds. From these records, active females were defined as cows with at least one test-day record within the previous 365 days, ensuring recent phenotypic contribution to herd-level production, with the most recent test day dated November 1, 2025. In addition, heifers in the herdbook records without a recorded herd-exit date were also classified as active females, as they represent potential contributions to future generations. In total, the predefined active female population comprised 11,107 Ayrshire, 2,066 Brown Swiss, and 31,704 Jersey females from 126, 35, and 391 herds, respectively. On the bull side, a total of 1,076 Ayrshire, 437 Brown Swiss, and 1,033 Jersey bulls were available. Bulls were further selected based on lifetime performance index values from the November 2025 official genetic evaluation release and were required to have at least 20 active daughters within the predefined female population. This selection resulted in 501 Ayrshire, 250 Brown Swiss, and 500 Jersey bulls being retained for analysis.

Genotype data. Among selected animals, 2,388 Ayrshire, 638 Brown Swiss, and 5,386 Jersey had genotype information. Animals were genotyped using the Illumina BovineSNP50 BeadChip (Illumina Inc., San Diego, CA), comprising 45,101 SNP markers. Quality control was applied to retain only SNP markers on autosomes with a minor allele frequency of at least 0.05, a call rate for animals and SNP markers of greater than 0.95, and a difference between observed and expected heterozygosity of less than 0.15 (Wiggans et al., 2009). After quality control, 38,542, 35,457, and 34,520 SNP markers were retained for Ayrshire, Brown Swiss, and Jersey, respectively, for subsequent analyses.

Pedigree data. Across all breeds, pedigree information was extracted for all selected bulls and active females. The pedigree records included 46,352 Ayrshire, 18,188 Brown Swiss, and 104,808 Jersey animals, with pedigree depths of 29, 37, and 31 generations, respectively.

Statistical Analyses. The average genetic relationships between each animal and the active females within each herd was estimated using the method developed by Van Doormaal *et al.* (2003). Pedigree genetic relationship values were estimated using the complete pedigree records of all active females and available bulls according to the following formula:

$$R_{ij} = \frac{\mathbf{e_i'Ax_j}}{n_j} \quad (1)$$

where R_{ij} is the R-value of i^{th} animal in the j^{th} herd, $\mathbf{e_i'}$ is a row vector with 1 corresponding to the i^{th} bull and 0 otherwise, $\mathbf{A}$ is the pedigree additive genetic relationship matrix, $\mathbf{x_j}$ is a column vector with 1 for all active females in the j^{th} herd and 0 otherwise, n_j is the total number of active females in the j^{th} herd.

Genomic relationship values were estimated using Equation (1) and replacing $\mathbf{A}$ with $\mathbf{G}$, which is the genomic relationship matrix.

Results & Discussion

The average pedigree and genomic relationship values between bulls and active females within herds across all breeds are summarized in Table 1. Ayrshire had the lowest average R- and GR-values at 13.06% and 16.91%, respectively, compared to 15.89% and 20.03% for Brown Swiss and 15.33% and 20.15% for Jersey.

Table 1. Within herd average and standard deviations of pedigree and genomic relationship values between bulls and the active females.

Breed	Number of bulls	R-values (SD) (%)	GR-values (SD) (%)
Ayrshire	501	13.09 (3.86)	16.91 (5.04)
Brown Swiss	250	15.89 (3.62)	20.03 (4.70)
Jersey	500	15.33 (3.45)	20.15 (4.86)

Since one-half of the genetic relationship is equivalent to the expected inbreeding of the progeny, the corresponding inbreeding values from the R-values were 6.55%, 7.95% and 7.65%, for Ayrshire, Brown Swiss and Jersey, respectively. These estimates are in line with the observed inbreeding levels of 6.89%, 7.10% and 7.56% reported by Van Doormaal (2025). Furthermore, within herd R-values between bulls and active females ranged from 4.43% to 14.61% in Ayrshire, 10.63% to 18.25% in Brown Swiss, and 0.74% to 17.32% in Jersey. The corresponding GR-values

ranged from 5.51% to 20.16% in Ayrshire, 12.25% to 24.13% in Brown Swiss, and 0.91% to 25.97% in Jersey. These findings demonstrate substantial within-herd variation in genetic relationships between bulls and active females and highlight the utility of these measures for identifying less-related sires for mate allocation strategies aimed at managing inbreeding.

The R-values of the top five lifetime performance index (LPI) bulls within the five herds exhibiting the highest genetic relationships across all breeds are presented in Tables 2–4. The corresponding GR-values followed a similar pattern and were approximately 1.2 times greater than the R-values. Therefore, only R-values are reported in this study. The R-values of the top five bulls within the top five herds ranged from 0.80% to 20.34% in Ayrshire, 7.72% to 27.37% in Brown Swiss, and 9.03% to 31.09% in Jersey, indicating substantial variation in bull genetic relationships across herds. These ranges are consistent with those reported by Makanjuola *et al.* (2025) for the Canadian Holstein breed, although the Canadian Holstein breed exhibited a narrower range of R-values for the top 100 LPI bulls. This difference is expected, as Holsteins are the most widely used dairy breed in Canada and were the first to implement genomic selection, which has resulted in higher levels of inbreeding compared to other dairy breeds (Van Doormaal *et al.,* 2025).

Table 2. Average pedigree relationship values between top five lifetime performance index (LPI) bulls and active females within five herds exhibiting the highest genetic relationships in the Ayrshire breed.

	Herd 1	Herd 2	Herd 3	Herd 4	Herd 5
Sire 1	18.75	16.24	18.19	19.81	20.34
Sire 2	0.80	1.55	0.68	1.35	0.82
Sire 3	16.01	18.53	17.29	16.75	18.46
Sire 4	1.18	4.25	1.50	3.72	2.53
Sire 5	17.12	17.10	16.49	18.10	18.71

Table 3. Average pedigree relationship values between top five lifetime performance index (LPI) bulls and active females within five herds exhibiting the highest genetic relationships in the Brown Swiss breed.

	Herd 1	Herd 2	Herd 3	Herd 4	Herd 5
Sire 1	7.83	7.72	8.61	8.04	8.22
Sire 2	16.36	16.36	17.44	16.66	19.71
Sire 3	27.37	22.61	22.16	24.76	21.96
Sire 4	15.93	16.04	16.14	15.80	17.08
Sire 5	16.26	13.32	14.55	17.75	12.69

Table 4. Average pedigree relationship values between top five lifetime performance index (LPI) bulls and active females within five herds exhibiting the highest genetic relationships in the Jersey breed.

	Herd 1	Herd 2	Herd 3	Herd 4	Herd 5
Sire 1	22.25	18.52	23.41	20.48	17.68
Sire 2	14.83	18.56	13.76	16.43	15.09
Sire 3	28.57	19.84	31.09	20.32	20.89
Sire 4	19.89	19.97	17.24	20.52	16.66
Sire 5	9.28	9.94	9.29	9.03	9.80

To maintain genetic progress, producers and artificial insemination (AI) companies strive to use top-ranking bulls. However, given the existing variation in genetic relatedness, targeted mate allocation strategies can be implemented by selecting high performing bulls that are less genetically related to the active female population within a herd. These results demonstrate that outcross top bulls can be identified and utilized to achieve continued genetic improvement while maintaining inbreeding at desirable levels.

Conclusions

This study demonstrate that pedigree- and genomic-based relationship metrics can be applied at the herd level to quantify and manage genetic relationships and inbreeding in Canadian dairy breeds. Substantial variation in genetic relationships between bulls and active females exists within and across herds, creating opportunities to identify less-related, top-ranking bulls for targeted mate allocation. Effective herd-level inbreeding management can ultimately translate into improved control of inbreeding at the population level.

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