COUNCIL ON DAIRY CATTLE BREEDING

June 27, 2025

Changes in Calving Ease and other calving traits due to phenotypic and genetic base change

Introduction

The output of genetic evaluation models is typically what – after several corrections and transformations – the end user sees as the Predicted Transmitting Ability (PTA) of an animal. The PTA, therefore, is derived from the raw numerical outputs of the genetic model solvers, adjusted by a number of factors and standardized through the addition of a constant (the breed mean).

The scale in which a PTA is reported must be meaningful and usable for producers. In the U.S. dairy industry, there is a strong preference for expressing PTAs in actual trait units – such as pounds of milk, disease incidence rates, or the probability of calving difficulty – to make the results practical and easy to interpret. PTAs released to the public are typically adjusted relative to a “zero” value, which represents the average genetic merit of a recent reference group, known as the “genetic base population.” This adjustment ensures that PTA values remain intuitive and comparable over time.

Although the term “genetic base of the population” might sound complex, it is quite straightforward. It refers to a selected group of animals, usually cows born in a specific year, whose average genetic values are calculated to establish the baseline. To develop the final PTAs that producers see, the genetic base value is subtracted from each animal’s initial PTA. As a result, published PTAs can have positive or negative values: generally, a positive PTA means the animal is above the genetic base, whereas a negative PTA means the animal is below the genetic base.

Over time, as genetic progress accumulates, more and more animals surpass the existing genetic base. To maintain meaningful comparisons, the genetic base is updated every five years by the Council on Dairy Cattle Breeding (CDCB). Each update uses a newer generation as the reference group, which naturally leads to higher breed averages and causes individual PTAs to shift lower (in absolute terms), even though the animals’ genetic values themselves have not changed.

This dynamic helps producers consistently identify animals with superior genetic potential, even as the overall population improves.

The base change for the four calving-related traits was excluded from the routine April 2025 genetic base change due to unanticipated results while assessing the base change impact. The further analysis, captured here, describes these results that have since been confirmed as accurate.

Overall, while the findings point to a significant reduction of dystocia on U.S. dairy farms in Holsteins, recording and reporting calving ease scores remains vitally important. Brown Swiss rates of dystocia on the other hand have increased.

Genetic and phenotypic base explanation for calving ease traits

CDCB conducts genetic evaluations for calving ease traits in both the Holstein and Brown Swiss breeds, while evaluations for stillbirth traits are conducted for the Holstein breed only.

In the calving ease and stillbirth evaluations a sire-maternal grandsire threshold model is used, where outputs are expressed in terms of probabilities or frequencies of difficult calvings (or stillbirth). In this model, the observed calving difficulty (or stillbirth) is understood as a combination of two factors: genetics (which we aim to improve through selection) and environment (management factors such as feeding and gestation practices). Environmental effects are incorporated into the final PTA because, for example, sires' daughters calving in a "poor" environment will generally experience more difficult calvings, while daughters calving in a "good" environment will tend to have easier births.

When USDA revisited the calving ease evaluation 20 years ago (Van Tassell et al., 2003), they decided to define the environmental contribution based on the observed calving difficulty of bulls born in a particular year. This approach created what we call the phenotypic base, reflecting the contemporary environment in which most of the calvings are taking place.

In 2020, the calving trait model was also updated to account for, among others, the increasing use of sexed semen. The data showed a strong trend in the sex-ratio of calves that has since been accounted for. More information on this change can be found here: https://uscdcb.com/april-2020-changes-to-evaluation-system/

Therefore, in the evaluations for calving ease and stillbirth, both genetic and phenotypic bases are considered. These bases are referenced to sire averages rather than cow averages, due to the sire–maternal grandsire structure of the evaluation model.

In Sire Calving Ease (SCE) and Sire Stillbirth (SSB), we use the service sire's year of birth as the reference for the base. The genetic base is computed as the average genetic value of the bulls born in a specific year. The phenotypic base is defined as the percentage of difficult calvings among their calves (both males and females) born from heifers (first-parity cows). With the upcoming base change in August, the base population will consist of bulls (i.e., service sires) born in 2020.

In Daughter Calving Ease (DCE) and Daughter Stillbirth (DSB), we use the maternal grandsire's year of birth as the base reference. The genetic base is computed as the average genetic value of the bulls born in a specific year. The phenotypic base is the percentage of difficult calvings among calves (both males and females) born from their first-parity daughters. With the August base change, we will be using bulls (i.e., maternal grandsires) born in 2015.

The phenotypic base is recalculated at every triannual evaluation and is breed-specific, making it difficult to precisely predict in advance the average dystocia rate for the specific group of bulls used as the genetic base. This uncertainty is especially pronounced in the first evaluations following a base change. As mentioned earlier, a base change involves switching to a younger group of animals, meaning the bulls used to compute the new phenotypic base typically have fewer progeny. As more progeny records become available over subsequent evaluations, the phenotypic average may shift slightly before stabilizing once a sufficient amount of data has accumulated.

Because the phenotypic base is defined by the average observed difficulty of calvings from a recent cohort of bulls, we expect the PTAs of these bulls to be evenly distributed around the phenotypic base. However, older bulls will typically lag behind. Their PTAs will reflect a greater tendency for dystocic calvings compared to more recent bulls as a result of both genetic and management improvements over time.

In Holstein, back in 2005 considering bulls born in 2000, the phenotypic base was approximately 8%. By 2024 (considering Holstein bulls born in 2015), it had decreased to approximately 2.29%. The August 2025 base change places the phenotypic base at 1.36%. This substantial reduction reflects genetic improvement, better management practices, and the increased use of sexed and beef semen, all of which contribute to easier calvings.

For Brown Swiss, the frequency of dystocia was already low, even before the August 2025 base change, and given the small numbers in the phenotypic case and the flat genetic trend, some continued changes are expected beyond August 2025.

Assessing the impact of the base change in the last April evaluation, the initial expectation was that the entire population would shift in roughly the same direction and magnitude as the phenotypic base change. However, due to the interaction between the phenotypic and genetic base for calving ease traits in particular, this did not happen. As a reminder, calving traits have never undergone a base change of this nature before. When CDCB last updated the genetic base in 2020, the phenotypic base had been fixed for years at an old phenotypic level, so the only observed impact was of the genetic base at that time. More information on that change to the trait group is available here: https://uscdcb.com/wp-content/uploads/2020/06/NAAB-CDCB-HAUSA-Calving-Traits-June-2020-August-2020-Calving-Trait-Adjustment-06_2020.pdf

While this paper focuses on SCE, each calving trait behaves somewhat differently, but because of the same reasons: a phenotypic base, a genetic base change, and a threshold model.

Consequences

Every five years, CDCB updates the genetic base for all traits and also revises the phenotypic base for calving ease traits.

The effects of these changes in the Holstein breed, based on actual numbers from the April 2025 evaluation for Sire Calving Ease (similar logic with different averages can be applied to all calving ease traits), are summarized below:

- The new phenotypic base for Sire Calving Ease (SCE) is 1.36%, calculated as the average frequency of difficult calvings on first-parity cows from bulls born in 2020. This is lower than the previous base of 2.29%, which was calculated using bulls born in 2015 (associated with the 2020 base change).

- As expected, the PTAs of recent A.I. bulls are roughly evenly distributed above and below the new phenotypic base. Most older bulls now have PTA values above the base, indicating a greater likelihood of dystocic calvings compared to more recent bulls. This is the result of continued genetic improvement in calving ease over time. These shifts in distribution (more bulls above and fewer bulls below the base) were not observed with the previous base, and are a clear result of significant genetic progress in calving ease in recent years.

- PTA variability has decreased as a consequence of the phenotypic base approaching zero. As the incidence of reported dystocic calvings becomes very low, PTAs are naturally constrained – values cannot fall significantly below the base because frequencies of dystocia below 0% are biologically impossible.

Figure 1. All bulls average PTA (traditional) changes due to the combined effect of phenotypic and genetic base updates computed for calving ease and stillbirth.

Breed	Trait	Current base (%)	New base (%)	Average PTA Change	New base year
Holstein	SCE	2.53	1.77	**-0.76**	2020
	DCE	3.10	2.59	**-0.51**	2015
	SSB	6.48	4.29	**-2.19**	2020
	DSB	7.09	6.13	**-0.96**	2015
Brown Swiss	SCE	2.27	2.85	**+0.58**	2020
	DCE	3.01	3.46	**+0.45**	2015

Figure 2. A.I. bulls (NAAB status "A" and "G") average PTA (traditional) changes due to the combined effect of phenotypic and genetic base updates computed for calving ease and stillbirth.

Breed	Trait	Current base (%)	New base (%)	Average PTA Change	New base year
Holstein	SCE	2.08	1.44	**-0.64**	2020
	DCE	2.16	1.78	**-0.38**	2015
	SSB	5.8	3.8	**-2.00**	2020
	DSB	4.88	4.17	**-0.71**	2015
Brown Swiss	SCE	2.43	3.05	**+0.62**	2020
	DCE	2.93	3.37	**+0.32**	2015

Figure 3. Standard deviations for calving traits comparing the old and new base years.

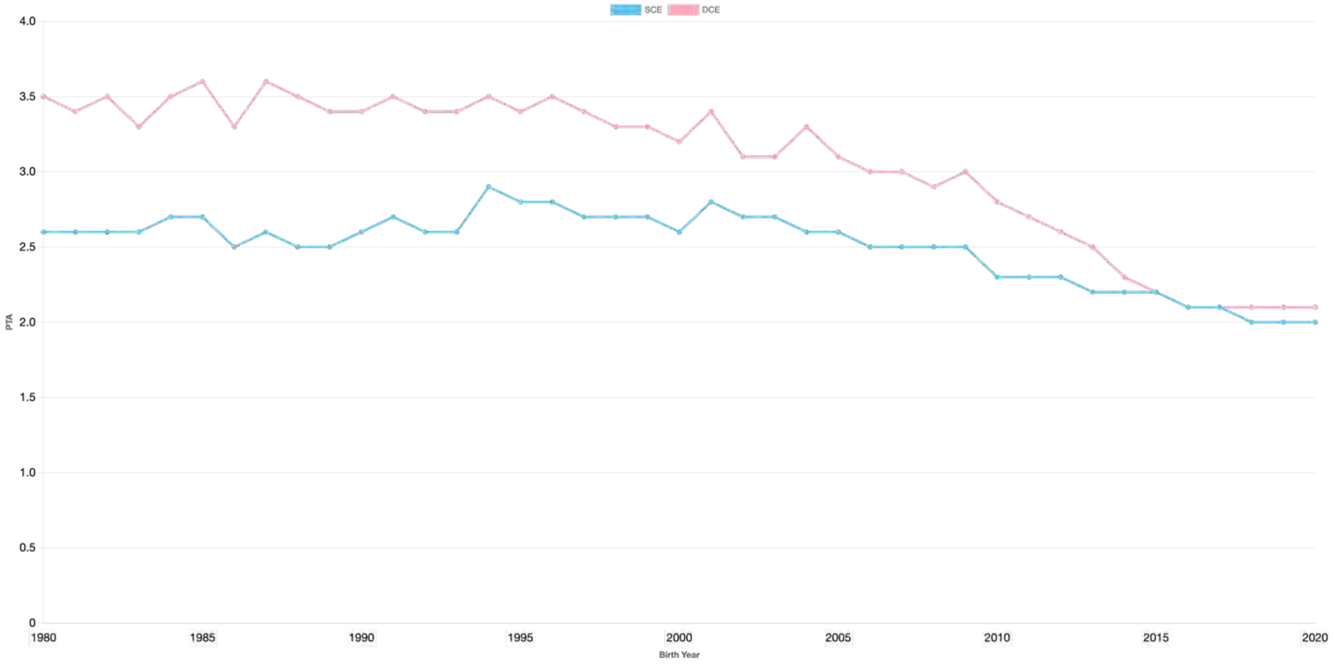
Breed	Trait	Current base (%)	New base (%)	New base year
Holstein	SCE	0.61	0.45	2020
	DCE	0.78	0.67	2015
	SSB	0.66	0.48	2020
	DSB	1.39	1.24	2015
Brown Swiss	SCE	0.47	0.57	2020
	DCE	0.55	0.62	2015

Numerical details

The following values and trends apply specifically to the Holstein breed.

Genetic trend

Below is the official CDCB genetic trend for the calving ease traits – Sire Calving Ease (SCE) and Daughter Calving Ease (DCE) – based on results from the April 2025 evaluation but utilizing the phenotypic base of bulls born in 2015. The trend is expressed in PTA units, where a value of 2% corresponds to an expected 2% incidence of dystocic calvings on first parity cows.



Phenotypic trend

Current (old) phenotypic base

From April 2020 to April 2025, the old phenotypic base consisted of the average calving difficulty on first parity cows for bulls born in 2015 (SCE, 2.29%) and maternal grandsires born in 2010 (DCE, 2.71%)

August 2025 (new) phenotypic base update

The upcoming phenotypic mean (the new phenotypic base) will shift to the average calving difficulty of first-parity cows for bulls born in 2020 and maternal grandsires born in 2015, which will be approximately 1.36% and 1.76%, respectively.

The jump from 2.29% (old base) to 1.36% (new base) or the phenotypic base of bulls born in 2015 and 2020, respectively, represents a significant change. This difference is partly due to genetic progress and partly due to management improvements, such as better animal handling and increased use of sexed semen. According to the genetic trend (above), the reduction in PTAs (indicating easier calvings) was about 1%, which helps explain the shift. Prior to 2005, the trend was essentially flat.

How bulls compare to the phenotypic base

The phenotypic base is defined as the average risk of dystocia (on first-parity cows' calvings) for a group of contemporary bulls at a specific point in time.

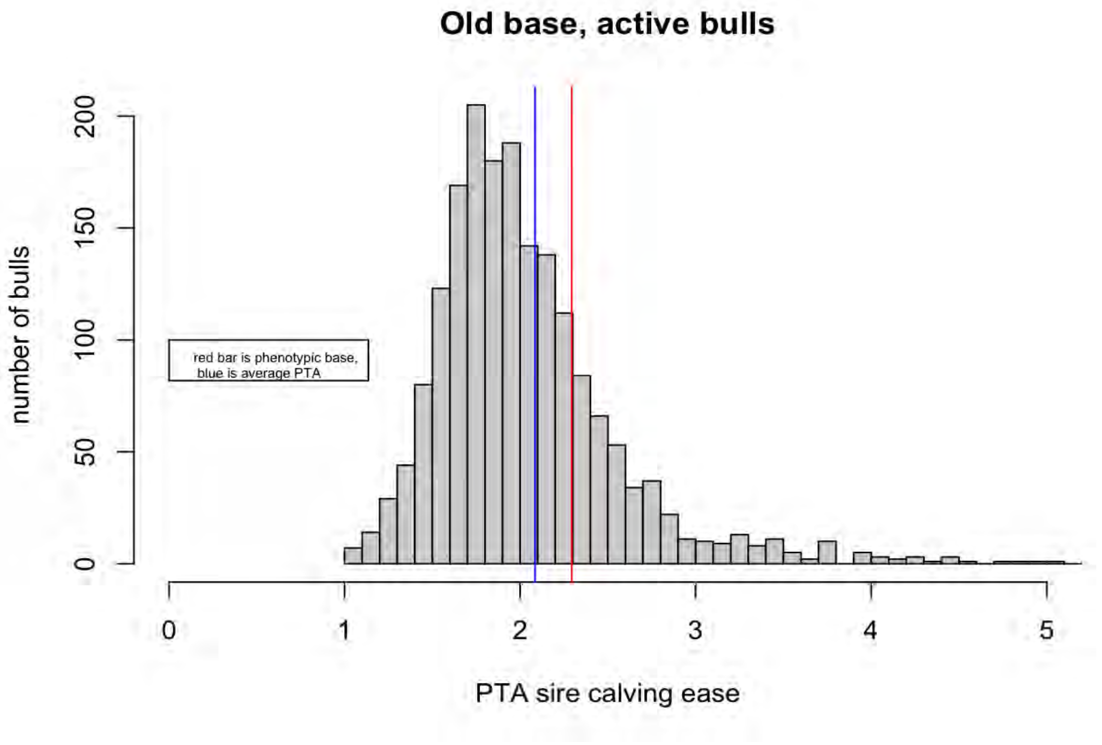
Sire calving ease (SCE) = Calves from bulls of a given birth year (new base at August 2025, set to 2020)
Daughter calving ease (DCE) = Calvings of daughters from bulls born five years earlier than those used for SCE (new base at August 2025, set to 2015).

By construction, some bulls will be above this average and some bulls will be below. If genetic selection improves the trait over time, and if the phenotypic base remains unchanged, eventually all bulls' PTAs will be better than the phenotypic base. Also, recent bulls will tend to have better PTAs than older bulls. Outlined below are the main consequences of this process.

*How **active A.I. bulls'** PTAs for SCE compare using the old base*

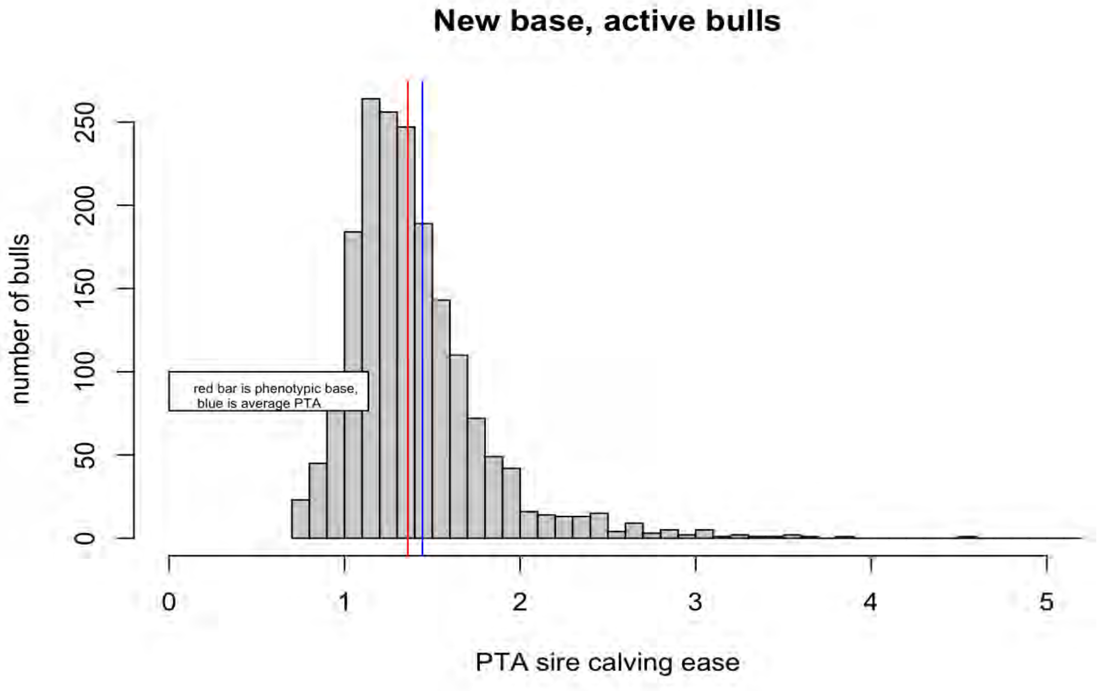
The histogram below shows the distribution of PTAs for SCE, expressed on the old genetic and phenotypic basis, for "active" A.I. bulls. Here, "active" A.I. bulls consist of both Active (A) and Genomically Tested (G) bulls.

In the plot, the red line represents the old phenotypic base, while the blue line marks the mean PTA of the active A.I. bulls. Visually, about 70% of the active A.I. bulls fall to the left of the red bar, indicating that most bulls today are slightly better (i.e., easier calving) than the bulls whose calves contributed to establishing the old phenotypic base. This is expected, as today's bulls are younger and have benefited from the ongoing genetic improvement for SCE.



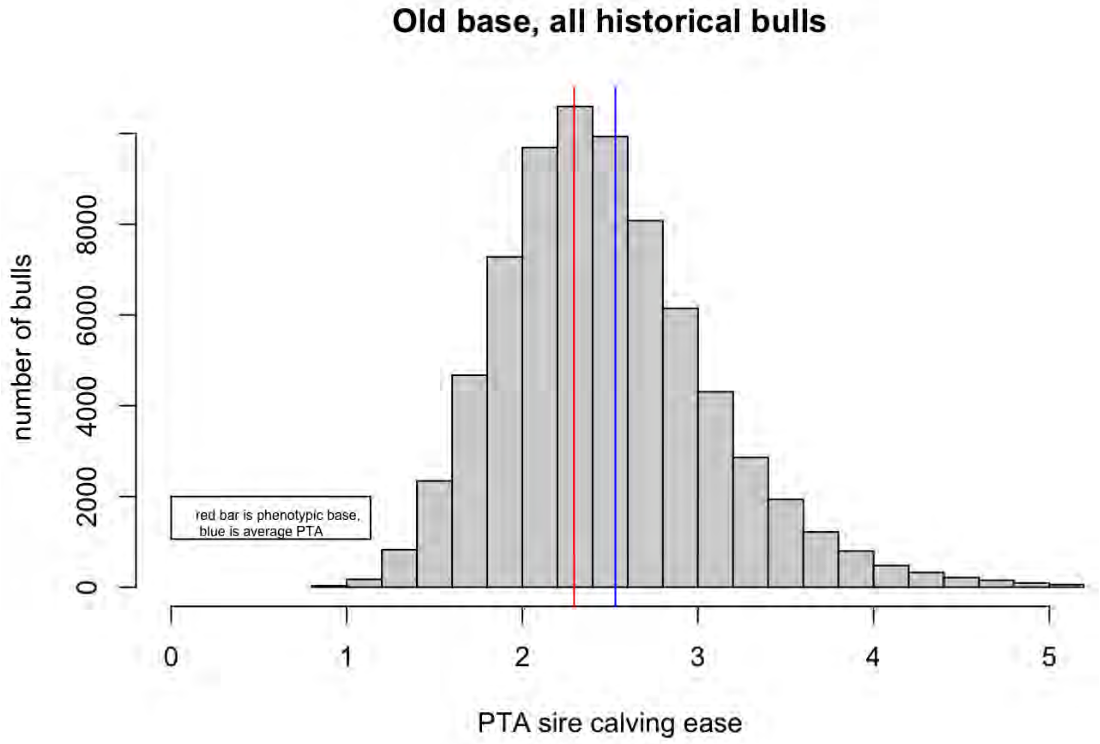
*How **active A.I. bulls**' PTAs for SCE compare using the new base*

The histogram below shows the active A.I. bulls' distribution and average PTA for SCE expressed on the new genetic and phenotypic base. In this case, the red line represents the new phenotypic base. The average PTA of the active bulls (blue line) falls almost exactly on the red one. This outcome is expected by definition: the phenotypic base for SCE reflects the average calving difficulty of calves born from contemporary bulls. As a result, 47% of the active bulls have a PTA for SCE lower than the phenotypic base.



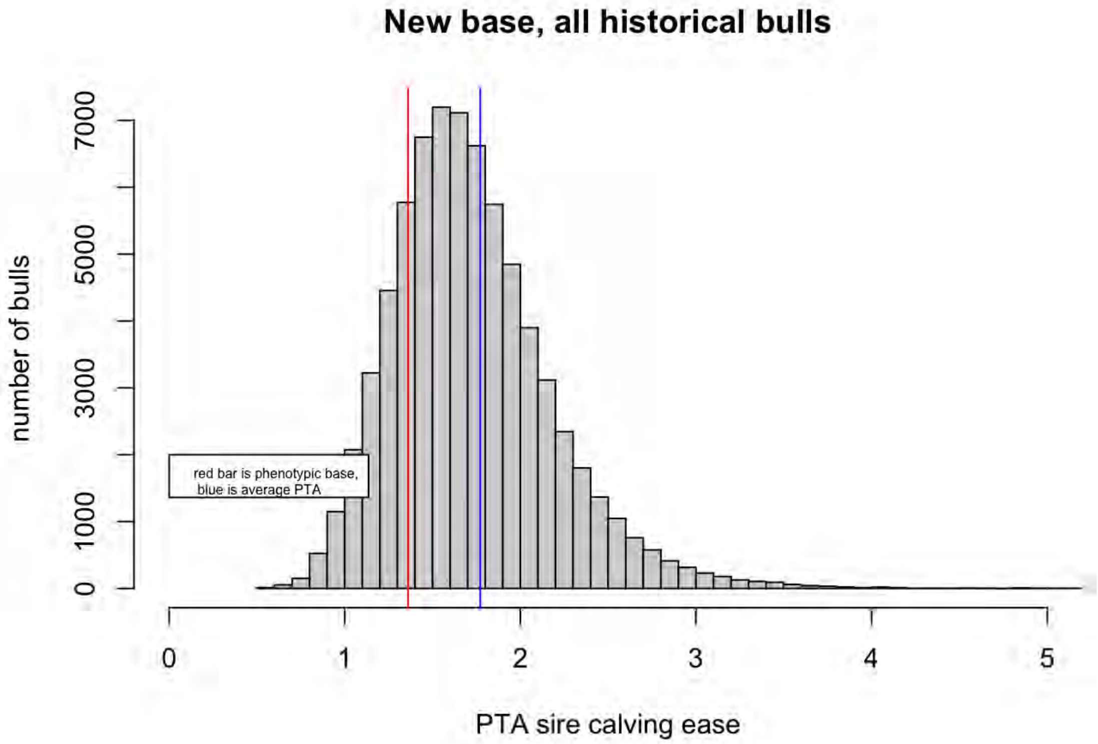
*How **all bulls'** PTAs for SCE compare using the old base*

By *all bulls*, we mean every bull with a traditional evaluation for the trait SCE. The histogram below shows the distribution of these bulls' PTAs (expressed on the old genetic and phenotypic base), with the average PTA indicated by the blue line. The PTAs are 35% to the left (better) and 65% to the right (worse) of the old phenotypic base (red line). This is expected because the phenotypic base reflects calvings from bulls born in 2015, a group that had already improved somewhat for SCE but not to the extent seen in bulls born in 2020, as illustrated in the genetic trend shown earlier.



*How **all bulls'** PTAs for SCE compare using the 2020 base*

The histogram below shows the distribution of SCE PTAs for "all" bulls expressed on the new genetic and phenotypic base. Most historical bulls (approximately 84%) are to the right (worse) relative to the phenotypic base (red line), as indicated by the average PTA (blue line) also falling to the right. This shift occurs because the new phenotypic base reflects calvings from bulls born in 2020 and therefore genetically improved compared to the ones born in 2015. The histogram below illustrates the ongoing genetic progress in SCE, with younger bulls consistently outperforming older ones.



More differences between the 2020 and 2015 phenotypic base

Upon closer inspection, there are two notable differences between the last two histograms comparing “all” bulls’ PTAs expressed in the old versus new base.

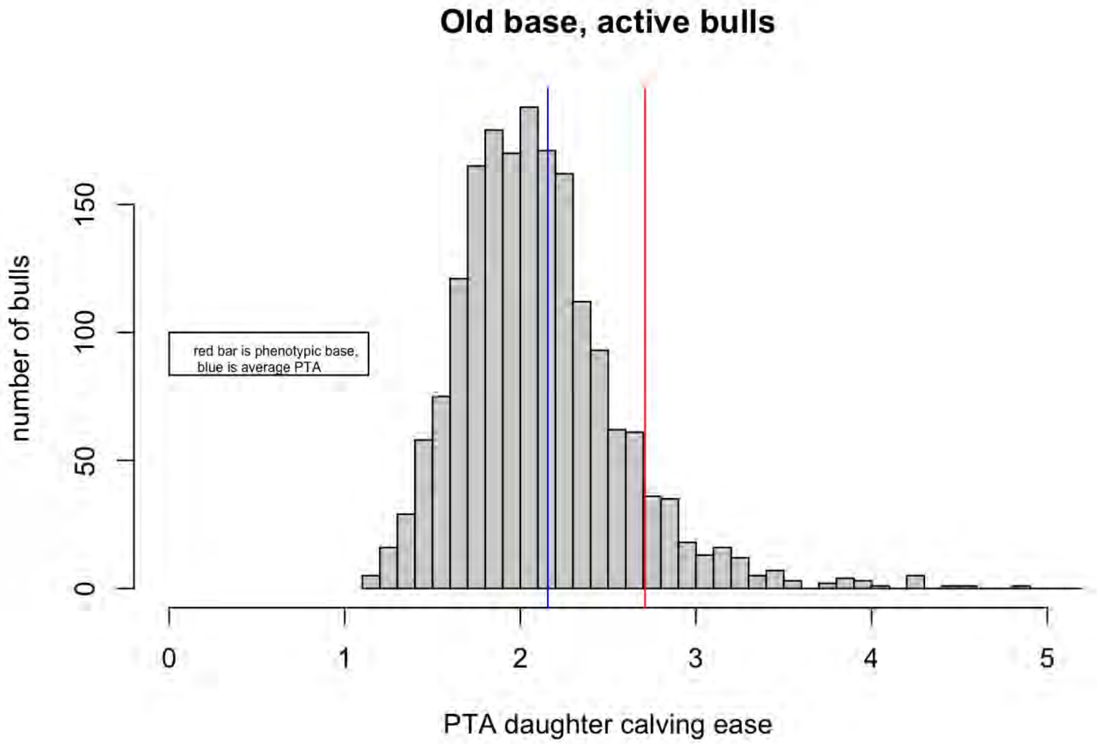
First, the average PTA of all bulls (blue line) has shifted from approximately 2.53% in the old phenotypic base to 1.77% in the new base. However, in both graphs, the blue line was computed using the same bulls. The shift reflects improved environmental conditions: the same bull used in 2020 conditions creates less dystocia than in 2015.

The second difference is the reduction in PTA variation. This results from the general reduction in dystocia rate. The less dystocia, the less variation of PTAs. If both the environment and the genetics result in (much) lower dystocia, at the limit, we could eventually reach a point where dystocia is nearly eliminated and PTAs approach zero. In fact, the differences in dystocia are now very small, with nearly all historical bulls having less than 2.5% PTA for SCE under the new phenotypic base.

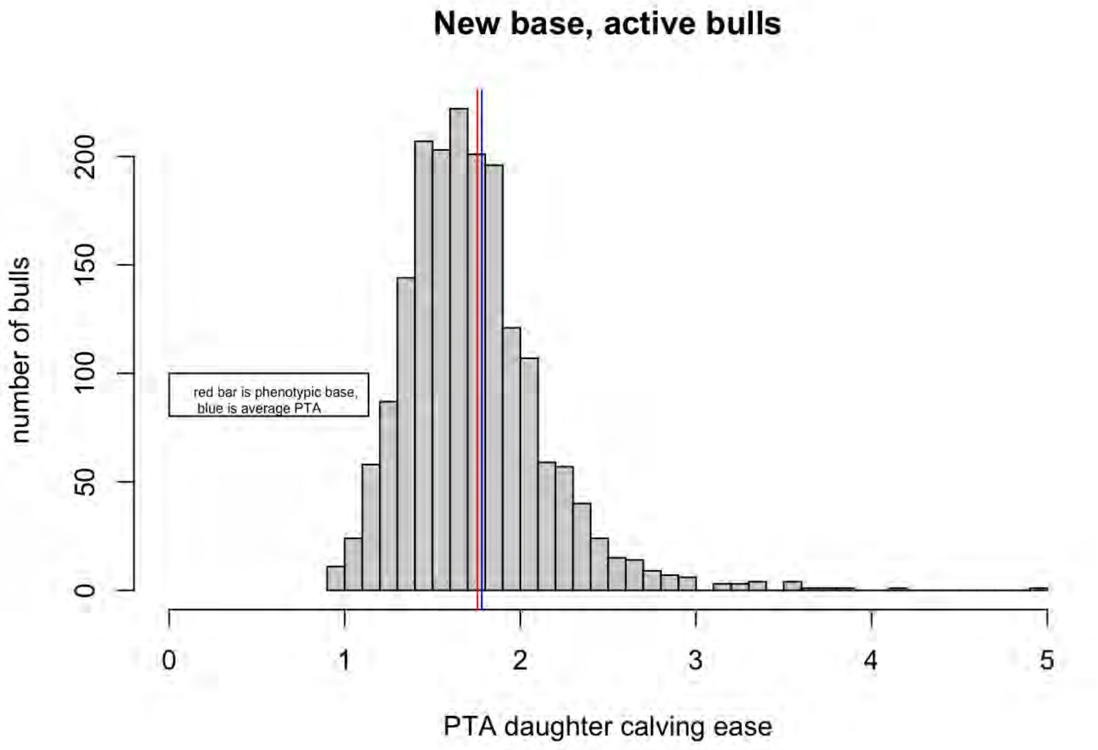
Daughter calving ease

We observe similar patterns in the change of base for the Daughter Calving Ease (DCE) trait, comparing the old base — defined by the dystocia frequency of calves with maternal grandsires born in 2010 — with the new base from calves with maternal grandsires born in 2015.

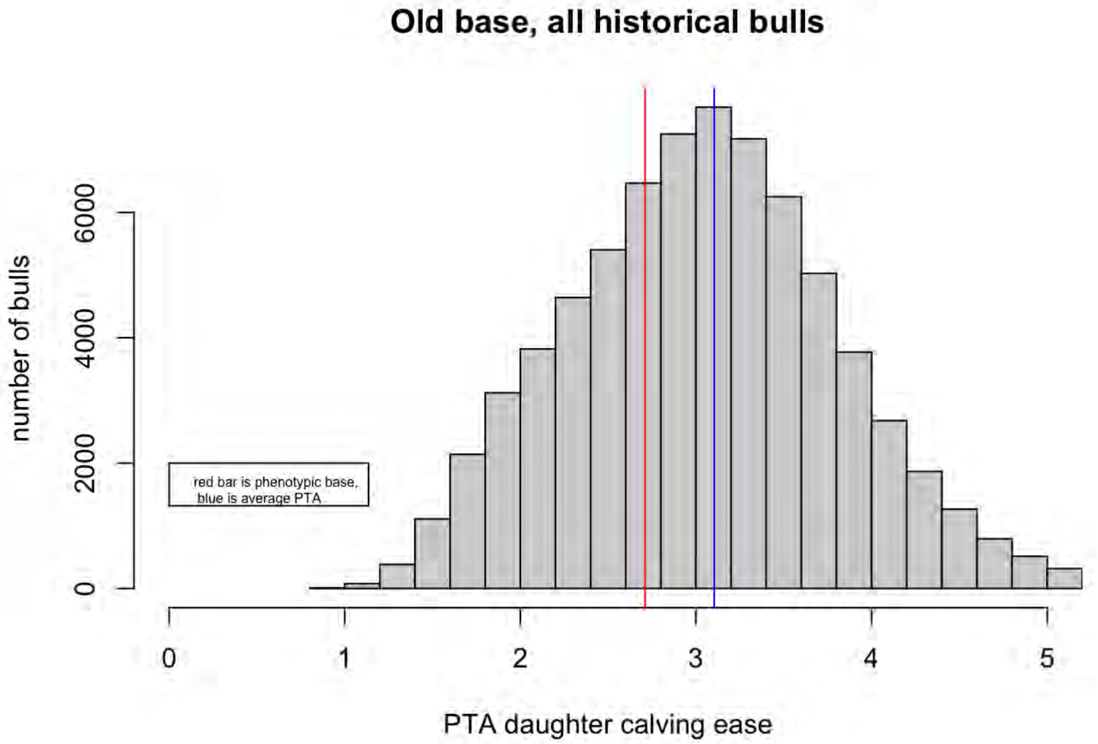
The same trend appears: active bulls PTAs are centered around the new phenotypic base (with 52% falling below the red line), while most historical bulls have higher dystocia rates than this new phenotypic base (only 11% are below the phenotypic base), reflecting the impact of genetic progress.

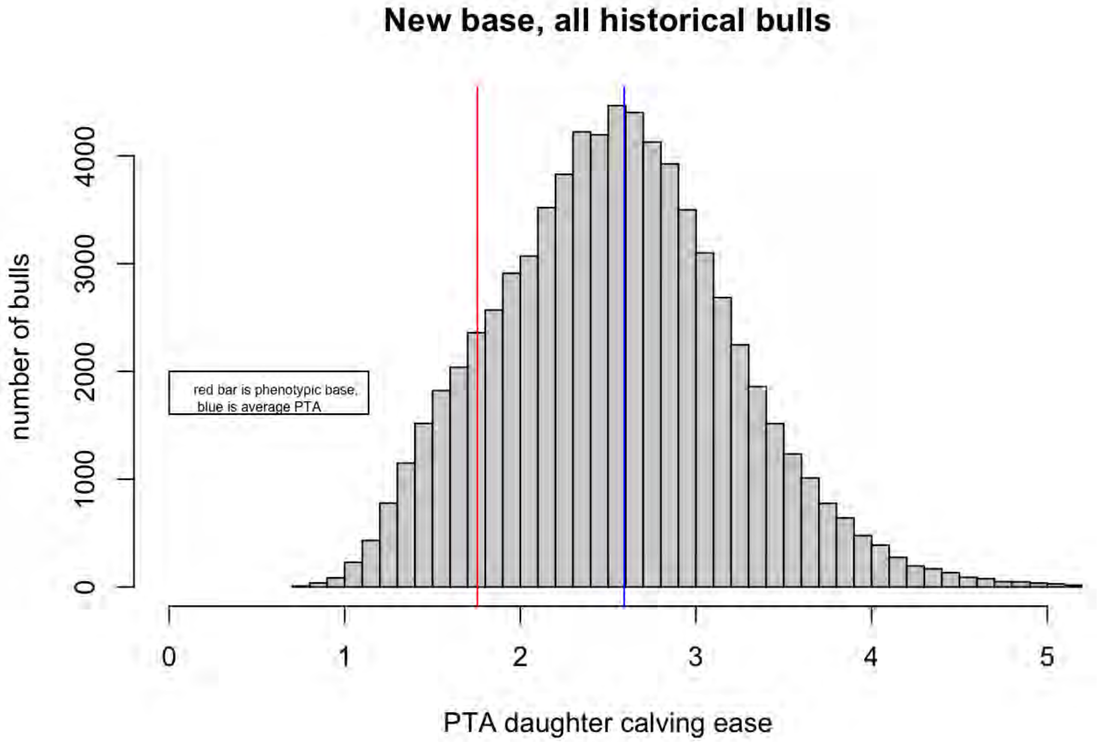


Old base, active bulls



New base, active bulls


Old base, all historical bulls
number of bulls
0
2000
4000
6000
red bar is phenotypic base,
blue is average PTA
0
1
2
3
4
5
PTA daughter calving ease


New base, all historical bulls
number of bulls
0
1000
2000
3000
4000
red bar is phenotypic base,
blue is average PTA
0
1
2
3
4
5
PTA daughter calving ease