

How genomics transformed intensive dairy genetic improvement

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Genomic selection has successfully increased rates of genetic gain for intensively managed dairy cow populations. For example, the rate of gain for protein yield has almost doubled for US Holstein bulls, and fat yield has increased by approximately 50%. Field data show that generation intervals have decreased substantially across all breeds implementing genomic selection, and they are now nearing biological limits. While these results were anticipated before genomic evaluations were introduced, the number of genotyped animals – primarily cows – has dramatically exceeded expectations. The National Cooperator Database in the US now includes more than 10 million genotypes (677,705 males, 9,452,839 females) from 56 different genotyping chips, reflecting a high level of demand for genomic PTA.

Abstract

Several factors have contributed to this success. The availability of extensive historical data collected through national milk recording systems was essential for this success, as were mature genetic evaluation programs, widespread use of artificial insemination, progeny-test programs by genetic companies, and the presence of high-value animals worth the cost of genotyping. However, these systems require a nationwide network of people and resources to operate, and it can be very challenging to make major changes. Furthermore, the perceived value of these programs is also changing as dairy farms in North America continue growing to maximize economies of scale in a commodity market.

The widespread availability of genomic information, coupled with the decreasing genotyping cost, increasing fertility of sex-sorted semen, refinement of estrous synchronization protocols, and rising beef prices has resulted in the development of very sophisticated breeding schemes that leverage embryo transfer, timed AI, sexed and conventional dairy semen, and conventional beef semen. Such integrated programs drive accelerated rates of genetic gain in lactating cows, permit precision management of replacement heifers, and produce high-value terminal beef-on-dairy calves that are very profitable. Genomics has empowered intensive dairy producers to achieve faster genetic gain than before while simultaneously increasing the value of the calves born on their farms. As dairy systems continue to evolve, genomic selection will remain a critical driver of genetic improvement and economic efficiency in the industry.

Key words: Genetic improvement, genomic selection, intensive management

Introduction

There have been three major revolutions in dairy cattle breeding since the dawn of the 20th century. The first of these is the establishment of national milk recording programs and purebred cattle associations, which collected the data that served as the foundation for genetic evaluations (Hutchins and Hueth, 2023). The second step forward was the adoption of frozen semen for artificial insemination, which made practical the dissemination of elite male genetics on a large scale (Foote, 2002). Finally, genomic selection allowed us to double the rate of genetic gain (Wiggans and Carillo, 2002). Perhaps in the future, the widespread adoption of embryo-based technologies will produce a fourth revolution (Hansen and Block, 2004). These new technologies have contributed to the growing complexity of decisions about animal breeding that can sometimes lead to suboptimal benefits (e.g., Martin-Collado *et al.*, 2018). Nevertheless, tools such as sexed semen, embryo transfer, and heifer genotyping are being used to increase dairy farm profitability.

Influence of genomic selection on rates of genetic improvement

The general concept of genomic selection was first described by Nejati-Javaremi *et al* (1997) and Meuwissen *et al* (2001), although it took some time for commercial technology to catch up with theoretical developments. Schaeffer (2006) used simulation to show that a doubling of the rate genetic gain might be achievable, which was later confirmed by García-Ruiz *et al* (2016) and Guinan *et al* (2022) using national datasets. As an example, Figure 1 shows the genetic trend for the Lifetime Net Merit \$ total merit index used in the United States. The first official genomic evaluations in the USA were released in January 2009, and the change in genetic trend is striking. A recent validation study by Toghiani *et al* (2024) used data from genotyped heifers to show that realized gains from genomics may exceed expectations in some cases. Figure 2 shows phenotypic gains partitioned into the level of production in 1970, gains from the adoption of better management practices, and increases from genetic improvement. Over the 55-year time period represented in that figure, genetics have been responsible for an average of 60% of gains, while improved management has been responsible for 40% of gains, but since 2009 genetics has averaged 67% of gains. This is a clear demonstration of the value of genetic improvement in general and genomics in particular. However, this is not a call to ignore the importance of herd management: cows cannot perform to their genetic potential in substandard environments.

The rapid adoption of genomics has resulted in shorter generation intervals (Figure 3), as predicted by Schaeffer (2006), which are now approaching biological minima. This trend is most pronounced for bulls, which showed an immediate and rapid decrease. Generation intervals have also decreased on the female side of the pedigree, but that trend has been more gradual. At this point, generation intervals are unlikely to decrease further without the use of advanced laboratory approaches (e.g., Goszczynski *et al.*, 2019). This has resulted in the collection of semen from bulls at younger ages than before, as well as the collection of oocytes from heifer calves for use in embryo transfer programs. A potentially unanticipated consequence has been the need for artificial insemination companies to collect semen from a larger cohort of young bulls than in the past because semen volume and quality is lower from juvenile animals.

Factors enabling the success of genomic selection

Several characteristics of dairy cattle populations make them an ideal use-case for genomic selection (Wiggans *et al.*, 2017; Wiggans and Carillo, 2022). Extensive historical data are available in many Western countries, which have milk-recording programs that date back to the end of the 19th century. National genetic evaluation systems use those data in concert with progeny-test programs to produce genetic

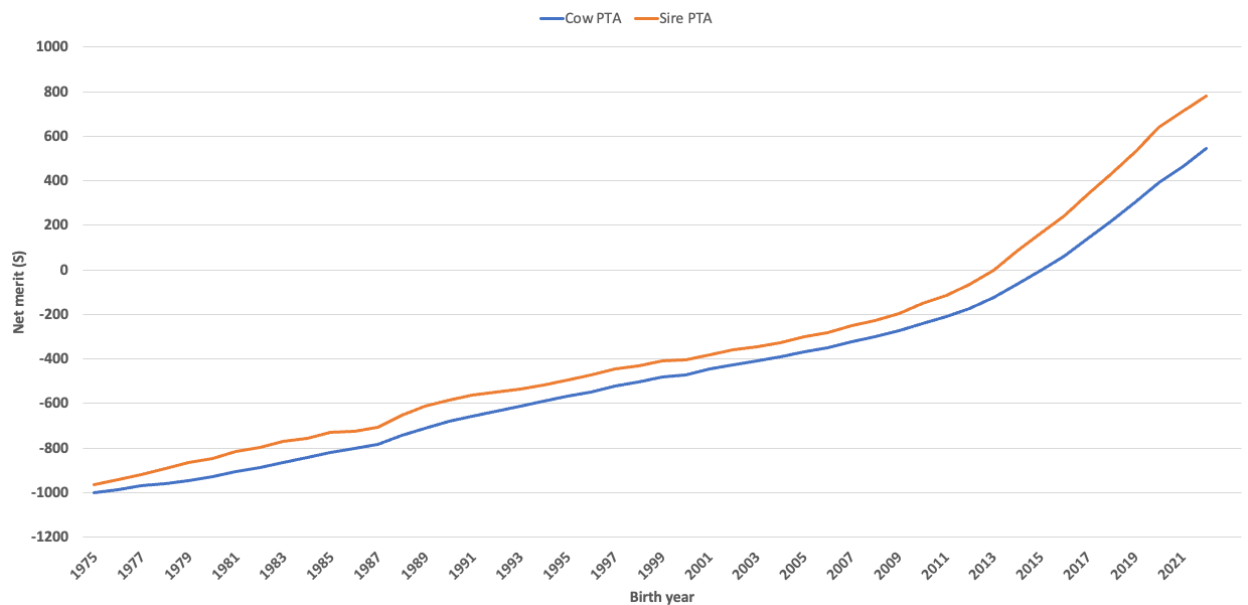


Figure 1. Genetic trend for Lifetime Net Merit \$ in US Holstein bulls (orange) and cows (blue) born between 1975 and 2022 based on December 2024 genomic evaluation run (Source: <https://webconnect.uscdcb.com/#/summary-stats/genetic-trend>).

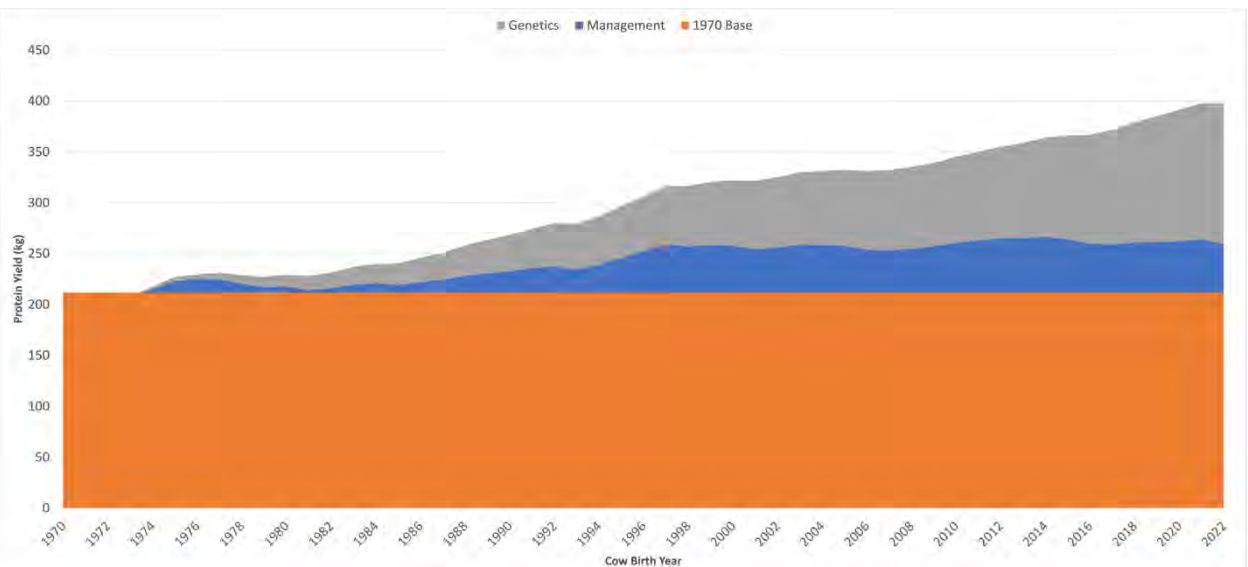


Figure 2. Phenotypic trend in protein production (kg) for US Holsteins partitioned into the 1970 level of production (orange), improvement due to management (blue), and gains due to genetic improvement (grey).

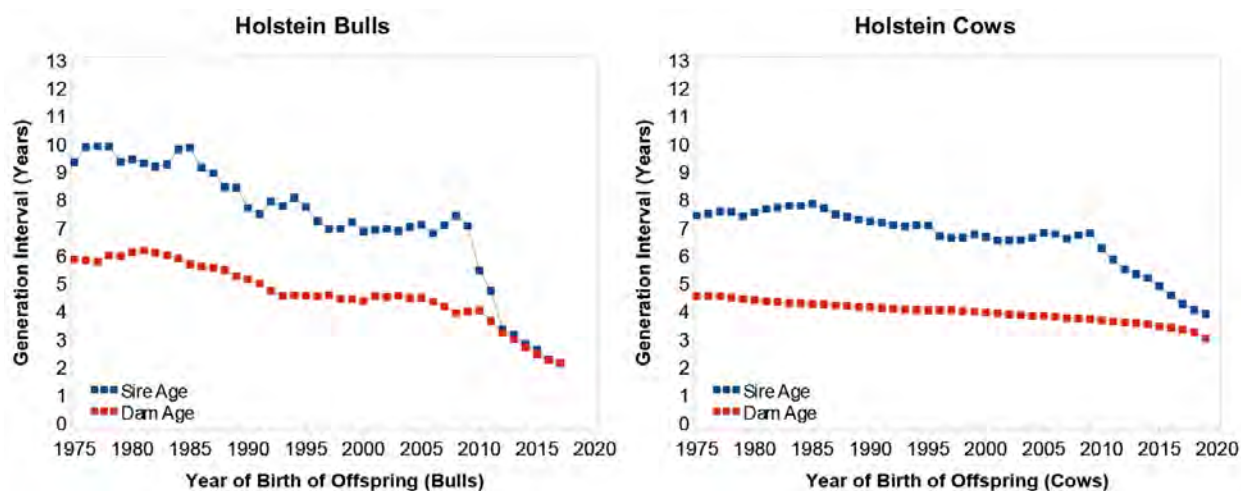


Figure 3. Generation intervals in year of sires (blue) and dams (red) of US Holstein bulls and cows (Source: Guinan et al., 2022, <https://doi.org/10.3168/jds.2022-22205>).

evaluations for bulls which produce semen for use in artificial insemination, which is widespread. Individual animals have high values, and the cost of genotyping is low relative to the cost of producing a replacement. Finally, cattle have long generation intervals that can be reduced substantially by genomics. Countries that adopted genomics early also had bio-banks of frozen semen, which made it possible to construct predictor bull populations from animals with high traditional reliabilities, which could then be genotyped and used to estimate single nucleotide polymorphism (SNP) effects. While genetic improvement at the population level is driven principally by sons of sires, cows in commercial dairy herds are commonly used to breed replacement animals, so genotyping costs are often justified by their use in improving the genetic potential of replacements.

Ultimately, genomic selection has been successful because herds with better genetics have lower production costs and are therefore more profitable than their contemporaries. A difference between herds of \$447 in PTA NM\$¹ means the cows in the better herd will average \$894 more net profit over their lifetime. Assuming that cows produce 26,264 pounds² of milk per lactation on a 305 d age-adjusted basis and average 3 lactations, they will make 78,492 lbs (784.92 cwt) of lifetime milk³. If the cost of production is \$21.64⁴, then a cow in the herd with better genetics has a lifetime production cost of \$16,091.01 versus an average cow \$16,985.67. This translates to a production cost of \$20.50 per cwt $[(784.92 \text{ cwt} \times \$21.64/\text{cwt}) - \$894.00] / 784.92 \text{ cwt}$ in

¹This is 1.96 SD of NM\$ on a PTA basis (VanRaden et al., 2025).

²English units of measurement are used in this example instead of SI units because milk pricing in the USA is based on hundred-weights (cwt) of milk in pounds.

³Average 305-AA standardized lactation yield for USA Holstein cows (<https://webconnect.uscdcb.com/#/national-performance-metrics>).

⁴October 1, 2024 values for the State of Wisconsin from the United States Department of Agriculture's Economic Research Service (<https://www.ers.usda.gov/data-products/milk-cost-of-production-estimates>).

the herd with better genetics, an advantage of \$1.14 (5.26%). In a low-margin business such as dairying, a 5% advantage in production costs can be substantial over time.

Figure 4 demonstrates the rapid adoption of genotyping by dairy producers. This was a surprise to many of us because we initially assumed that only genetics companies would be interested in genotyping bulls, and possibly a few embryo donors. The rate of bull genotypes is constant over time because the numbers of bulls does not change very much from year to year. However, the number of cows genotyped has increased each year and shows no signs of slowing. These genotypes have been used in concert with other management tools, including sexed, conventional, and beef semen and embryo transfer to develop sophisticated strategies for maximizing farm profit.

The production of crossbred beef-sired calves (Berry, 2021) represents an appealing source of revenue when replacement heifers are readily available through sexed semen and USA beef prices are very high because of a substantial reduction in the size of the national beef herd. Cabrera (2022) recently described several situations in which the use of beef-on-dairy matings are beneficial to USA dairy producers. They proposed that beef-on-dairy is a desirable strategy when a herd's reproductive performance is better than average, when crossbred beef calves are more valuable than dairy calves, and when a herd has the opportunity and willingness to buy and sell calves. The greatest returns are seen when beef semen is used in combination with sexed dairy semen, a pattern which is generally consistent across breeds (Ettema *et al.*, 2017; Clasen *et al.*, 2021) and production systems (Ruelle *et al.*, 2021; Pereira *et al.*, 2024).

Impact of genomic tools on farm management

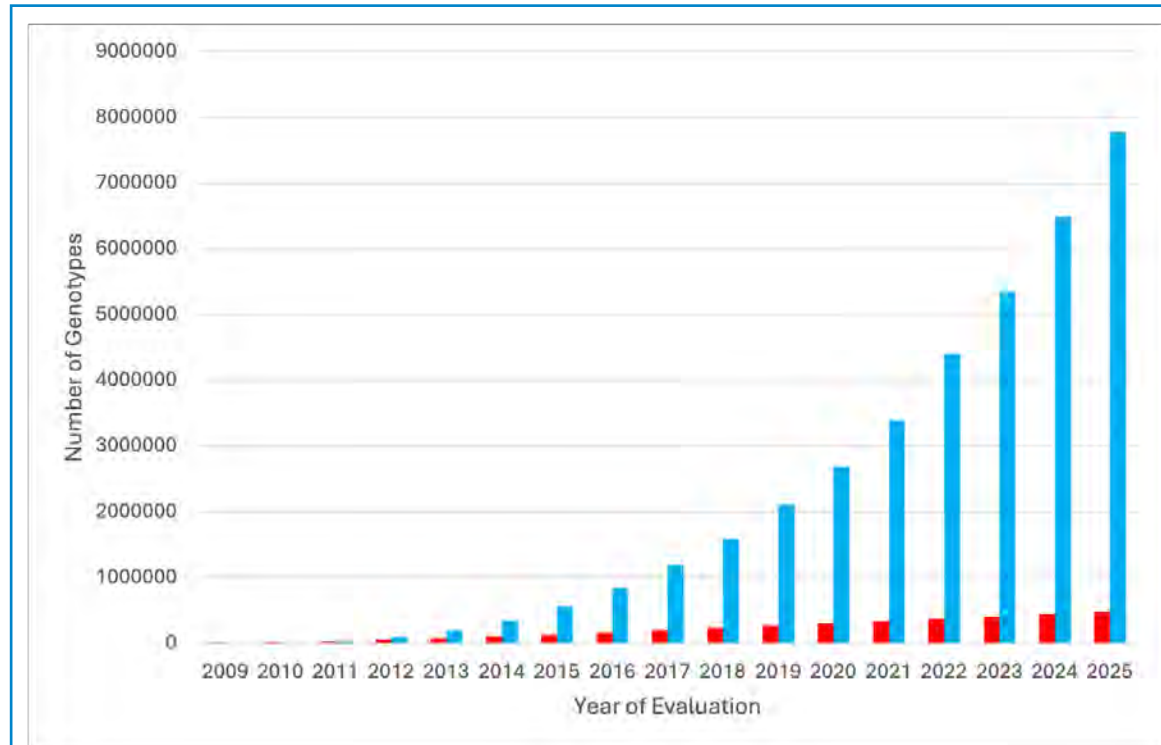
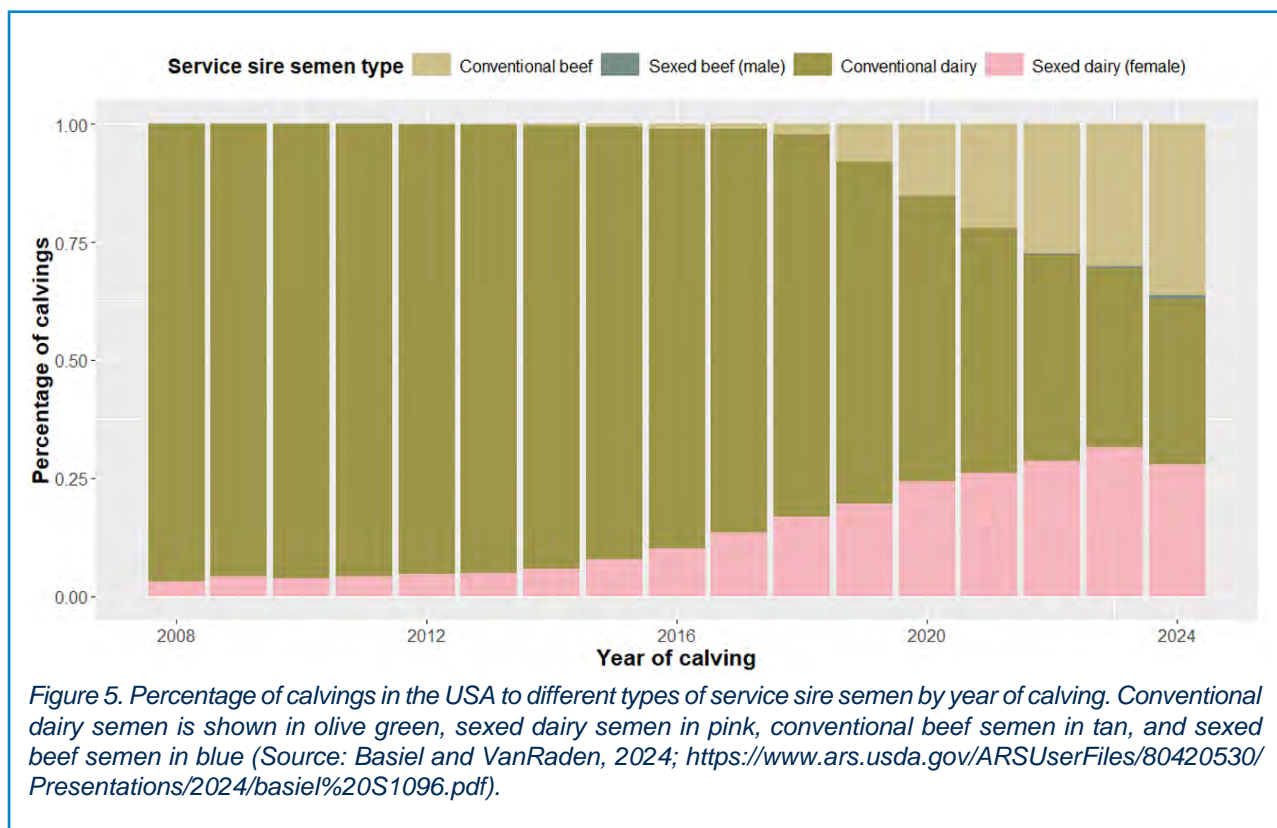


Figure 4. Holstein bull (red) and cow (blue) genotypes included in US national genomic evaluations, 2009–2025 (Source: <https://webconnect.uscdcb.com/#/summary-stats/genotype-count/evaluation-run>).



Basiel and VanRaden (2024) have recently described some of these strategies as they are used in the USA, including their impacts on semen type allocation and the genetic merit of resulting offspring. The production of sexed semen has increased steadily (Seidel and DeJarnette, 2022) since 2006, and is used principally to produce female-sorted units. This lets dairy farmers to meet their replacement needs with fewer matings, allowing them to . Over the last several years, there has been a clear shift from conventional dairy semen accounting for >95% of matings, to the current mix of conventional dairy, female-sexed dairy, and conventional beef semen in roughly equal portions (Figure 5). Male-sexed beef semen is available in limited quantities but does not yet account for many matings. Farms that genotype their heifers are also more likely to use advanced mating strategies (Basiel and VanRaden, 2024), which is consistent with the findings of Wellmann *et al* (2024) that herds can maximize revenue by genotyping their heifers and using that information to inform mate allocation decisions.

About 11% of dairy herds in the USA use embryo transfer, with larger herds (>500 animals) using it at higher rates than small (<100 animals) herds (United States Department of Agriculture, 2018). Fuerniss *et al* (2023) showed that beef embryos gestated by Holstein and Jersey recipients had more moderate frames sizes and more muscular phenotypes than beef-on-dairy crossbred calves, suggesting the use of embryo transfer may produce more valuable calves than the use of beef semen on dairy dams.

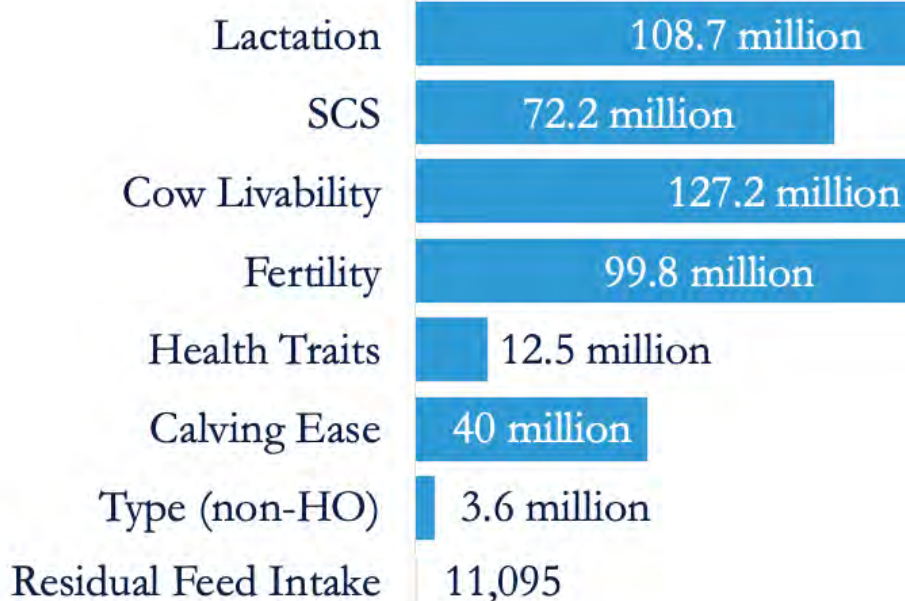


Figure 6. Number of records for different phenotypes in the US National Cooperator Database as of January 2025 ('HO = Holstein and SCS = Somatic cell score).

When genomics was first introduced, there was a lot of discussion about the need for continued data collection, with many people asking if phenotyping costs could be reduced. While this is a question that should be discussed, it is now clear that ongoing data collection is essential for continued genetic improvement (Gonzalez-Recio *et al.*, 2014). In most countries with intensive dairy production systems, national databases continue to grow, both in terms of records associated with “traditional” phenotypes and observations of new traits (e.g., Figure 6).

The development of new technologies and changes in demand for replacement heifers and beef steers has led many dairy producers to develop complex strategies which use a variety of reproductive tools to increase farm revenue. These alternative sources of revenue have been very important for USA farmers during a time of volatile milk prices that have often been lower than the cost of production. Embryo transfer is sometimes used to produce replacements but the use of purebred beef embryos remains relatively uncommon. The adoption of artificial insemination in the 1950s and 1960s and genomic selection in the late 2000s were very high in the USA because the value to farmers and genetic companies was clear. Future technologies will also have to demonstrate clear financial benefits if they are to be as successful.

Discussion and conclusions

The example of how better genetics translates to lower production costs is based on a presentation by Dr. Thomas J. Lawlor of Holstein Association USA (Brattleboro, Vermont, USA).

Acknowledgment

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