# Current genomic applications for improved reproductive performance in beef and dairy

Kent J. Andersen, Jason B. Osterstock
Zoetis
Centennial, CO

## Abstract

Genetic improvement in beef and dairy cattle reproductive traits has historically been hampered by the availability and accuracy of applicable genetic predictions. Reproductive trait phenotypes are generally time-consuming to measure, categorical and/or threshold in nature, often are not collected in the context of inventory-based performance recording systems, and typically of lower relative heritability. Introduction of the Illumina® Bovine SNP50 BeadChip, and subsequently other related genotyping platforms, has provided useful marker information for inclusion in beef and dairy genetic evaluations and performance programs. Increasingly, marker information is used to authenticate recorded pedigree information or assign parentage, enhance the non-parent accuracy of Expected Progeny Differences (EPD) and Predicted Transmitting Abilities (PTA), derive and manage haplotypes affecting fertility, as well as help manage inbreeding. In Angus seedstock, Genomic-Enhanced (GE) EPD and/or genomic predictions for the following reproductive traits are computed weekly by Angus Genetics Inc. (AGI): Calving Ease Direct (CED), Scrotal Circumference (SC), Heifer Pregnancy (HP), and Calving Ease Maternal (CEM). The average GE accuracy values associated with Angus non-parent GE-EPD for CED and SC are .31 to .36, respectively. In Holsteins, genomic-enhanced PTA (GPTA) computed by the Council on Dairy Cattle Breeding (CDCB) are available for the following major reproductive traits and indexes: Daughter Pregnancy Rate (DPR), Productive Life (PL), Sire Calving Ease (SCE), Daughter Calving Ease (DCE), and Net Merit (NM$). The reliability values for non-parent dairy reproductive trait GPTA range from .49 to .66 for tested Holstein heifers, as compared to .23 to .28 for untested animals. Enhanced accuracy and reliability values enable increased response to selection and commercial productivity.

**Keywords:** Angus, Holstein, genomics, accuracy, reliability

## Introduction

Notable production and economic losses are incurred across the beef and dairy industries due to females with untimely or failed conception and/or calving difficulty. In beef cattle, the calving percentage ─ proportion of exposed females that calve ─ is documented as 91.5 percent.[1] In beef herds with 200 or more cows, pregnancy status and other reproductive problems accounted for 47.9 percent of cow culling decisions, and 20.0 percent of cull cows were sold because of reproductive failure at less than five years of age.[1] Among beef heifers and cows, 11.6 and 4.3 percent, respectively, required some level assistance during calving.[1] Reproductive problems were the highest ranking category of reasons why dairy cows were permanently culled, and accounted for 26.3 percent of removals.[2] Almost one in five (17.2%) dairy calves required assistance during delivery, and 6.5% were either born dead or died prior to 48 hours of age.[2] Both environmental and genetic factors contribute to reproductive outcomes in beef and dairy cattle. Increasingly, genomic technology is available to enhance the dependability of genetic predictions for reproductive and calving performance, to help reduce associated economic losses.

Since shortly after introduction of the Illumina® BovineSNP50 Genotyping BeadChip[3] in 2008, leading beef and dairy cattle breed associations and genetic evaluation service providers have incorporated marker information into their genetic evaluations and performance programs. Specifically, of the various beef and dairy breeds, such integration of genomic information is most advanced and has been of most commercial impact in Angus and Holstein, respectively. While initial use of genomic-enhanced breeding information was centered on seedstock, there is now growing adoption by commercial users of Angus genetics and dairy producers with non-registered Holsteins. The purpose of this paper is to describe current use of marker information to improve the accuracy of selection, mating and marketing decisions for improved reproductive performance and calving ease in these breeds.

## Materials and methods

Collaboration among respective breed associations, genetic evaluation service providers, research and development personnel and genomic companies was and remains the key to unlocking the benefits of genomic technology. Cooperation among these entities was essential for appropriate technical integration of evolving marker information, along with continuously accumulating pedigree and performance data, into the existing beef and dairy genetic evaluation infrastructure. This integration into evaluation systems used and trusted by breeders and commercial producers was critical for adoption.

While the Illumina® BovineSNP50 Genotyping BeadChip that included just over 54,000 markers (typically referred to as 50K) was the foundational technology from which current genomic-enhanced predictions were developed, other lower density commercial genotyping platforms ranging from roughly 3,000 to 20,000 markers are now widely used in the dairy industry, particularly as applied to females that are less influential in the population. A process called imputation is then employed, whereby lower density marker information from tested animals is used to effectively infer their unknown genotypes to the higher 50K density. The impact of this strategy is that the costs of acquiring genotypes can be reduced while still affording the benefits of higher density genomic data; namely, greater accuracy of genomic predictions. As of July 29, 2013, across all dairy breeds and genotyping platforms, marker information from 439,528 animals contributed to the most recent dairy evaluations, with Holstein comprising 382,386 head of that total.[4] In contrast, while the total number of beef animals commercially genotyped across major breeds on comparable platforms is not documented, approximately 35,000 Angus animals are known to have been commercially genotyped on the 50K platform.

There are a number of different methods currently used to integrate genomic information into beef and dairy cattle genetic evaluations. In Angus, externally calibrated molecular breeding values (MBV) are incorporated as correlated traits. The higher the correlation between the MBV for a given trait and performance phenotypes, the greater the boost in accuracy associated with GE-EPD versus traditional EPD. In dairy genetic evaluations including Holstein, marker genotypes are primarily used along with recorded and verified parentage and production data to more precisely quantify pedigree relationships and gene sampling in the computation of Genomic Predicted Transmitting Abilities (GPTA). It follows that a valuable feature of genomic testing in beef and dairy cattle includes the verification or correction of recorded parentage, as well as the assignment of candidate parents, as is the case in multiple-sire breeding schemes. As well, primarily for more informed mating decisions, marker information is used in dairy to quantify inbreeding and assess carrier status for important haplotypes affecting fertility.

## Results and discussion

Angus Genetics Inc. computes GE-EPD on a weekly basis for 14 traits, including the reproductive measures CED and SC[5] (Table 1). The correlations between MBV from 50K and expressed performance for CED and SC, estimated and used in genetic evaluation by AGI, are .61 and .73, respectively. These correlations indicate that 37 percent of the additive genetic variation for CED and 45 percent for SC, are explained by the marker information. When 50K marker information is incorporated into GE-EPD along with verified parentage, the average accuracy achieved in non-parent animals is .31 and .36 for CED and SC, respectively. In contrast, animals with only pedigree information are assigned an accuracy of .05 in the genetic evaluation conducted by AGI.

To help Angus seedstock producers and commercial users of Angus genetics better understand the increased accuracy due to integration of 50K information and verified parentage, AGI and Zoetis approximated the number of progeny with associated performance information in genetic evaluation that would be required to achieve equivalent accuracy.[6] The number of progeny equivalents associated with the accuracy of non-parent GE-EPDs from HD 50K tested animals for CED and SC was approximated to be 21 and 11, progeny respectively. It follows that this added accuracy from 50K marker information is roughly equivalent to a typical yearling bull's first calf crop with calving ease score information and sons with yearling scrotal circumference data incorporated into traditional EPDs.

In addition to GE-EPDs for CED and SC, genomic predictions for HP and CEM were developed through collaborations between AGI and genomic companies, and are provided for 50K tested animals. Genomic predictions for these traits are expressed as Percent Ranks, benchmarked against tested Angus reference populations. Lower Percent Ranks indicate more desirable genetic merit for likelihood of successful HP and unassisted CEM. Eventually, it is anticipated that the EPD that are also available for these traits will be genomic enhanced. In the meantime, selection of young animals for improved HP and CEM must be based on pedigree-based EPDs and separate genomic Percent Ranks for these traits.

Genetic evaluations that incorporate genomic information for dairy cattle are provided on a monthly basis by the CDCB for the following reproductive and calving traits: PL, HCR, Cow Conception Rate (CCR), Daughter Pregnancy Rate (DPR), Sire Calving Ease (SCE), Daughter Calving Ease (DCE), Sire Still Birth (SSB), Daughter Still Birth (DSB), and Sire Conception Rate (SCR). Along with predictions for other economically relevant production, health and type traits, PTA for these traits also contribute to a variety of bio-economic selection indexes, including: NM$, Cheese Merit (CM$), Fluid Merit (FM$) and Calving Ability (CA$). The USDA-Animal Improvement Programs Laboratory routinely provides comparative average reliability values associated with GPTA from traditional versus genomic evaluations for a subset of these traits and indexes, including NM$, PL, DPR, SCE and DCE.[7]

Accuracy and reliability values associated with beef EPD and dairy PTA, respectively, quantify the relationship between predicted and actual genetic merit. While calculated differently and possessing different statistical properties (given similar amounts of information, accuracy is lower than reliability), each range from zero to .99. The higher the accuracy or reliability value, the less likely an EPD or PTA is to change as additional individual or progeny performance information accumulates.

Following each official dairy genetic evaluation provided by the CDCB, comparisons of average percent reliability associated with certain trait PTA for traditional as compared to genomic enhanced predictions are published for various classes of animals.[7] For the major reproductive traits (PL, DPR) and NM$ index, on average the reliability values associated with genomic PTA (GPTA) were .41 units higher in Holstein heifers (.62 to .66 versus .22 to .25, depending on the trait/index) than traditional PTA based on parent average (Table 2). Relative to sire and daughter calving ease (SCE and DCE), the GPTA for these animals had average associated reliability values that were .26 units higher (.28 and .23 versus .54 and .49, for SCE and DCE, respectively).

In addition to GPTA for reproductive traits, important haplotypes impacting fertility in Holstein, Jersey, Brown Swiss and Ayrshire have been identified through high density genomic testing. A haplotype is a segment of the single strand of DNA that parents pass to offspring through oocyte and sperm cells, detected by combining genomic marker information from progeny and parents.[8] Nine different haplotypes, or chromosome segments, that are not found in the homozygous state have been identified (Table 3). Inheritance of two copies of the detrimental version of these haplotypes, one from each parent, results in failed conception or early embryonic loss. The exact biological pathways related to fertilization and embryo development impacted by these haplotypes are unknown. Five of these haplotypes were found in Holstein (frequency of .7 to 4.8 percent).[9] Fertility haplotype information is reported to customers, included in GPTA for associated traits and indexes, and included in computerized mating programs.

## Conclusion

Genomic technology for improved reproductive performance and calving ease in beef and dairy cattle has increased the accuracy and reliability values associated with genetic predictions for young, non-parent animals. In beef cattle, adoption of genomic technology by Angus seedstock producers has increased in response to demand from commercial users of Angus genetics for yearling bulls that have more dependable GE-EPD. Early and aggressive adoption of genomic technology in dairy cattle by the A.I. industry has now spread to increased use by commercial producers for improved accuracy of replacement heifer selection, mating, and application of various reproductive technologies for increased productivity.

Table 1. High Density 50K for Angus impact on EPD, accuracy values, associated progeny equivalents and interpretation of HD 50K percentile ranks.

| Trait | Correlation (%GV) for GE-EPDs[1] | Average (+/-) EPD Change[2] | Average Accuracy[3] | Progeny Equivalents[4] | HD 50K Percent Rank Interpretation |
|---|---|---|---|---|---|
| Calving Ease Direct (CED) | .61 (37) | 3.0 | .31 | 21 | Lower Number, Easier Calving |
| Birth Weight (BW) | .64 (41) | 0.8 | .35 | 11 | Lower Number, Lower BW |
| Weaning Weight (WW) | .54 (29) | 3.0 | .29 | 19 | Lower Number, Heavier WW |
| Yearling Weight (YW) | .66 (44) | 5.0 | .32 | 22 | Lower Number, Heavier YW |
| Dry Matter Intake (DMI) component of Residual Average Daily Gain (RADG) | .59 (35) | 0.03 | .26 | 10 | Lower Number, Higher RADG |
| Residual Feed Intake (RFI) | NA | NA | NA | NA | Lower Number, More Efficient |
| Yearling Height (YH) | .70 (49) | 0.13 | .35 | 9 | Lower Number, Taller YH |
| Scrotal Circumference (SC) | .73 (53) | 0.23 | .36 | 11 | Lower Number, Larger SC |
| Docility (Doc) | .67 (45) | 5.0 | .30 | 10 | Lower Number, Calmer Doc |
| Heifer Pregnancy (HP) | NA | NA | NA | NA | Lower Number, Higher HP |
| Calving Ease Maternal (CEM) | NA | NA | NA | NA | Lower Number, Easier Calving |
| Milking Ability (Milk) | .38 (14) | 2.0 | .20 | 15 | Lower Number, More Milk |
| Mature Weight (MW) | .51 (26) | 11.0 | .25 | 7 | Lower Number, Heavier MW |
| Mature Height (MH) | NA | NA | NA | NA | Lower Number, Taller MH |
| Carcass Weight (CW) | .57 (32) | 5.0 | .19 | 6 | Lower Number, Heavier CW |
| Marbling Score (Marb) | .63 (40) | 0.12 | .31 | 16 | Lower Number, More Marb |
| Ribeye Area (RE) | .63 (40) | 0.10 | .25 | 9 | Lower Number, Larger REA |
| Fat Thickness (Fat) | .53 (28) | 0.01 | .25 | 11 | Lower Number, Less Fat |
| Tenderness (Tend) | NA | NA | NA | NA | Lower Number, More Tender |

[1] Correlation between HD 50K genomic predictions and expressed performance, and associated percent explained additive Genetic Variation (GV) – Genomic Update January 2013, American Angus Association/Angus Genetics Inc.

[2] Average absolute change in EPD versus GE-EPD from 50K for non-parent animals – Fast Forward EPDs, Accuracy Values Quick Tips, Zoetis and Angus Genetics Inc.

[3] Average accuracy of GE-EPDs from 50K based on verified parentage and 50K information – Fast Forward EPDs, Accuracy Values Quick Tips, Zoetis and Angus Genetics Inc.

[4] Approximate progeny equivalents associated with accuracy of GE-EPDs based on pedigree and 50K information. Progeny equivalents for carcass traits are actual progeny carcass records – equates to ultrasound scans from over 30 progeny

NA (Not Available) – designates that either an EPD is not available for the trait (RFI, Tend) or that 50K information for the trait is not yet directly integrated into the EPD (HP, CEM, MH)

Table 2. Comparison of percent reliability values associated with PTA from the April 2013 genomic and traditional evaluation of Holstein heifers (n=174,003).

| **Trait** | **Reliability (%)** | | |
|---|---|---|---|
| | **Genomic average** | **Traditional average** | **Difference**[1] |
| Net merit (NM$) | 66 | 25 | 41 |
| Productive life (PL) | 63 | 22 | 41 |
| Daughter pregnancy rate (DPR) | 62 | 22 | 40 |
| Sire calving ease (SCE) | 54 | 28 | 26 |
| Daughter calving ease (DCE) | 49 | 23 | 26 |

[1] Genomic minus traditional.

Table 3. Identified haplotypes impacting fertility in Holstein, Jersey, Brown Swiss and Ayrshire breeds.

| Breed | Haplotype Name | Carrier Frequency | Impact on Conception Rate | Impact on Return Rate | Earliest Known Ancestor(s) |
|---|---|---|---|---|---|
| Holstein | HH1 | 4.5% | -3.1% | -1.1% | Pawnee Farm Arlinda Chief |
| | HH2 | 4.6% | -3.0% | -1.7% | Willowholme Mark Anthony |
| | HH3 | 4.7% | -3.2% | -3.1% | Grey View Skyliner & Glendell Arlinda Chief |
| | HH4 | 0.7% | -3.0% | | Besne Buck |
| | HH5 | 4.8% | -3.5% | | Thornlea Texal Supreme |
| Jersey | JH1 | 23.4% | -3.7% | -3.7% | Observer Chocolate Soldier |
| Brown Swiss | BH1 | 14.0% | -3.4% | -2.5% | West Lawn Stretch Improver |
| | BH2 | 20.5% | 0.3% | | Rancho Rustic My Design |
| Ayrshire | AH1 | 26.1% | -4.4% | | Selwood Betty's Commander |

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