

Progress Requires Change

A great step of progress in dairy cattle improvement was taken with the December 2018 genomic evaluations, which utilize the more robust 80k SNP and the new-and-improved genome assembly. With progress, change can be expected, and production traits and Net Merit for some bulls may be noticeably affected in the December evaluations.

In recent comparison of results based on 60k or 80k SNP, there was no noticeable trend in the general population or among all the young genomic bulls within any breed. Some variation could be observed only in single top young genomic bulls. However, when comparing August to December individual results, a reduced trend was observed in yield traits for all young genomic bulls in Holstein, Jersey and Brown Swiss breeds.

What is the new genome assembly?

Over the last years, USDA AGIL researchers helped develop a greatly improved cattle DNA reference genome, or “map.” The new map showed improved imputation of genotypes and other benefits. Furthermore, the relatively recent availability of a large set of new information (HD SNP chip and fully-sequenced animals) provided benefits. For example, the identification of a large amount of SNPs enabled better estimates to producers for a number of CDCB services, compared to the 60k SNP set previously used in genomic evaluations. The SNP set initiated in December 2018 evaluations included 79,294 SNPs to enhance trait estimation (higher genomic reliability) and haplotype determination (more gene tests included in the haplotypes).

What effects can be expected?

USDA AGIL and CDCB analyzed effects of the 60k and 80k SNP sets via a side-by-side comparison using November 2018 data. Comparing the 60k and the 80k SNP sets – with all other factors constant – no noticeable trend was observed in the general population or among all the young genomic bulls in any breed. However, a downward trend could be seen in the very top young genomic Holstein, Jersey and Brown Swiss bulls.

When comparing August to December evaluations, the downward trend could be observed on **all** young genomic bulls for the aforementioned breeds.

There is no single reason responsible for the observed change between triannual runs. It’s the result of a combination of factors. The new SNP set certainly impacts the evaluations, but its impact on the bull population is limited, as explained above. Potential negative variation for individual genomic young bulls occurs through a combination of factors, such as new phenotypes, high inbreeding, genomic-only (no daughters) evaluations and reduced parent averages (since most sires of top bulls are genomic bulls also). The impact of inbreeding is not negligible. As the population becomes more related to top bulls, PTAs of top bulls are expected to decline. CDCB evaluations penalize the increase in inbreeding to promote outcross animals. The known underestimations of the traditional evaluations (referenced later in this report), summed to an expected greater variability in the genomic-only evaluations of top young animals, are other factors that contribute to the variability.

Reliability estimates changed only slightly, which might be surprising considering the expectation was an increase of 1.5% on average across traits. However, as [noted by AGIL researchers](#), observed versus published genomic reliabilities were already 2% overestimated for Holsteins and 3% underestimated for Jerseys. Holstein reliabilities should now be correct, whereas an upward adjustment to Jersey reliabilities is still needed and will be investigated.

How do we describe the variation alongside progress?

We remember the “old” days – before genomic evaluations – when bull evaluations were based on parent averages and daughter performance when available. Popular sires often obtained highly reliable evaluations based on hundreds or thousands of daughters. Certainly, time was a big factor, taking four to five years for a bull to receive a progeny-based evaluation and usually two or three more years to reach high reliabilities. Today with

genomic evaluations and genotyping, newborn calves (or even unborn embryos) can obtain a genomic evaluation that is ~70/75% reliable depending on the trait.

Genomics have boosted genetic progress, and progress requires change. The use of genomics changed selection processes toward animals based on genomic information only. When combining traditional and genomic information, this pre-selection is not accounted for in the traditional evaluations, resulting in somewhat biased (underestimated) traditional results. In addition, generation interval has shrunk almost to a physiological minimum (puberty of the bulls). It is common to see genomic bulls (with lower reliability than top proven bulls) having sons being marketed before having a single daughter in production. While ~70/75% reliability at birth is a giant advancement, one must remember that with lower reliability, variation can be expected from run to run.

What about haplotype determination?

Other important features of the 80k SNP set and the new map are better definition of the haplotypes (better SNP positioning), inclusion of a large number of gene tests, and more surrounding SNPs for fertility haplotypes determination. Although the direct inclusion of gene tests is a great advancement per se, the comparison between the 60 and 80k SNP sets showed very stable results. In other words, the accuracy of the results published by AGIL first and now by CDCB was already very high. A gene test (HH5) was intentionally not included at this stage, as many homozygous animals were detected whereas the haplotype results shown none. The performance of the gene test is under investigation at Neogen.

[CDCB recently announced](#) important information affecting the haplotype predictions of Polled in this run, as an issue in the merge of SNP data coming from four recent SNP chips and breed association information was recently discovered. Finally, be aware that BH1 and JH2 will be discontinued, effective December 2018. For more on haplotypes, please see <https://www.uscdcb.com/cdcb-changes-to-evaluation-system-december-2018/>.