Cow Reference Population – Benefit for Genomic Evaluation System and Farmers

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Abstract

Cow reference population is a tool to introduce genomic selection for new traits within a manageable time. Furthermore it is an instrument to control the bias in more and more pre-selected bull reference populations. Whole herd genotyping by farmers for management purposes becomes more and more popular. This results in cow reference populations for classical traits. Beside this several projects are set up in Europe by breeding organizations to support this trend and collect data especially on new traits.

The German Holstein herdbook organizations introduced the project KuhVision in June 2016 to achieve a reference population of 120.000 cows from whole herd genotyping within 3 years until June 2019. The goal of 550 participating herds with average 200 milking cows was reached already at the beginning of 2017. Meanwhile over 50,000 cows are in milk and provide phenotypes.

First results after adding 20,000 cows to the EuroGenomics bull reference population show improvement of gEBV reliability for all routinely evaluated traits (see Alkhoder *et al.*, 2017).

The benefit of whole herd genotyping for dairy farmers management is demonstrated by the prediction power of young stock gEBV (not including own performance information) for differences in later phenotypic performance. The phenotypic difference e.g. in 305d milk production of 1st lactation between the bottom 25% for gEBV milk kg (-440kg) and the top 25% (+909kg gEBV) was 1,495 kg milk (8,340 versus 9,835 kg). Even for low heritable traits like fertility and calving traits differences in young stock gEBV correspond to big variation in phenotypic performance. These results encourage additional farmers to start whole herd genotyping outside the project. Therefore there is a realistic chance to establish whole herd genotyping on a commercial base parallel to and after the project even adding more cows to the reference population than the 30,000/year expected from the 550 farms in the project.

Key words: genomic prediction, whole-herd-genotyping, genomic management, Holstein

Introduction

In Germany 2.4 million active Holstein cows are milk recorded and 1.9 million of those are herdbook registered. Routine genomic evaluations and official publication of gEBV was introduced in August 2010. Farmers were allowed to genotype females by the regional Holstein associations since 2011. But the number of genotyped females increased only slowly up to 1,000 animals per month until the end of 2015. This means less than 2% of all new Holstein females born in herds participating in milk recording and only 10% of all herds are genotyping females at all. The majority of the genotyped females were (pre)selected for elite breeding purpose (e.g. potential bull dams). Different to e.g. North America whole herd genotyping for management purposes did not become a common tool for herd management. There may be many reasons, but the costs are most probably not the main reason for not genotyping females, they are similar to e.g. North America.

Cow reference populations are necessary to extend routine genomic evaluations to new traits within a reasonable time. Furthermore adding cows to the bull reference populations for standard traits can compensate the reduced number of newly daughter proven bulls caused by the reduced number of bulls in A.I. compared to former number of test bulls due to genomic selection. The strong preselection of new A.I. bulls entering the bull reference population means that they no longer represent the full variation within the cow population that leads to bias. Including cows in the reference population could help to control this effect. Ideally reference cows should represent the entire variation of the cow population in terms of genetic structure and management conditions. Reference cows from representative herds and whole herd genotyping would be ideal.

Materials and Methods

Based on the idea of having a cow reference population that represents the entire genetic structure of the current German Holstein cow population kept in the whole range of relevant German management systems, the project KuhVision (cow vision) was initiated under the roof of German Holstein Association (DHV) and genetic evaluation center vit. As goal were defined 100,000 unselected reference cows from whole herd genotyping within 3 years. All members of the German genetic consortium i.e. all 11 regional Holstein associations participate and contribute to the 100,000 reference cows according to the percentage of Holstein cows in their region from total German Holstein cows. KuhVision was open for dairy farmers participating in official DHI, herd classification scheme and willing to record and deliver data on health traits and results of routine hoof trimming at least for three years. For this period they are offered subsidized prices for genotyping reduced up to 60% i.e. below 20€ package price per animal. Another advantage for participating farmers is an exclusive internet based management platform not just providing the results, but enabling e.g. horizontal benchmarking with other farmers. KuhVision started June 2016 at the peak of the milk price crisis. Nevertheless already at the beginning of 2017 more than 550 farmers with more than 100,000 cows participated and no more farmers could participate in the specific project. Meanwhile whole herd genotyping is offered with a reduced subsidization level and already 100 additional farmers (August 2017) signed.

Whole herd genotyping starts with an initial phase where all young stock is genotyped for the reduced fee plus all cows in first lactation for free.

In August 2017 180,000 females in total were genotyped including 75,000 cows in milk and about 27,000 having completed 1st lactation. This includes about 19,000 cows first calved 2013/2014 from the feasibility study KuhL.

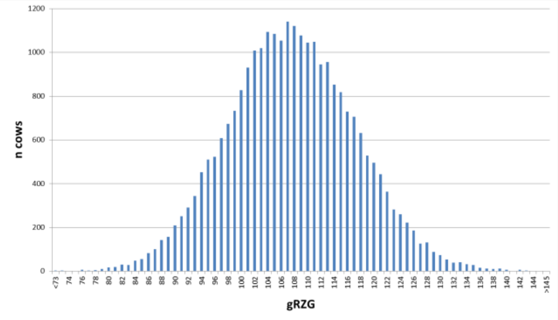

Figure 1. Distribution of genomic total merit index gRZG for 26,877 reference cows with completed 1st lactation (305 d).

Figure 1 shows the distribution of genomic total merit index gRZG of all cows having completed 1st lactation. Like intended these reference cows represent the full spreading of the entire German Holstein population. The average genetic level with a gRZG of 107.6 is only slightly higher as expected from the average birth year 2012.

All genomic breeding values (gEBV) are calculated without including own performances i.e. comparable to young stock genomics with direct genomic value (dGV) plus sire pedigree index (s-P.I.).

Results & Discussion

First results from the genomic evaluation based on reference cows only respectively adding reference cows to the EuroGenomic bull reference population are presented by Alkhoder *et al.* (2017). Despite these first results being based on a limited number of up to 19,000 cows they prove that genomic evaluation based on cow reference population is possible and adding cows to a big bull reference population improved the reliability of gEBV for all traits.

The main benefit of whole herd genotyping for the farmer is the selection among females with high accuracy including young stock and low heritable traits. Furthermore gEBVs can be used as base for individual mating of cows and heifers. Therefore it is important to show the farmer how accurate gEBVs (of young animals) predict differences in the phenotypic performance. To do so deviations of animal phenotypic performances from the herd average are compared to the corresponding trait gEBVs of that animal calculated without own performance information. Cows were deviated in quantiles for gEBV (lower 25%, 25-49%, 50-74%, highest 25%).

Figure 2 shows the results for 1st lactation milk yield (kg, 305 days) for 26,877 cows.

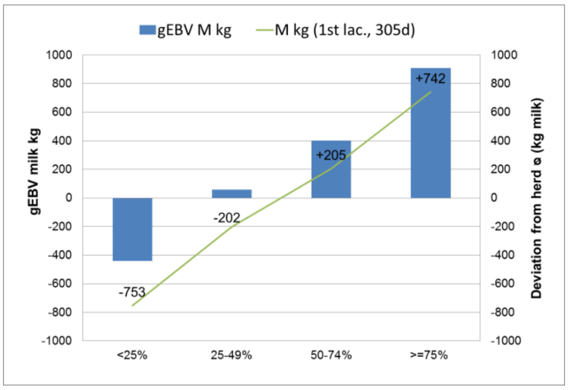

Figure 2. Comparison of 1st lactation milk yield (kg, 305 d) for classes of gEBV milk kg (n total = 26,877).

The difference in gEBV milk yield between the two extreme quantiles is 1,349 kg. This corresponds to 1,495 kg difference in milk production 1st lactation (305d) or 8,340 versus 9835 kg compared to the average production of 9,093 kg for all cows. There is variation within the groups but the overall expectation that within bigger groups of cows in same management conditions gEBV differences reflect differences in phenotypic performance is fulfilled.

For farmers it is more difficult to understand the relations between relative breeding values and phenotypic performances. gEBVs for all traits except milk production traits are expressed as relative breeding values on a scale of 100 for base animals and a genetic standard deviation of 12. Base for all traits are 4-6 years old cows (for 2017: all cows born 2011-2013). The base is shifted every year with the April publication.

Figure 3 gives the differences in somatic cell count (SCC) from the average of first 3 test days in 1st lactation for the 4 classes of gRZS (relative breeding value SCS, low SCS = higher RZS). A difference of 22 relative points for gRZS (1.85 genetic standard deviations) between the upper and lower quantile results in 97,000 cells/ml milk phenotypic difference or 111,000 versus 208,000 cells (average of 42,617 cows: 153,000 cells/ml).

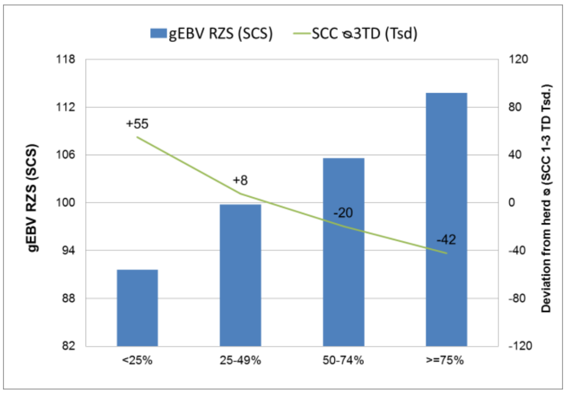

Figure 3. Comparison average of first 3 test day results for SCC (in tsd, 1st lac.) for classes of gRZS (n total = 42,617).

For still birth (including losses up to 48 h) data on 41,106 purebred Holstein calves born from heifers were available. Figure 4 illustrates that 13.9 points difference for relative breeding value maternal still birth rate (SBm) gave almost 16% difference in percentage dead born calves (6% versus 22%).

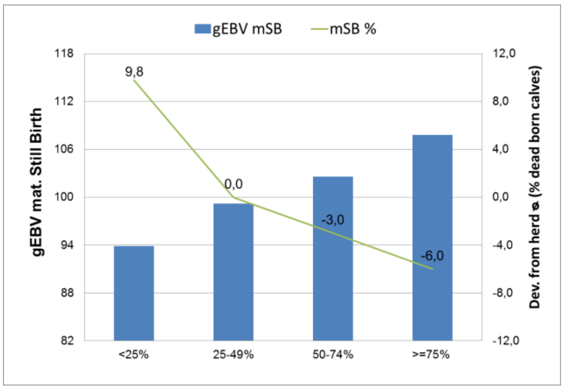

Figure 4. Comparison of % dead born calves (and died within 48 h) at 1st calving for classes of gEBV for maternal still birth rate gSBm (n total = 41,106).

Even for a low heritable fertility trait like non-return-rate-56days (NR56) phenotypic differences between classes of gEBV NR56 were big. 20.9 points of gEBV correspond to almost 11% of phenotypic difference NR56 in first lactation cows (47% versus 58% NR56).

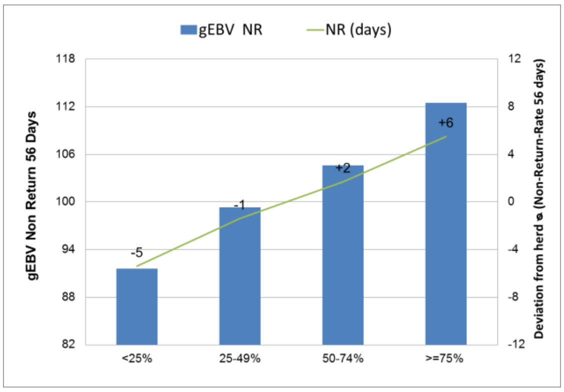

Figure 5. Comparison of % non-return-rate 56 days in 1st lactation for classes of gEBV NR56 (n total = 33,692).

For farmers conformation gEBV – besides animal selection – have a special importance in mating strategy. The use of mating programs including the definition of cow individual needs is widespread in German Holsteins. Most cow individual needs are defined for conformation traits. But for non-genotyped heifers there is no classification result or EBV based on own performance. Therefore gEBVs offer the first time a good information base to define heifer needs for individual mating. A good prediction of differences in phenotype is important to convince farmers for the benefit of whole herd genotyping.

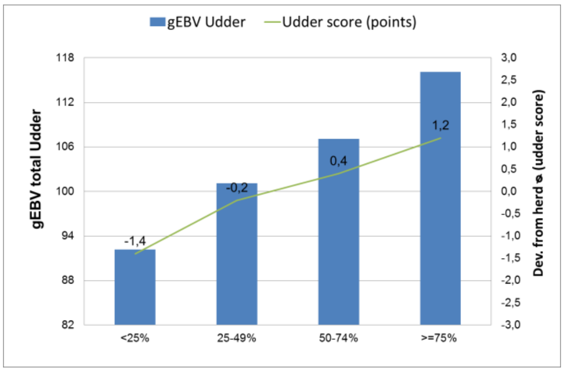

Figure 6. Comparison of Udder Score for classes of gEBV for overall udder (n total = 36,711).

Figure 6 shows the prediction of udder score by gEBV for overall udder. 23.9 points difference in gEBV between the extreme classes correspond to 2.6 points differences in classifiers score (80.3 versus 82.9).

These results are a very effective tool to confirm the farmers participating in the project KuhVision that they had taken a good decision and especially to convince more farmers to invest in whole herd genotyping to get effective additional management tools.

Conclusions & Outlook

In June 2016 the project KuhVision started to initiate a German Holstein cow reference population of 120,000 unselected cows from whole herd genotyping within 3 years. The project is very successful as planed number of herds/cows was reached within 7 month representing the entire genetic variation and all management conditions. Expected improvements of genomic evaluations seem to become reality as first results indicate. The advantages for farmers especially in early selection can already be approved in practice by the described first results. There is high probability that these proven advantages encourage the participating farmers to continue with whole herd genotyping after the end of the initial project in 2019 and with no or reduced grants on genotyping costs. Meanwhile already more than 100 additional farmers started whole herd genotyping outside the project KuhVision. There is a good chance that the predicted 30,000 additional reference cows per year after 2019 will be outreached.

References

Alkhoder, H., Liu, Z. & Reinhardt, F. 2017. Impact of adding cows to the current EuroGenomics bull reference population. *Interbull Bulletin 51*.