Why switch to a mixed reference population?

*Genetic evaluation is undergoing a constant development and is adapted to changing conditions. From next evaluation run in April onward genomics will be based on a mixed bull-cow reference population. Friedrich Reinhardt from **vit** explains reasons and consequences.*

So far genomic evaluation for Holsteins in Germany is based on a bull reference population with about 38,000 daughter proven bulls including performance data of over 50 million daughters. The older reference bulls born until 2010 were selected as calves by pedigree index and became test bulls. This selection of test bulls by pedigree index was in-precise and resulting selection intensity was low. Therefore the test bulls represented (almost) the entire variation of the cow population.

Younger reference bulls born after 2010 are pre-selected on the base of genomics. This pre-selection became more intensively and meanwhile just the best out of 40 candidates is entering AI and gets daughter proofs. But in genetic evaluation performance data of all offspring from a sire of sons is needed. If we have daughter performances exclusively from the best this results in biased breeding values.

In future a bull reference population represents less and less the entire variation in the cow population and the correct estimation of genetic level of AI bulls in classical evaluation becomes more difficult. But this correct estimation is pre-condition for unbiased genomics.

The solution is genotyping all females in commercial herds. Even if later not all genotyped female calves provide performance data for the reference population they are almost unselected and therefore representative for the entire cow population.

The so far bull reference population will be extended in future mainly by new reference cows. In the mixed reference population unselected cows will have increasing impact over time. This mixed reference population has another advantage. Because of many young cows the mixed reference population in genetically closer and better related to the current selection candidates. A small genetic gap between reference population and selection candidates has a positive effect on the reliability of genomic breeding values of young selection candidates. In the past this gap has become wider because more and more sires and grandsires of selection candidates have no daughter proofs and were therefore not in the bull reference population.

Validation studies with a mixed reference population of ca. 34,000 bulls and ca. 65,000 cows show that the resulting gEBV for selection candidates predict the later average daughter performances slightly better. This means that realized/true reliabilities of gEBV based on a mixed reference population are higher (+0.02 to +0.05).

With the switch in April 2019 ca. 150,000 reference cows will be added to the >38,000 reference bulls. Based on this massive increase in animals and different composition of reference population, the genomic formula and gEBV will change more than usual. Even in the subsequent runs in August and December more changes than usual between routine runs are expected because of further massive increase of about 40,000 new reference cows from the KuhVision project.

Cows provide data on new traits

Because of economic reasons - and demand from the society – animal health must get more emphasis in modern dairy breeding programs. Breeding and selection is always based on performance data as only way to detect superior animals. Despite many regional projects to record

animal health data the gathered data are not sufficient for an effective bull reference population. Just few, mostly older second crop bulls have classical breeding values for health traits with high reliabilities as base for a reference population. Furthermore foreign bulls can not contribute, too, because there is no international conversion for health traits. Therefore recording health data in herds participating in the whole-herd-genotyping program KuhVision is important. With this an effective reference population for new traits can be created within short time.

For traits like (true) feed efficiency and reduction of Methane emission this holds, too. Therefore some of the meanwhile 1,300 KuhVision herds should be equipped with modern automated recording technology –like in other countries – to achieve phenotypes for a cow reference population. Because data recording for feed intake and feed efficiency is expensive, international cooperation should be achieved. But this is only possible if the German Holstein population can contribute, too.

Conclusions

With close cooperation of all parties (dairy herds, breeding organizations, BRS, data center **vit** and science) German Holsteins realized the whole-herd-genotyping project KuhVision to ensure that genomic evaluations in future   are solid based and work like expected. This applies not just for all classical traits but for news traits needed for breeding and marketing, too.

Additionally dairy herds participating in KuhVision form a kind of nucleus for future breeding programs. Breeders are therefore more actively integrated in breeding programs.