

## **New method to calculate genomic breeding values for Dairy breeds**

*Single step is a new method to calculate genomic breeding values. It will gradually replace the current two-step method for all traits with the result of more accurate breeding values. The index for Saved feed is already based on this new type of model and will be followed by type traits in November 2022.*

Genetic evaluation is constantly improving due to more knowledge and more computer capacity. In the Nordic countries we have previously used a two-step method for all traits except Saved feed. In the first step traditional breeding values without genomic information are calculated. In the second step these breeding values are combined with genomic information. However, larger computer capacity has made it possible to use the single step method where pedigree, phenotypes and genotypes are combined simultaneously. This method has several advantages.

### **Higher accuracy – now and in the future**

When all information from both genotyped and non-genotyped animals are used simultaneously in the single step method it will increase reliability. This is because pedigree, phenotypes, and genotypes will be weighted together in a more optimal way.

The traditional genetic models we are using today as part of the two-step method builds on the assumption that AI bulls and dams of next generation of heifer calves have a genetic level that is equal to parent average. This is not the case after we gradually uses genomic selection more intensive and thereby are able to select the males and females that have got the best genes. The result is that we introduce a bias in our traditional breeding values – a bias that will be even more profound in the future. The bias may have an influence on the genetic trend in the future.

### **All information's are used during the AI bull's life**

In the present Nordic publication of breeding values for AI bulls, we use all available information, however when a bull gets a high reliability based on own daughters, the genomic information is excluded. When using the single step method all information is always used.