

Genomic selection in cattle industry: achievements and impact

Dr. Fritz Schmitz-Hsu, Senior Geneticist, Swissgenetics, CH-3052 Zollikofen

1 Introduction

Advances in analyzing the genome combined with new statistical procedures made it possible, that genomic selection became a very widely used tool in cattle breeding. Genomic selection - besides gene and marker tests - can be considered as the most influential technology since the introduction of artificial insemination (AI).

2 Fundamentals of genomic selection

Genomic selection is based on analyzing thousands of markers spread over the whole genome of an individual. Markers are differences in one single base pair = Single Nucleotide Polymorphism (SNP). Nowadays, ten thousands of SNPs can be determined at large and with rather small costs using SNP panels. By correlating SNPs with the breeding values of a reference population, equations to estimate genomic breeding values can be derived. Based on those equations and the SNP genotype, a Direct Genomic Value (DGV) can be calculated. A DGV can be combined with a traditionally estimated breeding value, resulting in a Genomically enhanced Estimated Breeding Value (GEBV). The major benefit of a GEBV is the higher reliability than a traditional breeding value in the case of young animals. Using GEBVs, young animals can be selected more successfully and with a shorter generation interval, resulting in a substantial increase of genetic progress. As long as a sufficient large reference population is available (>1000 genotyped animals with breeding values with high reliability), GEBVs can be derived for any measured trait within the same population.

3 Application in dairy cattle breeding

Genomic selection was introduced in dairy cattle breeding within a very short time. Less than a decade after the theoretical framework of Meuwissen et al. (2001), all principal countries published GEBVs of their young bulls in large dairy breeds. The long period needed to progeny-test a bull, the high costs associated with it, the widely spread artificial insemination and the willingness of AI industry and other organizations to invest into this new technology fostered the swift introduction of genomic selection. Now already millions of cattle are genotyped worldwide.

4 Achievements and impacts

In the US Holstein population, GEBVs of young animals have for most traits a 20 - 48 percent points higher reliability than breeding values based on pedigree information only. Therefore young bulls are marketed at large scale already as soon as they produce semen, shortening the generation interval drastically. With reproduction technologies (embryo transfer, ovum pick-up, in vitro fertilization etc.), genetic providers reduce the generation interval even further. In the context of genomic selection, many new genetic disorders were discovered, which have a negative impact on fertility.

The hope, that many new genetically superior families could be found, that inbreeding could be reduced, that the reliability of GEBVs could be increased further by using SNP panels or even sequence data, or that the estimation equations of one population could be applied successfully in other breeds (avoiding the establishment of an own reference population) have not been achieved, yet.

Besides further reducing generation interval, organizations in dairy cattle breeding are working on introducing genomic selection into smaller breeds, and are applying it for management purposes and on new traits (health traits, feed efficiency, methane emission etc.). But there is no way to get around a sufficient amount of well recorded phenotypes.