Genomic selection in dairy cattle: Progress and challenges

Genomic selection has revolutionized cattle breeding during the last several years. This article nicely summarizes the short history of genomic selection, its current applications in various countries and some challenges. For tree breeders, it is time again to look at animal breeders to see if we can adopt their applications to use in tree improvement.

The authors link the genomic selection revolution with two developments: (1) sequencing of the bovine genome accompanied by discovery of thousands of SNP markers and inexpensive genotyping platforms, and (2) the demonstration by Meuwissen et al. (2001) showing that breeding values can be predicted very accurately using markers alone.

The authors describe the genomic selection in two steps: First, the effects of small chromosome segments or SNP markers are estimated in a reference or training population using a linear mixed model. Significant SNPs from the first model are then fit simultaneously in a second linear mixed model to obtain predictions for each SNP. In the subsequent generation, the progeny are genotyped and only marker information is used to estimate breeding values without progeny testing.

The authors summarize the application of genomic selection in dairy cattle breeding around the world and compare the results. A common finding in 3 countries (United States, New Zealand, and Australia) was that a straightforward BLUP method for estimating the marker effects gave reliabilities of genomic estimated breeding values almost as high as more complex methods, such as Bayesian methods.

The criterion for successful genomic selection is measured by the accuracy of breeding values. The authors discuss the parameters that affect the accuracy of genomic selection. The parameters are linkage disequilibrium, population size, heritability and the distribution of QTL effects. The authors conclude that in order to be successful in genomic selection, the single markers must be in sufficient LD with the QTL. For forest trees, this suggests that large number of markers are required because the genome size of trees is large and LD decays rapidly. The authors suggest that there should be large number of animals with phenotypic records to estimate the effects of SNPs. Another important parameter is heritability. A high heritability requires fewer phenotypic records. Finally, if there are many QTL of small effects, a large number of phenotypic records will be required to estimate marker effects accurately.

The implications of genomic selection summarized by the authors are profound. According to some estimates, using genomic selection, progeny testing can be avoided in cattle breeding which saves up to 92% of the cost of testing. The increase in reliability is sufficiently high that at least two dairy breeding companies are already marketing bulls for commercial use based on their genomic estimated breeding values only, at 2 year of age. The authors predict that the genomic selection strategy should at least double the rate of genetic gain in the dairy industry, mainly by reducing the breeding cycles and eliminating progeny testing.

At the end of the paper, the challenges with genomic selection and its implementation are discussed. The major challenges are (i) increasing the accuracy of genomic selection, (ii) integrating genomic information into national and international genetic evaluations, and (iii) managing long-term genetic gain.

If genomic selection works for forest trees, it will surely revolutionize tree breeding. The impact on tree breeding would be much larger than any other crop and animal species because forest trees have a longer cycle of breeding. Conifer Translational Genomic Network (led by David Neale, UC-Davis) is working towards this goal.

Reviewed by Fikret Isik