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Theo Meuwissen Wins Prestigious John J. Carty Award

NMBU's Professor Theodorus Meuwissen has received the 2016 John J. Carty Award from the US National Academy of Sciences along with his collaborator Michael Goddard for their pioneering work on genomic selection. According to the award announcement, this work united quantitative genetic theory with genomics technology, revolutionizing the genetic improvement of livestock and also having implications for fields from crop improvement to human medicine.

At the time when the key article (1) was published in 2001, agricultural science had reached the stage where a limited number of DNA markers were available per genome for breeding. These markers could be used to identify QTLs (quantitative trait loci) by calculating the probability that a given SNP was associated with a specific phenotype. Because only strong correlations would be registered as reliable QTLs using these statistics, only a few markers turned out to be useful for breeding selection.

Foreseeing the development of multi-DNA marker technologies with high density SNP collections for several agricultural animal and plant genomes, the novel approach that Meuwissen et al. (1) introduced was to base decisions for breeding on the joint merit of all markers across the genome. Instead of calculating
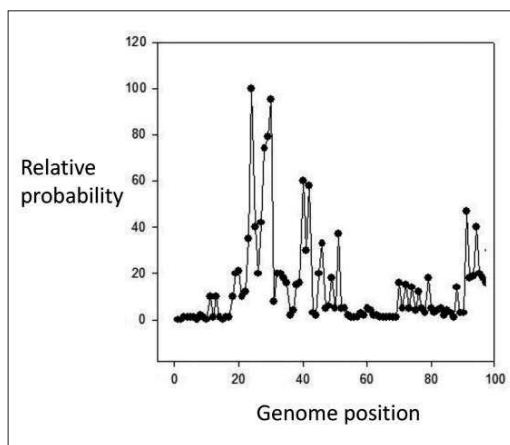

Fig. 1. Bayesian statistics gives higher resolution for phenotype/DNA marker data compared to classical QTL analysis. The Bayesian approach identified several markers contributing to phenotypic variance (e.g. at 24, 30 and 40) while the classical QTL approach failed to identify any markers representing as much as 2% of the total variance using the same phenotype/DNA marker data set. This figure is redrawn from results presented in reference 1.
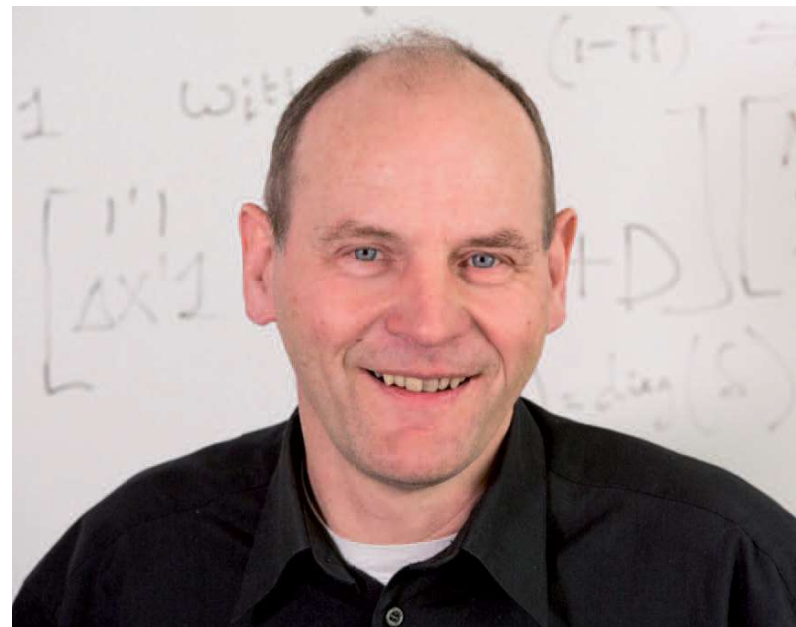
correlations for specific phenotypes and DNA markers, the Bayesian formula is used to calculate phenotype/DNA marker probabilities using a prior probability that a marker has a phenotype correlation >0. This alternative strategy increases resolution (Figure 1) and has significantly improved the accuracy of selection in breeding schemes.

One successful application of genomic selection involves dairy cattle where a doubling of dairy cattle improvement per generation has occurred during the last 15 years. At NMBU, researchers use the Bovine Affymetrix 25K MIP-SNP chip for genotyping Norwegian Red cattle (2). Phenotype records have been collected for 96% of the total herd in relation to milk and meat quality as well as

fertility and health characteristics.

Another application of genomic selection involves fish (3). A simulated study at NMBU demonstrated that multi-marker genomic selection is the best method for transferring traits (e.g. disease resistance) from wild fish populations into farmed fish populations.

So, theoretically the genomic selection approach ought to be useful for analyzing any data set relating phenotypes and DNA markers using high density SNP collections. Examples would include projects for crop improvement of grains and vegetables as well as studies of determinants involved in such human diseases as cancer, Alzheimers, hypertension and diabetes. In several respects, genomic selection represents

a paradigm shift in methodology for genomic analysis compared to classical QTL.

The John J. Carty Award is presented annually in fields such as agricultural science, genome biology, physics, mathematics, ecology or computational science. The last time the award was given for agricultural science was in 1984.

References
1. Meuwissen, THE et al.: Prediction of total genetic value using genome-wide dense marker maps. Genetics 157 (2001) 1819
2. Ødegård, J et al.: Genetics 181 (2009) 737
3. Luan, T et al.: Genetics 183 (2009) 1119