

**DR DAVE JOHNSON'S CONTRIBUTION TO DAIRY CATTLE GENETIC
EVALUATION IN NEW ZEALAND**

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SUMMARY

Dr Dave Johnson's contributions to New Zealand's dairy cattle genetic evaluation over the last 20 years are outlined. Five major research areas are highlighted: animal model introduction, variance component estimation, reliability of breeding values, on-demand test-day model results and genomic selection. A key measure of the success of Dr Johnson's research is that many of the findings and systems are still being used every day in New Zealand and around the world.

INTRODUCTION

In this paper, the contributions of Dr Dave Johnson to New Zealand's dairy cattle genetic evaluation will be discussed. This review will cover the period from 1993 to the present. Over this time there have been major changes in the genetic evaluation of dairy cattle. In the early 1990s many countries, including New Zealand, were adopting the animal model methodology for routine genetic evaluation. This was followed by the broadening of breeding objectives to include fertility, survival and other functional traits, which necessitated the need for genetic evaluations of these traits at a national level. The last decade has seen the adoption of the test-day model methodology for routine genetic evaluation of the production traits in dairy cattle. The latest change has been the adoption of genomic selection in dairy cattle that took place over the last six years. LIC, in collaboration with industry partners has been responsible for the research, development, maintenance and routine operation of the New Zealand's dairy cattle national genetic evaluation over the last 20 years. Dr Johnson has been closely involved in, and has made significant contributions to, all these research areas throughout his career at Livestock Improvement Corporation (LIC). Rather than list all the contributions over this 20-year period, I will highlight five areas that have had a major impact.

ANIMAL MODEL INTRODUCTION

In June 1996, a new animal model was implemented in New Zealand whereby dairy cattle were genetically evaluated using an across-breed animal model (Harris, 1996 and Garrick *et al.*, 1997). The animal model used was a single-trait repeatability model. The model allowed for heterogeneous subclass variation, that arose from the inclusion of mixed breed contemporary groups, by including fixed breed and group effects directly in to the additive relationship matrix. Also, a new methodology to predict total lactation yields from individual test-day information was developed to provide phenotypic production records for the mixed model analysis. This method was developed by Dr Johnson during 1994 and 1995. This method accounted for any number of herd tests over any testing frequency and allowed for variable information among herd-mates and for the effects of culling (Johnson 1996). The advantages of this approach were that all the phenotypic records were adjusted to a common 270-day length, additionally, a computationally efficient method to calculate the accuracy of prediction which weighted the records according to the amount of available information was devised. Although this phenotype is no longer used in the production national genetic evaluation it is still used to provide milk volume, fat yield and protein lactation yield phenotypic records are still used in a multiple-trait model to calculate fertility and longevity breeding values (BVs).

Acknowledging and honouring the contribution of Dave Johnson to animal evaluation

VARIANCE COMPONENT ANALYSIS

An algorithm was described that estimated variance components for a univariate animal model using REML in a paper by Dr Johnson and Professor Robin Thompson titled “Restricted maximum likelihood estimation of variance components for univariate animal models using sparse matrix techniques and average information” published in 1994 (Johnson and Thompson 1995). Sparse matrix techniques were employed to calculate those elements of the inverse of the coefficient matrix required for the first derivatives of the likelihood. The method made use of an average information (AI) restricted maximum likelihood (REML) algorithm. At that time, variance components were commonly estimated using derivative free (DF) REML methods or expectation-maximization (EM) algorithms. The AI REML procedure was found to be about 5 times faster than DF method and about 15 times faster than EM algorithm. The research led Dr. Johnson to develop variance component software based on the AI REML algorithm. Both univariate and multivariate analyses could be undertaken with this software. This software was subsequently used to estimate genetic and phenotype parameters from the data recorded in progeny test herds. These analyses were based on 100,000s of records across multiple traits. These types of analyses would have been computationally infeasible with any of the other available software at that time. Many of the estimates of the genetic and phenotype parameters are still in use in the current national genetic evaluation.

CALCULATION OF RELIABILITY OF BREEDING VALUES

The reliability of a BV is a measure of its accuracy. Exact reliabilities can be calculated from the inverse of the mixed model equations. However, in national evaluations the mixed model contains more than 10,000,000 equations, making them computationally infeasible to invert. A method of approximating reliability that was computationally fast and provided estimates with low amounts of bias was needed for the national evaluation. A new method was developed for calculating approximate reliability of breeding values for national systems of evaluation by Johnson and Harris in 1998 (Harris and Johnson 1998a). The method combined the reliability of three information sources: parent average, animal’s own records, and progeny records. This method provided good approximation to the actual values with minimal upward bias and was better than the current method used in New Zealand at that time. One of the major advantages of the method was that it could be extended to accommodate more complex models by altering the selection index equations within the method. This method has been now been extended to several complex models including test-day models (Ducrocq and Schneider 2007) and genomic selection models (Harris and Johnson 2010). This method was also extended to the estimation of reliability for Interbull multiple across country sire genetic evaluations (MACE) (Harris and Johnson 1998b). The motivation was to address concerns relating over-estimation of MACE reliabilities and its flow-on effects on the weighting of foreign information being included in national genetic evaluations. The proposed method was found to be a significant improvement over the method used at that time. The method was adopted by Interbull in 1999 and still used.

ON DEMAND TEST-DAY MODEL

In 2007, a testday model (TDM) was developed to provide national genetic evaluation for the production traits (Harris *et al.* 2006). A TDM can simultaneously account for fixed environmental effects such as herd-testday contemporary groups, and genetic, permanent environmental (PE) and temporary environmental (TE) random effects. In the TDM model, each test day is modelled, thereby taking into account the temporary environment, resulting in an improved accuracy of evaluation over a lactation model. Also, the TDM can include functions of the cows’ days in milk to account for cow-to-cow differences in the shape of the lactation curve. Dr. Johnson was an integral member of the development team. One aspect of the TDM development that has gone

unrecognised was Dr Johnson's on-demand TDM build for herd-testing customers. Because the national TDM model is only run approximately every 3 weeks, a system to provide updated results at the time of an individual herd-test was required thereby enabling farmers to make breeding and culling decisions based on the most up-to-date information. Dr. Johnson developed a simple system of selection index equations, that incorporated the latest herd-test results into the most recent TDM evaluation. The solution was computationally simple allowing up 1000 herds (300,000 cows) to be processed daily at the peak of the season.

GENOMIC SELECTION

Over the last five years, a considerable amount of research effort was being directed to the application of genomic selection to a national evaluation system for number of livestock species, including dairy cattle. In New Zealand we had the additional complication of requiring an across-breed genomic evaluation system in order to get genomic evaluations on progeny-tested Jersey Holstein-Friesian crossbred sires. Johnson and Harris (Harris and Johnson, 2010) describe a method for the prediction of breeding values incorporating genomic information in an across-breed evaluation. The first stage involved the prediction of genomic breeding values for genotyped individuals. The novel component of this method was the estimation of the genomic relationship matrix in the context of a multi-breed population. The paper outlines a selection index procedure to blend genomic predictions with the ancestral information that is lost between the process of deregression of the national breeding values and subsequent re-estimation using the genomic relationship matrix. Finally, the paper describes how the genomically-enhanced predictions are filtered through to non-genotyped descendants using a regression procedure. This is basis of the current national and LIC genomic selection methods used to select the genomic young bulls to be progeny tested.

CONCLUSIONS

This paper has only covered a small number of the contributions that Dr Dave Johnson has made to New Zealand's dairy cattle genetic evaluation over the last 20 years. However, each of these contributions has had a major impact. The many case the contributions are unique, in that they solve real research problems facing the New Zealand industry, such as the need for an across-breed genetic evaluation system and as such solutions were not readily available from the scientific literature. A key measure of the success of Dr Johnson's research is that many of the findings and or systems are still being used every day in New Zealand and around the world. Another important the contribution that Dr. Johnson has made is to his colleagues' work, most of which is unrecognised through co-authorship, by providing daily guidance across many areas within statistical research. His colleagues have found this guidance invaluable to their own research projects.

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