

## DAVE JOHNSON



Dave Johnson was born and bred in Southland, New Zealand. After completing his BSc and MSc at Otago University, Dave undertook a PhD at the University of Toronto (his thesis was titled "The symmetric structure theorem for reductive Lie algebras"). He then joined Ag Research as a research statistician: analysing numerous field experiments, as well as providing animal breeding expertise to New Zealand's sheep and beef cattle breeding programs.

Dave also worked in the area of variance component analysis during his years at Ag Research, and this led to the development of variance component software based on the AI REML algorithm. The software enabled both univariate and multivariate analyses and was subsequently used to estimate genetic and phenotype parameters from the data recorded in progeny test herds at Livestock Improvement. These analyses were based on 100,000s of records collected on multiple traits: analyses that would have been computationally infeasible with any other available software at that time. Many of the genetic and phenotype parameter estimates are still in use in the current national genetic evaluation.

Dave joined Livestock Improvement in 1993 and continued there until now. Over this period Dave has made a significant contribution to New Zealand's dairy cattle genetic evaluation. In the early 1990s many countries, including New Zealand, were adopting the animal model methodology for routine genetic evaluation. During the introduction of the animal model, Dave developed a new methodology to predict total lactation yields from individual test-day information thus providing phenotypic production records for the mixed model analysis. These records 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.

Dave was involved in research to improve the methods for estimating the reliability of estimated breeding values. Exact reliabilities can be calculated from the inverse of the mixed model equations. However, in national evaluations, the mixed model contains more than 10 million equations, making them computationally infeasible to invert. A new method of approximating reliability that was computationally fast and provided estimates with low amounts of bias was developed and published by Dave Johnson and Bevin Harris in 1998. This method has been extended to several complex models including test-day and genomic selection models, and to estimation of reliability for Interbull multiple across country sire genetic evaluations (MACE).

In 2007, Dave was an integral member of the team that developed a test-day model (TDM) to provide a national genetic evaluation for dairy production traits. One aspect of the TDM development that has gone unrecognised was Dave's on-demand TDM build for herd-testing customers. The national TDM model is only run approximately every 3 weeks, but farmers required a system to provide updated results at the time of an individual herd-test to enable breeding and culling decisions based on the most up-to-date information. Dave developed a computationally simple solution that incorporated the latest herd-test results into the most recent TDM evaluation, allowing up to 1000 herds (300,000 cows) to be processed daily in peak season.

Over recent years, considerable research effort has been directed towards the application of genomic selection in a national evaluation system for a number of livestock species, including dairy cattle. In New Zealand there was 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. Dave made valuable contributions to a method for the prediction of breeding values incorporating genomic information in an across-breed evaluation: the novel component being the estimation of the genomic relationship matrix in the context of a multi-breed population.