

Fellows Elected 2023



Ken G. Dodds

Dr Ken Dodds is a statistician located at Invermay Research Centre and is part of AgResearch's Statistics team. Ken has made a massive contribution to the New Zealand's genomic research over the course of his more than 35-year career working primarily in partnership with the Animal Genomics team at Invermay.

Ken was brought up on his parent's dairy farm near Mataura where they farmed pedigree Friesians. Ken did his undergraduate study at Otago University and then completed his PhD with Bruce Wier in statistical genetics at North Carolina State University before returning to New Zealand to work at the Ministry of Agriculture and Fisheries which subsequently became AgResearch.

Ken has guided numerous summer and PhD students, many of whom were formally supervised by others, in the delicate arts of appropriate statistical and genetic analyses for their projects. He has also been behind the statistical rigor of the Invermay group's many publications. His current tally of more than 12 000 citations of published papers where he is an author or co-author clearly demonstrates a significant impact on his field. Ken has contributed to research and subsequent industry implementation of many novel traits including carcass composition, meat quality, disease resistance and methane emissions, as well as the industry implementation of animal model and then genomic selection in New Zealand sheep, salmon, deer and goats. He is still actively working on bringing improvements to the NZ sheep and deer system some 25 years after its creation.

He has also played a similar role in the GenomNZ genotyping service over nearly 30 years. Several aspects of his work have made major contributions to statistical techniques which have had significant impacts both scientifically and industry. Although often overlooked, linkage mapping is still a difficult and developing field with

considerable issues relating to the travelling salesman problem of analysis complexity and the effect of genotyping errors. Ken has been instrumental in many papers in adapting and utilising linkage mapping techniques to solve real world problems, whether it was producing the first linkage map in the world for sheep, which was then used to identify the location of some key major genes and in the longer term contributed to the sheep and cattle genome assemblies. However, more recently with Timothy Bilton they solved the problem of using uncertain genotypes to create linkage maps. Then in another paper they also addressed the problem of estimating linkage disequilibrium with error prone genotypes.

Ken has also provided the primary statistical expertise in a series of papers mapping gene variants that have a major effect on sheep production including: Inverdale, Booroola, Woodlands, myostatin, parasite resistance, microphthalmia, horns and yellow fat. Genotyping for these variants is still routinely undertaken commercially today. The discovery of the causal mutations for Inverdale and Booroola was a world first in sheep for production traits. He has also made a major contribution in pedigree assignment and estimation of breed proportions from marker data and the software he has written underlies New Zealand's pedigree and breed assignment in commercial breeding programs in sheep, goats, salmon and deer.

In two areas this work has been rather unique. The first was the development and industry implementation of the fractional-parentage system which uses DNA marker information to calculate the pedigree of animals in breeding program. The fractional-parentage DNA pedigree system that Ken developed made the use of DNA parentage cost-effective in the New Zealand sheep industry by using relatively low numbers of DNA markers while maintaining the high rates of genetic progress. In more recent years he has developed and

maintains the KGD software suite available on Github. This population genetics software allows pedigree assignment, breed proportion estimation, and creation of genomic relationship matrices for subsequent use in many applications including genomic selection. At its core it transparently handles low depth genomic sequencing data which produces uncertain genotypes. This development has led to at least a ten-fold reduction of the cost of developing and deploying genomic selection in a new species. The method has been widely used

in more than 100 species to date including in conservation and production genetics in plants, mammals, birds, fish, decapods and shellfish.

Over his career Ken has presented or been co-author on 50 papers at AAABG, the first in 1991. He has also served on the AAABG committee. For his outstanding contributions to the science of genetics and animal improvement, the Association for the Advancement of Animal Breeding and Genetics is pleased to elect Ken Dodds as a Fellow of the Association.