## HELEN NEWTON TURNER MEDAL TRUST

The Helen Newton Turner Medal Trust was established in 1993 following an anonymous donation to the Animal Genetics and Breeding Unit. The Helen Newton Turner Medal is awarded to provide encouragement and inspiration to those engaged in animal genetics. The Medal is named after Dr Helen Newton Turner whose career with CSIRO was dedicated to research into the genetic improvement of sheep for wool production. The Medallist is chosen by Trustees from the ranks of those persons who have made an outstanding contribution to genetic improvement of Australian livestock.

The Helen Newton Turner Medal was first awarded in 1994 to Associate Professor John James and a list of all recipients to date is given below. The recipient of the Medal is invited to deliver an Oration on a topical subject of their choice. The Oration of the 2013 Medal recipient, Prof. Michael Goddard, is reproduced in these proceedings.

**Trustees of the Helen Newton Turner Trust are:**

### MEDALLISTS

*1994* J.W. James
*1995* L.R. Piper
*1997* J. Litchfield
*1998* J.S.F. Barker
*1999* C.W. Sandilands
*2001* G.A. Carnaby
*2003* F.W. Nicholas
*2005* K. Hammond
*2007* L. Corrigan
*2009* R. Hawker
*2011* R. Banks
*2013* M. Goddard
*2015* A. Gilmour

## HELEN NEWTON TURNER AO

# LIVESTOCK GENETIC IMPROVEMENT IN THE 21$^{ST}$ CENTURY – OPPORTUNITIES AND CHALLENGES

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## INTRODUCTION

It is a great honour to receive the Helen Newton Turner medal. I knew Helen at the beginning of my career and towards the end of hers. Her knowledge and passion were an inspiration to all of us. In this Helen Newton Turner oration to AAABG I will attempt to take a broad view of the opportunities and challenges facing genetic improvement of livestock, especially cattle and sheep, in the early part of the 21$^{st}$ century.

We are frequently told that the development of an Asian middle class will increase the demand for livestock products especially meat and dairy products. The frustration for producers is that this increased demand does not translate into higher prices. I suspect this is due to competition among suppliers. There are other suppliers of livestock products including the intensive poultry and pig industries and there are plant based substitutes. However, the price of farm inputs does rise. I can only see further rises in the price of feed grain, water, labour and the costs of compliance with animal welfare and environmental regulation. Therefore, to remain profitable I suggest that farm businesses need a 2% per annum increase in economic efficiency, that is, in the ratio of income to costs.

This implies a doubling of efficiency over 35 years. Is that possible? The poultry meat industry has easily achieved this increase, largely through genetic improvement of broilers. Between 1980 and 2010 the Victorian dairy industry increased production per ha 3 fold. The challenge is to do this again. In northern Australian beef production a doubling of production per ha could be achieved if weaning rates were lifted to 80% with reduced cow losses, on farm growth rates averaged 0.7 kg/day and the feedlot finishing phase was shortened. This is a tall order. Perhaps it could be achieved with a cross breeding program using a small, fertile, adapted dam breed and a fast growing sire breed producing calves that graze a feed source of high nutritional quality?

Doubling economic efficiency could be achieved by a combination of increasing the price for products, decreasing cost per ha and increasing production per ha. I suggest it will have to come mostly from increasing production per ha because I cannot see that the prices for farm outputs will increase enough or that costs for farm inputs will decrease enough. Therefore this paper will concentrate on the opportunities to increase production per ha by genetic improvement. While acknowledging that non-genetic improvements will be important they are not the subject of this paper.

Genetic improvement in economic efficiency depends on breeding objectives being aligned with economic efficiency and the use of tools that will deliver genetic progress.

## BREEDING OBJECTIVES

The objective should be to increase profit where profit is understood to include all objectives including non-monetary ones such as safety, animal welfare and environment. In the past the most common mistake has been to ignore some traits such as fertility, health and feed conversion efficiency. Especially if there are unfavourable correlations between these traits and other selection criteria, this risks undesirable and costly changes in these traits that are ignored. Fortunately most industries have moved to a more comprehensive breeding objective. However, there are aspects of the objective that are still ignored. For instance, where the commercial animal is crossbred but selection is within purebreds or where breeding stock are selected in a different environment to the one where their offspring will be farmed. As discussed later, genomic selection offers a better opportunity to select for the traits in the breeding objective than we have had before.

What changes in breeding objectives can we anticipate in the future? The risk of predicting the future is high and, fortunately, objectives change relatively slowly so selection for today's objectives is satisfactory. However, possible changes might be an increased community concern for animal welfare and environmental outcomes, changes in production systems such as robotic milking, sexed semen, cows with twins, once-bred heifers, adaptation to a hotter , drier climate, inclusion of the effect of one animal on the performance of herd mates (so-called social breeding values), and the use of lines specialised for a certain product or environment. We need to include changes in objectives as soon as they become apparent.

## TOOLS FOR GENETIC IMPROVEMENT

The tools considered are choice of breed, crossbreeding, avoidance of inbreeding, selection, transgenesis, use of major genes, specialised lines to account for GxE or differences in objectives and mate allocation.

Breed differences can be large but the choice of the best breeds is a once only improvement. Often obvious changes are made quickly by industry and after that the gain from changing breed is small because each breed has some advantages and disadvantages.

Heterosis is also a once only improvement but is an almost cost free improvement in efficiency that is under-utilised.

If heterosis is nearly always an economic advantage, inbreeding depression is nearly always an economic loss. Inbreeding is an inevitable result of small effective population size ($N_e$) and many breeds have $N_e$ about 100-200. Consequently, inbreeding slowly increases with the expected outcomes such as a rise in frequency of a succession of recessive abnormalities. The management of these recessives is an increasing problem which needs to be put in the usual economic index approach. That is, selection should be based on estimated breeding value for profit including the effect of recessive abnormalities. This will result in culling of animals carrying the more common recessives and culling animals that carry multiple, undesirable genes. However, overall inbreeding levels should be held down by optimising selection decisions to maximise breeding value while minimizing future inbreeding.

Selection is a major opportunity to drive long term improvement in livestock but it is not a new opportunity and in the absence of new technology we can perhaps not expect sudden improvements in its use. The new technology is genomic selection. This is already adopted in the dairy industry and being introduced in other industries. By itself it is beneficial but it is synergistic with 3 other technologies. Traditionally, recording of performance had to be done on selection candidates or their close relatives. This was a problem where the trait was difficult or inconvenient to measure on stud animals. For instance, meat quality is hard to measure on live animals; disease traits are difficult to select for because stud animals are managed to minimise disease; crossbred performance cannot be recorded on purebred animals; feed intake is too expensive to measure routinely. Genomic selection can potentially overcome these problems because the training population can be separate from the elite breeding population. Therefore, the training population can consist, in part, of commercial animals not closely related to the stud animals. This opportunity may be difficult to utilise because traditionally the cost of recording is paid by the owners of elite or stud animals. However, the opportunity is important enough that we should find a new method of paying for the costs. For instance, we could train a genomic prediction equation using crossbred lambs slaughtered and evaluated for FCE and meat quality and yield. Automatic measurement technology would be a synergistic technology with genomic selection because it could reduce the cost of collecting the data for the training population. Another synergistic technology is reproductive technology that allows reproduction at an early age so that generation interval can be reduced. Since DNA can be obtained from an animal at birth or before, selection decisions can be made earlier in life when using genomic selection than when selection is based on phenotype.

The technology to make transgenic animals has recently improved with the invention of CRISPR and talens. However, this improvement does not overcome the main obstacles to use of transgenesis in agricultural livestock and I suspect we are still years away from adoption of this technology in livestock.

Genotype by environment interactions (GxE) are not uncommon if we interpret E to include the market for which the livestock or their products are intended, the management system and the physical environment. Therefore, one might expect that efficiencies can be gained by breeding a line of animals for a particular environment – management- market combination (EMM). For instance, a line of dairy cows for cheese production or a line of meat sheep carrying the booroola gene for crossing with Merinos. However, the economies of scale work against this idea. It may be more economical to breed a general purpose line that can be sold to many customers rather than a specialist line that is sold to a few customers. This conflict deserves further consideration.

Most of the traits in the breeding objective of sheep and cattle are quantitative traits controlled by a very large number of genes, most of which have a small effect. However, in a few cases, there are known genes of large effect such as booroola for litter size in sheep and myostatin mutations causing double muscling in cattle and sheep. Few of these genes of large effect are deliberately used partially because they have unfavourable side effects. Generally their logical use would be in a line used for crossbreeding for a particular EMM and so utilisation of them depends on specialised lines as discussed above.

## CHALLENGES FOR YOUNG SCIENTISTS

The biggest opportunities to increase the rate of genetic gain are in utilising the synergy between genomic selection, reproductive technology and automatic phenotyping. Therefore we should aim to make genomic selection very accurate by using a large, across breed training population including commercial animals under commercial conditions and automatically recorded for traits in the breeding objective. To achieve high accuracy regardless of breed, we need a Bayesian statistical method rather than BLUP, based on genome sequence data from which we have identified the causal mutations or markers in near complete linkage disequilibria with them. To identify these causal mutations we will need to make use of biological information from which we can predict which sites in the DNA cause an effect on phenotype when mutated. Capturing phenotypic information on commercial animals is partly a technology problem (to make measurement very cheap) but also an organisational problem requiring support from industry leaders. To gain full benefit from this technology we need much cheaper reproductive technology such as JIVET and very cheap DNA testing. Cheap DNA testing will lead to more animals being tested and hence, potentially, a large training population provided phenotypic information on these animals can be captured and used for improving the accuracy of the genomic prediction equation. Among many advantages, this will allow animals to be allocated to their most profitable EMM based, in part, on DNA tests.

## CONCLUSIONS

For sheep and cattle farming to remain profitable, the economic efficiency will need to double over the next 35 years mainly by increasing production per ha. Genetic improvement can contribute to this objective by careful choice of breeding objectives, use of new technology such as genomic selection, reproductive technology and automated phenotyping

## 2015 HELEN NEWTON TURNER MEDALLIST CITATION

### DR ARTHUR GILMOUR

Dr Arthur Gilmour has made an outstanding contribution to the genetic improvement of Australian livestock, in particular through his development of and support for, software for analysing complex data for research and implementation.

Arthur joined NSW Agriculture in 1970, and spent 10 years as a Biometrician before completing a PhD at Massey under Professors Al Rae and Robert Anderson. He returned to NSW Agriculture where he continued working to 2009, retiring from the role of Principal Research Scientist with 41 years' service.

In his roles in NSW Agriculture, he assisted countless researchers in the design and analysis of experiments, particularly in sheep and plant breeding, as well as developing software used widely in Australia and overseas. These software tools have become "tools of the trade" for researchers and practitioners. An example of implementation software developed by Arthur is BVEST, which was the genetic analysis tool for LAMBPLAN in its formative decade, configured both for use by LAMBPLAN scanning operators and later for centralised analysis of increasingly large across-flock datasets.

Arthur is perhaps best known for the ASREML software, the development of which was stimulated by Arthur's interaction with Dr Robin Thompson, to apply REML methods efficiently, and with Dr Brian Cullis, leading to greatly enhanced models for analysis of plant breeding data. ASREML grew out of REG, which was attractive to users because it was comprehensive and allowed a wide choice of models – features central to ASREML. ASREML is cited in thousands of publications world-wide, and continues to be developed under Arthur's guidance and with his inputs.

Key to Arthur's contribution has been that the tools are backed by seemingly inexhaustible willingness to help others – in his own words: "My role has been to make new ideas in the area of mixed models accessible to general researchers so they can effectively explore their data."

This willingness to share was encapsulated in the citation for Arthur's 2001 Fellowship of the AAABG: "*Not only has ASREML been made readily available to researchers throughout the world, but a discussion group has also been set up that is better described as 'ask Arthur a question'. His generosity in time to individually answer and his resistance to describing perhaps 50% of the questions as stupid are exemplary.*"

Without accurate estimates of genetic parameters, understanding of how traits work genetically and hence genetic evaluation and improvement, are impossible. Arthur Gilmour's life work has enabled this fundamental task of genetics research, development and implementation to be conducted rigorously and accordingly is an extremely important underpinning contribution to the genetic improvement of livestock (and plants) in Australia.

*Footnote:*
*The full text of Dr Gilmore's oration will be published in the 22nd Proceedings of AAABG 2017.*