TABLE OF CONTENTS

Preliminary pages
President's Message ii
25th Conference Committee and Citation of Papers iii
Reviewers iv
Sponsors v
AAABG Rules vii
AAABG Fellows ix
AAABG Honorary Members x
Helen Newton Turner Medal xi
Helen Newton Turner Bright Futures Award xii
Table of Contents xiii

John Vercoe Memorial Lecture
The role of animal genetic resources in the sustainable livestock transformation 1
P. Boettcher, R. Baumung, G. Leroy and B. Besbes

Plenary Papers
Animal breeding is part of the solution to environment, climate, and animal-welfare challenges facing animal production 5
M. Henryon T. Ostersen, P.E. Vercoe and A.C. Sørensen
Livestock breeding, where have we been and what lies ahead? 10
S.P. Miller

Breeding Plans A
An optimal contribution selection technique that utilises on-additive genetic components 23
Z. Loh, J.H.J. van der Werf and S. Clark
Ewe genotype effects in genetic evaluation of Merino fleece traits across ages 27
S.I. Mortimer, K.L. Egerton-Warburton, T.L. Bird-Gardiner and A.A. Swan Evolution of sheep breeds within LAMBPLAN and the rise of the Composites 31
A.J. McMillan, S.F. Walkom and D.J. Brown
Genetic and economic effects of genomic selection amongst surplus dairy heifers in Australian dairy herds 35
J.M. Morton and G.J. Nieuwhof
Effects of selection and data truncation on estimates of genetic parameters obtained fitting a single-step model 39
K. Meyer
Genetic benchmarking of Maternal sheep flocks using genomic testing 43
D.J. Brown, P.M. Gurman and A.A. Swan
Preliminary evaluation of the impact of visual traits on lifetime ewe performance 47
P.K. Wahinya, D.J. Brown, S.F. Walkom, T. Bird-Gardiner, B.E. Clarke, J.L. Smith and A.A. Swan

Breeding for Reproductive Traits A
Comparison of udder and teat traits in Merino ewes recorded at lambing and weaning 51
E.G. Smith, G.A. Acton, A.M. Bell and J.L. Smith

Age at puberty, days to calving and first parity return to oestrus in Australian temperate beef breeds 55
K.A. Donoghue, R. Rippon, M. Wolcott, K.L. Moore, S.A. Clark and B.J. Walmsley
New module for prediction of reproductive traits EBV in BREEDPLAN 59
M.G. Jeyaruban and D.J. Johnston
Fibre diameter variation as a measure of resilience in sheep 63
E.G. Smith, S.F. Walkom and S.A. Clark
Development of female fertility indicator traits for the Angus HeiferSELECT genomic tool 67
P.A. Alexandre, L.R. Porto-Neto, B.C. Hine, A.M. Samaraweera, A.I. Byrne, A.B. Ingham, C.J. Duff and A. Reverter

Multinomics
Library preparation method affects observed microbiome variation when using Oxford Nanopore sequencing 71
E.M. Ross, Z. Chen, L.T. Nguyen, S. Meale and C. T. Ong
Simultaneous investigation of genomic regions of interest - the use of adaptive sampling 75
R.M. Clarke, A. Hess, A, Caulton, R. Brauning, K.M. McRae, A. Chen and S.M. Clarke
Gene network prediction for bull fertility traits 79
W.L.A Tan, N. Hudson, L.R. Porto-Neto, A. Reverter, J. Afonso and M.R.S. Fortes
Methylome profiling in response to stress: mycotoxin (sporidesmin) exposure in sheep 83
A. Caulton, K.M. McRae, K.G. Dodds, R. Brauning, N.K. Pickering, P.L. Johnson and S. M. Clarke

Breeding Plans B
Resources assessment for determination of ancestral alleles in cattle 87
J. Dorji, L.R. Porto-Neto, A.J. Chamberlain, C.J. Vander-Jagt, J. Kijas and A. Reverter
Incorporating genomic information in evaluations for farmed deer in New Zealand 91
R. Costilla, R. Brauning, J. Ward, S. Newman, A. Hess, S. Hickey, T. van Stijn, J. McEwan, K. Dodds, S. Clarke and S. Rowe
Understanding trait preferences and views on genetic tools for the New Zealand beef industry 95
L. Kok, S. Harburg, B. Santos, P. Amer, J. Archer, A. Boyd and G. Jenkins
The economic value of gestation length 99
E. Ooi, N. Howes, F. Hely, M. Stephen, P. Amer and C. Quinton
Australian beef cattle breeding objectives 103
B.W. Gudex, P.J. Williams and B.J. Walmsley
Signatures of positive selection for scrotal circumference in three beef cattle breeds 107
Z. Manzari, D.J. Johnston, N.K. Connors and M.H. Ferdosi
BREEDPLAN single-step genomic evaluations deliver increased accuracies across all breeds and EBVs 111
D.J. Johnston, M.H. Ferdosi, N.K. Connors, J. Cook, C.J. Girard and A.A. Swan

Breeding for Reproductive Traits B
Genotype by trait-specific season interactions for farrowing rate and average piglet birthweight 115
A.M.G. Bunz, K.L. Bunter, J. Harper, R. S. Morrison, B.G. Luxford and S. Hermesch

Translating multibreed genomic prediction of bull fertility traits into on-farm selection of bulls 119
L.R. Porto-Neto, P. Alexandre, J. Dorji, M.R.S. Fortes and A. Reverter
The highs and lows of recording calf and calving traits 122
M. Axford, M. Khansefid E. Jewell, A. Chamberlain and J.E. Pryce
Using foetal age estimates to substitute birth date recording in beef cattle evaluations 126
J. Kang, F. Weik, N. Sanderson, D. Robertson and J.A. Archer
Prediction of gestation length and days to conception from foetal age scans for genetic improvement of maternal fertility in beef cow herds: a simulation study 130
F. Weik, J. Kang and J.A. Archer
Match birthweight ASBVs to flock fecundity for lamb survival 134
S. Hatcher, S. Robertson, D.J. Brown and K.L. Bunter
FecB carrier Deccani crossbred ewes in Maharashtra, India have moderately higher litter sizes than non-carrier ewes 138
C. Nimbkar, P.M. Ghalsasi, S.W. Walkden-Brown and J.H.J. van der Werf

Prediction/Genomic Prediction Beef
Using genomic and phenotypic data to characterise the genetic structure of Brahman cattle populations in Southern Africa 142
W.M.S.P. Weerasinghe and B.J. Crook
Application of an empirical approach for predicting accuracy for genomic evaluations 146
K.L. Moore, P.M. Gurman and D.J. Johnston
Genomic prediction using imputed whole-genome sequence in Australian Angus cattle 150
N. Kamprasert, H. Aliloo, J. van der Werf, C. Duff and S. Clark
Comparing genomic prediction accuracies for commercial cows' reproductive performance using GA2CAT and two machine-learning methods 154
Y. Li, S. Hu, L. Porto-Neto, R. McCulloch, S. McWilliam, J. McDonald, C. Smith, P. Alexandre, S. Lehnert and A. Reverter
Assessing the value of metafounders for genomic prediction in Australian Simmental beef cattle 158
D.J.A. Santos, N.K. Connors, P.M. Gurman, M.H. Ferdosi, S.P. Miller and A.A. Swan
Imputation accuracy for missing alleles in crossbred beef cattle 162
P.K. Wahinya and M.H. Ferdosi

Prediction/Genomic Prediction Dairy
Estimation of SNP effects in Lacaune dairy sheep depending on the reference population composition 166
M. Wicki, J. Raoul and A. Legarra
Genetic evaluation of longevity using productive life and survival scores in Australian Holstein cattle: prediction of early survival 170
M. Haile-Mariam, M. Khansefid, M. Axford, M.E. Goddard and J.E. Pryce

Novel Traits: Environment and Greenhouse Gas
Heritability and repeatability of methane emissions and feed intake in young dairy sires 174
R.C. Handcock, D.J. Garrick, D.P. Garrick, R.J. Spelman, P. van Elzakker, P. Beatson, G. Worth and L.R. McNaughton

Towards selecting for lower methane sheep 178
P.T Fitzgerald, E.H. Clayton, A.J. Donaldson, D.J. Brown, V.H. Oddy and J.H.J van der Werf
Using rumen microbial predictors for genomic prediction of feed efficiency 182
T.P. Bilton, P.L. Johnson, F. Booker, H.H. Henry, M.K. Hess, R. Jordan, S.M. Hickey, H. Baird, N. Amyes, J.C. McEwan and S.J. Rowe
Implementing genetic tools to reduce methane emissions in NZ sheep flocks 186
J.A. Archer, M.D. Aspin, D.E. Brier, S-J. H. Powdrell, D. Campbell, C.L. Winkworth-Lawrence, S.J. Rowe, J.C. McEwan and M. Lee

Genetic Diversity and Inbreeding A
A comparison between the use of pedigree or genomic relationships to control inbreeding in optimum-contribution selection 190
M. Sharif-Islam, M. Henryon, J.H.J. van der Werf, A.C. Sørensen, T.T. Chu, B. J. Wood and S. Hermesch
Detection of signatures of selection in Australian beef cattle 194
H. Aliloo, B.J. Walmsley, K.A. Donoghue and S.A. Clark
Demonstrating differences in survival and fertility of high and low genetic merit cows within and across herds 198
J.E. Newton, M. Haile-Mariam and J.E. Pryce
Population scale long-read sequence databaseses: are they useful for accurate SNP and indel discovery? 202
I.M. MacLeod, T.V. Nguyen, J. Wang, C.J. Vander Jagt and A.J. Chamberlain
Epigenetic repression of genes associated with ribeye area of Nelore cattle 206
J. Afonso, M.R.S. Fortes, W.J. Shim, T.F. Cardoso, J.J. Bruscadin, A.O. de Lima, W.J.S. Diniz, B. Silva-Vignato, W.L.A. Tan, A.S.M. Cesar, M. Boden, G.B. Mourão, A. Zerlotini, L.L. Coutinho and L.C. de Almeida Regitano

Meat Quality
Genomic prediction of consumer satisfaction traits of Australian beef 210
A.M. Lynn, P. McGilchrist, H. Aliloo, R. Polkinghorne, M. Forutan, B.J. Hayes and S.A. Clarke
Relationships of sire breeding values for Merino production traits with eating quality of lamb 214
S.I. Mortimer, B.W.B. Holman, S.M. Fowler, T.I.R.C. Alvarenga, D.L. Hopkins, K.L. Egerton-Warburton, J.L. Smith, B.C. Hine and A.A. Swan

Epigenetics, Structural Variants & Transcriptomes
Cost effective detection of deleterious structural variants in long-read sequence – How deep is enough? 218
T.V. Nguyen, J.Wang, A.J. Chamberlain and I.M. MacLeod
Heritability and repeatability of paternal haplotype recombination rate in beef cattle autosomes 222
M.H. Ferdosi, S. Masoodi and M. Khansefid

Genetic Diversity and Inbreeding B
Characterising heterozygosity of the X chromosome in the Australian Wagyu population 226
D.P. Garrick, R.C. Handcock and C. Teseling

Measured Goats in the Rangelands: An overview of a meat goat reference population 230
T. Granleese, S.I. Mortimer, T. Atkinson, G. Refshauge, T. Bird-Gardiner, F. Haynes, D.J. Brown, P. Alexandri and S.F. Walkom
Selecting for more methane efficient sheep 234
J.H.J. van der Werf

Novel Traits and Phenotyping Tools B
Investigating the genetic cause of Wry Face in the Australian Jersey cattle population 238
C.J. Vander Jagt, C.M. Reich, I.M. MacLeod, M.E. Goddard, B.J. Hayes, T.T.T. Nguyen, G.J. Nieuwhof and A.J. Chamberlain
Importance of incorporating feeding rate when developing predictions of feed intake 242
P.L. Johnson, K. Knowler, T.P. Biton and S.J. Rowe
Remote sensor collars measure age at puberty in tropical beef heifers in northern Australia 246
D.J. Johnston, M. Dayman, T.P. Grant, K. Hubbard, K. Goodwin, A.K. Doughty and J.D. Cook

Understanding and Utilising Genetic Diversity
Genetic diversity of domestic goats from Central Laos 250
S.V. Le, S. de las Heras-Saldana, P. Alexandri, L. Olmo, S.W. Walkden-Brown and J.H.J. van der Werf

Infectious Diseases/Disease Resistance
Immune competence and micro-environmental sensitivity 254
M.D. Madsen, J.H.J. van der Werf, A. Ingham, B. Hine, A. Reverter and S. Clark
An across-flock analysis on faecal worm egg counts in Merino sheep in South Africa 258
S.W.P. Cloete, Z. Mpetile and K. Dzama
Genetic variation in susceptibility to facial eczema in dairy cattle in New Zealand 262
A. Ismael, E. Donkersloot, F. Wallace, G. Worth, S. Davis, L. McNaughton and R.J. Spelman
Faecal microbiota of Angus cattle with divergent immune competence 266
B.N. Maslen, B.C. Hine, C. Duff, P.A. Alexandre, S.A. Clark, J.H.J van der Werf, J.D. White and S.D. Pant

GWAS
Multi-trait genome wide association meta-analysis of body weight, carcase composition and eating quality traits in Australian sheep 270
N. Moghaddar, A.A. Swan and J.H.J. van der Werf
Discovering the missing variation in the bovine genome; a long read sequencing pilot study into the structural variation in two dairy breeds 274
A. Chamberlain, T. Nguyen, J. Wang and I. Macleod
X and Y chromosome SNPs as indicators of sex in quality assurance checks for genomic analysis in Wagyu 278
C. Teseling and D.P. Garrick
Genome wide association study and heritability estimates for ram semen traits 282
M.J. Hodge, S. de las Heras-Saldana, S.J. Rindfleish, C.P. Stephen and S.D. Pant
Online Mendelian Inheritance in Animals (OMIA) – looking to the future 286
I. Tammen, M. Mather, D. Vanichkina, J. Nothman, Z. Li, S. Jufri and F.W. Nicholas

Novel Traits and Phenotyping Tools A

Genetic evaluation of coat type for Australian Angus 290
A.M. Samaraweera, H. Aliloo, A. Byrne, C.J. Duff and S.A. Clark
Genetic parameters for linear type traits in Hungarian Charolais beef cattle 294
B.J. Crook, W.M.S.P. Weerasinghe and M. Torok
Validation of breeding values for robustness in Australian Merinos 298
D.L. Waters, J.H.J. van der Werf, D.J. Brown, S.F. Walkom and S.A. Clark
Merits of using new intramuscular fat measurement technologies in genetic evaluation of Australian lamb 302
P. Alexandri, S.F. Walkom, S. Stewart, P. McGilchrist, C. Steel and D.J. Brown
Merits of using DEXA to measure lean meat yield for the genetic evaluation of Australian lamb 306
S.F. Walkom, P. Alexandri, S. Connaughton, G. Gardner, A. Williams and D.J. Brown
Progress of the Southern Multi-Breed Resource Population: Hard-to-measure phenotypes to drive genomic selection 310
B.J. Walmsley, K.L. Moore, S.F. Walkom, S.A. Clark, T. Granleese and K.A. Donoghue

Genetic Evaluation A

Estimate the genetic parameters and analysis of culling reasons in Iranian Holstein dairy cattle 314
H. Keshavarzi, E. Dehnavi and A. Small
Genetic parameters and lambda values for post-weaning production traits in Merino sheep 318
S. de las Heras-Saldana, P. Gurman, A.A. Swan and D.J. Brown
Longevity of reference populations in a trans-Tasman genetic evaluation: Review of the Angus Sire Benchmarking Program 322
S.F. Walkom, C.J. Duff, C. Girard and K. Moore
Angus BreedCHECK – Validation using industry data 326
C.J. Duff, A.M. Samaraweera, A.I. Byrne, A.B. Ingham, P.A. Alexandre, L.R. Porto-Neto and A. Reverter
Quantifying the linkage between genetics represented in the Southern Multi-Breed project and the wider Australian beef populations 330
K.L. Moore, S.F. Walkom, J.P. Siddell and B. Walmsley
Utility of pooled DNA samples for estimating a flock profile 334
P.M. Gurman, K. Gore and D.J. Brown
Assessing the influence of BayesR and GBLUP SNP effects in the correlation scan methodology 338
B.S. Olasege, I. van den Berg, E.J. Breen, M. Haile-Mariam, P.N. Ho, L.R. Porto-Neto, B.J. Hayes, M. Goddard, J.E. Pryce and M.R.S. Fortes

Health and Welfare A

The value of research and industry flocks for predicting breech strike resistance in Australian Merino sheep 342
E. Dehnavi, A.A. Swan, J.L. Smith, T.L. Bird-Gardiner, G. Burbidge and D.J. Brown
Development of a new BREEDPLAN objective body composition EBV to allow selection to improve cow survival 346
M.L. Wolcott, D.J. Johnston, M.G. Jeyaruban and C.J. Girard

Serum health biomarkers are significantly correlated with gene expression during the transition period of dairy cows 350
A. Kudriashova, A.J. Chamberlain, J.E. Newton, C.R. Bath, C.J. Vander Jagt, C.M. Reich, B.A. Mason, J.E. Hemsworth and M.E. Goddard
Preliminary genetic parameters for flystrike and its association with production traits in Australian Merino sheep 354
E. Dehnavi, A.A. Swan, A.M.M. Ramsay, G. Burbidge and D.J. Brown

Breeding for Reproductive Traits - Dairy
Milk production and fertility of spring-calved Holstein-Friesian, Jersey and crossbred cows milked once daily or twice daily in New Zealand 358
J.M.D.R. Jayawardana, N. Lopez-Villalobos, R.E. Hickson and L.R. McNaughton
Conception based fertility trait for genetic evaluation of New Zealand dairy cattle 362
K. Stachowicz, E.C. Ooi, B. Santos and P.R. Amer
Attributes of lactating cows ranked divergently for fertility using a milk mid-infrared spectroscopy based prediction model 366
A.R. Bird, J.E. Newton and P.N. Ho

Genetic Evaluation B
Appropriateness of combining carcass data from Angus sire benchmarking program and breeder herds in a single genetic evaluation 370
A.M. Samaraweera, A. Byrne and C.J. Duff
Infoherds, genomic selection for dairy cattle in New Zealand 374
B. Santos, N. Howes, S. Harburg, E. Ooi, S. Meier, A. Fear and P. Amer
Validation of calving ease EBVs examining the impact of genetic groups and single-step on predictive ability 378
P.M. Gurman, L. Li, M.G. Jeyaruban, D.J. Johnston, C.J. Girard, and A.A. Swan

Resource Allocation & Genetics of Intake and Efficiency
Remodelling the genetic evaluation of NFI in beef cattle - Part 1: Developing an equivalent genetic model 382
L.Vargovic, K.L. Moore, D.J. Johnston, G.M. Jeyaruban, C.J. Girard, J. Cook, J.A. Torres-Vázquez and S.P. Miller
Remodelling the genetic evaluation of NFI in beef cattle - Part 2: Shortening the length of the feed intake test 386
L.Vargovic, K.L. Moore, D.J. Johnston, G.M. Jeyaruban, C.J. Girard, J. Cook, J.A. Torres-Vázquez and S.P. Miller
Across-breeds systems biology analysis reveals key genes contributing to feed efficiency in beef cattle 390
K. Keogh, D.A. Kenny, P.A. Alexandre, M. McGee and A. Reverter

Producer Day
Identification of climate-resilient Merino sheep using satellite images 394
S. de las Heras-Saldana, L.A. Suarez, P.K. Wahinya, K.L. Bunter and D.J. Brown