

TABLE OF CONTENTS

Preliminary pages	
President's Message	iii
26 th Conference Committee and Citation of Papers	iv
Reviewers	v
Sponsors	vi
AAABG Rules	viii
AAABG Fellows	x
AAABG Honorary Members	xxi
Helen Newton Turner Medal	xxii
Helen Newton Turner Bright Futures Award	xxiii
2023 Helen Newton Turner Medalist Oration	xxiv
John Vercoe Memorial Lecture	xxviii
Table of Contents	xxix
Plenary Papers	
Global regulations governing genome editing in food animals <i>A.L. Van Eenennaam</i>	1
Growing Aotearoa New Zealand's aquaculture industry through breeding and genomics: Progress, challenges and opportunities <i>J.E. Symonds, M.R. Scholtens, K.G Dodds, S.M. Clarke, R. Costilla, S.P. Walker, N. King, N.L.C. Ragg, M. Camara, J.A. Ericson, J. Vignier, M. Wellenreuther, Z. Waddington, J. Bailey, R.D. Roberts, E. Malpot, M.L. Tate and T. Slattery</i>	6
John Vercoe Memorial Lecture	
Climate change mitigation through genetic improvement – A deeply worthwhile challenge in the spirit of John Vercoe <i>R.G. Banks</i>	13
Sustainability – Feed Efficiency and Methane	
Measurement of feed intake in sheep using "off the shelf" technologies <i>P.T. Fitzgerald, R.L. Hergenhan and J.H.J. van der Werf</i>	18
Feed-intake and methane efficiency for weight and growth pre-slaughter of MLA resource flock lambs <i>B. Paganoni, B. Bolt, A. Bowden, P. Fitzgerald, S.F. Walkom and J.H.J. van der Werf</i>	22
Selecting for efficiency in long-fed cattle is important <i>W.S. Pitchford</i>	26
Genetic insights into methane emission traits in indoor-fed growing cattle <i>S.B. Crowley, D.C. Purfield, S.B. Conroy, D.N. Kelly, R.D. Evans and D.P. Berry</i>	30
Methane emissions of low and high methane yield selection line sheep fed ryegrass-based pasture across multiple periods <i>A. Jonker, S. Hickey, J.C. McEwan, E. Sandoval, S. MacLean and S. Rowe</i>	34
Effect of winter forage brassica grazing on methane selection line sheep <i>F.L. Booker, S.M. Hickey, T.P. Bilton, I. Hampton, B. Bryson, M. Ward, P.L. Johnson, J.C. McEwan and S.J. Rowe</i>	38

Table of Contents

Portable accumulation chambers for measuring enteric methane in cattle <i>T.P. Bilton, S.M. Hickey, A. Searle, I. Hampton, F. Booker, C. Rodgers, S. Sevier, S. Gebbie, K.G. Dodds, G.M. Jenkins, J.A. Archer, J.C. McEwan and S.J. Rowe</i>	42
Factors affecting methane production of composite and crossbred cattle grazing tropical and subtropical pastures in Northern Australia <i>C. Whistler, K. McCosker, C. Warburton, D. Johnston, T. Grant, B. Taylor, K. Goodwin, M. Dayman, N. Scott, S. Cullen, M.H. Dekkers, S. Clark and B.J. Hayes</i>	46
Novel Traits	
Genetic analysis of sensor-based activity traits in Australian Merino sheep <i>H. Keshavarzi, E. Dehnavi, J. McNally, J.L. Smith and S. Schmoelzl</i>	50
Assessing behavioural rigidity and its genetic influences in Australian Wagyu cattle <i>A. Lloyd, M. Facy and J. Grose</i>	54
An examination of multibreed temperament measures recorded in the Southern Multi-Breed Resource Population <i>B.J. Walmsley, K.L. Moore, R. Woodgate, S.A. Clark, F.E.M. Haynes and K.A. Donoghue</i>	58
Genetic risk factors for tail biting in Australian pigs as determined by binomial regression models <i>D. van Winden, R.Y. Galea, M.N. Aldridge, P.M. Gurman and S. Hermesch</i>	62
Genetic parameters of being a tail-biting recipient in pigs <i>A.A. Reda, M.N. Aldridge, P.M. Gurman and S. Hermesch</i>	66
Genetic correlations between purebred and crossbred pre- and post-weaning piglet mortality <i>J. Harper and K.L. Bunter</i>	70
Genetic analysis of sow udder treatments <i>A.M.G. Bunz, J. Harper and K.L. Bunter</i>	74
Implementation and delivery of the Wagyu Feeder Check <i>C.F. Teseling, M.B. McDonagh and D.P. Garrick</i>	78
Genomic Prediction 1	
Cost-benefit of a genomic reference population for goats in Australia <i>T. Granleese and S.F. Walkom</i>	82
Genomic models for estimating genetic parameters for lifetime wool traits in Merino sheep <i>P.K. Wahinya, D.J. Brown, B.E. Clarke, J.L. Smith, T. Bird-Gardiner, A.A. Swan</i>	86
Evaluating the accuracy of SNP-BLUP and admixture for breed composition prediction in rare and well-represented cattle breeds <i>C.A. Ryan</i>	90
IBS versus IBD - new insights from whole genome sequence data <i>C.L. Warburton, R. Costilla, M.E. Goddard, B.J. Hayes and T.H.E. Meuwissen</i>	94
The molecular cattle for precision breeding <i>R. Xiang, M.E. Goddard, A.J. Chamberlain and J.E. Pryce</i>	98
Recovering the obscured genetic architectures through deconvolution of GWAS statistics <i>Z. Loh</i>	102
Sort & Paste: A numerical method to render any random variable heritable given a genotype <i>A. Reverter and P.A. Alexandre</i>	106

Table of Contents

Assessing the effectiveness of low-coverage nanopore sequencing in genomic selection: A comparison between Clair3 and QUILT pipelines <i>L.T. Nguyen, H. Lamb, J. Copley, B.J. Hayes and E.M. Ross</i>	110
Aquaculture	
Estimating thermal tolerance in selectively-bred New Zealand Greenshell mussels (<i>Perna canaliculus</i>) <i>M.R. Scholtens, R. Roberts, N.J. Delorme, N. King, N.L.C. Ragg, R. Costilla and J.A. Ericson</i>	114
Genotype-by-environment interactions in Yellowtail Kingfish: Implications for genetic improvement. <i>M. Camara, A. Setiawan, J.W.M. Bastiaansen and N.K. Jacob</i>	118
Marker-based family assignment without parent genotypes <i>K.G. Dodds, J.E. Symonds, S.J. Rowe and J.C. McEwan</i>	122
Applying machine learning to unlock genomic insights in snapper breeding <i>J. Blommaert and M. Wellenreuther</i>	126
Fast-tracking farmed king salmon climate change adaptation <i>J.E. Symonds, M.R. Scholtens, K.G. Dodds, R. Costilla, S.M. Clarke, J. Arinez, N.J. Kenny, S.P. Walker and Z. Waddington</i>	130
Sustainability – Methane	
Methane and carbon dioxide emissions in Australian Angus – past and present <i>M.D. Madsen, C.J. Duff, M. Samaraweera, L.A. Mowbray, T. Granleese, R. Hergenhan, T. Bird-Gardiner, P.F. Arthur and S.A. Clark</i>	134
Validation of genomic prediction for methane emissions in Australian Merino sheep <i>M.N. Aldridge, S.I. Mortimer, D.J. Brown, P.T. Fitzgerald, E.H. Clayton, A. Donaldson, B. Paganoni, A. Thompson, V.H. Oddy and J.H. van der Werf</i>	138
Building a reference population to enable genomic selection for methane related traits in beef cattle <i>S. Clark, M. Madsen, R. Hergenhan, C. Duff and T. Granleese</i>	142
Repeatability and heritability of dairy cow methane concentration using sniffer sensors <i>F. Almasi, S.R.O. Williams, C.J. Vander Jagt, L.C. Marett, J.L. Jacobs and J.E. Pryce</i>	146
Methane index explorer: Optimising a breeding value format for simultaneous inclusion of enteric methane emissions in breeding schemes and national inventories <i>P.C. Ariyarathne, S.M. Hickey, T.P. Bilton, P. Johnson, N.K. Pickering, S.J. Rowe and J.C. McEwan</i>	150
Incorporation of direct methane traits in national breeding objectives <i>F. Hely, D. Kenny, N. Howes and P. Amer</i>	154
The Green Cow project: developing a methane efficiency genomic breeding value for the Australian dairy industry <i>C.J. Vander Jagt, F. Almasi, B.J. Sepulveda, L.C. Marett, S.R.O. Williams, R. Xiang, S. Bolormaa, M. Shaffer, J. Penry, C. Hill, D. Gibson, J.L. Jacobs and J.E. Pryce</i>	158
Dairy	
Industry perspectives on calf traits <i>M.M. Axford, M. Khansefid and J.E. Pryce</i>	162
Correlation of cow mortality and culling (sale) rate with selected type traits in Australian Holstein and Jersey cattle	166

Table of Contents

<i>M. Haile-Mariam, M.E. Goddard, M. Axford, J. Newton and M. Khansefid</i>	
Updating the genetic prediction model for cow survival in Australia <i>M. Khansefid, J.E. Pryce, J.E. Newton, M. Axford, G. Nieuwhof, M.E. Goddard and M. Haile-Mariam</i>	170
Selection for first parity linear-type traits in the New Zealand dairy cattle population <i>M.A. Nilforooshan, R.G. Sherlock and B.L. Harris</i>	174
Evaluating genetic and phenotypic relationships of six traits other than production (TOP) in dairy cattle prior to their adoption in New Zealand <i>R.C. Hancock, D.P. Garrick and M.A. Stephen</i>	178
Dual-purpose Norwegian red cattle for sustainable dairy and beef productions in pasture-based systems <i>C. McKimmie, H.A. Najafabadi, E. Noble-Campbell, J. Hoffmann and J. Jenko</i>	182
Agriculture Institute Australia's Student Compendium is building a sustainable research, development and adoption workforce <i>B. Hancock and T. Manning</i>	185
Genomic Prediction 2	
Multi-trait genomic models with trait and marker specific weights can substantially increase the accuracy of genomic breeding values <i>T. Meuwissen and V. Boerner</i>	189
Integrating whole genome sequence variants selected from large-scale association analysis into a single-step marker model in New Zealand dairy cattle <i>Y. Wang, M.A. Nilforooshan, R.G. Sherlock, A.M. Winkelman and B.L. Harris</i>	193
A linkage disequilibrium method to reposition single nucleotide polymorphism and improve genotype imputation accuracy <i>Y. Fazel, K. Moore, S. Miller and M.H. Ferdosi</i>	197
Multi-breed genomic estimated breeding values predict liveweight production in North Australian beef cattle <i>B.J. Hayes, G. Fordyce, E. Dodd, S. Speight and K. McCosker</i>	201
Estimates of accuracy for genomic-only breeding values and flock profiles in Australian Merino sheep <i>L. Li, P.M. Gurman, A.A. Swan and D.J. Brown</i>	205
Helical: A full-stack agile platform enabling data flywheels and data sharing to empower modern breeding programs <i>D.P. Garrick, D.J. Garrick and J.E. Howse</i>	209
Alignment of pedigree and genomic information in a combined terminal sire and maternal sheep analysis <i>P.M. Gurman, P. Alexandri, D.J. Brown, K.L. Bunter, S. de las Heras-Saldana, K.P. Gore, L. Li, A.J. McMillan, S.F. Walkom and A.A. Swan</i>	213
Implementing genomic outcomes for simulated progeny to support mating decisions <i>D.P. Garrick, J.E. Howse and C.F. Teseling</i>	217
Sustainability Methane Prediction	
Association between rumen and faecal microbiome and enteric methane emissions in dairy cattle <i>B.J. Sepulveda, C.J. Vander Jagt, A.J. Chamberlain, J. Wang, L.C. Marett, S.R.O. Williams, J.L. Jacobs and J.E. Pryce</i>	221
Metagenomic predictions for enteric methane emissions in sheep using long-read sequencing of rumen fluid samples	225

Table of Contents

<i>Y. Li, L.T. Nguyen, C.T. Ong, S. Yadav, M. Aldridge, P. Fitzgerald, J. van der Werf and E. M. Ross</i>	
Proxies in practice: Implementing rumen metagenomic profiles for genomic selection of methane emissions <i>T.P. Bilton, P.L. Johnson, H. Henry, B.J. Perry, F. Booker, J. Peers-Adams, M. Ward, B. Bryson, S.M. Clarke, J.C. McEwan, L.W. Coleman, N.K. Pickering, K.G. Dodds and S.J. Rowe</i>	229
Tissue-specific RNA expression data enhances genomic prediction of methane emissions in sheep <i>S.W. Alemu, T.P. Bilton, B.J. Perry, H.M. Henry, K.M. McRae, K.G. Dodds, J.C. McEwan, S.M. Clarke and S.J. Rowe</i>	233
Use of mid-infrared spectroscopy data for improving accuracy of genomic prediction for methane emissions <i>S. Bolormaa, P.N. Ho, I.M. MacLeod, M. Haile-Mariam, L.C. Marett, S.R.O. Williams, J.L. Jacobs, C.J. Vander Jagt, M.E. Goddard, R. Xiang, and J.E. Pryce</i>	237
Exploring adaptive sequencing for efficient profiling of methanogenic microbiomes in cattle oral samples as a proxy for methane prediction and mitigation studies <i>Z. Chen, J. Silaban, E.M. Ross and C.T. Ong</i>	241
Evaluating oral swabbing as a practical alternative to rumen sampling for large-scale methane emission studies in grazing animals <i>C.T. Ong, Z. Chen, A.S. Cavallaro, M.R.S. Fortes, M. Dekker, A. Boulton, B. Kniwesky and E.M. Ross</i>	245
Maternal traits & survival	
Effects of adding a new fertility trait to the Angus Australia HeiferSELECT index <i>C.D. Quinton, S. Harburg, L.E. Proctor, P.R. Amer, C.J. Duff and A.M. Samaraweera</i>	249
The influence of spermatozoal motility on conception and scan count following artificial insemination in sheep <i>M.J. Hodge, S.J. Rindfleish, L. Li, C.P. Stephen, S.D. Pant and S. de las Heras-Saldana</i>	252
Genetic parameters for cause of death traits in lambs and indicator traits linked to neonatal survival <i>M. Hebart, R. McEwin and F.D. Brien</i>	256
A revisiting of the genetics of lamb survival and related traits, as part of the Fit to Lamb Project <i>R.A. McEwin, M.L. Hebart and F.D. Brien</i>	260
An ex-post cost benefit analysis of the Ovita lamb survival project <i>K.M. McRae, J.M. Everett-Hincks, S.-A. Newman, W.E. Bain, G. Greer, H. Baird, H. Manley, G. Shackell, S.M. Clarke, K.G. Dodds, N. Amyes, N. Jopson, M. Lee, P.L. Johnson, S.J. Rowe and J.C. McEwan</i>	264
Genetics parameters for gestation length with early in life growth traits in an Australian Wagyu population <i>M. Facy, A. Lloyd and J. Grose</i>	268
Across-breed analysis of maternal traits in New Zealand beef cattle <i>J. Kang, D.J. Garrick, M.A. Lee, F. Weik and J.A. Archer</i>	272
Breeding Programmes	
Multi-trait selection with desired gains and non-linear indexes <i>J.H.J. van der Werf</i>	276

Table of Contents

Digital twin: Modelling breeding program approaches in Australian Wagyu <i>J. Copley, B. Hayes, G. Moser, B. Engle, K. Villiers and M. Kelly</i>	280
Routine diagnosis of genetic evaluations and auto standardisation to non-linear cost function <i>X. Zhang, F. Hely, K. Stachowicz and P. Amer</i>	284
Micron premiums and their role in Merino breeding programs <i>S.F. Hatcher, A.E. Casey, S.F. Walkom, D.J. Brown and A.A. Swan</i>	287
Cost - benefit of genotyping commercial Merino sheep <i>G. Rose, S. Martin, D.J. Brown, L.P. Kahn and J.H.J. van der Werf</i>	291
A comparison of progeny of selected and unselected sires within the setting of a community-based breeding programme catering to women smallholder goat rearers in Bihar, India <i>S. Abeykoon, P. Amer, P. Wilcox and C. Nimbkar</i>	295
Optimal breeding programs for Lao native goats in smallholder systems <i>S.V. Le, S. de las Heras-Saldana, P. Alexandri and J.H.J. van der Werf</i>	299
Genetic diversity & inbreeding	
Identification of relationships and pedigree simplification using graph theory <i>M.H. Ferdosi and D. Johnston</i>	303
Assessing the genetic diversity of Australian goats <i>P. Alexandri, T. Atkinson, D.J. Brown, K. Gore, K. Smith, S.F. Walkom and T. Granleese</i>	307
Breed comparisons in combined LAMBPLAN: Genetic group and linkage assessment <i>A.J. McMillan, P. Alexandri, P.M. Gurman, D.J. Brown, K.L. Bunter, K.P. Gore, S. de las Heras-Saldana, L. Li, S.F. Walkom and A.A. Swan</i>	311
Using genotyping by sequencing to monitor the genetic diversity of Australian honey bees <i>P. Alexandri, S.P. Miller, E.A. Frost, N.C. Chapman, S.F. Walkom, R.G. Banks and K.L. Bunter</i>	315
Breed-of-origin of alleles and genomic breed composition estimation in New Zealand crossbred dairy cattle <i>Y. Wang, A.M. Winkelman and B.L. Harris</i>	319
Ascertaining the breed composition of an admixed sheep populations using genomic information: a simulation study <i>S. Sahoo, M.H. Ferdosi, J.H.J. van der Werf and S. de las Heras-Saldana</i>	323
Genomic inbreeding measures for Australian Wagyu - methods and implications <i>D.P. Garrick, D.J. Garrick and C.F. Teseling</i>	327
Absence of C>T polymorphism in the intron (5'-UTR) region of the MTHFR gene in Indian Barbari goats <i>A. Kumar, S.P. Singh, D. Sharma, G. K. Gupta, Pooja, A. Chauhan, V. Aditya and B. Kumari</i>	331

Table of Contents

Meat and Growth	
Genetic correlations of Merino meat colour traits with lean meat yield and eating quality <i>S.I. Mortimer, S.M. Fowler, B.W.B. Holman, T.I.R.C. Alvarenga, D.L. Hopkins, K.L. Egerton-Warburton, J.L. Smith, B.C. Hine and A.A. Swan</i>	335
Genetic parameter estimation of carcase quality phenotypes measured with cameras in Australian Wagyu <i>E. de Bruyn, K.L. Moore and S.P. Miller</i>	339
Multibreed genomic evaluation for sensory eating quality of lamb using consumer assessments <i>D.J. Brown, S.Z.Y. Guy, S.I. Mortimer, L. Pannier, P. McGilchrist, D. Pethick and A.A. Swan</i>	343
Estimated frequencies of myostatin mutations (double muscling) in Australian tropically adapted beef breeds <i>K.L. Moore, D.J. Johnston and T. Grant</i>	347
Identification of genes harbouring mutations affecting eating quality traits in beef cattle using Bayesian genomic prediction methods <i>M. Forutan, H. Aliloo, S. Clark, P. McGilchrist and B. Hayes</i>	351
Genetic correlations between mature body condition, weight, and hip height and early fat-depth traits in Australian Angus cattle <i>M. Samaraweera, H. Aliloo, C.J. Duff and S.A. Clark</i>	355
Joint modelling of mean and dispersion increases the accuracy of random regression on simulated growth curves <i>C.L. Nel and A.R. Gilmour</i>	359
Accuracy of genomic predictions for beef eating quality traits <i>H. Aliloo, M. Forutan, P. McGilchrist, B. Hayes and S. Clark</i>	363
Yearling weight and horn traits in South African Merino lines divergently selected for and against number of lambs weaned <i>S.W.P. Cloete, C.L. Nel and J.J.E. Cloete</i>	367
Alternative Omics Approaches	
Microbiability and heritability of deer seasonality traits <i>J.L. Clarke, T.P. Bilton, H. Henry, K.M. McRae, F. Booker, B. Veenvliet, W. Bain, J.A. Ward, B. Thompson, D. Stevens, J.C. McEwan, B.J. Perry, M.A. Black and S.J. Rowe</i>	371
Characterisation of short tandem repeats (STRs) in cattle using long read sequencing <i>Q.H. Tran, I.M. MacLeod, T.V. Nguyen, J. Wang and A.J. Chamberlain</i>	375
Considerations in imputation of Skim Sequenced data <i>M.S. Tahir, J. Wang, A.J. Chamberlain, C.M. Reich, B.A. Mason and I.M. MacLeod</i>	379
The feasibility of an imputation reference population for structural variation in cattle <i>A.J. Chamberlain, T.V. Nguyen, J. Wang, X. Wang, C.J. Vander Jagt and I.M. MacLeod</i>	383
Insights from population-scale long-read sequencing: structural variant characterisation and annotation <i>T. Nguyen, J. Wang, A. Chamberlain and I. Macleod</i>	387

Table of Contents

Exploring blood biomarkers as potential intermediate phenotypes for transition cow diseases: a foundation for future multi-omics integration <i>A. Kudriashova, A.J. Chamberlain, J.A.A. McArt, J.E. Hemsworth, C. M. Reich and M.E. Goddard</i>	391
Using multi-omics data to identify candidate genes for milk lactose percentage in dairy cattle <i>M. Ghoreishifar, R. Xiang, T. Lopdell, M. Littlejohn, A. Chamberlain, J. Pryce and M. Goddard</i>	395
Evidence of chromosome x association with knobbed acrosomes <i>B.S. Firewski, W.L.A. Tan, T. Melo, L.R. Porto-Neto, A. Reverter, M. McGowan and M.R.S. Fortes</i>	399
Health and Welfare	
Preliminary investigation of the genetics of shedding in maternal sheep <i>S.F. Walkom, J.R. Keiller, M.P. Kelly and D.J. Brown</i>	402
Genetic evaluation of tail length in Australian sheep <i>M.J. Hodge, D.J. Brown and S.F. Walkom</i>	407
Assessing genetic variability in flystrike resistance across expression levels in Australian Merino sheep <i>E. Dehnavi, A.A. Swan, B.C. Swain, J.C. Greeff, J.L. Smith, G. Burbidge, A.M.M. Ramsay, T.L. Bird-Gardiner and D.J. Brown</i>	411
The role of conformation traits in evaluating heat tolerance in dairy cattle <i>L.M. Jensen, M. Haile-Mariam, S. Bolormaa and J.E. Pryce</i>	415
Linear analysis of rumen themologger data to compare tolerance to heat challenge in eight sheep breeds <i>C.L. Nel, K. Mafunga, S.K. Maloney, T.S. Brand, K. Dzama, P.G. Theron and S.W.P. Cloete</i>	419
The effect of tree shade and breed on heat stress indicators in Dormer and South African Meat Merino ewes and lambs <i>K. Mafunga, C.L. Nel, K. Dzama and S.W.P. Cloete</i>	423
Preliminary analysis of immune competence traits in northern Australian tropically adapted beef breeds <i>K.L. Moore, D.J. Johnston, T. Grant and J. Croaker</i>	427
Associations between immune competence breeding values and health traits in Australian Angus cattle <i>L.A Mowbray, M. Samaraweera, C. Duff, B.C. Hine, A. Reverter, P.A. Alexandre, L.R. Porto-Neto and A.B. Ingham</i>	431
Including resilience in the breeding objective of sustainable Merino sheep <i>E.G. Smith, S.F. Walkom, A.A Swan and S.A. Clark</i>	435
Genetic Evaluation	
Latest developments in genomic tools for Angus Australia: SteerSELECT, HeiferSELECT and BreedCHECK <i>A. Reverter, C. Duff, M. Samaraweera, P.A. Alexandre, B.C. Hine, A.B. Ingham, L.A Mowbray and L.R. Porto-Neto</i>	438
The 2025 National Breeding Objective review for Australian dairy cattle: insights from stakeholder consultation <i>T.T.T. Nguyen, M. Axford, P. Thurn, L. Monks, G. Nieuwhof, P. Williams, D. Watson, H. McLaren and M. Shaffer</i>	443

Table of Contents

Exploring adoption factors, and preferences to the use of beef genetic tools in Northern Australia <i>P. Menchon, J.K. Manning, D.L. Swain and A. Cosby</i>	447
Combined LambPlan: Expanding the mulit-breed nature of the LambPlan evaluation <i>S.F. Walkom, P. Alexandri, D.J. Brown, K.L. Bunter, N.K. Connors, S. de las Heras-Saldana, K.P. Gore, P.M. Gurman, L. Li, A.J. McMillan, S.P. Miller, P.E. Bradley and A.A. Swan</i>	451
Expanding Australian sheep genomic reference population <i>P. Alexandri, P.M. Gurman, D.J. Brown, K.L. Bunter, K.P. Gore, S. de las Heras-Saldana, L. Li, A.J. McMillan, S.F. Walkom and A.A. Swan</i>	455
Fixed effects and genetic parameters for the combined LambPlan evaluation of Australian sheep <i>S. de las Heras-Saldana, D.J. Brown, P.M. Gurman, P. Alexandri, K.L. Bunter, K.P. Gore, L. Li, A.J. McMillan, S.F. Walkom and A.A. Swan</i>	459
Genotyping reduces preselection bias on MERINOSELECT ASBVs in Merino flocks <i>B.E. Clarke, D.J. Brown, P. Bradley and A.A. Swan</i>	463
Implementation of genomic mate selection and other non-additive issues <i>B.P. Kinghorn and A.J. Kinghorn</i>	467
Factors affecting genetic gain by geographic location for Australian and New Zealand MERINOSELECT flocks <i>C.J. Bunter, P.E. Bradley, M.J. Hodge and K.L. Rummery</i>	471
Genetic progress in industry	
Seven Years On: What has Single-Step BREEDPLAN meant for the Australian Brahman breed? <i>C.A. Millen, B.J. Crook and P.J. Williams</i>	475
BREEDPLAN: 40 years of accelerating genetic progress in the beef industry <i>B.W. Gudex, C.A. Millen, D.J. Johnston and N. Turner</i>	479
Genetic trends in Australian beef cattle and sheep populations and their impact <i>R.G. Banks, D.J. Brown, K.L. Moore, B.J. Walmsley and A.A. Swan</i>	483
Breeding for facial eczema tolerance - A success story <i>P.L. Johnson and R. Proffit</i>	487