Final report

A genetic approach to internal parasite control in Australian cattle

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Abstract

The main source of pasture contamination with infective strongyle eggs is from faeces of calves, especially weaners. However, not all calves contaminate the pasture at the same rate. The half-sibling progeny groups of different sires grazing the same pasture contribute unevenly to the total load of strongyle eggs on that pasture.

Lower faecal worm egg output is a phenotypic expression of enhanced genetic resistance to internal parasites. The heritability of this trait is 41%, which provides adequate opportunity for selection for enhanced resistance of cattle to internal parasites. Large half-sibling progeny groups provided by Breedplan herds using link sires facilitate accurate selection.

This study has developed preliminary estimated breeding values (EBVs) for internal parasite resistance in 99 Angus sires across southeastern Australia. Breedplan offers the ability to monitor developments in enhanced resistance to parasites alongside continuing genetic gains in the production traits.

Executive summary

The primary objective of this project was to demonstrate that parasite resistance in cattle herds could be established and maintained via genetic selection without compromising enterprise profitability.

The control of the effects of internal parasites on production and profitability presents a significant cost to Australian beef cattle producers. Current methods of internal parasite control rely heavily on the strategic use of chemicals. The useful life of these chemicals is shortened by the rapid development of resistance by the parasites. Failure of these chemicals is widespread. In addition, there is growing pressure on cattlemen to reduce costs whilst remaining open to increasing scrutiny and traceability regarding safe, residue free food. There is also an increasing interest in organic food production with emphasis on chemical free production methods.

This project demonstrated that it is possible to select cattle with enhanced resistance to internal parasites in pasture based breeding herds in southeastern Australia. Using faecal egg counts (FEC) of paternal half-sibling lines of weaner cattle as a phenotypic indicator of internal parasite resistance, it was possible to develop EBVs for parasite resistance for sires. The heritability of this trait was found to be 41%.

With 41% of the total variation in faecal egg output within weaner groups being due to genetics, there is ample opportunity for selection if half-sibling sire-lines containing adequate numbers are made available. Breedplan, with its use of link sires, provides genetic linkages and large half-sibling sire groups from herds over a wide range of environments and management situations. The Angus Long Fed/CAAB Dollar index was very similar for animals with high or low parasite resistance EBVs. This gives an early indication that progress could be made in selection for parasite resistance without compromising progress with production traits.

The potential benefits to industry from adopting the technology include:

1. Increased usage of genetic selection (via sire EBVs) for enhanced parasite resistance within breeds.
2. Decreased reliance on chemical control of internal parasites.
3. Improved productivity and profitability of beef enterprises.
4. Improvements in aspects of animal welfare and environmental stewardship.

Initial benefits will be to progressive seedstock producers who adopt the technology to obtain a marketing advantage. The gathering of phenotypic information for this trait is cumbersome. Therefore, future research on seedstock herds with wide commercial acceptance would provide the maximum industry benefit. Benefits would be transferred to those clients who use EBVs in their selection decisions. This process will be facilitated by the dissemination of useful information via such mechanisms as targeted media outlets, sire catalogues, extension activities and field days, as well as via scientific discourse.

The collection of phenotypic data for calculation of EBVs for enhanced genetic resistance presents difficulty in comparison to easy to measure traits such as 400day weight. Therefore, future progression of research would preferably involve collecting data from Breedplan enrolled herds using link sires selected by Australian Genetics and Breeding Unit (AGBU) at New England University. From these herds, sires can be identified for commercial industry and to be used in breeding trials to establish populations of cattle for genomic studies. Development of marker

assisted EBVs for enhanced parasite resistance would serve as a realistic objective of future research on this hard to measure trait.

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1. Background

Trichostrongyle nematode parasites, notably *Ostertagia ostertagi* and *Cooperia oncophora* are a major cause of production loss in Australian beef enterprises. Their control is also a source of significant cost to beef producers. Annual cost of strategic *Ostertagia* control in a 100 cow spring calving herd in southeastern Australia is $1,240.[1] Estimates in the US of the cost of not controlling internal parasites range from $10 to $40 per cow per year.[2]

Effective anthelmintic chemicals have only been available since the 1950's. Since then, treatment of individuals or small groups for clinical illness has been discouraged in favour of strategic programs which focus on pre-emptive treatment of whole herds or of all the animals in specified management categories. These treatments have been designed to control parasite build up over the cattle-pasture ecosystem. However, the adoption of strategic programs has in some cases lead to failure through development of parasite resistance.[3]

Resistance to the macrocyclic lactones (ML) is now widespread. In US beef herds the failure to eliminate worm egg shedding following several years of ML pour-on application has been identified.[4] A recent survey from 13 cattle properties in southeastern Australia demonstrated widespread failure of all groups of anthelmintics to significantly reduce faecal worm egg count.[5]

The outcome of the failure of current management practices is increasing the opportunity for parasite transmission in the grazing environment. Reducing the opportunity for worm transmission and subsequent exposure of parasites to anthelmintics would curtail the opportunity for resistant parasite strains to develop. The useful life of the chemical could be extended.

Increased awareness of food safety, environmental concerns, the growth of interest in organic agriculture and the development of parasite resistance to chemotherapy therefore encourages the development of modified approaches to internal parasite control.

It is possible to breed cattle with improved resistance to parasites.[6] Cattle bred to demonstrate improved host immunity are able to minimize parasite transmission by reducing faecal egg output. Faecal egg count (FEC) - expressed as eggs per gram of parasite eggs from calves - has been shown to be a phenotypic indicator of parasite resistance with a moderate heritability of 0.3 to 0.4.[7,8,9] It has been demonstrated that there is much variation in FEC amongst calf cohorts in a herd situation.[10] Variation in FEC with this level of heritability allows for progress to be made in breeding populations of cattle for enhanced resistance to internal parasites.

2. Objectives

The primary objective of this project was to demonstrate that enhanced parasite resistance in cattle herds can be established and maintained via genetic selection without compromising enterprise profitability.

Potential Outcomes would include:

1. Increased usage of genetic selection (via sire EBVs) for enhanced parasite resistance within breeds.
2. Decreased reliance on chemical control of internal parasites.
3. Improved productivity and profitability of beef enterprises.

4. Improvements in aspects of animal welfare and environmental stewardship. Initial benefits will be to progressive seedstock producers who adopt the technology to obtain a marketing advantage. Subsequently, benefits would be transferred to those clients who use EBVs in their selection decisions. This process will be facilitated by the dissemination of useful information via such mechanisms as media targeting the beef industry, sire catalogues, extension activities and field days, as well as via scientific discourse.

3. Methodology

MLA is committed to investing in top quality scientific research, performed by suitably qualified, experienced and registered researchers and organisations. In experiments that involve livestock, MLA acknowledges that such research needs to be done under the auspices of a recognised Animal Care and Ethics Committee (AEC). The responsibility for obtaining AEC approval lies with the researcher. MLA has in the past not specifically asked for evidence that such AEC approval had indeed been obtained.

3.1 Animals

Angus cattle were sampled from 8 herds with strong genetic links to the Temania Angus stud enterprise. Genetic linkage was achieved through the use of common sires across the participating herds through artificial insemination with frozen semen. All sires were recorded with Breedplan. Genetic linkage provided half-sibling sire lines across a range of climatic and management situations. These herds were located from Coolah in northern NSW to Mortlake in the Victorian western district. Weaner cattle were sampled at what was considered to be a susceptible age of between 6 months and 17 months. Calves included in the project had (a) not been treated with an anthelmintic or, (b) been treated at least six weeks prior to being sampled. This time interval in the latter group was designed to negate the residual effects of anthelmintics. Calves born in the spring of 2010 and calves born in the autumn of 2011 were included in the project. Age, sex, dam lactation number and sire were known for each calf. The selection of dams was assumed to be random, therefore maternal genetic contribution to each half-sibling sire group was ignored.

3.2 Parisitology

Samples were collected manually from the rectum of each animal and the sample container was labeled with either animal identity or sample number related to animal identity. Samples were kept cool by refrigeration or ice coolers before being transported to the Veterinary Diagnostic Laboratory at CSU, Wagga. Faecal egg counts of strongyle eggs were carried out within four days of collection, employing the VDL Standard Operating Procedure for Ruminant Faecal Egg Counts.[11] Technicians performing FECs were checked against each other to ensure consistency of results. Cultures revealed that *Cooperia spp*. and *Ostertagia spp.* were the predominant strongyle species represented.

3.3 Statistical analysis

Following deletion of animals with incomplete records or when sires were represented fewer than four times, 2556 records were included in the data set. Calf sex profiles were not evenly represented across herds. In one herd, only steer calves were sampled. Two herds had unmarked bull calves and heifers. The remainder of the herds sampled steers and heifers. There were 99 sires sampled of which 12 were used as link sires on multiple properties.

All analyses were conducted using the GenstatV13.1 (VSN international). Fixed effects that were included in the final model were Property/Date (as there was a confounding effect of property and sampling date), calf age, dam lactation number and calf sex. Sire was fitted as a random effect.

Fourthroot transformations were applied to ensure model assumptions of normality and homogeneity of residual variance were met. The predicted means and standard errors for each sire were derived by refitting the model in Average Information (S language) Residual Maximum Likelihood (ASREML). Similarly, the heritability was calculated in ASREML.

4. Results

4.1 Fixed effects

Property/Date: (P<0.001) As expected there was a wide variation in FEC due to time collected and location.

Age: (P<0.001) Overall, there was a trend for decreasing predicted mean FEC as calves aged. However, on one property, an older cohort was sampled which had gone longer without treatment and had built up higher counts.

Dam Lactation Number: (P <0.001) From the second lactation there was a gradual increase in predicted mean FEC as the number of lactations in the dam increased. Sex: (P<0.001) There was a highly significant difference between predicted means for sex of calf. Bull calves had significantly higher counts than steers, which in turn had significantly higher counts than heifers.

4.2 Random effects

Sire Effects (Estimated Breeding Values):
Table 1 shows the predicted sire EBVs and 95% confidence intervals for progeny of each of the 99 sires represented in the study. These represent the best linear unbiased prediction (BLUP) of the true means with all other terms in the model held constant. These means give a meaningful estimate of the paternal contribution to variation in FEC. EBVs are sorted in order of decreasing parasite resistance with the most favourable at the top of the list. Sires are identified by their EBV ranking.

Table 1 Estimated Breeding Values and Standard Error for 99 sires

SIRE	EBV	SE
1	2.639825409	0.231822
2	2.707646207	0.140092
3	2.846702636	0.197837
4	2.871847962	0.199325
5	2.904061749	0.19391
6	2.911617478	0.354361
7	2.96645459	0.217908
8	2.972475608	0.241808

9	2.97642507	0.232043
10	3.01139003	0.0976593
11	3.019902712	0.252398
12	3.060848195	0.213379
13	3.065710876	0.354243
14	3.072705081	0.292495
15	3.121475829	0.123914
16	3.132451309	0.15876
17	3.142749684	0.353988
18	3.14741523	0.387318
19	3.163040022	0.316966
20	3.182574819	0.230761
21	3.200673785	0.23375
22	3.202520171	0.20886
23	3.203896932	0.276999
24	3.205496591	0.370413
25	3.214817377	0.223166
26	3.227056271	0.231142
27	3.228995307	0.303221
28	3.248570346	0.253136
29	3.251787315	0.354969
30	3.254095137	0.369273
31	3.261250055	0.387998
32	3.283249274	0.217568
33	3.292314376	0.226907
34	3.293109774	0.158533
35	3.304986746	0.125819
36	3.331609619	0.369415
37	3.332372177	0.388144
38	3.346719597	0.281266
39	3.348046175	0.27431
40	3.352976884	0.370472
41	3.359614321	0.147477
42	3.362433107	0.277212
43	3.370782135	0.321765
44	3.377467253	0.239832
45	3.396745593	0.388101
46	3.403541835	0.218604

47	3.405062004	0.387626
48	3.407895826	0.294896
49	3.408791043	0.387773
50	3.410905193	0.124101
51	3.416253041	0.30243
52	3.416562188	0.188399
53	3.416962733	0.265706
54	3.422888388	0.354913
55	3.42496829	0.369497
56	3.42534498	0.293149
57	3.434198673	0.156065
58	3.435384796	0.165436
59	3.442535212	0.387837
60	3.44402392	0.260341
61	3.456108313	0.299706
62	3.460477917	0.149361
63	3.471483198	0.370183
64	3.475531909	0.355099
65	3.481005805	0.321951
66	3.48242024	0.284608
67	3.492644588	0.194757
68	3.497333337	0.354476
69	3.506653379	0.237264
70	3.51115073	0.29151
71	3.535508587	0.240174
72	3.545131703	0.369857
73	3.545331383	0.209234
74	3.548859958	0.132408
75	3.549598392	0.387955
76	3.562098327	0.25511
77	3.568397947	0.388533
78	3.585466307	0.369609
79	3.600662626	0.271896
80	3.609015403	0.191444
81	3.63034553	0.388357
82	3.642719841	0.298829
83	3.675696662	0.354973
84	3.692813335	0.24618

85	3.697554538	0.304597
86	3.698881795	0.33182
87	3.705671481	0.356208
88	3.711507104	0.277938
89	3.72059328	0.222638
90	3.745075577	0.369776
91	3.77606321	0.262024
92	3.811614481	0.292903
93	3.814844533	0.182937
94	3.830680179	0.286786
95	3.914027151	0.316339
96	3.961573954	0.229208
97	4.018015065	0.280884
98	4.158605811	0.244431
99	4.240021387	0.285093

Figure 1. Transformed predicted means for 21 sires with lowest Standard Errors and including 12 link sires

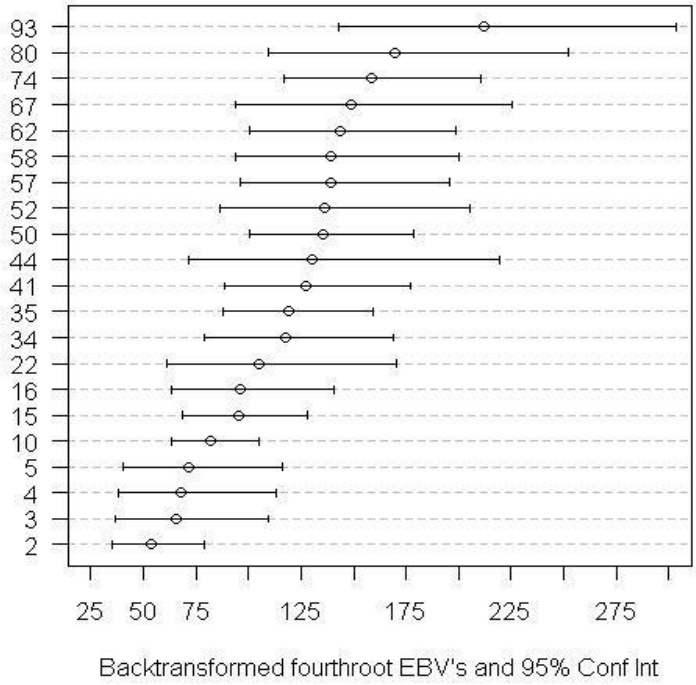
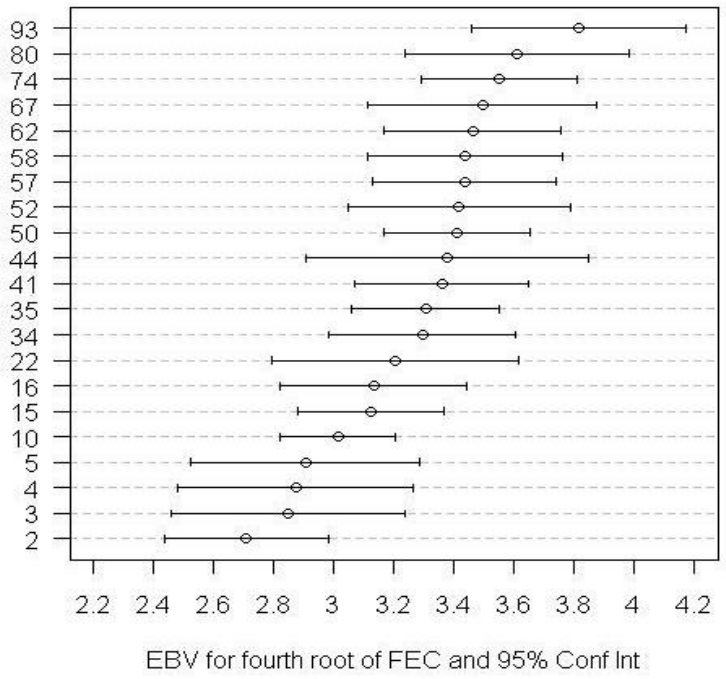


Figure 2. Backtransformed predicted means of FECs for 21 sires with lowest Standard Errors and including 12 link sires



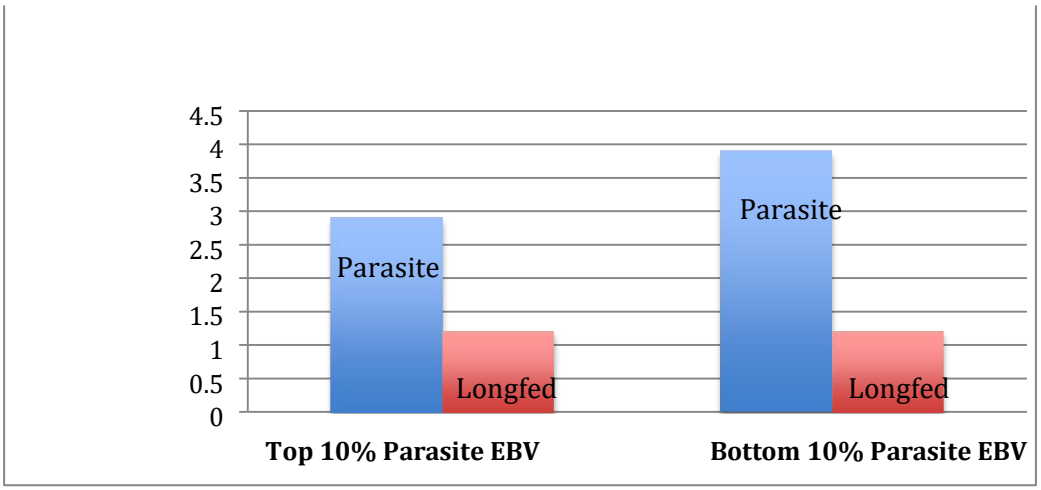
4.3 Heritability

Analysis of fourthroot EBVs estimated a heritability of 0.4085 with a standard error of 0.0965.

4.4 Effect of Enhanced Parasite Resistance on Production Traits

Dollar index values for Long Fed/CAAB[26] showed little variation between the animals with the highest 10% and the lowest 10% of Parasite Resistance EBVs.

Figure 3. Mean Long Fed/CAAB Dollar Indices for Highest and Lowest 10% Parasite resistance EBVs



5. Discussion

In unselected cattle populations, faecal egg count (FEC) values for strongyle eggs per gram of faeces do not follow a normal distribution. A small number of calves account for a large proportion of the pasture contamination that occurs. The likelihood of certain sires to produce calves that cause high parasite transmission has been found to be up to 20 times that of other sires.[12]

Calves can be separated into three types: (1) Never demonstrate high FEC values, (2) Rises in FEC values after introduction to contaminated pastures for 2 months then falling to low levels, (3) High FEC value persisting for the duration of testing. The approximate percentage of these phenotypes is 25:50:25 respectively.[12]

In addition, Type 1 and Type 2 calves maintain low FEC values but the Type 3 calves continue to shed eggs in high numbers. The three FEC phenotypes were classified as: innately immune, acquired immune, and immunologically non-responsive.[12] These results have been verified to be true in different areas with different parasite fauna and different transmission conditions.[13] The existence of phenotypic ratios strongly suggests a genetic influence.

Host genetics accounts for a large part of the variation in FEC values, and for a very significant part of transmission patterns. Tissue samples for gene expression analysis have been collected from the FEC phenotypes. Microarray techniques identified that immune responses could involve small but replicable differences in expression patterns of multiple genes or groups of genes.[14] Genes expressed in resistant sheep have been identified with involvement in an acquired immune response and the structure of intestinal smooth muscle.[14]

Identification of quantitative trait loci (QTL) affecting known phenotypes is underway in a closed pedigree herd of Angus cattle.[16] QTL have been identified on bovine chromosomes 2, 3, 5, 6, 14 and 15 for EPG and on chromosomes 3, 11 and 18 for serum pepsinogen. These QTL have been linked to levels of infection, where *Cooperia* correlate well with FEC, and *Ostertagia* correlate well with serum pepsinogen levels.[17]

Genetic improvement of beef cattle based on measurement of economic traits and peer group comparisons alongside pedigree information has been very effective.[18] Success has been largely due to easily measurable phenotypes for highly heritable economic traits and existing genetic variation. However, traits of low or moderate heritability such as parasite resistance and other fitness traits are not easily measured in a commercial setting without negatively affecting other commercial traits.

Best linear unbiased prediction (BLUP) methodology allows for simultaneous analysis of multiple traits.[19] Negative effects on production traits caused by selection for parasite resistance would therefore be detected in herds enrolled in Breedplan.

Development of gene marker assisted selection would greatly speed up the genetic improvement for parasite resistance. However, determining the accuracy of QTL is dependent on population size, pedigree structure and measuring phenotypic differences within a population. Although QTL have been identified using populations derived from founder animals identified phenotypically, this is a costly exercise in a research situation. In the dairy industry large half-sibling families are available through extensive use of AI and progeny testing and these have been used to detect QTL.[20] In the beef industry we now have large half-sibling families recorded on Breedplan. In January 2009 some 585,695 calves were analyzed for 200day weight representing the progeny of 51,179 sires.[21] Many of the animals on this and other large breed registries have genetic linkages through the use of

common elite sires by artificial insemination. Identifying a significant number of phenotypes in the commercial cattle population is now possible and affordable.

Arguments have been put forward that there may be a tradeoff between disease resistance and production traits.[22] In a composite sub-tropically adapted beef breed, relationships between tick and worm counts and growth, male and female fertility and flight-speed scores were found to be close to zero. Tick and worm resistance were therefore assumed to be traits that were independent of other economic traits.[9] The statistical power of Breedplan using BLUP technology with its multitrait selection of up to 18 traits would detect any negative correlation between production and disease resistance. Breedplan selection indexes are also able to place different emphasis on traits according to production environment and markets targeted. Large commercial herds can select for multiple phenotypes, with each individual component fitting into the overall economic framework.[23]

Selection for resistant lines of cattle is possible within a commercially acceptable time frame.[24] However, there is currently no emphasis given to parasite resistance in the selection of commercial seedstock. In fact, in some environments, selection for growth could result in reduced resistance to parasites.[25]

It is possible to select cattle for resistance to parasites using FEC phenotypes. Breedplan recording and AI is widespread in the Australian beef seedstock industry and large half-sibling groups exist in the seedstock population. Through pedigree analysis of identified phenotypes, families or strains of cattle may be identified as having increased resistance to parasites. These resistant lines of cattle would be useful in their own right as seedstock. They would also be valuable to researchers in locating QLT for the development of marker assisted EBVs.

6. Conclusion

Cattle can be bred for enhanced resistance to worm parasites. However, this fact has not been widely promoted to the commercial seedstock sector. Much research work is being done at the DNA level using populations that have been phenotypically identified as resistant or susceptible but these populations are confined to research centres and their genetics are not generally available to commercial producers. Once QLT have been identified and genomic maps refined, identification of genes controlling resistance will offer a wider option for disease control.[10]

In the US expected progeny differences (EBV equivalents) have been calculated from data using half-sibling groups ranging from 1 to 24.[6] In Australia, use of Breedplan allows sire-lines to be identified through FEC data from large groups of half-siblings spread over a wide range of environmental and management situations. In addition, the effects of selection for parasite resistance on production traits can be monitored through Breedplan. Data from this study were re-analysed at the Animal Genetics and Breeding Unit (AGBU) at the University of New England.[27] Additional pedigree information was used from the Angus Breedplan database. This provided a dataset representing 93 sires with 3 generations of ancestors, and included 7,115 animals. Cohort groups were more precisely defined. Although heritability estimates were reduced, the EBV rankings of sires followed similar trends. (Appendix 1)

The identification and removal of parasite susceptible strains of cattle from a cow/calf operation would include the synergistic benefit of greatly reducing disease transmission and costs involved in parasite control. Environmental benefits would stem from reduced chemical use on farm. Reduced

cattle handling and disease would have animal welfare benefits. The economic prospects of management options such as chemical free organic beef production would improve.

This project has demonstrated that the tools are available to develop EBVs for enhanced internal parasite resistance in beef cattle in southern Australia. Seedstock herds using Breedplan, and which have high industry acceptance, offer an opportunity to identify sires which pass on enhanced parasite resistance to a high number of commercial herds.

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Ann Cowling of CSU carried out the initial complex statistical analyses. Subsequent analysis, using additional information provided by the Angus Breedplan data base, was carried out by David Johnston of the Animal and Genetic Breeding Unit at the University of New England, Armidale. Professors Peter Chenoweth and Nick Sangster of CSU provided insight into navigating the academic channels.

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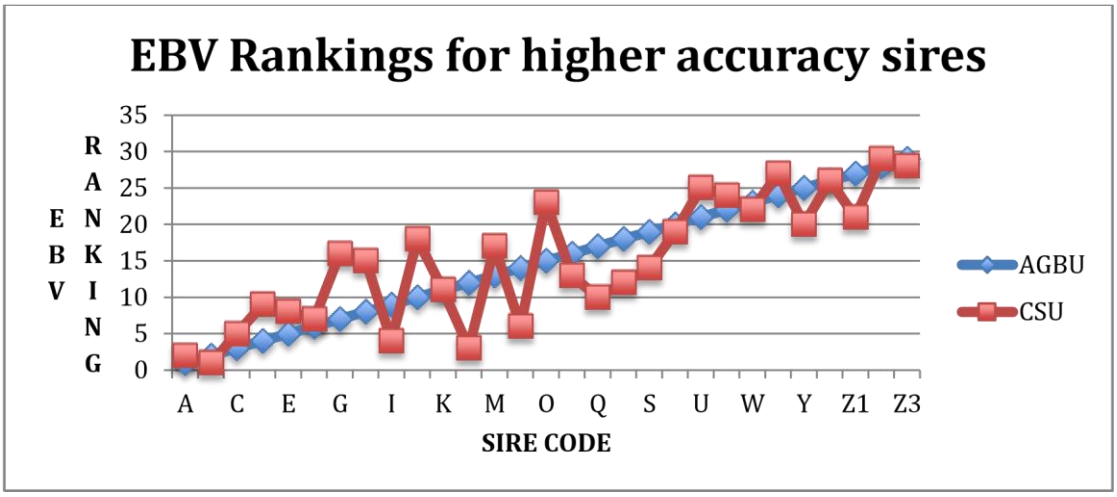
Peter Honey

9. Appendix

9.1 Appendix 1

Comparison of rankings for higher accuracy sires from the AGBU and CSU analyses



9.2 Appendix 2 Faecal egg count genetic analyses and trial EBVs

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Background

Faecal egg count (FEC) data on Australian Angus cattle in Southern Australia were provided to AGBU as part of MLA project B.AHE.066 managed by Dr Peter Honey. The aim of this part of the project (milestone 5.1 and 5.2) is to generate estimated breeding values (EBVs) from existing FEC data using additional information (fixed effects and pedigree) and applying appropriate fixed and random effects models.

Data

Data were provided by Peter Honey in Excel. The data required significant time to correct the animal identification numbers to allow merging across databases (i.e. between this dataset and the full Angus Society database). A total of 2,649 animals were in the original files however 162 could not be matched with Angus Society identification numbers and were excluded. These records were mainly from herds Baillie and Atkinson and it may be possible with additional information to get the correct idents. The remaining animals were merged with the latest Angus BREEDPLAN files to get full fixed effects and pedigree information (this includes all parents and grand-parents and other relatives back in the pedigree – this inclusion improves the accuracy of the estimates of genetic variance and hence the EBVs). A further 68 animals did not appear in files with a weaning weight and after removing any duplicates the final dataset contained 2,398 animals and a total of 3,899 records (i.e. 1,501 repeat records from 4 herds). The final dataset represented a total of 93 sires with number of FEC recorded progeny ranging from 1 -183 (mean = 26). FEC were recorded as eggs/gram (epg) and for analysis the FEC records on each individual were classified as either first record (FEC1) or second record (FEC2). There are possibly some animals are misaligned with the definition of their FEC1 or

[1] AGBU is a joint venture of NSW Department of Primary Industries and the University of New England

FEC2 records because some herds did not measure all animals at first measurement time (e.g. herd Walmsley).

A total of 6 herds are represented in the data, with 44% of data from a single herd. For FEC1 records, a contemporary group was formed by concatenating the herd and FEC recording date with the BREEDPLAN constructed contemporary group for 200d weight (Graser *et al.* 2005). This yielded a total of 174 FEC contemporary groups (FCG). For second FEC records (FEC2), there were only two recording months (June and July) and a total of 60 FEC contemporary groups were formed that also commonly used the BREEDPLAN 200d weight contemporary group definition (but in some case the 400 day contemporary group was used). Preliminary analyses revealed the FEC statistics varied greatly across contemporary groups. For example, for contemporary groups with more than 10 records the mean FEC varied from 3.5 epg to 1,759 epg and standard deviations ranged from 1.9 to 428. Table 1 presents raw means and standard deviations for FEC1 and FEC2 records. Given the nonnormal distribution of the FEC records the trait was transformed using a cube root transformation (cFEC1 and cFEC2). This transformation followed recommendations of many analyses of FEC data in sheep and beef, including the method used currently in the Sheep Genetics Australia genetic evaluation (Brown *et al.* 2007). The distribution of residuals revealed a vast improvement in normality however possible issues still may remain with the large number of FEC records equal to zero.

Table 1. Raw statistics for FEC at first (FEC1) and second (FEC2) measurement times.

Variable	N	Mean	Std	Min	Max
FEC1	2398	334.5	593.5	0	7680
cFEC1	2398	5.6	3.0	0	19.7
WT1	2398	251.7	38.8	104	422
Age1	2398	215.8	26.6	134	288
AoD1	2398	3.8	1.7	1.8	11.0
FEC2	1501	105.1	160.1	0	1420
cFEC2	1501	3.5	2.4	0	11.2
WT2*	1501	247.2	38.1	136	405
age2*	1501	212.9	24.6	162	317
AoD2*	1501	3.9	1.7	1.8	10.9

* mostly same previous weight and age information used as for FEC1

Analyses

Significant fixed effects were determined using SAS fitting all effects and first order interactions, with sire included as a random effect. The initial models included FEC contemporary group (FEC measurement date + herd + BREEDPLAN 200d or 400d defined management group), age of dam (linear and quadratic), age of animal (linear and quadratic) and first order interactions. Contemporary group included herd, sex, weigh date and 45 day slice. Age of dam (AoD) was calculated at birth of calf and for ET calves was age of the recipient dam. Age of calf was simply the age at 200d weight record, and while not specifically age at FEC it allowed differences in age (pooled across fixed effects) to be removed. Final models were determined by sequentially removing all non-significant effects (P>0.05). For FEC1 and FEC2, the final fixed effect model was FEC CG, age of dam (linear and quadratic) and age. Trait heritabilities were estimated from univariate animal model

analyses using restricted maximum likelihood procedures in ASReml (Gilmour *et al.* 2009) and fixed effects identified using SAS. A relationship matrix based on up to 3 generations of paternal and maternal pedigree was utilised for all analyses and contained a total of 7115 animals.

Three single analyses were run using the FEC data. Firstly, FEC1 and FEC2 were analysed as separate traits and the third analysis was performed treating the FEC2 as a repeat record. Estimated breeding values (EBVs) were generated from each analysis and back-transformed to the observed FEC scale. Genetic correlations were also estimated between FEC1 and FEC2 (and FEC1 and WT) using bivariate analyses in ASReml with the same models used in the univariate analyses. No maternal genetic or permanent environmental effects were estimated as the data would not support these models.

Results

Solutions to fixed effects showed a very large FEC CG effects, clearly some herds had greater levels of worm burden than others, which may result simply from location or management. Age of dam also had a significant effect on FEC, in particular, calves from 2 years old had higher FEC1 than those from older cows. Figure 1 plots the effects of age of dam (modeled in pooled yearly age classes) on FEC1. Age of calf also showed a significant effect with older calves (within a contemporary group) had lower FEC1 (-1.68 egg/grams/day of age).

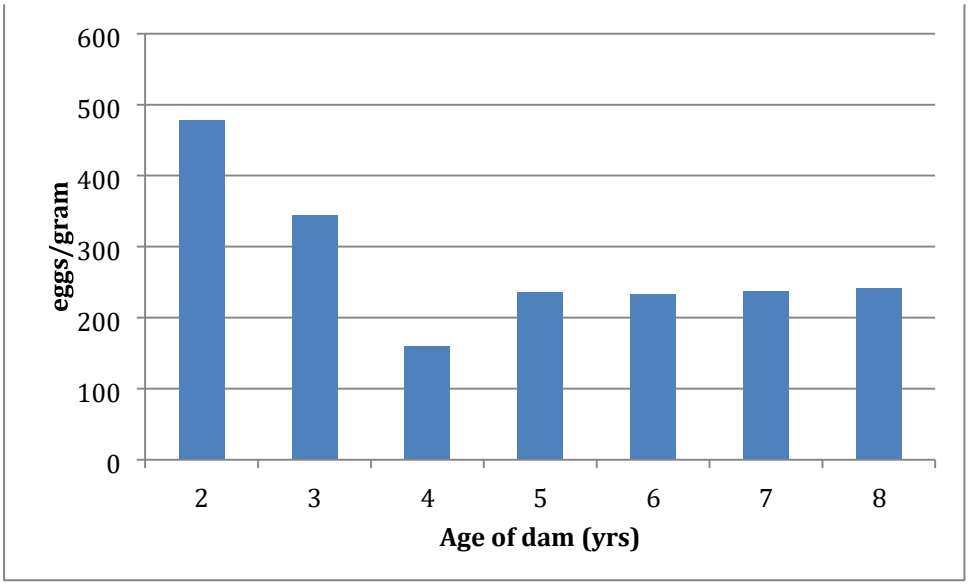

Figure 1. Least squares means of FEC1 by age of dam (in years).

Heritabilities and repeatability are presented in Table 2. FEC1 and FEC2 had similar heritabilities (0.26 and 0.31, respectively). When the data was analysed using a repeatability model the heritability was slightly lower (0.23) with a 0.29 repeatability.

Table 2. Variance components*, heritabilities (h^2) for FEC from 3 models, and repeatability (t^2) of FEC across the two measurement times. Approximate standard errors in brackets.

Model	V_a	V_{pe}	V_p	h^2	t^2

FEC1	1.32	-	5.09	0.26 (0.06)	-
FEC2	1.69	-	5.50	0.31 (0.09)	-
FECR	1.22	0.28	5.22	0.23 (0.05)	0.29 (0.03)

*V_a = additive genetic variance; V_{pe} permanent environmental variance of the animal; V_p = phenotypic variance

Genetic correlations presented in Table 3 show a 0.69 genetic and 0.29 phenotypic correlation between FEC1 and FEC2. The genetic correlation between FEC1 and WT1 was 0.18 (with a large standard error) with a -0.02 phenotypic correlation. EBVs from the repeatability model are summarised in Table 4 for all animals and for sires with progeny with a FEC record. For all animals the cube root transformed EBVs (CEBV12) ranged from -3.03 to +2.46. The cEBV12 was also back-transformed onto the observed scale using the level of FEC of 250 epg from these data. The EBVs (FEC_EBV12) ranged from -215 epg to +422 epg, where lower EBV represents lower expected FEC. The interpretation of these EBVs would be if the top and bottom sires were joined to similar cows we would expect the progeny to be ½ difference in sire's EBVs of 320 epg (i.e. ½ -215-422) in a herd with a mean count of a 250 epg. Sire accuracies averaged 67% with a top of 94% and list of sire with > 5 progeny recorded are presented in Appendix A.

Given the 0.69 correlation between FEC1 and FEC2 the EBVs on high accuracy sires for both traits (N=30) were also computed from the 2 single trait analyses (see Appendix B). The two single trait EBVs were well correlated with the EBV12 (i.e. from the repeatability model) but the two EBVs themselves were only moderately correlated and there is some evidence of sire re-ranking across measurement times.

Table 3. Genetic (r_g) and phenotypic correlations (r_p) between FEC1 and FEC2 and between FEC1 and WT1. Approximate standard errors in brackets.

Trait1,2	**Trait 1 h^2**	**Trait 2 h^2**	**r_g**	**r_p**
FEC1,FEC2	0.26 (0.07)	0.28 (0.08)	0.69 (0.15)	0.29 (0.03)
FEC1, WT1	0.26 (0.06)	0.43 (0.08)	0.18 (0.17)	-0.02 (0.03)

Table 4. Mean EBVs and accuracies from repeatability model for cube root transformed EBVs (cEBV12) and backtransformed on the observed scale EBVs (FEC_EBV12).

Group	**Variable**	**Mean**	**Std**	**Min**	**Max**
All animals	cEBV12	0.05	0.49	-3.03	2.46
(N=7115)	FEC_EBV12*	10.9	6.1	-215	422
	accuracy	0.44	0.19	0.02	0.94
Sires with progeny	cEBV12	0.03	0.70	-1.99	1.66
(N=93)	FEC_EBV12*	12.8	82.3	-170	256

accuracy	0.67	0.16	0.26	0.94

* back-transformed to observed scale assuming a 250 epg mean expression

Discussion

This study has shown FEC is heritable in Angus cattle and agrees with other beef cattle literature in British (Morris and Amyes 2012) and tropical cattle (Prayaga *et al.* 2009; Henshall *et al.* (2001). Sire differences were evident however EBVs on the cube root scale are difficult to interpret and therefore EBVs were transformed back to observed scale assuming a particular mean level of worms. The EBVs computed are project trial EBVs and not Angus Society or BREEDPLAN EBVs. Any release of these trial EBVs will require the approval of the project and individual cooperators.

All analyses were performed without accounting for any heterogeneity of variances (see Brown and Tier 2003) or for removing groups with low means (as done by Morris and Amyes 2012). Clearly in these data big difference in the mean egg counts occurred between herds and because not all sires were cross-classified across herds it is possible that this may be affecting the EBVs on particular sires. Future work would need to consider developing diagnostics for determining if whole contemporary groups should be dropped due to low mean (i.e. lack of appropriate nature challenge) or low variance. Alternatively a more sophisticated method of analysis could be considered (e.g. MCMC and Gibbs Sampler).

The significant fixed effects of contemporary group, age of dam and age demonstrate the necessarily of this information for any development of a genetic evaluation for FEC. Also the significant effect of age of dam suggests there could also be the possibility of maternal effects but at this stage it is not known if these would have a genetic component. The increased FEC of calves from 2 year old cows is an interesting phenomenon that with further investigation might help inform the mechanisms by which calves acquire immunity to worm infestations.

The genetic correlation between FEC1 and FEC2 (r_g<1) suggests that weaning and postweaning measures of FEC are different traits, and positively correlated. This difference may be due to genetic differences in the response to drenching but may also represent different worm species present during the autumn versus the winter or even different rates of achieving natural immunity. This has ramifications for the development of a genetic evaluation in terms of determining which of the two time points might be most important. If both are deemed necessary, then clear guidelines will be needed to define two traits, including age ranges and requirements for knowledge on any drenching treatments. Morris and Amyes (2012) estimated a genetic correlation of 0.89 between Angus and Hereford cattle measured at weaning and again 3 months later (including a drench), however the heritability of their second measure was only 0.11 (compared to 0.28 for the first). The genetic correlation with weight estimated here suggests that selection for faster growth rate will lead to a small correlated response of increased worm counts.

Future work could include: estimation of genetic correlations with other traits and overall $indexes; investigate possibility of a major gene contributing significantly to these traits (see Henshall *et al.* 2001), modeling maternal effects (would require additional data) and determining the trait's economic value in a range of beef cattle production systems (i.e. for inclusion in selection indices). For the any future development of a genetic evaluation (e.g. BREEDPLAN) there will be a need for clear trait definition, including industry recording protocols and data submission. For breeds other

than Angus several thousand records will be required to establish the heritability of FEC in their breed and production systems.

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9.3 Appendix 2A.

Trial EBVs from repeatability model for cube root transformed EBVs (cEBV12) and backtransformed on the observed scale EBVs (FEC_EBV12) in eggs/gram.

Sire ID by ranking	nprog	cEBV12	FEC EBV12*	accuracy
1	43	-2	-170	0.81
2	17	-2	-169	0.68
3	104	-1.6	-144	0.92
4	18	-1.5	-141	0.75
5	12	-1.1	-106	0.71
6	45	-1.1	-106	0.71
7	26	-1	-97	0.74
8	12	-0.9	-94	0.67
9	67	-0.6	-67	0.89
10	14	-0.6	-64	0.67
11	148	-0.6	-64	0.93
12	183	-0.5	-52	0.94
13	139	-0.4	-49	0.93
14	60	-0.4	-47	0.87
15	33	-0.4	-42	0.79
16	10	-0.3	-39	0.64
17	31	-0.3	-39	0.83
18	29	-0.3	-36	0.77
19	30	-0.3	-35	0.8
20	82	-0.3	-35	0.9
21	11	-0.3	-31	0.6
22	24	-0.2	-25	0.73
23	10	-0.2	-25	0.62
24	19	-0.2	-23	0.7
25	22	-0.2	-19	0.72
26	20	-0.1	-16	0.76
27	86	-0.1	-14	0.91
28	34	-0.1	-8	0.79
29	39	-0.1	-7	0.84
30	7	0	-2	0.62
31	76	0	2	0.9
32	8	0	3	0.61
33	35	0.1	11	0.69
34	37	0.1	16	0.81
35	33	0.1	17	0.79
36	20	0.2	21	0.73
37	35	0.2	21	0.79
38	9	0.2	24	0.63
39	9	0.2	25	0.58
40	10	0.2	27	0.64

41	8	0.2	28	0.45
42	8	0.2	30	0.61
43	16	0.2	30	0.68
44	12	0.3	38	0.61
45	34	0.4	48	0.82
46	21	0.4	49	0.78
47	10	0.4	52	0.7
48	18	0.5	61	0.73
49	13	0.5	63	0.65
50	11	0.5	64	0.58
51	8	0.5	65	0.55
52	20	0.5	65	0.8
53	9	0.5	66	0.62
54	12	0.5	67	0.63
55	13	0.6	78	0.68
56	42	0.7	88	0.82
57	156	0.7	90	0.93
58	83	0.7	100	0.91
59	15	0.8	106	0.74
60	12	0.9	117	0.69
61	22	1	140	0.7
62	11	1.1	153	0.64
63	48	1.1	157	0.84
64	8	1.4	205	0.69
65	11	1.5	216	0.64
66	23	1.5	222	0.76
67	46	1.7	255	0.9

* back-transformed to observed scale assuming a 250 epg mean expression

9.4 Appendix 2B

Trial EBVs of higher accuracy sires for FEC_EBV12, FEC1 and FEC2 from single trait analyses

Sire ID by ranking	FEC_EBV12*	EBV FEC1#	EBV FEC2$
1	-170	-245	-3
3	-144	-226	-39
4	-141	-162	-64
9	-67	-102	-12
11	-64	-87	-17
12	-52	**-139**	**45**
13	-49	-52	-16
14	-47	-60	-21
15	-42	-107	40
17	-39	-72	1
18	-36	17	-42
19	-35	-102	46
20	-35	-27	-15
26	-16	-89	42
27	-14	8	-6
28	-8	22	-15
29	-7	-57	44
30	2	49	-5
34	16	0	30
35	17	**201**	**-50**
37	21	76	0
45	48	70	22
46	49	94	-21
52	65	57	62
56	88	58	70
57	90	28	134
58	100	70	84
63	157	**40**	**193**
66	222	227	111
67	255	209	194

* back-transformed to observed scale assuming a 250 epg mean expression
# back-transformed to observed scale assuming a 350 epg mean expression
$ back-transformed to observed scale assuming a 100 epg mean expression