final report

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Limousin Information Nucleus and Young Sire Testing Project

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Executive Summary

DNA marker discovery was moving from searching for genes of large effect and small marker panels to the use of high density Single Nucleotide Polymorphism (SNP) panels to discover many SNPs with small effects. In order to validate the predictions from the currently available small marker panels marketed by genomic companies and to enable Genome Wide Scans (GWS) to search for informative SNPs for production traits the availability of a large number of animals phenotyped for a wide range of traits became important. It also became increasingly evident that prediction equations from the high density SNP panels were likely to be breed specific. For the Limousin breed to take advantage of new genomic technologies it was essential to establish a database of Limousin or Limousin cross animals with known pedigree,a comprehensive phenotypic profile and stored DNA.

The most effective way to produce the database was an Information Nucleus which involved a progeny test of young bulls where all progeny are grown out and slaughtered. Additional advantages of the progeny test model are that some young bulls would gain accurate genetic information (EBVs) for a wide range of traits and could be utilised to increase the genetic progress of the breed.

The project ran over three cohorts of calves each sired by 10 young Limousin sires, a group of Charolais bulls and a group of Shorthorn bulls mated predominantly to mature Angus cows Some high content Limousin cows which were mated only to the Limousin bulls in each cohort. All progeny were backgrounded on pasture or forage oats after weaning and were finished in a commercial feedlot or the Tullimba research feedlot for a minimum of 100 days except for cohort 1 heifers (finished on grass).

An extensive range of phenotypic measures was taken on each calf including birth traits, growth traits, carcase traits docility and MSA and laboratory eating quality traits. All progeny and their measurements were recorded in the ABRI crossbred register. Those traits currently analysed by BREEDPLAN were routinely analysed in the Limousin BREEDPLAN analysis. High quality DNA extracted from blood was stored at the University of Queensland Animal Genetics Laboratory for all sires and progeny.

Progeny from the first cohort were tested with an Illumina 50K genomic test by the CRC for Beef Genetic Technologies. Along with the genotypes from 345 influential Limousin sires the genomic results for cohort 1 progeny were used to test the veracity of the CRC multibreed genomic prediction equations for the Limousin breed and also to test prediction equations developed for the Limousin breed in the USA by Merial through their subsidiary,Igenity. In both cases the the prediction equations were not sufficiently accurate to justify the inclusion of genotype predictions into the Limousin BREEDPLAN analysis.

The industry benefit of this project is that the accurately measured and genotyped animals along with 345 genotyped influential sires will allow the Limousin breed to take advantage of the Single Step BREEDPLAN genetic analysis which utilises genomic test results to increase the accuracy of EBVs and Indexes and to get EBVs for hard or expensive to measure traits such a NFI and carcase traits. This will increase the rate of genetic gain for Limousin seedstock herds which will in turn benefit the Australian beef industry.

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1 Background

As an outcome of the mid term review of the Co-operative Research Centre (CRC) for Beef Genetic Technologies (2007 to 2012) the major goal of “identifying 6 to 10 genes of large effect to explain 50 percent of the genetic variation for hard to measure traits” was changed to “ using genome wide scans (GWS) with high density Single Nucleotide Polymorphism (SNP) panels to explain 15 percent of the genetic variation for hard to measure traits” High density genome wide SNP tests were not available when the project commenced. A marker based genomic test for traits such as feed efficiency, and marbling was being marketed in Australia and a specific Limousin marker test was being marketed by Merial. At the time there was a lack of data to verify the accuracy of these tests for any breed including the Limousin breed.

It was becoming increasingly evident that gene markers have different frequencies and also the size of the effect was different between breeds. For the Limousin breed to be able to test the accuracy of gene markers tests being promoted by genomic companies (or coming to market) and to also take advantage of new genetic technologies such as GWS it was essential to establish a significant database of Limousin or Limousin cross animals with known pedigree, a complete phenotypic profile and stored DNA . The most effective way to produce such a database was an Information Nucleus based on a progeny test of young bulls where all progeny are grown out and slaughtered. Additional advantages of the progeny test model was that some young bulls would get accurate genetic information (EBVs) for a wide range of traits which could then be utilised to increase the genetic progress of the breed.

2 Project Objectives

1. A total of 240 progeny for 10 Limousin sires per year will be born in co-operator commercial herds for three consecutive years.
2. 240 progeny per year will be finished on grass or grain to an average carcase weight of 310 kg at 18 months of age.
3. Measurements on 240 calves to include gestation length, birth weight, 200 day wt, 400 day wt, 600 day wt, docility score and flight time. All of these records to be stored on the ALBS database at ABRI
4. Additional measurement on the 240 calves to include carcase weight, fat depth, eye muscle area, marble score, pH, meat colour, shear force, compression, IMF%, Cooking Loss,
5. DNA samples will be taken and stored at the University of Queensland for 240 calves each year.

3 Methodology

3.1 Nomination of sires

Nominations for young bulls for each cohort were sought from members of the Australian Limousin Breeders Society (ALBS) with a preference for young bulls in the top 10 percent of the breed for some or all of the breed indexes. Where more sires were nominated than the required 10 young sires the highest indexing sires were selected. In addition a selection of six representative sires was sought from the Charolais and Shorthorn breeds to provide head to head comparisons between Limousin and these breeds. The number of progeny recorded for each sire is shown in Appendix 1

3.2 Mating to commercial cows

Three hundred cows were randomly mated to the Limousin, Shorthorn and Charolais sires using a synchronised AI program. Cows were inseminated to one Shorthorn and one Charolais sire in rotation with the 10 Limousin bulls. In the first two years two rounds of AI were used but for the third cohort a single round of AI was used. Limousin bulls were used for natural mating with each herd 10 days after the AI program.

3.3 Measurements taken to weaning

All calves were tagged and weighed within 24 hours of birth with calving ease also recorded as well as those calves which were twins. At approximately 200 days of age all calves were weighed, hair samples taken as back up and blood samples taken and sent to the University of Queensland Animal Genetics Laboratory for extraction of high quality DNA and aso for sire verification. Calves were scored for docility using the ALBS nine point scoring system

3.4 Backgrounding

Calves were grown from approximately 240kg liveweight to 400k liveweight on pasture or grazing oats. At the conclusion of backgrounding 400 day weights together with ultrasound scanning for carcase traits was taken on all progeny. Calves were vaccinated with Bovilis MH prior to entry to the feedlot.

3.5 Finishing

With the exception of cohort 1 heifers all progeny were finished in a feedlot for a minimum of 100 days. The cohort 1 steers were finished at the ICM Feedlot in Victoria as the Growsafe equipment had not been installed at the Tullimba Feedlot at the time of measurement. Cohort 2 and cohort 3 steers and heifers were lot fed at the Tullimba research feedlot and underwent a 70 day feed intake measurement during their 100 day plus feedlot period.

3.6 Slaughter

The first cohort were slaughtered at Teys, Wagga and cohorts 2 & 3 were slaughtered at John Dee abattoirs at Warwick, Qld. In each case the NLIS identification number was cross referenced with the kill number to ensure correct identification of carcases. The eye muscle area measurement was taken by Alex McDonald using a plastic grid for all slaughter groups. The p8 fat depth measurement was taken by abattoir staff and all carcases were measured by accredited MSA assessors for all MSA traits. A one rib meat sample was taken from all carcases and transported to the UNE Meat Science Laboratory.

3.7 Meat Science Measurements

The UNE Meat Science Laboratory measured ultimate pH, Intramuscular Fat Percentage Warner Bratzler Shear Force and Cooking Loss on all meat samples.

3.8 Data recording

All measurements of birth traits, weight traits, docility, ultrasound carcase scans, carcase traits and eating quality traits were recorded on the ABRI multibreed database. (Appendix 2). Measurements analysed in the Limousin BREEDLAN analysis were analysed in the monthly BREEDPLAN run.

4 Results

4.1 Genomics

The first cohort was tested with an Illumina 50K genomic test by the Co-operative Research Centre for Beef Genetic Technologies. Along with the genotypes from 345 influential Limousin sires the genomic results for cohort 1 were used to test the veracity of the CRC multibreed genomic prediction equations for the Limousin breed and also to test prediction equations developed for the Limousin breed in the USA by Merial through their subsidiary,Igenity. In both cases the the prediction equations were not sufficiently accurate to justify the inclusion of genotype results into the Limousin BREEDPLAN analysis.

4.2 Progeny testing of young sires

An extensive range of phenotypic measures were taken on each calf including birth traits, growth traits, carcase traits docility and MSA eating quality traits. All progeny were recorded in the ABRI crossbred register and the measurements of traits were added to this database Those traits currently analysed by BREEDPLAN were routinely analysis in the Limousin BREEDPLAN analysis.

As expected the EBVs and Indexes for some young bulls increased, some decreased and some remained relatively unchanged. The accuracy of all traits also improved significantly especially for carcase traits.

4.3 Use of the young sires by Limousin breeders

Semen from most of the young sires was offered for sale by auction at the National Show and Sale following the completion of all data entry and analysis. Prices paid ranged widely.

A sire in the top 1% for all traits was a late addition to the Cycle 1 program to replace a young sire that failed a health test and was already being used by AI as he was in the top 5% for all $Indexes. After progeny testing the sire was in the top 1% for all $Indexes. The sire was used even more widely by Limousin breeders and his semen has been exported to the USA and Europe.

5 Discussion

5.1 Data collected

The measurements collected on the three cohorts of progeny is the most complete set of phenotypes collected for the Limousin breed in Australia. In addition to the standard data used to calculate EBVs and Indexes in the standard Limousin BREEDPLAN analysis measurements of traits including feed efficiency (two cohorts), the eating quality traits, objective tenderness (shear force), chemical intramuscular fat percentage, cooking loss and MSA Index has been recorded. The data also included the first significant quantity of actual abattoir carcase measurements for the breed.

5.2 Multibreed data

Data collected on the progeny of Charolais and Shorthorn sires and recorded in the ABRI multibreed database is available for future multibreed analyses.

5.3 Genomic tests

The cost of genotyping calves was not included in the budget for the Limousin BIN because of the uncertainty at the time (2009) of the most appropriate genomic test and its cost. Genomic testing of the first cohort along with 345 influential sires was carried out by the Co-operative Research Centre for Beef Genetic Technologies to enable verification of the multibreed prediction equations for the Limousin breed.

With the impending introduction of the Single Step BREEDPLAN analysis it is important that genomic testing is done on cohort 2 and cohort 3 animals for incorporation into the Single Step analysis for the Limousin breed along with the genomic results from the 345 influential sires, new AI sires registerd since 2012 and cohort 1 progeny

5.4 Specific Objectives

6. A total of 240 progeny for 10 Limousin sires per year will be born in co-operator commercial herds for three consecutive years.
7. 240 progeny per year will be finished on grass or grain to an average carcase weight of 310 kg at 18 months of age.
8. Measurements on 240 calves to include gestation length, birth weight, 200 day wt, 400 day wt, 600 day wt, docility score and flight time. All of these records to be stored on the ALBS database at ABRI
9. Additional measurement on the 240 calves to include carcase weight, fat depth, eye muscle area, marble score, pH, meat colour, shear force, compression, IMF%, Cooking Loss,
10. DNA samples will be taken and stored at the University of Queensland for 240 calves each year.

The actual number of calves born in co-operator herds each year met the objective of 240 calves born but some of these calves were not suitable to be included in the project due to being twins, illness or death

The heifers from cohort 1 were finished on grass and the steers from cohort 1 and all progeny in cohort 2 and cohort 3 were finished on grain for a minimum of 100 days. The average carcase weight of the cohort 1 heifers was 247kg with heifers in cohort 2 and 3

being an average of 323kg carcase weight and the three cohorts of steers averaged 341kg carcase weight.

All of the measurements were taken on all calves and stored in the ABRI multibreed database
All of the above measurements except compression were recorded on all animals
Blood samples were taken from all progeny and high quality DNA is stored at the University of Queensland Animal Genetics Laboratory

6 Conclusions/Recommendations

The utilisation of genomic technology to help determine the genetic potential of individual animals is now widely used in the Australian dairy industry and is well advanced in the Australian beef industry. The key to utilisation of genomic technology is a large number of extensively phenotyped animals which also have genotypes. This project has put the Limousin breed in a position to start utilising genomic technology through the Single Step BREEDPLAN analysis. The animals measured in this project which have not yet been genotyped need to be genotyped so that they are part of the resource population for the breed. The Limousin breed needs to continue to build the number of animals in this resource population in a strategic way.

7 Key Messages

Limousin seedstock breeders will need to embrace genomic technology in the same way that seedstock breeders from other breeds such as Angus, Hereford, Charolais and Brahman are embracing the technology. The reference population of genotyped animals with high accuracy EBVs and genotyped young animals with comprehensive and accurate phenotypes needs to be continually increased. This will enable breeders to use genotyping to increase the accuracy of the main traits and also to provide EBVs for expensive or difficult to measure traits such as feed efficiency and carcase eating quality traits.

8 Appendix

8.1 Sires and progeny measured

Cohort 1

Sire	Progeny born	Progeny with Carcase data
BPLPD830	13	12
JWMFD3	22	19
MDNPY329	18	16
MGWFC225	16	15
MGWPC210	16	16
PKVPC706	17	15
RBMPD102	16	14
RKKPD12	14	12
TJGPC11	19	17
WLPD46	16	16
LMLPD46*	14	13
MGWPW840*	8	8
PLAPC15*	12	12
Charolais sires	13	11
Shorthorn sires	15	13

** Follow up sire

Cohort 2

Sire	Progeny born	Progeny with Carcase data
BCTPB64	17	15
BPLPD842	16	15
DJGPE1419	15	12
GCNFY309	16	14
GHSPB2	16	13
KCCPE50	8	7
MATPE148	11	10
MDNPE1385	18	16
MRJPE7	13	13
MUWFE24	22	20
MGWPB65**	25	23
MGWPD400**	18	16
SLTPE7**	18	18
Charolais sires	9	8
Shorthorn sires	7	7

**Follow up sire

Cohort 3

Sire	Progeny born	Progeny with Carcase data
AMSPC7020	15	13
DENPC20	17	14
GHLPC3	36	33
IMUPE555	14	13
KCCPF85	16	13
MCFPE55	25	21

MGWFE647	13	11
PKVPC717	16	14
PKVPF48	15	15
PREPD99	13	12
BCTPC64**	26	24
MDNPB734**	10	9
MDNPC925**	3	3
MDNPE1558**	2	2
MDNPF1645**	2	2
Charolais sires	11	10
Shorthorn sires	8	7

**Follow up sire

8.2 Data recorded

Birth, Growth Traits & Docility

	Gest Length	Calving Ease	Birth Wt	200 D Wt	400 D Wt	600 D Wt	Docility Score
Cohort 1	185	226	226	228	223	145	226
Cohort 2	157	231	165	227	226	0	227
Cohort 3	147	235	235	231	231	0	231

Scan Traits

	EMA	Rib Fat	P8 Fat	IMF%
Cohort 1	223	223	223	223
Cohort 2	221	221	221	221
Cohort 3	231	231	231	231

Abattoir Carcase traits

	Carcase Wt	EMA	Rib Fat	P8 Fat	Marble Score	Meat Colour
Cohort 1	216	216	216	216	216	216
Cohort 2	211	211	211	211	211	211
Cohort 3	222	222	222	222	222	222

Meat quality traits

	WB Shear Force	IMF %	Cooking Loss	pH	MSA Index
Cohort 1	214	214	214	214	214
Cohort 2	211	211	211	211	211
Cohort 3	222	222	222	222	222