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Evaluation of the genetic basis of polledness in Australian goats

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Executive summary

The Australian goat industry is a comparatively small but important enterprise given the demand for goat meat both domestically and within many regions of the world. Development of the industry in Australia is at an early phase, meaning the benefits from research in genetics and genomics are yet to be realised. This project represented a first step towards a better understanding of the genetic characteristics of Australian goats. The objectives of the project were to 1) investigate the genetic basis for polledness (lack of horns) in Australian goats and a related intersex condition and 2) obtain a baseline genetic diversity survey of Rangeland goats. A total of 175 goats were sampled from three populations; Boer and Cashmere goats from studs in Queensland and Rangeland goats from far western NSW. In each case, blood was collected from both horned and polled animals and in the Rangeland population a small number of animals were sampled with the intersex condition (sex reversed genetic females that display both sets of sex organs). The DNA from each animal was genotyped at 52,088 single nucleotide polymorphisms (SNP) and the genetic data analysed against their phenotype (presence or absence of horns). This revealed a strong association signal on goat chromosome 1 in both the Boer and Rangeland goats. Importantly, the chromosomal location of this association signal matched exactly with the results of previous research into polled European dairy goats. The conclusion was therefore that the same genetic mechanism underpins poll in Australian and European goats. Analysis of the intersex animals revealed unexpected results, indicating a more complex association with polledness than previously thought. This leaves open the possibility that a genetic test can be developed to breed for poll animals without generating intersex kids. The SNP data was analysed to determine the population history of Rangeland goats. The animals carry exceptionally high levels of genetic diversity, as might be expected of an unmanaged population. Further, a clear genetic signal was observed that suggested Boer genetics are present with the Rangeland animals. The results of the project form an important first step towards a deeper understand of the genetics of production traits in this livestock species.

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1 Background

1.1 History of rangeland goats in Australia

Goats were bought to Australia by a series of European settlers and have been part of the landscape ever since. Goats were aboard the first fleet on arrival from England via Africa in 1787 and introductions are recorded from India soon after in 1791 (Parsonson 1998). It is also possible Portuguese, Dutch and other explorers may have released goats in Australia prior to British settlement. Their adaptability to the arid environment that characterises much of the Australian continent has meant that goats have flourished without human management. The resulting population of feral or 'Rangeland' goats has an unknown genetic composition but likely includes contribution from dairy breeds such as the Alpine and Saanen as well as exotic breeds from Asia and Africa. The animals display a diverse range of phenotypic characteristics, including coat colour, body conformation and fibre type (Figure 1). Information concerning their distribution and abundance is summarized in MLA's Goat RD&E Strategy (2012).

1.2 Genetic basis of poll in European goats

For a long time, breeders have shown a preference for animals without horns (referred to as 'polled'). Polled animals are less likely to injure each other or their animal handlers during transportation and yarding. Further, they don't get caught in fencing and those that naturally lack horns don't need to be physically dehorned. Breeding for poll has been common place in sheep and cattle breeds for centuries, with many commercially important breeds uniformly polled. Most goat breeds carry horns, however there are polled animals and the genetic basis in European goats has been elucidated. A positional cloning study identified an 11.7 Kb deletion on chromosome 1 that causes both the absence of horns and an intersexuality condition (Pailhoux *et al.* 2001). Poll is inherited as a dominant trait, while the associated sex reversal occurs as a recessive trait in XX individuals. This has a practical consequence for breeders with a preference for polled animals, as the associated intersex condition often dissuades them from breeding hornless animals together. Interestingly, the poll intersex locus (*PIS*) in goats is non-syntenic to the loci underpinning poll in sheep (Johnson *et al.* 2011; Kijas *et al.* 2012) or cattle (Medugorac *et al.* 2012). This raises the prospect that the *PIS* locus is not the only cause of poll in goats given reports that poll is not associated with the intersex condition in all breeds (Quanwu *et al.* 1996). This prompted analysis in this project, to better understand what causes poll in Australian goats and to see if it can be genetically 'uncoupled' from the intersex condition.

Figure 1 Goats from three populations. Cashmere goats (n = 48) were sampled from a single stud breeder in Queensland (panels 1 and 2). The majority of animals were horned (panel 1) but four animals were polled (panel 2). Rangeland goats (n = 66) were sampled from a single property in far western New South Wales (panels 3 – 6). These feral and largely unmanaged animals displayed a wide variety of phenotypic variation in colour, hair type and body composition. Some Rangeland individuals were phenotypically similar to Boer goats (eg panel 5). Boer goats (n = 61) were sampled from a single stud breeder in Queensland (panels 7 – 9). The three populations offered the opportunity to assess the genetic basis of poll while performing a survey of genetic diversity across breeds.

1.3 Molecular tools now available for the goat genome

The availability of SNP arrays has prompted an acceleration in our understanding of domestication and genetic diversity in cattle (Bovine HapMap consortium, 2009), sheep (Kijas *et al.* 2012) and other domestic animals (Muir *et al.* 2008; Vonholdt *et al.* 2010). These arrays allow the genotyping of tens of thousands of genetic loci distributed across the genome. The large amount of genetic information that can be rapidly obtained have powered association studies into both monogenic diseases (Becker *et al.* 2010; Charlier *et al.* 2008; Lequarré *et al.* 2011; Zhao *et al.* 2012) and complex traits (Hayes *et al.* 2010; Heaton *et al.* 2012). To date this has not been possible in goat, however through the work of the International Goat Genomics Consortium a SNP chip has recently been made available that assays in excess of 50,000 loci distributed across the goat genome. In this context, the project sought to apply the goat SNP chip for two objectives. Firstly, we performed a fine-grain analysis of the genetic diversity and admixture that links three breeds of goats with a shared population history. Secondly, we sought to investigate the genetic basis of poll and

the associated intersex condition within non-European animals. This searched for the presence of genetic heterogeneity and loci that may control poll in addition to the *PIS* locus.

2 Project objectives

The project had the following objectives:

1) investigate the genetic basis for polledness and the related intersex condition
2) explore if a DNA test can be developed to 'uncouple' poll from the intersex condition
3) obtain a baseline genetic diversity survey of Rangeland goats
4) evaluate the effectiveness of recently developed genomic tools for goat research
5) explore future opportunities for genetics and genomics to assist the goat industry

3 Methodology

3.1 Animal sampling

Three goat populations were sampled (Figure 1). 61 Boer goats were sampled from the Yarrabee goat stud in Queensland, including polled (20) and horned (41) animals. A total of 66 Rangeland goats were sampled from the Orana property in outback New South Wales. Of these, 31 had horns and 35 were polled. Five of the polled individuals appeared to be hermaphroditic, a condition previously reported in goats arising from karyotypically XX (sex reversed) male animals that are infertile. This is referred to throughout as the 'intersex' condition. The third population was 48 Cashmere goats sampled from the Tarampa stud in Queensland. This consisted of 44 horned and 4 polled females. Sampling of each animal involved collection of 8 ml of whole blood, and all animal handling and sample collection was performed in accordance with Animal Ethics, CSIRO Brisbane Animal Ethics Committee, Registration Number A12/2011.

3.2 Genotyping and data quality checking

DNA was extracted from whole blood using the Qiagen Blood and Tissue extraction kit following the manufacturer's instructions. A total of 183 DNA samples were genotyped using the goat SNP50 BeadChip on the Illumina HiScan machine. Raw signal intensities were converted into genotype calls using GenomeStudio software v2011.1. Intensity values from 53347 SNP were analysed against a cluster file provided by the International Goat Genomics Consortium before three filters were applied to remove unreliable markers. Firstly, metrics describing cluster separation and heterozygote intensity were utilised within GenomeStudio to identify 644 underperforming SNP. Secondly, call rate was calculated for each SNP across the set of 183 DNA samples. A total of 1145 SNP with call rate less than 90% were removed. Finally, a concordance test was applied after genotyping two independent samples from the same animal. Investigation of 52164 loci that returned a genotype call in both duplicates identified 24 discordant SNP. A total of 1259 SNP that failed at least one of the three filters were removed from the project.

3.3 Methods for data analysis

Basic indices of genetic diversity including the proportion of polymorphic markers (P_N), observed heterozygosity (H_O) and expected heterozygosity (H_E) were calculated using PLINK (Purcell *et al*. 2007). In preparation for model based clustering using STRUCTURE (Pritchard et al 2000), a subset of SNP were selected as follows. First, markers in linkage equilibrium were identified using the LD based pruning approach implemented in PLINK (- - indep-pairwise 50 10 0.15). This removed 35,671 SNP that exceeded an r^2 threshold of 0.15. Markers without known genomic location and SNP on the X were removed. From the remaining markers, a random set of 8000 SNP were used. Genotypes from 182 animals were used for three replicate runs performed using K = 2 - 4, where K is the number of assumed subpopulations. The admixture model was applied and runs comprised 5000 MCMC burnin replications and 5000 run length. Solutions were checked for variability between replications and to ensure convergence before visualisation was performed using DISTRUCT v1.1 (Rosenberg, 2004).

To perform linkage mapping of the genetic cause of poll / horn, polled and horned animals were assigned as cases and controls respectively, before allelic association testing were performed for each SNP using the - - assoc function in PLINK. Association testing was first performed separately within Boer and Rangeland goats. A chi-squared test for association was performed for each marker using the - - assoc flag within PLINK, before the negative Log10 of each p-value was plotted in genomic order. A GWAS was subsequently performed using all of the animals in a single analysis (Table2). The Cochran-Mantel-Haenszel (CMH) test was used to investigate the association between case and control after adjusting for stratification (Dobbins and Simpson 2002). The CMH test was applied as an I x J x K stratified table where: I equalled 2 to represent case and control; J equalled 2 to represent bi-allelic SNP allele frequencies; K equalled 3 to represent the three breed clusters of Boer, Rangeland and Cashmere individuals. The CMH test was performed using the - - mh flag within PLINK.

4 Results and discussion

4.1 Genetic mapping of poll horn

The genetic basis for horn poll was investigated separately within Boer and Rangeland goats. A genome wide association study (GWAS) was performed using 20 polled and 41 horned Boer goats. Analysis of the genotype and phenotype of each animal revealed a strong signal on chromosome 1 (Figure 2). Perfect association was observed for two SNP (*snp3443* P = 2.51 x 10-12; *snp29531* P = 2.51 x 10-12). Each polled animal was heterozygous while every horned animal was homozygous, consistent with a dominant mode of inheritance for poll. The fact every polled animal was heterozygous, and none were observed that were homozygous for poll, is also consistent with the breeding performed at the Boer stud. Specifically, matings that include two polled animals have been avoided. The consequence of using a horned animal in every cross is that all of the progeny will carry at least one wild type allele (and can therefore not be homozygous for poll).

The two SNP markers with perfect association were located at Mb position 127.7 and 148.1 on chromosome 1 which is adjacent to the poll intersex syndrome (*PIS*) locus (Mb position 127.5). Independent GWAS using 35 polled and 31 horned Rangeland goats revealed an association signal in the same region (Figure 2). The two SNP with the strongest association (*snp3460* P = 1.02 x 10-9; *snp3455* P = 6.80 x 10-8) were located within a 175 Kb region (Mb position 126.9 – 127.1) slightly upstream of the *PIS* locus. The finding that both populations contained a single and strong association peak in the *PIS* region prompted a third GWAS analysis. All animals were used for association testing following correction for

breed based genetic stratification (refer to the methods for details). Plotting the results for chromosome 1 separately for all three GWAS revealed that the combined analysis served to reduce the critical interval. Five of the ten highest SNP were located in a 769 Kb region (Mb position 126.9 – 127.7) when estimated using all animals. This region is centered on the *PIS* locus.

Interpretation: The conclusion from this first part of the study was that the genetic determinant for poll in Australian goats is:

1) the same in Boer and Rangeland goats as it mapped to the same region of the genome

2) in the same chromosomal position as previously found in European diary goats. ***This strongly suggests that the cause of poll in Australian populations is present due to the introduction of European poll goats during the foundation of today's local populations.***

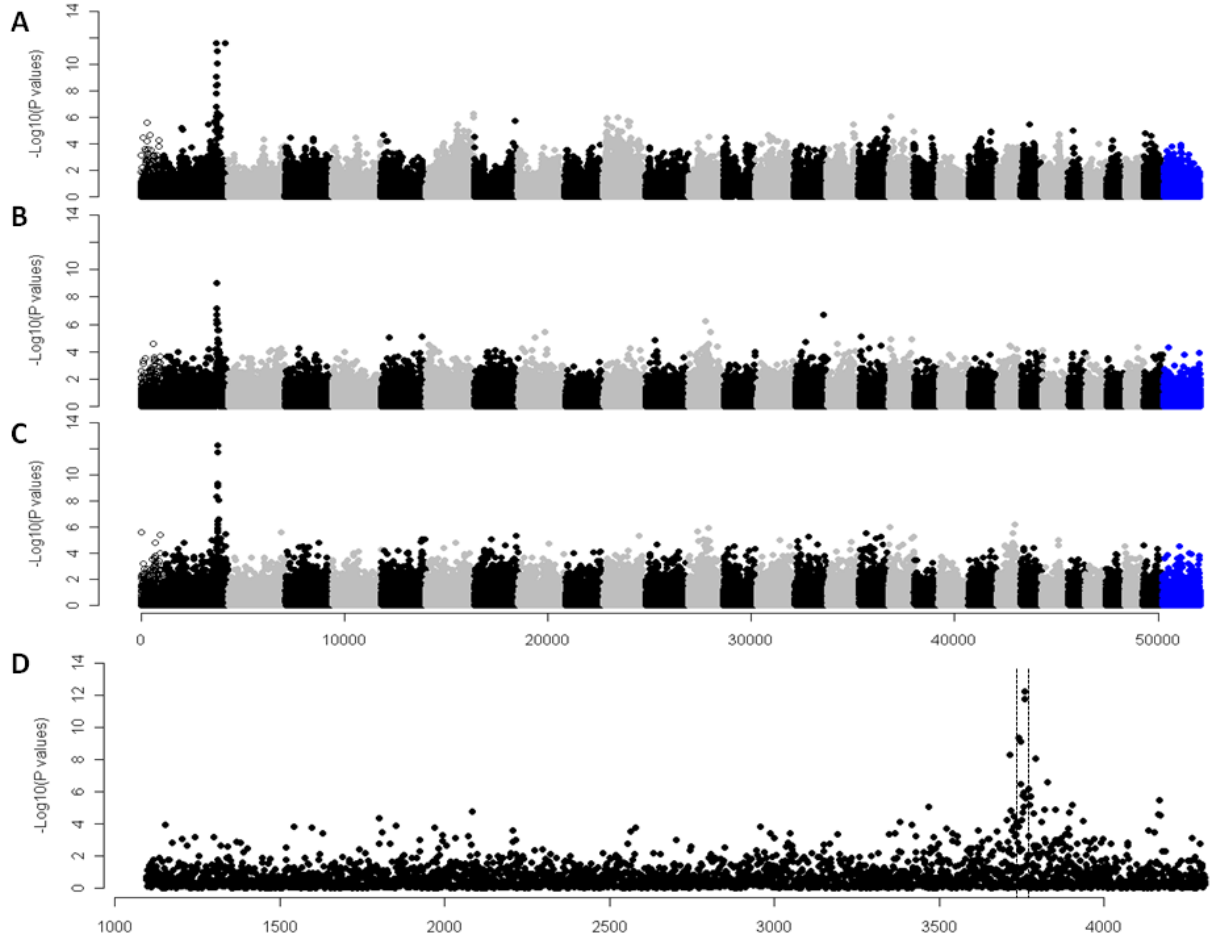

Figure 2 Genome wide association study for poll (absence of horns) in goat. Genome wide plots of –log10 (*P* values) are shown following analysis using Boer goats (**panel A**), Rangeland goats (**panel B**) or a combined analysis of all animals that includes Cashmere **(panel C**). SNP are plotted in genomic order with odd and even numbered chromosomes given in black and grey symbols respectively. SNP without known chromosomal position are plotted at left using open symbols, while markers on the X are given in blue (far right). The association results obtained using all animals is shown for chromosome 1 (**panel D**). Five of the top ten SNP defined a critical interval of 769 Kb (vertical lines) centered on the *PIS* region previously shown to cause Poll in European goats (Pailhoux *et al.*, 2001).

4.2 Analysis of intersex goats

Initial characterisation of the *PIS* locus and its effect on poll included testing 17 XX sex-reversed European (intersex) animals. This revealed that all 17 intersex goats were homozygous for the *PIS* deletion (*PIS* -/-) (Pailhoux *et al.* 2001). This was an important finding **that set the expectation in this work that each intersex animal should carry two copies of the poll mutation**. This expectation matches the observations of breeders, who report that intersex animals are only produced from crossing polled males and females.

To test this expectation (that intersex animals should be homozygous for poll), we developed a PCR test that directly assays for the presence or absence of the 11 Kb deletion at the *PIS* locus (Figure 3). The test was performed on DNA from all 175 goats. Figure 3 confirmed two intersex animals (IS200 and IS500) were homozygous for the presence of the deletion (*PIS* -/-). These were the only two animals that were homozygous for the deletion out of all 175 goats investigated. These two animals conform to the expectation that intersex goats are homozygous poll (and carry the deletion on both versions of chromosome 1). Interestingly, analysis of the remaining intersex animals revealed all three carried at least one copy of the non-deleted or wild-type chromosome (the PCR test was not able to distinguish between *PIS* +/- heterozygotes and *PIS* +/+ wild-type homozygotes).

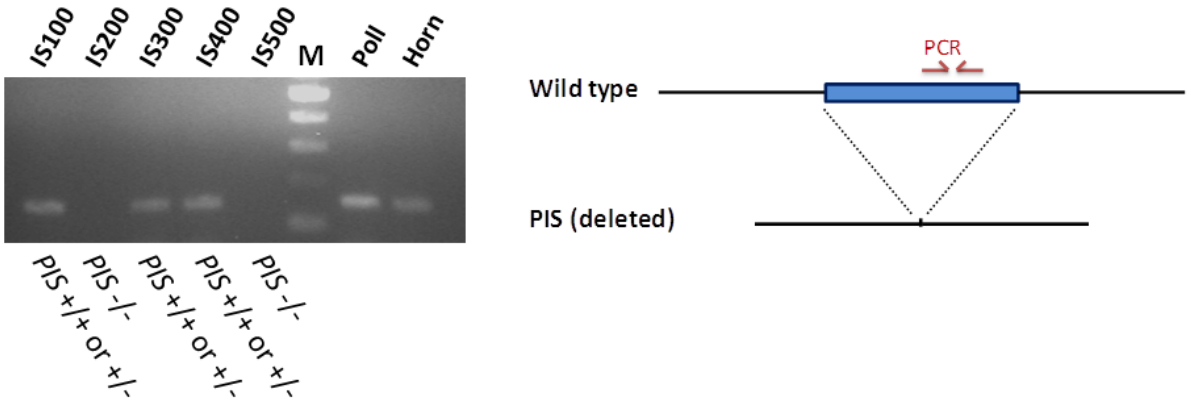

Figure 3 Direct PCR testing of five intersex goats. A direct PCR test was developed to detect the presence of the wild type chromosome associated with horns (see the schematic at right). PCR primers were used that hybridise within the deleted region of chromosome 1 that is unique to poll causing *PIS* chromosomes (DelTestE, Pailhoux *et al.* 2001). Production of the 148 bp PCR fragment occurs only from the non-deleted wild-type chromosome associated with horns (*PIS* +). Five intersex animals were tested (IS100 – IS500), along with a sexually normal polled (Poll) and horned (Horn) goat. PCR products were loaded on to a gel along with a size marker (M) (the gel is seen at left). Only two of the intersex animals (IS200 and IS500) appear to be homozygous for the *PIS* deletion (*PIS* -/-). The remaining animals carry at least one copy of the wild-type chromosome.

Interpretation: The finding that some of the intersex animals have a 'wild-type' or normal chromosome at the poll locus was unexpected. The interpretation is that there may be more than two chromosomal versions present in the population. To date, the assumption was that chromosomes were either 'wild-type' or 'poll'. The finding in this research was that there may be a third chromosome, however the results are not conclusive and additional analysis will be required. The finding does, however, indicate two things:

1) the relationship between the appearance of poll and the intersex condition is more complicated than previously thought

2) this complication increases the chance the two traits can be uncoupled, leaving open the opportunity to breed for poll without generating intersex kids.

4.3 Genetic diversity

To address the second objective of the project, the SNP genotypes were used to estimate the relative level of genetic diversity present within each population. Genetic diversity is important, as it reflects the ability of a population to adapt and change in response to selection for traits of interest. Very low genetic diversity (and high levels of inbreeding) stifles genetic progress whereas high diversity in a population suggests plenty of the raw material for genetic gain is available. A key metric of genetic diversity is the proportion of genetic loci that display polymorphism within a given population. SNP loci are bi-allelic, so the percentage of SNP that displayed both alleles was calculated within each population (termed P_n, Table 1). For the Rangeland goats, this revealed 99.6% of SNP tested were polymorphic. This is an exceptionally high level of polymorphism. The rate of SNP polymorphism was only slightly lower within Cashmere (98.0%) and Boer (97.1%) goats. When viewed against the results obtained in other studies, it appears goats (in general) contain a lot of genetic variability. For example, analysis using the ovine SNP50 BeadChip returned lower levels of diversity in 74 breeds of domestic sheep (all sheep breeds had P_n < 97%, Kijas *et al.* 2012). Similarly, testing 47 cattle breeds with the bovine SNP50 BeadChip showed the proportion of loci with non-zero MAF ranged between 70 and 85% (Gautier *et al.* 2010). Variation in the number of animals per breed and differences in the development of the species specific SNP arrays mean that it is difficult to draw firm conclusions, **however the high rate of diversity observed here strongly suggests goats are likely to be more polymorphic than cattle, sheep and other livestock species such as the pig**.

Table 1 Diversity metrics comparing goat populations

Population	Origin	n	P_N	H_O	PH_O	H_e
Boer	Australia	61	97.1	0.363	0.374	0.355
Rangeland	Australia	66	99.6	0.411	0.413	0.409
Cashmere	Australia	48	98.0	0.384	0.392	0.371

Basic indices of genetic diversity were compared between populations. The number of animals within each group is given as n. The proportion (%) of 52088 SNP that displayed both alleles within each group is given as P_N. The average observed heterozygosity was measured using all SNP (H_O) or using only polymorphic SNP within each population (PH_O). Expected heterozygosity, based on the observed genotype frequencies is given as (H_E).

Ranking the diversity between the three goat populations revealed the Rangeland animals had the highest diversity using each metric. This is consistent with their population history,

as the Rangeland goats are largely unmanaged feral goats expected to contain genetic contributions from a number of diverse breeds. In contrast, both the Cashmere and Boer goats were sampled from a single stud with established pedigree records but still retained high levels of diversity. This suggests that where selection pressure for target traits is maintained, genetic progress can be expected to continue and inbreeding is not a concern.

4.3 Genetic links between populations

The SNP data can be used to search for evidence that breeding has occurred between populations (termed 'admixture'). To search for admixture between the populations, model based clustering was performed that partitioned the genome of each individual into a user defined number of components (*K*). At *K* = 2, the Boer and Cashmere goat genomes appear to carry different ancestral components that are both present within Rangeland goats (Figure 4). At *K* = 3, Rangeland animals carry an ancestral component largely absent from either the Boer or Cashmere animals (shown in green, Figure 4). This likely reflects the past genetic contribution of a breed that has not been sampled in this study. Within each breed, the proportion of each ancestral component was averaged across individuals (Table 2). This revealed that for the Rangeland animals, around 22% of their genome has a common ancestry with Boer goats while approximately 15% is in common with Cashmere goats (Table 2). Repeating the analysis using *K* = 4 differentiated a small number of Rangeland animals that in each case were of the intersex phenotype.

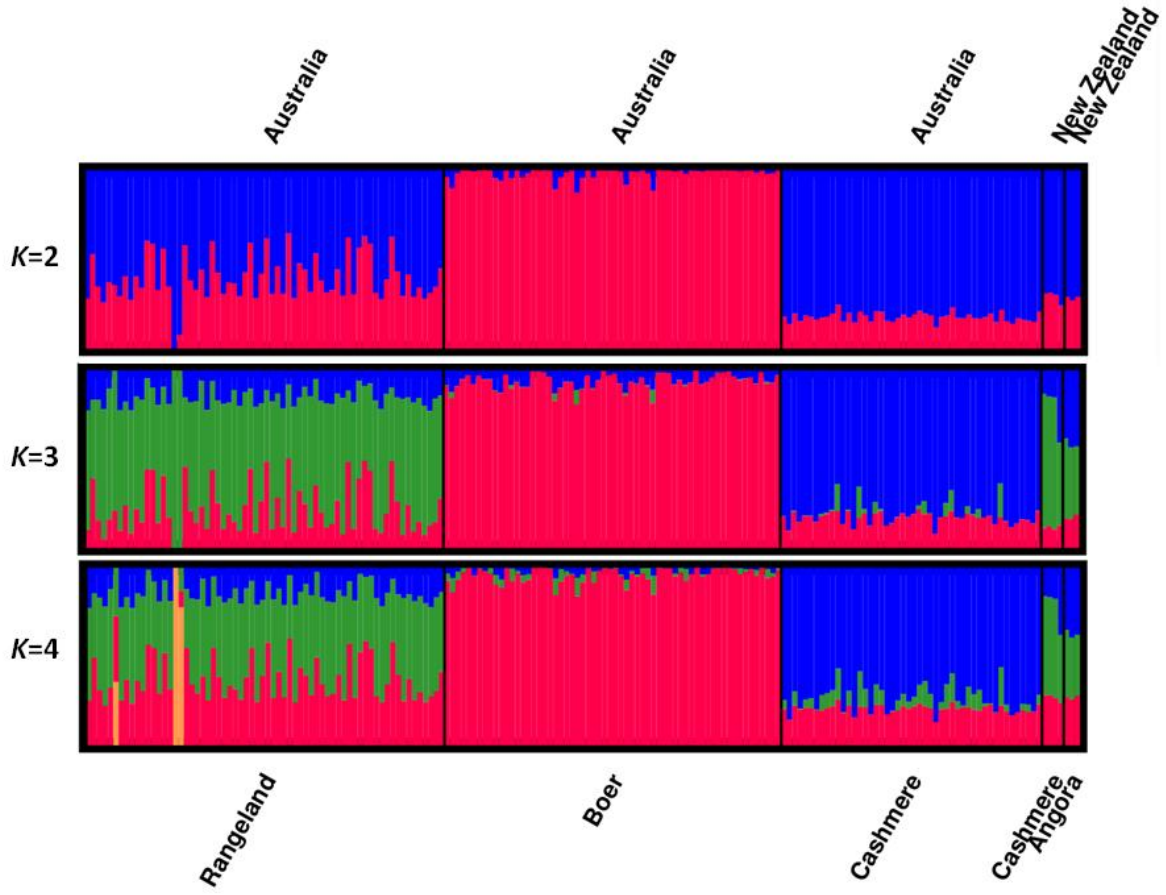

Figure 4 Model based clustering of goat populations. The genome of each goat was decomposed into a pre-determined number of *K* components, and typical results are shown for *K* = 2 – 4. The analysis relied on genotypes at 8000 SNP, selected to be unlinked. Assuming two components, a division can be observed between Boer goats and other animals. At *K* = 3, the composition of Boer, Cashmere

and Rangeland animals appear distinct. Inspection of the Rangeland animals indicates a varied contribution of Boer and Cashmere genomes. The within breed average for the proportion of each sub-population is given in Table 2.

The model based clustering analysis showed clear evidence that admixture has occurred and genetic links exist between the populations. For example, a number of Rangeland goats shared up to 50% of their genome with Boer goats (Figure 4). This may reflect anecdotal information concerning the intentional release of Boer goats into rangeland environments to facilitate introgression of Boer genetics and their associated superior carcass traits. On average, around 22% of the Rangeland goat genome was in common to that found in Boer goats (Table 2), and the physical appearance of some Rangeland animals certainly suggests Boer genetics are present (panel 5, Figure 1). The majority of the Rangeland goat genome was largely absent from the other Australian goats (green component, 64 %, Table 2). Comparison with an expanded set of breeds will be required to determine the origin of this diversity, as Africa, Indian, Chinese and other European breeds are all likely to have contributed to the feral population. Perhaps the most likely breeds to have contributed this genomic component are Alpine and / or Saanen, as these played a large part in the development of Rangeland goats and have not been genotyped in this experiment (Pers. Comm., Blair Brice).

A note of caution is required concerning the interpretation of the model based clustering presented. Links (perceived co-ancestry) may be found between populations that would not arise if an expanded set of populations was sampled. Given only three breeds were evaluated, it is therefore possible that inclusion of additional goat breeds may alter the signatures of admixture detected.

Interpretation: The clustering analysis (Figure 4) indicated:

1) Rangeland goats have the most ‘mixed’ genomes of the three breeds tested. This can be seen by the presence of multiple genomic components represented by the different coloured sections in Figure 4.

2) Comparison between the breeds showed genetic mixing has occurred between the Boer and Rangeland populations. Some of the Rangeland goats had a DNA profile that was up to 50% the same as purebred Boers. This confirms that Boer genetics have been introduced into the Rangeland animals, probably with the view to grade up their carcass traits.

3) A chunk of the Rangeland genetic profile comes from a population not sampled in the experiment (seen as the green component in Figure 4). Given neither Alpine nor Saanen were included, these seem like the most likely contributors based on the recorded use of these European breeds during colonial Australia.

4) The SNP data proved to be highly informative for tracking the mixing of genetics.

Table 2 Ancestral Proportions for Each Breed

	Sub-population Proportions			
Population	**green**	**red**	**dark_blue**	**orange**
Assuming *K* = 3 subpopulations				
Rangeland	0.636	0.218	0.146	na
Boer	0.006	0.936	0.058	na
Cashmere	0.023	0.167	0.810	na
Assuming *K* = 4 subpopulations				
Rangeland	0.471	0.358	0.138	0.033
Boer	0.025	0.958	0.016	0.000
Cashmere	0.062	0.204	0.734	0.000

Assuming either 3 or 4 subpopulations, each breed was tested using model based clustering. The table shows the average proportion of each subpopulation assigned within the three goat breeds.

5 Conclusions and recommendations

5.1 Conclusions regarding poll

The experiment convincingly answered a number of questions concerning the genetics of poll in Australian goats. The key conclusions were:

- the same genetic cause underpins poll in both the Boer and Rangeland goat

- this genetic cause has been inherited from European dairy goats

The SNP data could be used to develop a diagnostic test for poll, however given it is a dominant trait this may have limited impact. One possible application would be to distinguish between polled animals that are homozygous (two copies of the genetic determinant) and heterozygous (only one copy). While both classes of animal carry horns, the kids they produce will be different and so goat farmers may benefit from a test where they want to increase the proportion of polled animals.

5.2 Recommendations regarding poll

If a service to distinguish homozygous from heterozygous polled animals has value, more information about the likely application and uptake within industry could be obtained. This might take the form of a survey for producers to estimate indicative interest. The technical provision of a service would not be difficult through a laboratory such as the University of Queensland who already offer DNA based tests for the cattle and horse industries. The SNP markers have been identified in this project that would form the basis of a diagnostic test.

5.3 Conclusions regarding intersex

The conclusions concerning the genetic basis of the intersex condition were less clear cut. The analysis was based on investigation of only 5 intersex animals, however this was sufficient to discover that they were not all homozygous for the poll chromosome as expected. From this first experiment, therefore, we can only say that the cause of the intersex condition is more complex than initially thought. Additional research will be needed to better understand the genetics of how intersex animals are generated, and a brief outline of how this might be approached is given below.

5.4 Recommendations regarding intersex

If the industry benefit to flow from ‘uncoupling’ poll from intersex is strong, a follow-up project should be considered. The strategy for additional experimentation would involve:

- collection of a small number of animal trios (say up to 10 trios). Each trio needs to consist of both parents and their progeny where the offspring exhibits the intersex condition. Where available, inclusion of full-sibs that did not develop the intersex condition would also assist.

- if trios are not available within industry, a series of directed matings using embryo transfer should be considered. Matings would be performed where both parents are polled (heterozygous *PIS*/+). This would generate each genotypic class (*PIS/PIS*, *PIS*/+ and +/+) and allow for a re-sequencing experiment to identify the sequence differences between *PIS/PIS* animals that are sexually normal and those that display the intersex condition.

- SNP genotyping of each trio member, and sequence analysis of the intersex individuals.
- If there is an interest to pursue this, CSIRO has the expertise to conduct the molecular genetics and analysis. Other project participants (Ben Swain, BCS Agribusiness) would be needed to identify and collect the required trios. Given the modest size of the goat industry and the limited levy funds available for research, a project could be designed to proceed at a similar level of investment that was used to drive this project.

5.5 Conclusions concerning rangeland goats

Analysis of the SNP data revealed that Rangeland goats are perhaps the most genetically polymorphic population of (semi)-domestic animals recorded to date. SNP genotyping technology has only been available for livestock species for the last couple of years, however a search of the published results indicates that the Rangeland goats contain higher levels of diversity than any other population (of any livestock species). This is perhaps not surprising given the animals randomly mate and diversity is not being reduced through application of AI or the preferential use of high value sires. What does a high genetic diversity mean? It can be thought of as meaning that the population contains a broad range of genes that have been accumulated from a variety of different historical sources. A practical conclusion would be that if selection pressure was applied to almost any trait, the population would quickly respond and exhibit strong genetic gain.

5.6 Recommendations concerning the genetic history of the rangeland goats

Additional SNP data derived from European, African and Asian goat breeds is needed to better understand the genetic contributions that have been involved to develop Australia's Rangeland population. These datasets are likely to become available through international collaboration (at no cost) within the next 12 months. Once available, the recommendation is that the same analysis performed here is repeated using the expanded set of animals.

5.7 Other recommendations

Communication materials are developed to communicate the results in non-scientific language for goat producers and the wider rural community.

6 Acknowledgements

Ben Swain did an outstanding job coordinating the collection of blood samples from the Boer and Rangeland goat populations. Helen Darlington (Yarrabee goat stud) allowed us access to her Boer goats and Russell McCulloch assisted with the collection of blood samples. John Vagg allowed us access to his Rangeland animals and arranged for the poll and intersex animals to be available for blood sampling. Andrew James arranged for access to his Cashmere goats, and Russell McCulloch and Judit Salces Ortiz assisted with the sample collections. Judit subsequently assisted with the PCR based testing of the *PIS* locus, and Russell performed the DNA extractions and SNP50 genotyping using the new goat SNP50 beadchip. Gwenola Tosser (INRA) provided the cluster file for analysis using the SNP50 chip.

Alex Ball reviewed a draft version of the report. Both Terry Longhurst and Felice Driver assisted in discussions and interpretation of the results, and Blair Brice commissioned the work.

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