Animal Genetic Resources Information, 2009, 45, 113–119. © Food and Agriculture Organization of the United Nations, 2009
doi:10.1017/S1014233909990435

Genetic variation of the reference population for quantitative trait loci research in South African Angora goats

C. Visser and E. van Marle-Koster

Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria 0002, South Africa

Summary
The South African Angora goat industry makes the largest contribution to global mohair production. Mohair is a luxury fibre and production of a high quality clip is essential. For many years genetic improvement of Angoras in South Africa was based on quantitative selection. Genome mapping efforts provided new avenues for improvement and a quantitative trait loci (QTL) study was initiated to identify QTL associated with mohair traits. The aim of this study was to describe the genetic diversity of the reference population using the available stud and commercial herds with full phenotypic records. The most appropriate QTL design was identified based on the population structure with regard to the families and number of bucks available for breeding. Four herds, consisting of 1067 pure bred goats in 12 half-sib families, were included. Blood samples were obtained from the herds, 94 markers were tested and diversity parameters were estimated. The average number of alleles per marker varied between 5.4 and 7.2 amongst the herds, whereas the observed heterozygosity varied between 0.59 and 0.67. The genetic structure of these herds was found appropriate for use as a reference population as they showed sufficient genetic variability.

Keywords: *Angora goats, mohair, genetic variation, quantitative trait loci design*

Résumé
L'industrie de la chèvre angora de l'Afrique du Sud apporte la plus grande contribution à la production mondiale de mohair. Le mohair est une fibre de luxe et la production d'une tonte de haute qualité est essentielle. Pendant de nombreuses années, l'amélioration génétique des chèvres angoras en Afrique du Sud était basée sur la sélection quantitative. Les activités de cartographie des génomes ont fourni de nouvelles voies pour l'amélioration et une étude sur le QTL a été lancée pour identifier le locus à effets quantitatifs associé aux caractères du mohair. Le but de cette étude était de décrire la diversité génétique de la population de référence en utilisant les troupeaux reproducteurs et commerciaux disponibles ayant des contrôles phénotypiques complets. Le plan de QTL le plus approprié a été identifié sur la base de la structure de la population considérant les familles et le nombre de boucs disponibles pour la sélection. Quatre troupeaux de 1067 chèvres de race pure dans 12 familles à descendance uniparentale ont été inclus. On a effectué des prises de sang sur les animaux des troupeaux, on a testé 94 marqueurs et estimé les paramètres de la diversité. Le nombre moyen d'allèles par marqueur variait entre 5,4 et 7,2 dans les troupeaux, tandis que l'hétérozygosité variait entre 0,59 et 0,67. La structure génétique de ces troupeaux a été considérée adéquate pour son utilisation en tant que population de référence car les troupeaux ont montré une variabilité génétique suffisante.

Mots-clés: *chèvres Angora, mohair, variation génétique, schéma des locis à effets quantitatifs*

Resumen
La industria de la cabra Angora de Sudáfrica es la que representa el mayor porcentaje de producción de mohair a nivel mundial. El Mohair es una fibra considerada de lujo, y la producción donde se lleve a cabo una esquila de alta calidad es esencial. Durante muchos años la mejora genética de cabras Angora en Sudáfrica ha estado basada en la selección cuantitativa. Los esfuerzos llevados a cabo en relación con el mapeo genético abrieron nuevos caminos para mejorar, y se inició un estudio QTL para identificar el QTL asociado con los rasgos de mohair. El propósito de dicho estudio consistió en describir la diversidad genética de la población de referencia utilizando el semental disponible y rebaños comerciales con registros fenotípicos completos. El diseño más apropiado de QTL fue identificado en base a la estructura poblacional con respecto a las familias y al número de machos disponibles para la cría. Se incluyeron cuatro rebaños que sumaban 1067 cabras de raza pura en 12 familias de medios hermanos. Se obtuvieron muestras de sangre de los rebaños, se probaron 94 marcadores, y se estimaron parámetros de diversidad. El número promedio de alelos por marcador varió entre 5.4 y 7.2 entre los rebaños, mientras que la heterocigosidad observada varió entre 0.59 y 0.67. La estructura genética de estos rebaños se consideró apropiada para ser utilizada como población de referencia, dado que mostraba suficiente variabilidad genética.

Palabras clave: *Angora, mohair, variabilidad genética, loci de rasgos cuantitativos*

Submitted 6 July 2009; accepted 17 August 2009

Correspondence to: C. Visser, Department of Animal and Wildlife Sciences, University of Pretoria, Pretoria 0002, South Africa. email: carina.visser@up.ac.za

Introduction

South Africa is the major producer of mohair in the world, with a contribution of between 55% and 60% of the product to the world market (Loots, 2007). It is therefore imperative to maintain a good quality clip through selection for the desired

mohair traits, that largely depend on accurate genetic improvement programs. For many years quantitative studies and research were undertaken with regard to mohair traits and production of Angora goats, and the results contributed to increased and improved production (Snyman and Olivier, 1996; Snyman, 2002). Despite the progress made with quantitative selection, it has certain limitations, including the selection of breeding values does not account for population effects or genetic diversity and selection is optimised for a general response in the next generation, rather than the highest long-term response (Andersson, 2001). Advances in genomics have provided new opportunities for animal geneticists and breeders where knowledge of the underlying molecular mechanisms of fibre and fleece characteristics should lead to more efficient selection programs in the long term (Purvis and Jeffery, 2007). Microsatellite markers have been widely applied as a suitable DNA marker for diversity and genome-wide studies in goats (Iamartino *et al.*, 2005), because no single nucleotide polymorphisms are yet available for this species (Maddox and Cockett, 2007).

Quantitative trait loci (QTL) studies have been performed in poultry and beef and dairy cattle for some time (Sonstegard *et al.*, 2001; Tuiskula-Haavisto *et al.*, 2002; Casas *et al.*, 2004; Boichard *et al.*, 2006), and the prerequisites include a suitable reference population. It is also requisite to test for sufficient within-breed variation of the reference population, because this knowledge is the first step towards responsible exploitation of domestic animal biodiversity (Beuzen *et al.*, 2000; Iamartino *et al.*, 2005; Li *et al.*, 2008). The necessity of global diversity surveys for further integration into QTL detection studies was also highlighted by Gibson (2003) (http://www.fao.org/biotech/docs/Gibson.pdf).

A QTL identification study was identified in South African Angoras for potential QTL affecting mohair traits. The most appropriate designs for outbred populations with relatively large families are full- or half-sib designs (Weller, 2001). The challenge of these designs is that there is a force towards a small number of sire families with large progeny groups, but there is the probability that the sires used in the project are not heterozygous (Bovenhuis, 2005). A half-sib design was identified as being the most appropriate for the South African Angora industry.

The aim of this paper was to describe the establishment of the reference population for QTL research in South Africa through the appropriate selection of stud families and evaluation of the genetic variation within the herds using microsatellite markers.

Material and Methods

Selection of suitable herds

The majority of Angora goats are farmed in the Eastern Cape province of South Africa. This region referred to as the Karoo has a dry climate and bush type vegetation, that is suitable for Angora goat production. Angora goat breeders taking part in the National Small Stock Performance Scheme were approached in the selection of the herds for this study. Only families with complete pedigree and phenotypic records were considered for inclusion. The breeders agreed to use at least two of the same bucks over a 3-year period to generate sufficient offspring for the reference population. Phenotypic recordings were made on growth (birth and weaning weights, average daily gain) and mohair (fleece weight, fibre diameter, staple length, standard variation of fibre diameter etc.) traits for all goats.

Animal sampling and genotyping

Blood samples were collected over a 3-year period from the animals of the selected herds, and the blood was stored in a DNA bank for small stock research (GADI, National Department of Agriculture). A total of 1124 individual blood samples were used in the study from four different Angora stud herds with suitable families, sufficient progeny and required records.

DNA was extracted from whole blood using the Qiagen DNEasy Tissue kit at the University of Pretoria and the Invisorb blood mini HTS kit (Invitek) for the XtractorGene (Corbett Robotics) at Wageningen University and Research Center according to the protocols of the respective manufacturers. An initial volume of 100 µl of blood was used for both protocols.

DNA samples were amplified with 94 microsatellite markers as selected for the QTL study. Incorrect parentage attributable to recording errors and overmating was identified with Cervus 3.0, and all aberrant individuals were removed from the study. Markers were selected on levels of polymorphism, heterozygosity, allele size range and amplification success. The markers were divided into 8 genotyping sets, averaging 12 markers per set. Polymerase chain reaction (PCR) was performed in an I-Cycler (Bio-Rad) and Ti Thermocycler (Biometra) using 100 ng of DNA, 2.94 µl of ABgene® PCR Master Mix (ABGene, UK) and 0.03 µl each of 40 pmol/µl reverse and forward primer. The PCR amplification was conducted in a 6-µl final volume in 384-well PCR plates under the following conditions: 95°C for 5 min followed by 35 cycles of 96°C for 30 s, 45 s at annealing temperature and 90 s at 72°C with a final extension step of 10 min at 72°C.

Statistical analysis

The statistical power of a half-sib design depends on the number of sires used, offspring per sire and statistical parameters (*i.e.*, the heritability of traits, heterozygosity and magnitude of the QTL; acceptable type 1 error and the marker–QTL recombination fraction). The statistical power was calculated using the 'Power of Daughter Design' software by Bovenhuis (2005).

The genetic variability of the families selected for the reference population was analysed using MS toolkit (Park, 2001). The genetic parameters which were estimated included allelic frequencies, mean number of alleles and heterozygosity values per locus and for each population. The polymorphic information content for each locus and across loci were estimated using Cervus 3.0 software (Marshall *et al.*, 1998).

The FSTAT 2.9.3 program (Goudet, 1995) was used to compute Wright's *F* statistics for each locus, including *F*, θ and *f*, that are analogous to Wright's (1978) F_{IT}, F_{ST} and F_{IS}, respectively. The statistical significance of the obtained values was estimated by bootstrapping using 1000 replications.

Population structure and F_{ST} values were inferred by using the *structure* program (Pritchard *et al.*, 2000), a Bayesian approach based on the genotypes of the individuals collected. Individuals were assigned to *K* (unknown) populations, where *K* was varied across runs of the program, and individuals had membership assigned to them over all of the different clusters (number of clusters = *K*). The sum of the probabilities to belong to a population equals one. The *structure* program was run with 10^6 iterations and a burn-in period of 10 000 iterations to assure a random starting point for the algorithm. The runs were repeated 20 times for $2 > K < 10$ to check the consistency of the results. An admixture ancestry model was assumed, that provides for the individuals to have mixed ancestry. This is modeled by assuming that a certain individual (*i*) has inherited some fraction of its genome from ancestors in population *k*.

Results and discussion

The results obtained from testing for statistical power (Power of Daughter Design, Bovenhuis, 2005) of the half-sib design in this study were based on a heritability of 0.32, a type 1 error of 0.05 and a recombination fraction of 0.1. A 12 sire design with approximately 100 offspring per sire was predicted to yield sufficient (0.910) power to detect QTL, and this was identified as the most appropriate experimental design for QTL detection in the South African Angora goat population. The family structure of the four stud herds with full phenotypic and pedigree information selected for the reference population is provided in Table 1. These animals were part of 12 half-sib families, ranging between 44 and 140 offspring with an average of 88 half-sib offspring per sire. All possible sires were screened for heterozygosity over loci, and sires with the highest heterozygosity values were selected.

A total of 800 alleles from 94 loci were detected in the 1067 individuals which were genotyped. All markers were found to be polymorphic in each of the four evaluated herds. The number of alleles identified per locus averaged 7.99, with a variation from 2 (BM4630) to 23 (INRA011). The mean polymorphic information content value across loci was 0.57, indicating a medium level of information (Table 2), which closely corresponds to values reported by Kumar *et al.* (2005), Martinez *et al.* (2006) and Traore *et al.* (2009).

The observed and expected heterozygosity values over all loci for all herds averaged 0.63 and 0.62, respectively. Individual markers varied significantly, ranging from as low as 0.14 (CSSM32) to as high as 0.83 (BM1329) for unbiased heterozygosity. These mean values correspond closely to those reported by both Kumar *et al.* (2005; $H_O = 0.45$, $H_E = 0.63$) and Martinez *et al.* (2006; $H_O = 0.62$, $H_E = 0.66$), although both higher (Qi *et al.*, 2009) and lower (Gour *et al.*, 2006) values were reported previously for various microsatellite panels tested in different goat populations.

The *f*, *F* and θ values estimated for the 96 loci across all populations are indicated in Table 2. The mean θ value (= 0.069, range = 0.002–0.161) was similar to that found by Gour *et al.* (2006), but it was marginally higher compared to other previously reported estimates in goat breeds (Kumar *et al.*, 2005; Martinez *et al.*, 2006; Dalvit *et al.*, 2008). The highest within-population fixation index (*f*) was estimated for BM4630 (0.175), that indicates a heterozygote deficit. Of the 94 markers, 74 showed negative *f* values, indicating no inbreeding but rather outbreeding. Overall, the microsatellite loci included were useful to obtain a reliable assessment of the genetic variability within the population.

Genetic variability in the South African reference population was relatively high with the average number of alleles varying between 5.41 and 7.21 in the four herds. The estimated unbiased hetereozygosity or gene diversity was well above 60%, except for one herd with a value of 56.5%. These levels of heterozygosity for the different

Table 1. Family structure of herds for the reference population in the study.

	Offspring			
	Year 1	**Year 2**	**Year 3**	**Total**
Herd 1				
Sire 1	41	33	36	110
Sire 2	18	38	59	115
Sire 3	34	42	8	84
Sire 4	31	46	27	104
Herd 2				
Sire 1	9	99	32	140
Sire 2			84	84
Herd 3				
Sire 1		41	23	64
Sire 2	38	41	76	117
Sire 3	54	54		92
Sire 4		37		91
Herd 4				
Sire 1	27	40		67
Sire 2		37	7	44

Table 2. Number of alleles per marker (k), observed (Hobs) and expected (HExp) heterozygosity, polymorphic information content (PIC) and F statistics per marker.

Locus	No. of samples	k	Hobs	HExp	PIC	F (F_{IT})	θ (F_{ST})	f (F_{IS})
BM0121	848	9	0.64625	0.6685	0.61475	0.05	0.07	−0.023
BM0321	1101	9	0.54575	0.5175	0.484	−0.03	0.032	−0.063
BM0719	933	6	0.715	0.733	0.69025	0.075	0.06	0.016
BM1225	874	5	0.6175	0.57925	0.519	0.002	0.073	−0.077
BM1258	1098	10	0.71275	0.672	0.61975	0.046	0.1	−0.06
BM1312	524	10	0.5905	0.676	0.625	0.197	0.06	0.145
BM1329	635	7	0.8755	0.82525	0.64175	−0.05	0.036	−0.089
BM143	1018	6	0.70375	0.67075	0.62075	0.033	0.091	−0.064
BM1818	1051	9	0.7565	0.7215	0.67925	0.019	0.073	−0.058
BM2830	931	9	0.6425	0.606	0.52725	−0.038	0.02	−0.059
BM3205	467	9	0.50675	0.576	0.526	0.129	0.034	0.098
BM3517	681	12	0.722	0.723	0.6805	0.057	0.068	−0.011
BM415	919	9	0.842	0.785	0.7515	−0.011	0.058	−0.074
BM4208	874	11	0.8455	0.78825	0.7575	0.019	0.058	−0.041
BM4621	1002	6	0.54	0.51875	0.45975	0.046	0.089	−0.047
BM4630	959	2	0.37025	0.4105	0.32375	0.205	0.037	0.175
BM6526	627	12	0.6555	0.7115	0.6625	0.122	0.062	0.063
BM7160	848	6	0.6975	0.673	0.61425	0.074	0.051	0.024
BM8125	890	8	0.657	0.63	0.58625	−0.006	0.05	−0.058
BMC1009	897	8	0.64625	0.64275	0.589	0.058	0.063	−0.005
BMC1222	852	6	0.54875	0.6445	0.5885	0.182	0.112	0.079
BMC8012	872	3	0.526	0.4765	0.36825	−0.076	0.002	−0.078
BMS0712	904	9	0.745	0.737	0.6935	0.029	0.042	−0.013
BMS0745	860	10	0.8375	0.73575	0.69775	−0.021	0.078	−0.107
BMS1248	869	9	0.2375	0.25125	0.23625	0.082	0.051	0.032
BMS1332	1044	7	0.68575	0.6	0.53075	−0.009	0.012	−0.021
BMS1714	863	5	0.762	0.71975	0.66675	−0.03	0.029	−0.061
BMS1788	919	11	0.73925	0.69	0.644	0.021	0.063	−0.045
BMS2252	920	6	0.62825	0.61425	0.55675	0.001	0.034	−0.035
BMS2526	1085	7	0.756	0.737	0.6895	0.037	0.072	−0.037
BMS2782	781	11	0.7745	0.73	0.68775	−0.011	0.07	−0.087
BP28	855	9	0.62475	0.6995	0.6575	0.221	0.103	0.132
CSRD247	1083	8	0.691	0.64375	0.59275	0.049	0.1	−0.057
CSSM19	957	5	0.3155	0.3065	0.27275	−0.008	0.048	−0.059
CSSM32	892	5	0.1415	0.1385	0.132	0.034	0.059	−0.026
CSSM43	881	6	0.6175	0.59275	0.5215	−0.035	0.038	−0.075
CSSM47	945	6	0.317	0.29425	0.2745	−0.068	0.014	−0.083
CSSM54	893	12	0.42825	0.54425	0.48975	0.257	0.161	0.115
DRBP1	222	8	0.67575	0.673	0.619	−0.207	0.148	−0.417
HEL11	668	14	0.68775	0.7225	0.682	0.14	0.074	0.071
HUJ614	1108	7	0.55125	0.51275	0.423	−0.048	0.015	−0.063
IL2RA	936	8	0.599	0.5835	0.55	0.052	0.08	−0.031
ILSTS011	1076	7	0.73525	0.6765	0.6315	0.028	0.051	−0.025
ILSTS033	1104	9	0.5895	0.585	0.543	0.083	0.093	−0.012
ILSTS034	898	6	0.60625	0.5785	0.513	0.043	0.045	−0.002
ILSTS045	1094	6	0.633	0.6225	0.5555	0.082	0.116	−0.039
ILSTS058	814	11	0.7325	0.7455	0.7045	0.032	0.107	−0.084
ILSTS059	1111	4	0.50975	0.4965	0.4215	0.083	0.069	0.016
ILSTS087	1070	9	0.524	0.49075	0.46025	0.022	0.079	−0.062
INRA003	919	3	0.574	0.5	0.39475	0.028	0.068	−0.043
INRA005	957	4	0.52125	0.47075	0.37075	−0.027	0.098	−0.139
INRA006	1052	11	0.7745	0.74025	0.698	0.003	0.06	−0.06
INRA011	1097	23	0.74225	0.73125	0.70475	0.038	0.093	−0.061
INRA040	644	8	0.56575	0.5905	0.5525	0.011	0.034	−0.024
INRA063	1082	5	0.6705	0.66775	0.60525	0.032	0.033	−0.002
INRA177	858	9	0.45375	0.4435	0.396	0	0.054	−0.057
INRA206	729	8	0.76	0.7595	0.71875	0.033	0.059	−0.027
INRA210	820	7	0.44875	0.44275	0.38925	0.099	0.103	−0.004
INRABERN192	912	8	0.72525	0.66	0.616	0.025	0.102	−0.086
INRABERN172	1072	6	0.7265	0.6965	0.64925	0.003	0.036	−0.034
LSCV25	877	10	0.738	0.76375	0.728	0.112	0.055	0.06
LSCV36	1098	7	0.62625	0.60725	0.5515	0.001	0.025	−0.024
LSCV46	1114	3	0.284	0.2455	0.22	−0.126	0.009	−0.137

Continued

Table 2. Continued

Locus	No. of samples	*k*	Hobs	HExp	PIC	*F* (F_{IT})	θ (F_{ST})	*f* (F_{IS})
LSCV52	1114	7	0.71375	0.68025	0.62225	−0.02	0.025	−0.046
MAF050	894	9	0.74125	0.74325	0.69725	0.02	0.036	−0.016
MAF214	646	12	0.649	0.6745	0.61975	0.19	0.143	0.055
MAF64	1084	7	0.77525	0.75125	0.71125	0.043	0.072	−0.032
MAF70	1083	8	0.70925	0.6875	0.637	0.044	0.083	−0.043
MCM104	1115	6	0.7095	0.659	0.60425	0.003	0.075	−0.079
MCM136	1118	3	0.36425	0.358	0.3005	0.157	0.154	0.003
MCM210	788	6	0.57775	0.535	0.4655	0.03	0.078	−0.051
MCM527	923	5	0.64275	0.63225	0.5685	0.07	0.112	−0.047
MCM58	909	17	0.7455	0.73925	0.701	0.036	0.04	−0.004
MCM64	734	9	0.599	0.56025	0.52	0.08	0.116	−0.041
OARAE129	935	4	0.558	0.5635	0.4755	0.093	0.072	0.023
OARCP26	955	7	0.4475	0.525	0.47525	0.16	0.034	0.131
OARCP34	1004	8	0.74925	0.72025	0.67925	0.027	0.073	−0.049
OARCP73	719	15	0.837	0.801	0.7715	0.015	0.057	−0.044
OARFCB005	961	9	0.3515	0.412	0.3795	0.082	0.045	0.039
OARFCB11	891	4	0.34975	0.4195	0.354	0.106	0.035	0.074
OARFCB193	1032	6	0.703	0.66625	0.6205	0.017	0.1	−0.092
OARFCB48	898	8	0.76775	0.70425	0.65525	0.028	0.066	−0.04
OARHH35	728	10	0.77575	0.758	0.7195	0.005	0.031	−0.027
OARHH64	819	6	0.6805	0.68675	0.6285	0.049	0.053	−0.004
OARVH098	949	6	0.69325	0.69575	0.64425	0.098	0.101	−0.003
OLADRB	767	13	0.73825	0.72375	0.67775	0.022	0.051	−0.03
SRCRSP05	1111	8	0.75775	0.74475	0.7075	0.071	0.147	−0.09
SRCRSP08	1089	8	0.64	0.6255	0.57475	−0.005	0.063	−0.072
SRCRSP09	1073	9	0.73725	0.65975	0.604	0.02	0.139	−0.139
SRCRSP10	1098	11	0.775	0.727	0.68275	0.009	0.039	−0.031
SRCRSP24	1083	8	0.73475	0.69225	0.65825	0.02	0.064	−0.047
TGLA040	903	6	0.5135	0.55025	0.496	0.12	0.095	0.027
TGLA179	1088	9	0.82975	0.773	0.74075	−0.022	0.046	−0.072
TGLA304	977	8	0.6695	0.618	0.55525	0.007	0.067	−0.065
Over all loci		7.989	0.6346356	0.6210346	0.56934574	0.04	0.069	−0.031

herds (Table 3) were on the same order as that reported by Martinez *et al.* (2006) for Canary goat populations; but they were lower compared to values reported by Iamartino *et al.* (2005) for Italian goat populations, Li *et al.* (2008) for Chinese goat breeds and Dalvit *et al.* (2008) for Alpine sheep breeds. With regards to population subdivision, the F_{ST} value (0.182) for herd 2 indicated a reduction of heterozygosity which supports the unbiased heterozygosity estimation (Hartl, 1988). These levels of heterozygosity exceeded expectations as the Angora goat population in South Africa is relatively small, and high selection pressure has been applied to the animals over several generations.

The population structure and level of admixture were estimated using the *structure* program. The most likely number of clusters (K) was four (Figure 1) and inferred by the $\ln\Pr(X/K)$ value. The variability of this value across runs for a given K gives a good indication of the most likely number of clusters for the population. The smallest K with the least variability is often the one that bests explains the data (Pritchard *et al.*, 2000; Sollero *et al.*, 2009), as was the case when $K = 4$.

Table 4 shows the proportion of individuals of each of the herds in the four most likely clusters inferred by the *structure* program, and this corresponded to the four different herds included in the study. Herd 1 were mostly divided between clusters 1 (69%) and 3 (28%). A total of 97% of herd 2 was assigned together in cluster 2, whereas 96% of the population of herd 4 belonged to cluster 4. Animals in herd 3 were almost equally divided amongst clusters 1 (31%), 3 (36%) and 4 (31%). The considerable gene flow between herds 1 and 3 (as well as their almost

Table 3. Measures of genetic variation in the population studied.

Herd	Sample size	Loci typed	Unbiased Hz ± SD	Obs Hz ± SD	No. of alleles	F_{ST}
1	400	94	0.627 ± 0.015	0.637 ± 0.003	6.98	0.0658
2	218	93	0.565 ± 0.018	0.592 ± 0.004	5.41	0.1818
3	338	94	0.633 ± 0.014	0.652 ± 0.003	7.21	0.0659
4	111	93	0.634 ± 0.016	0.671 ± 0.005	6.87	0.0486

Note: Hz, heterozygosity.

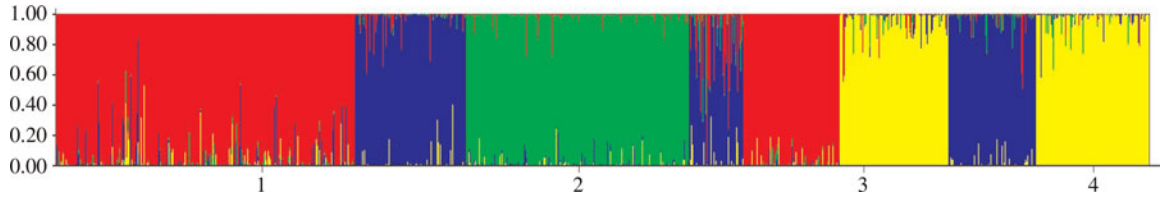

Figure 1. A summary plot of the estimates of *Q*. Each individual is represented by a single vertical line broken into *K* coloured segments, with lengths proportional to each of the four inferred clusters. The numbers (1–4) correspond to the herds.

Table 4. Proportion of membership of the analysed goat herds in each of the four clusters inferred in the *structure* program.

	Inferred clusters				
Herd	**1**	**2**	**3**	**4**	***N***
1	**0.691**	0.008	0.281	0.020	400
2	0.011	**0.969**	0.010	0.010	218
3	0.310	0.020	**0.360**	0.311	338
4	0.007	0.018	0.013	**0.962**	111

identical F_{ST} values) are most likely due to interchanging bucks during successive mating seasons, resulting in a lack of divergence attributable to the recent common ancestors of offspring. In contrast, herd 2 formed an individual cluster with a high F_{ST} value, that was probably due to the breeder buying in new bucks on an annual or bi-annual basis. The sources of this new genetic material are probably not included in this study.

The genetic structure of these herds was appropriate for use as reference populations because the genetic diversity was sufficient and the herds showed a level of differentiation. The levels of genetic diversity compared favourably with genetic diversity studies performed previously on various goat populations, indicating that there is a possibility to exploit natural variation on the molecular level within the population for improved production.

Current selection in the Angora goat breed in South Africa aims to establish a balance between production and survival traits because there is a limit to the harshness of the environment in which animals can produce viable amounts of mohair and a limit to the quality of mohair that such an adapted animal will be able to produce. Although the focus of the current project is on mohair production, all recorded traits (including body weights and efficiency parameters) will be included in future research programs. South Africa needs to develop a competitive, sustainable fast-growing economy and therefore needs to apply available modern technology. This study was the first attempt to explore the genetic variation available within the Angora goat reference population.

Conclusion

This study confirmed that there is sufficient genetic diversity within the South African Angora goat reference population to utilise molecular research in the genetic improvement of the breed. The establishment of this reference population forms part of a comprehensive, integrated approach in which both quantitative and molecular tools are applied for genetic improvement of South African Angora goats. An in-depth knowledge of the genetic diversity of the analysed populations will help to structure future molecular studies on this newly established reference population.

Acknowledgements

The authors convey their sincere appreciation to Drs H. Bovenhuis and R.M. Crooijmans of the Animal Breeding and Genetics Group, Wageningen University and Research Centre, for their expertise and contribution to the South Afrian Angora study, mainly focussing on the QTL identification project.

References

Andersson, L. (2001) Genetic dissection of phenotypic diversity in farm animals. *Nature Review of Genetics* 2, 130–138.

Beuzen, N.D., Stear, M.J., and Chang, K.C. (2000) Molecular markers and their use in animal breeding. *Veterinary Journal* 160, 45–52.

Boichard, D., Fritz, S., Rossignol, M.N., Guillaume, F., Colleau, J.J., and Druet, T. (2006) Implementation of marker-assisted selection: Practical lessons from dairy cattle. Presented at the 8th World Congress on Genetics Applied to Livestock Production, 13–18 August, Belo Horizonte, MG, Brazil.

Bovenhuis, H. (2005) *Power of a Daughter Design statistical program*. Animal Breeding and Genetics Group, Wageningen UR, The Netherlands.

Casas, E., Lunstra, D.D., and Stone, R.T. (2004) Quantitative trait loci for male reproductive traits in beef cattle. *Animal Genetics* 35, 451–453.

Dalvit, C., Sacca, E., Cassandro, M., Gervaso, M., Pastore, E., and Piasentier, E. (2008) Genetic diversity and variability in Alpine sheep breeds. *Small Ruminant Research* 80, 45–51.

Goudet, J. (1995) FSTAT (version 2.9.3): A computer programme to calculate *F*-statistics. *Journal of Heredity* 8, 485–486.

Gour, D.S., Malik, G., Ahlawat, S.P.S., Pandey, A.K., Sharma, R., Gupta, N., Gupta, S.C., Bisen, P.S., and Kumar, D. (2006) Analysis of genetic structure of Jamunapari goats by microsatellite markers. *Small Ruminant Research* 66, 140–149.

Hartl, D.L. (1988) *A Primer of Population Genetics* (2nd ed.). Sinauer Associates, Inc. Publishers, Sunderland, MA, USA. p. 78.

Iamartino, D., Bruzzone, A., Lanza, A., Blasi, M., and Pilla, F. (2005) Genetic diversity of southern Italian goat populations assessed by microsatellite markers. *Small Ruminant Research* 57, 249–255.

Kumar, D., Dixit, S.P., Sharma, R., Pandey, A.K., Sirohi, G., Patel, A. K., Aggarwal, R.A.K., Verma, N.K., Gour, D.S., and Ahlawat, S. P.S. (2005) Population structure, genetic variation and management of Marwari goats. *Small Ruminant Research* 59, 41–48.

Li, J.Y., Chen, H., Lan, X.Y., Kong, X.J., and Min, L.J. (2008) Genetic diversity of five Chinese goat breeds assessed by microsatellite markers. *Czech Journal of Animal Science* 53, 315–319.

Loots, F. (2007) Seisoenoorsig. *Angora Goat and Mohair Journal* 50, 11.

Maddox, J.F., and Cockett, N.E. (2007) An update on sheep and goat linkage maps and other genomic resources. *Small Ruminant Research* 70, 4–20.

Marshall, T.C., Slate, J., Kruuk, L.E.B., and Pemberton, J.M. 1998. Statistical confidence for likelihood-based paternity inference in natural populations. *Molecular Ecology* 7, 639–655.

Martinez, A.M., Acosta, J., Vega-Pla, J.L., and Delgado, J.V. (2006) Analysis of the genetic structure of the Canary goat populations using microsatellites. *Livestock Science* 102, 140–145.

Park, S.D.E. (2001) Trypanotolerance in West African cattle and the population genetic effects of selection. Phd thesis, University of Dublin.

Pritchard, J.K., Stephens, M., and Donnely, P. (2000) Inference of population structure using multilocus genotype data. *Genetics* 155, 945–959.

Purvis, I.W., and Jeffery, N. (2007) Genetics of fibre production in sheep and goats. *Small Ruminant Research* 70, 42–47.

Qi, Y., Luo, J., Han, X., Zhu, Y., Chen, C., Liu, J., and Sheng, H. (2009) Genetic diversity and relationships of 10 Chinese goat breeds in Middle and Western China. *Small Ruminant Research* 82, 88–93.

Snyman, M.A. (2002) Evaluation of a genetically fine mohair producing herd. *Small Ruminant Research* 43, 105–113.

Snyman, M.A., and Olivier, J.J. (1996) Genetic parameters for body weight, fleece weight and fibre diameter in South African Angora goats. *Livestock Production Science* 47, 1–6.

Sollero, B.P., Paiva, S.R., Faria, D.A., Guimaraes, S.E.F., Castro, S.T. R., Egito, A.A., Albuquerque, M.S.M., Piovezan, U., Bertani, G. R., and Mariante, A.d.S. (2009) Genetic diversity of Brazilian pig breeds evidenced by microsatellite markers. *Livestock Science* 123, 8–15.

Sonstegard, T.S., van Tassel, C.P., and Ashwell, M.S. (2001) Dairy cattle genomics: Tools to accelerate genetic improvement? *Journal of Animal Science* 79(Suppl), E307–E315.

Traore, A., Alvarez, I., Tamboura, H.H., Fernandez, I., Kabore, A., Royo, L.J., Gutierrez, J.P., Sangare, M., Ouedraogo-Sanou, G., Toguyeni, A., Sawadogo, L., and Goyache, F. (2009) Genetic characterization of Burkino Faso goats using microsatellite polymorphism. *Livestock Science* 123, 322–328.

Tuiskula-Haavisto, M., Honkatukia, M., Vilkki, J., de Koning, D.J., Schulman, N.F., and Maki-Tanila, A. (2002) Mapping of quantitative trait loci affecting quality and production traits in egg layers. *Poultry Science* 81, 919–927.

Weller, J.I. (2001) *Quantitative Trait Loci Analysis in Animals*. CABI Publishing, Wallingford, UK.

Wright, S. (1978) *Evolution and the Genetics of Populations. Variability within and among Natural Populations* (Vol. 4). University of Chicago Press, Chicago.