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Navajo-Churro sheep and wool in the United States

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Summary
Navajo-Churro sheep have been part of the subsistence of three cultures in the Southwest of the United States for over 400 years. These cultures include Navajo (a Native American nation), Hispanic and Anglo. The Navajo-Churro breed nearly became extinct in the 1950s to 1970s, but farsighted conservation programmes were then begun which involved all three cultures in saving this unique breed. Navajo-Churro sheep are a distinctive double-coated Criollo breed. The fleece type is superbly suited to the textiles produced in the local region and which are famous throughout the United States for their unique qualities and cultural relevance. A registry system involving ongoing inspection of each generation assures that the type remains traditional. Census numbers are now close to 3000 head as the breed moves beyond its original homeland to become more widely established throughout the United States.

Keywords: *Navajo-Churro, sheep, textile, wool*

Résumé
Pour plus de 400 ans, les moutons Navajo-Churro ont contribué à la subsistance de trois cultures du sud-ouest des Etats-Unis d'Amérique. Ces cultures sont la Navajo (une nation amérindienne), l'hispanique et l'anglo-américaine. Entre les années 50 et 70, la race Navajo-Churro a presque disparu, mais au cours de ces années, des programmes prévoyants de conservation impliquant les trois cultures ont été lancés pour sauver cette race unique. Le mouton Navajo-Churra est une race distincte Criollo, avec une double toison de poil et de laine. Ce type de toison est idéal pour la production des textiles de cette région, qui sont célèbres partout aux Etats-Unis pour leurs qualités uniques et leur intérêt culturel. Un régime d'enregistrement prévoyant les inspections continues de chaque génération assure le maintien du phénotype traditionnel. Les recensements indiquent que les animaux sont maintenant presque 3000 et que la race se répand au-delà de son territoire d'origine et s'établit un peu partout aux Etats-Unis.

Mots-clés: *Navajo-Churro, mouton, textile, laine*

Resumen
Los ovinos Navajo-Churro han contribuido a la subsistencia de tres culturas en el suroeste de los Estados Unidos por casi 400 años. Estas culturas incluyen Navajo (indígena), Hispánica, y Angla. La raza Navajo-Churro casi se extingue entre 1950 y 1970, pero en esos años empezaron varios programas de conservación que salvaron a esta raza única con el esfuerzo de las tres culturas. La Navajo-Churro es una raza criolla distinta, con un vellón de pelo y lana. Este tipo de vellón es muy bueno para la producción de tejidos regionales los cuales son famosos en los EEUU por sus cualidades únicas y su pertinencia cultural. Un sistema de registros incluye inspecciones de cada generación ovina para asegurar que el fenotipo tradicional se mantenga. Los censos de la raza indican que ya hay 3000 animales y que la raza ya se está criando fuera de su terreno original.

Palabras clave: *Navajo-Churro, ovino, textil, lana*

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Introduction

European livestock, including sheep, came to the Americas in 1494 when Spain established colonies in the Caribbean. Colonisation expanded to include Nueva España, currently the Southwest of the United States, and sheep were introduced here in 1598. Spanish ranches subsequently prospered in Texas, New Mexico and Arizona, with flocks numbering in the thousands (Christman *et al.*, 1997).

Navajos who lived on the edge of Spanish occupation initially acquired a few sheep and horses by trading and raiding. Following the turmoil of 1680 during the Pueblo Revolt, both the Pueblos and Navajos acquired many sheep. The Navajos expanded their flocks, becoming famed for their herds and their abilities as shepherds. Sheep became a defining element of Navajo culture to the extent that even today the Navajo hold the core belief that 'sheep is life'.

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Navajo flocks grew to 574 821 sheep by 1930. The large number of sheep, goats, horses and cattle became problematic because of the severe drought conditions of the 1930s. As a result, the US government conducted a stock reduction programme. Reduction by purchase progressed so slowly that eventually about 30% of each household's sheep, goats and horses were slaughtered by government agents and were then thrown into arroyos or burned. This terrifying stock reduction is still vivid in Navajo memory (Bailey, 1980).

At the same time, demand increased for fine wool in the American textile industry and the local landrace churros were increasingly 'graded up' by crossing with Merino and English longwools. A few traditional churros remained in remote Hispanic villages, among isolated Navajos and on the West Coast. These isolated flocks eventually formed the landrace sheep breed Navajo-Churro, that was named to recognize both the Spanish and Navajo influences that were so important in forming and maintaining the breed.

In 1934 the US Department of Agriculture established the Southwestern Sheep Breeding Laboratory to determine which sheep breeds might thrive in that region. They assembled some 'original old-type' Navajo sheep from local flocks, and for 30 years introduced fine wool breeds and long wool breeds both as pure breeds and as crosses with the local landrace sheep. They ultimately concluded that the best wool for the traditional weavers and the sheep most suitable for the high desert was the old-type landrace churro sheep, although this translated only poorly into efforts to save this breed (Blunn, 1943).

By 1977 the old-type Navajo sheep had dwindled to fewer than 500 head, so Dr. Lyle McNeal formed the Navajo Sheep Project to revitalize the breed. The Navajo-Churro Sheep Association was formed in 1986 through the efforts of individual breeders and with the assistance of nongovernmental organisations including the CS Fund, the American Livestock Breeds Conservancy and Ganados del Valle. Over 5000 sheep have been registered with the Navajo-Churro Sheep Association; an estimated 1500 unregistered sheep remain in traditional flocks on the Navajo Reservation, as well as several hundred undocumented sheep throughout the United States, Canada and Mexico.

The Navajo-Churro Sheep Association developed breed standards for conformation and wool by using historic records, oral descriptions from Navajo Elders, current sheep in Spain and research from the United States Department of Agriculture project. These included objective measurements and samplers woven to subjectively compare wool quality. Sheep from the remnant flocks of the Southwest and West Coast were evaluated and those which were typical were identified as Navajo-Churro. These sheep became the nucleus breeding pool. The Navajo Sheep Project targeted educational programmes to increase awareness of the breed throughout its original area of distribution.

Figure 1. A four-horned Navajo-Churro ram.

Geography and climate

The region in which the Navajo-Churro was developed and continues to thrive is an extensive area where Colorado, Utah, Arizona and New Mexico share borders in the Southwest of the United States. This area is mostly high desert with cold dry winters and hot dry summers. A few higher elevation areas receive more rainfall than the lower areas, and these areas support pinion and pine forest.

Breed description

The Navajo-Churro sheep is a small sheep with a long thin tail. The weight of the ewes ranges from 40 to 60 kg and the rams from 55 to 85 kg. The sheep have a double coat of fine under-wool (80% of total fleece weight) and coarse outer hair (20% of total fleece weight). The locks are long, tapered and open. The legs and faces of adults lack wool. The ears are usually medium sized and broad, with no evidence of drooping. A few animals have small vestigial ears as a consequence of a single dominant gene. Navajo-Churro sheep have a very strong flocking

Table 1. Frequency of different horn types in Navajo-Churro sheep registered in 1988, 1999, and 2008.

Sex/horn type	1988	1999	2008
Rams			
Polled	1%	5%	5%
Scurred	23%	0%	0%
2 Horns	38%	67%	65%
4 Horns	38%	28%	30%
Ewes			
Polled	68%	64%	66%
Scurred	9%	11%	12%
2 Horns	13%	19%	19%
4 Horns	6%	5%	3%

Note: The numbers are the percentages of the total of that sex registered that year.

instinct and are intelligent. The sheep are generally long lived and are productive up to 15 years in some cases.

Horn character varies in the breed. Ewes are usually polled, although a substantial number have two horns and a small minority have four or more. Rams are rarely polled and most commonly have two horns, with a substantial number having four horns or more (Figure 1). It can be appreciated from Table 1 that the relative frequency of four horns is greater in rams than in ewes, suggesting that several breeders are actively selecting rams with this trait. In addition, it can be seen that selection has acted against scurred rams in the years following the first establishment of the registration and inspection procedures. The breeders tend to value variation in the breed, so that rare variants, including polled rams, are kept at sufficiently levels within the breed to prevent their extinction.

Lambing averages about 1.4 lambs per ewe per year in those flocks that are mated once per year. Most Navajo-Churro sheep are non-seasonal breeders, so two lamb crops per year are likely if rams are left with ewes year round. In such systems the fecundity per lambing can be somewhat lower, but the overall productivity per ewe increases because of the additional parturitions. Ewes seldom require assistance of any kind at lambing. Both ewe and lamb bond quickly, and the lamb usually suckles within 5–10 min of birth and is ready to travel with the dam within that same short time.

Fleece

The fleece consists of both fine wool and longer, medullated hair. The locks are open and tapered with no defined crimp pattern. Fleeces weigh from 1.8 to 3.6 kg and yield 67–72% of clean wool. The outer coat of hair can range from 150 to 300 mm long while the wool inner coat is typically 75–150 mm long. Many breeders shear twice per year to avoid fibres that are too long for most commercial wool processing mills, although this is less of a concern for fleeces used for handcrafting.

The fibre diameter has an extreme range because of the dual-coat type of fleece. The fine wool fibres vary from 18 to 30 µm, whereas the hairy fibres vary from 30 to 47 µm. It is common for kemp fibres to compose 2–5% of the fleece, and these can be up to 60-µm diameter. Because of fibre migration, the fleece can felt and be ruined if not shorn before hot summer weather.

Wool colour is variable as shown in Table 2. Most of the identified colour patterns at the *Agouti* locus occur in the breed (Adalsteinsson, 1970; Sponenberg, 1997). Navajo-Churro sheep can be solid black or brown colour as a result of either A^a *nonagouti* and E^D *dominant black*, so genetic colour identification is not always straightforward and documenting the genotypes of individual sheep can be difficult. The estimated colour

Table 2. Frequency of different colours in registered Navajo-Churro sheep for 1986–1988 (beginning of registry, 373 sheep), 1989–1998 (1952 sheep) and 1999–2008 (3603 sheep).

Colour	1986–1988	1989–1998	1999–2008
White	45%	27%	25%
White and tan	4%	6%	11%
Black	22%	30%	24%
Brown	1%	15%	13%
Dark brown	2%	2%	1%
Grey	12%	4%	2%
Grey and tan	2%	0%	3%
Blue	<1%	<1%	3%
Badgerface	3%	10%	9%
Black and tan	1%	2%	5%
Spots	3%	3%	3%
Multi-coloured	4%	1%	1%

percentages are based on the visible (rather than genetic) classification of colour of registered sheep (Figure 2). White and grey sheep can be born displaying much tan and red phaeomelanin, and these are separated for reporting but are considered part of the *white* and *grey* genotype. The badgerface, as well as the black and tan, totals include black, brown and grey versions of these patterns. The blue coloured sheep figure includes both the *English blue* at the *Agouti* locus and a different blue grey colour that originated in Navajo Sheep Project sheep. 'Navajo Sheep Project blue' is uncharacterized genetically, although certainly not at the *Agouti* locus because it occurs on animals with the *dominant black* allele. It is a distinctive blue grey colour with high luster.

A trend for reduction of the proportion of white sheep in the registered population has occurred over time. Up to 1988 about 45% of the registered sheep were white or white and tan. In the decade ending in 2008 only 26% were white or white and tan. In 2003 the Navajo Sheep Project flocks were dispersed among the Navajos, and at that time several sheep in Navajo flocks were registered. Among 327 sheep registered, 54% were white. Non-Navajo sheep registrations for that year included only 29% white, indicating a difference in colour selection

Figure 2. A traditional Navajo sheep show with various colours of sheep.

Figure 3. Althea Theresa Johns, a young weaver, with a traditional Navajo rug that she handwove from natural coloured Navajo-Churro yarns.

based on the cultural affiliation of the breeder. Likewise, black and brown colours are increasing in frequency. A non-quantified impression from local wool buyers is that white and black or grey sheep are more common on the Navajo reservation, including non-registered sheep whose fleeces are indistinguishable from those of registered sheep and are sold along with them.

Handcraft use

Low grease content and open locks make hand processing of Navajo-Churro wool easy. This is important in the desert homeland of these sheep, as it conserves water. More than 14 natural colours offer weavers an extensive choice for highly desired naturally coloured handwoven rugs with intricate traditional patterns (Figure 3). Natural colours vary from black through blue greys to white, and from dark chocolate brown through rich medium browns and fawn to white. Contemporary weavers and knitters value this wool because it is durable and nonpilling without being harsh handling.

Navajo and Hispanic weavers have used Navajo-Churro wool for over 400 years, producing rugs and blankets for utility, collectors and museums. The wool has a relatively coarse grade but is soft handling, especially in lamb's fleeces. The traditional textiles have seen a large upsurge in value as the products have gained recognition as uniquely representing a combination of culture, technique and animal genetic resource. This is especially true of Navajo rugs of traditional designs that are woven with naturally coloured wools.

Current situation

In 1986 the Navajo-Churro Sheep Association began registering Navajo-Churro based on the phenotypic standard which was developed through historic investigation and traditional expertise. Even though standards are used, they allow for variability in a deliberate attempt to maintain diversity within this landrace population. Each sheep registered must be approved either by on-site inspection or by mail-in photos and fleece samples. All progeny must be inspected for registration, even if parents are registered. All inspectors have competence in both sheep and wool. Inspectors include university professors and long-term breeders, including Anglos, Hispanics and Navajos so that each community is served.

The flockbook remains open to conforming sheep that lack pedigree information in order to continually include sheep from traditional, unregistered flocks which formed the original foundation of the breed. Likewise, sheep with pedigrees of registered stock are denied registration if they themselves deviate from the traditional breed type. In past years only about 3.5% of sheep submitted for mail-in inspection have been denied registration. This low figure indicates a good level of education among breeders concerning breed type and the goals of the association, such that nonconforming sheep are not presented for inspection and registration. The percentage of sheep rejected after on-site inspection is not recorded. However, it is likely similar to or lower than the figure for mail-in inspections because most of these inspections are in traditional communities where the main circumstance is a tendency to not register all sheep that conform, rather than the opposite situation of trying to register sheep that do not conform.

Inbreeding is not a problem except in a few flocks. Committed breeders pay attention to the genetic structure of the breed and share expenses for the transportation of stock around the country. In 2004 the average inbreeding level for the population was 3.8% in three generations and was increasing slowly. A few flocks had inbreeding levels of 10.5% (Maiwashe and Blackburn, 2004). Breeders often refer to *A Conservation Breeding Handbook* and other resources from the American Livestock Breeds Conservancy for advice on sound breeding schemes for small populations (Sponenberg and Christman, 1995).

The breed is currently showing a slow increase in numbers. Many sheep persist in traditional flocks, as well as flocks away from the traditional homeland of the breed. The traditional systems include both Navajo and Hispanic communities of the Southwest in which the sheep have been used for 400 years for wool and meat production.

In Navajo culture the sheep also serve ceremonial purposes, and sheep with four horns are traditionally thought to have more power. Their meat is therefore sought after for use in traditional healing ceremonies. Such sheep are especially powerful if they have been eating specific desert flowers and herbs before slaughter and ceremonial use.

Superimposed over the traditional systems are an increasing number of breeders who raise and use the breed away from its original area. These breeders have historically been the

most likely to use the registry, because the registry serves to keep people informed of breed developments as well as providing important documentation about the legitimacy of breeding stock raised outside of the original home of the breed. The photographic and fleece evaluation assures that breeders from all geographic areas can participate equally in the breed registry, while also assuring trueness and continuity of breed type.

In recent years increasing numbers of traditional Navajo and Hispanic breeders have been registering sheep. In the last few years 400 sheep have been registered by the Navajos, and a number of Navajo-speaking inspectors have been added by the association to help facilitate registration of sheep on the Navajo Reservation. This has been at the request of the Navajo breeders and signals an interest in participation in the registry and association work of the breed. Roughly 20% of the sheep in Navajo flocks are registered (400 of about 2000).

In the traditional Hispanic community some of the breeders with larger flocks participate in the association. About 20% of the sheep in Hispanic flocks are registered (100 are registered of a total of about 500), but the total number of sheep is much lower than in Navajo flocks.

Production systems

The use of the breed involves several different communities, and each has unique aspects. The traditional Navajo flocks are increasing, and within the Navajo nation there is heightened awareness of the heritage and importance of this breed of sheep. Programmes to reintroduce traditional sheep have been successful. Tales of elderly shepherdesses tearfully and joyfully receiving traditional type sheep back into their flocks after years of absence point to the importance and resonance that these sheep have with Navajo culture. These sheep are used for subsistence meat production, as well as providing wool for traditional weaving. They are very extensively managed in subsistence situations. The Navajo value their sheep highly, and the sheep are a source of cultural identity for many Navajo.

Within the Hispanic community the sheep are also more secure than in previous decades. A few key breeders keep large flocks, and efforts to promote the traditional wool and meat from this breed have made it possible for these flocks to be economically viable. Meat from these flocks tends to enter commercial channels, while wool is usually used locally and then is marketed as finished textile products with local character and high demand. The flocks of the Hispanic community tend to be large and are raised extensively. Commercial exploitation through marketing channels is more common in this group than in the traditional Navajo community.

Outside of these two traditional communities are the more mainstream, generally Anglo-American flocks. These flocks have a tendency to be smaller than the other two, but their high number and participation in the Association and registry of sheep make these important for the genetic management of the breed. These flocks closely monitor colour variation and wool characteristics, as well as horn configuration. Exchange of sheep among all of the types of flocks assures that the breed continues to function as a single unit. The meat of these sheep is usually sold in local markets, but the wool is valued for handcraft use throughout the United States.

Social and economic aspects

The Navajo-Churro sheep breed is closely identified as a traditional and highly valued resource for the Navajo community. The resurgence of breed numbers and quality has been a great aid in recapturing certain aspects of traditional Navajo textiles. Although overall Navajo textile production was never diminished, an increase in the availability of the traditional wool (ideal for Navajo rug production) and the enhanced range of natural colours have met with increased production of the style of rugs based on them. The traditional rugs based on the wool of Navajo-Churro sheep meet with a brisk demand that is enhanced by their link to traditional Navajo ways of life and traditional resources.

The Navajo have also formed cultural networks based around the production and exchange of traditional sheep. Among these is the ‘Sheep is Life’ celebration that occurs annually in the Navajo nation and celebrates the sheep, their production and their use. This celebration includes traditional foods and procedures, as well as storytelling which is an important part of Navajo culture and relates very heavily to their keeping of sheep. The social networks and the celebrations all serve to more clearly define the Navajo relationship to the Navajo-Churro breed, with the result of assuring the breed’s appreciation and continuity. An indication of the centrality of the sheep to Navajo culture is the requirement that candidates for the title of Miss Navajo Nation be able to kill a sheep quickly and with dignity. The killing of sheep for food is seen as integral to Navajo identity.

Hispanic cooperatives geared at traditional sheep and wool production have also met with success. These have raised awareness and acceptance of the traditional sheep and have enhanced the dedication to this breed resource by the Hispanic community. This is in a geographic region of increasing economic growth and land development, so that the traditional systems are threatened by rising land prices and increased numbers of immigrants to the area that do not share the values or history of this traditional community. Marketing and promotion of traditional products in cities throughout the region have raised awareness of the importance of local resources and traditions and have helped to provide some support for the survival of

the traditional Hispanic community and its use of the Navajo-Churro sheep.

The use of traditional Navajo-Churro wool has resulted in an ongoing market for this wool. This has led to around 5000 kg of the wool going through commercial processing for each of the last 15 years. This is spun into yarn, that is then used for handweaving. To this amount must be added the wool that is handspun for use in knitting or handweaving. Although that figure is likely less than the amount being commercially spun, it tends to result in elite products at the high end of the price structure for these products. This results in increased return to producers involved in that aspect of the production.

Current developments

Slow Food, an international group dedicated to preserving traditional heritage breed foods with exceptional taste, has recognized the Navajo-Churro for its delicate flavor. Sheep can be butchered at any age, but lamb from 6 months to nearly a year is considered optimum. At 8 to 9 months the hanging carcass weight is generally 20–25 kg. Slow Food has done a preliminary taste test of older ram carcasses and found that 12-, 18- and 24-month rams all provide carcasses with high quality and flavorful meat. The relative lack of intramuscular fat in this breed may contribute to the longevity of good flavor in the carcasses, avoiding 'muttony' flavor which detracts from the consumption of meat from older animals of most breeds of sheep.

Genotyping has not been done on large numbers of Navajo-Churro, but recent data indicate a higher percentage of RR genotypes at Codon 171 than for commercial breeds. Because the Navajo-Churro breed is classified as a rare breed, the United States Department of Agriculture has begun collecting germplasm from Navajo-Churro rams to cryopreserve in the National Seed Bank. Collection is being done in collaboration with the American Livestock Breeds Conservancy and the National Animal Germplasm programme. This effort targets rams from the traditional flocks.

Because the Navajo Churro is so colourful, so adaptable and produces superb carpet wool, the limited population is highly prized by US sheep breeders and by artisans. The yarn is extremely durable for use in rugs, saddle blankets, carrying bags and outer garments. Some businesses and traders have now adopted the Churro as a name brand identifier for high quality weavings made with Navajo-Churro wool. This includes the Hispanic weaving cooperative Tierra Wools, as well as two traders working with the Navajo weavers. Pendleton Mills, a large commercial mill, collaborated with Black Mesa Weavers for Life and Land and has been able to buy and spin sufficient Navajo-Churro wool to offer limited runs of commercially produced textiles with traditional patterns.

A recent book highlighting the use of purebred wools for handcraft has helped to raise the demand for Navajo-Churro and other purebred wools by spinners and weavers outside of the original region for the breed. The link of demand for purebred products and breed survival has been brought to a wide audience, helping to assure a secure economic base for breeders providing the wool from purebred sheep (Sponenberg and Bixby, 2002).

Organisations

One of the most important organisations promoting the breed and monitoring its population and structure is the Navajo-Churro Sheep Association. The association has very effectively solved problems which arise in the conservation of landraces which come from traditional communities which survive outside of the mainstream culture of herdbooks and breed associations. The inclusiveness of the association and the mechanisms which they have developed for including sheep from the traditional systems as well as those which have moved into other, more mainstream, systems is of great value in serving as a model for landrace conservation in the United States. The success of this is reflected in that 60% of the 200 sheep registered in 2008 were from traditional Navajo flocks on the reservation. With a registered population hovering around 1500, the Navajo-Churro has endured a close call with extinction. The total figure of all sheep of this breed is roughly twice the number of registered sheep.

The Navajo-Churro Sheep Association is run by a board of directors. There are between five and nine directors, depending on the needs of the association. The bylaws require that at least one of the directors is Navajo and one is Hispanic. This assures that the various communities involved with the sheep are all involved in the association and its decisions. Each of the three major communities involved with the sheep (Navajo, Hispanic and Anglo) tend to organize and offer different efforts for the breed and invite the other communities to participate. This varies from more economically based promotional efforts to more culturally based efforts such as celebrations involving food, traditional storytelling and other cultural expressions related to the sheep and their keeping.

Local groups with roots in the traditional communities are actively involved in promoting the sheep and its wool. Currently two Navajo organisations, Sheep is Life and Black Mesa Weavers for Life and Land, are encouraging events that focus on the old-type sheep. Tierra Wools, a Hispanic weaving business owned in common, has successfully featured Churro wool for over 20 years. The sheep is culturally and economically vital in these groups.

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Chromosomal segments underlying quantitative trait loci for mohair production in Angora goats

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Summary
This study reports the results obtained in the search of chromosomal regions affecting fleece traits in a population of Angora goats in the Argentinean Patagonia. Six hundred thirty-four offspring from 14 parental half-sib families were used. Nine phenotypic fleece traits were recorded at 4 and 11 months of age. A genome examination using 85 informative molecular markers was conducted. A linkage analysis was performed using a regression interval analysis. Our study identified 10 genomic regions affecting the average fibre diameter, coefficient of variation of the average fibre diameter, percentage of fibres with diameters over 30 μm, greasy fleece weight, staple length, average curvature of fibres, percentage of continuous medullated fibres and percentage of kemp fibres located on five goat chromosomes (1, 2, 5, 13 and 19). These results show that the average size of the quantitative trait loci effect was 1.6 phenotypic standard deviations for different traits and families. The aims of quantitative trait loci detection is the potential use of these molecular markers to increase accuracy in predicting the genetic merit of breeding and its implementation in animal breeding schemes through marker-assisted selection.

Keywords: *Angora goats, mohair, quantitative trait loci*

Résumé
Dans cette étude, on signale les résultats obtenus dans la recherche des régions chromosomiques relatives aux caractéristiques de la toison des chèvres angora dans la Patagonie argentine. On a utilisé 634 descendants de 14 familles à descendance uniparentale et enregistré neuf caractères phénotypiques de la toison à 4 et 11 mois. Un examen du génome a été entrepris en utilisant 85 marqueurs moléculaires informatifs. L'analyse du groupe de liaison a été effectuée en utilisant une analyse de l'intervalle de régression. Notre étude a identifié 10 régions génomiques qui affectent le diamètre moyen de la fibre, le coefficient de variation du diamètre moyen de la fibre, le pourcentage de fibre ayant un diamètre supérieur à 30 μm, le poids de la laine en suint, la longueur de la fibre, la courbure moyenne de la fibre, le pourcentage de fibres médullaires continues et le pourcentage de fibre de jarre située sur cinq chromosomes de chèvre (1, 2, 5, 13 et 19). Ces résultats indiquent que la taille moyenne de l'effet QTL était des déviations phénotypiques standard de 1,6 pour les différents caractères et familles. Le but de la détection des QTL est l'utilisation potentielle de ces marqueurs moléculaires en vue d'accroître la précision dans la prévision de la valeur génétique de la sélection et sa mise en œuvre dans les programmes de sélection animale par le biais de la sélection assistée par marqueurs.

Mots-clés: *chèvres Angora, mohair, loci à effets quantitatifs*

Resumen
En este estudio, informamos sobre los resultados obtenidos en la búsqueda de regiones cromosómicas que afectan a las características del vellón en una población de cabras de Angora en la Patagonia Argentina. Se utilizaron seiscientos treinta y cuatro crías de 14 familias parentales de medios hermanos. A la edad de 4 meses y de 11 meses, se registraron nueve rasgos fenotípicos en relación al vellón. Se realizó una inspección del genoma utilizando 85 marcadores moleculares informativos. Se llevó a cabo un análisis de ligamiento utilizando un análisis de regresión de intervalo. Nuestro estudio identificó diez regiones genómicas que afectaban al diámetro promedio de fibra, coeficiente de variación de diámetro promedio de fibra, porcentaje de fibra con diámetro superior a 30 μm, peso de lana suarda, longitud de la fibra, valor promedio de la curvatura de la fibra, porcentaje de fibras meduladas continuas y porcentaje de fibras kemp localizadas en cinco cromosomas caprinos (1, 2, 5, 13 y 19). Estos resultados indican que el tamaño promedio del efecto QTL era de 1.6 desviaciones estándar fenotípicas para diferentes rasgos y familias. La detección de QTL tiene como propósito el uso potencial de estos marcadores moleculares para aumentar la precisión a la hora de pronosticar el mérito genético en la crianza, y su utilización en proyectos de crianza de animales a través de la selección asistida por marcadores.

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

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Introduction

Mohair production in Argentina is located mostly in the northern area of Patagonia (Neuquén, Rio Negro and Chubut provinces). Herds have an average of 150 head with low individual mohair production (1–2 kg/animal/

year). The quality of fleece is poor, leading to depreciated commercial value because of a high proportion of medullated fibre contamination. The 'Progama Mohair' was created in 1999 by the Secretaría de Agricultura, Ganadería, Pesca y Alimentos (SAGPyA), República Argentina (http://www.sagpya.gov.ar), and a breeding programme using a dispersed nucleus scheme to improve the quantity and quality of mohair production was implemented. Ten years after the Programa Mohair, the mohair fibre price rose from US $1.10/kg to US $6.15/kg (Arrigo and Sapag, 2007).

The classical quantitative genetics theory assumes that quantitative traits are controlled by an infinite number of genes, each with an infinitesimal effect, and are influenced by environmental factors. However, beyond this model, it is well known that there are *loci* which can have a major effect on quantitative traits (Falconer and Mackay, 1996). Such genes are called quantitative trait loci (QTL). QTL are defined as a region of the genome (i.e., segment of the chromosome) which harbours one or more genes affecting a quantitative trait (Geldermann, 1975).

The presence of QTL is inferred from significant differences in terms of phenotypic values between individuals which have inherited different QTL alleles from their parents. QTL alleles are not identifiable, because their position and determinism are unknown, so the information coming from molecular markers is used instead. A molecular marker is a *locus* with a known position on the genome which can take various forms (alleles) which are identifiable at the molecular level.

In recent decades, molecular biology techniques which have been developed coupled with advances in statistical genetics have made possible the mapping of QTL influencing economically important traits, including fleece and wool traits. Once the location of a trait is determined by linkage to the markers, possible candidate genes controlling the trait can be inferred. Some previous studies have indicated the presence of genes or gene families involved in fleece traits in sheep (reviewed by Purvis and Franklin, 2005). Identification of genes and molecular markers offers the opportunity to improve production efficiency, product quality and product diversity through utilising them in breeding programmes, developing transgenic lines and developing therapeutic agents which can be used to alter fibre attributes by altering gene expression (Purvis and Franklin, 2005).

Compared to other livestock species, there is very limited published literature on QTL identification in goat populations. Genome examinations for QTL in Angora goats conducted by Cano *et al.* (2007) and Marrube *et al.* (2007) reported the first results on putative QTL affecting fleece and conformation traits. In a recent partial genome examination, Abadi *et al.* (2009) also reported putative QTL affecting the growth and cashmere yield in Rayini goats.

This study reports the results obtained in the search of chromosomal regions affecting fleece traits using 85 informative molecular markers over 21 autosomes in a population of Angora goats in the Argentinean Patagonia.

Materials and methods

Animals and phenotype traits

The analysed population had a total of 634 kids from 14 Angora bucks. The number of half-sib offspring per buck ranged between 20 and 85 kids. The population was established in five batches (from 2000 to 2004).

Mid-side mohair samples were taken from kids at 4 and 11 months of age. Fleece samples were analysed at the Textile Fibres Laboratory of INTA Bariloche. Eight phenotypic fleece traits were recorded at 4^1 and 11^2 months of age, which are indicated by the superscript letters '1' and '2', respectively: average fibre diameter (AFD, μm), coefficient of variation of the AFD (CVAFD, %), percentage of fibres with diameters over 30 μm (F30), percentage of kemp fibre (KEMP, %), percentage of continuous medullated fibres (CONT, %), percentage of discontinuous medullated fibres (DISC, %), staple length (SL, mm), average curvature of fibres (ACF, °/mm) and greasy fleece weight (GFW, kg, recorded only at 11 months of age). The samples were analysed according to IWTO-8-97 (1997) and IWTO-12-03 (2003). The SL was measured with a caliper.

Molecular markers genotyping

The DNA isolation, polymerase chain reaction conditions and molecular markers (microsatellite) genotyping were the same as those described by Cano *et al.* (2007, 2009). All bucks were genotyped for 120 microsatellite markers distributed over 21 autosomes from the available Web goat genetic map (http://locus.jouy.inra.fr/).

Statistical analysis

An interval mapping analysis was performed under a half-sib model (Knott *et al.*, 1996) using the QTL Express programme (Seaton *et al.*, 2002) at http://qtl.cap.ed.ac.uk/. The fixed effects included in the analysis were sex, year of birth (2000–2004), birth type (single or twin) and flock (eight levels). Appropriate *F*-statistic thresholds for the chromosome type 1 error rate were generated by a permutation test of 10 000 iterations (Churchill and Doerge, 1994). The LOD drop-off method developed by Lander and Botstein (1989) was used to estimate the confidence intervals of the QTL locations.

Results

Table 1 provides the phenotypic measurements (means and standard deviations) for fleece traits in 14 families'

Table 1. Phenotype data (means ± SD) of the progeny from 14 Angora goat families.

	Traits						
Family (n)	AFD[1] (μm)	CVAFD[1] (%)	F30[1] (%)	KEMP[1] (%)	CONT[1] (%)	SL[1] (mm)	ACF[1] (^{0}/mm)
1 (36)	24.0 ± 2.5	27.8 ± 2.5	17.4 ± 10.7	0.7 ± 1.3	1.5 ± 1.8	89.6 ± 11.6	34.7 ± 2.3
2 (87)	23.4 ± 1.8	27.3 ± 3.7	12.5 ± 8.7	0.8 ± 1.1	2.0 ± 3.0	89.5 ± 10.6	34.4 ± 3.5
3 (47)	23.2 ± 1.9	29.1 ± 3.6	13.0 ± 8.3	0.5 ± 0.7	1.6 ± 1.9	68.1 ± 14.5	34.2 ± 2.0
4 (40)	23.1 ± 1.5	28.5 ± 2.4	13.5 ± 8.2	0.4 ± 0.3	0.4 ± 0.5	79.5 ± 17.2	34.2 ± 1.9
5 (64)	23.2 ± 1.6	27.2 ± 3.2	12.0 ± 7.2	0.8 ± 1.0	0.9 ± 0.7	92.8 ± 13.9	33.9 ± 4.5
6 (72)	23.7 ± 1.6	27.6 ± 2.8	14.8 ± 7.1	0.5 ± 0.4	0.9 ± 0.6	92.6 ± 14.7	34.0 ± 3.3
7 (69)	23.6 ± 1.5	28.7 ± 2.9	15.2 ± 2.9	0.4 ± 0.5	1.2 ± 1.5	90.6 ± 13.5	34.1 ± 2.8
8 (50)	23.5 ± 2.5	30.1 ± 3.7	17.4 ± 10.4	0.3 ± 0.4	2.0 ± 3.5	96.4 ± 9.1	33.5 ± 2.5
9 (38)	–	–	–	–	–	–	–
10 (37)	22.8 ± 1.2	27.8 ± 2.6	10.7 ± 5.3	0.6 ± 0.5	1.9 ± 2.1	77.8 ± 9.1	32.6 ± 2.4
11 (25)	24.0 ± 2.4	30.1 ± 2.4	21.1 ± 10.8	0.5 ± 0.9	0.8 ± 1.1	79.1 ± 11.9	33.4 ± 3.2
12 (20)	23.0 ± 1.3	30.1 ± 3.0	14.1 ± 3.1	0.3 ± 0.3	0.7 ± 0.8	68.5 ± 13.3	34.5 ± 3.1
13 (31)	24.3 ± 1.8	28.5 ± 2.4	18.3 ± 9.0	0.6 ± 1.1	1.1 ± 1.8	87.3 ± 17.4	33.3 ± 2.4
14 (20)	–	–	–	–	–	–	–

	Traits							
Family (n)	AFD[2] (μm)	CVAFD[2] (%)	F30[2] (%)	KEMP[2] (%)	CONT[2] (%)	SL[2] (mm)	ACF[2] (^{0}/mm)	GFW (kg)
1 (36)	25.0 ± 2.2	25.4 ± 3.2	18.8 ± 9.9	0.3 ± 0.8	0.4 ± 0.4	177.8 ± 35.7	37.4 ± 3.4	1.5 ± 0.4
2 (85)	23.8 ± 2.1	25.6 ± 3.3	13.8 ± 9.9	0.4 ± 0.6	0.5 ± 0.6	170.1 ± 33.5	43.4 ± 7.4	1.3 ± 0.3
3 (47)	24.3 ± 1.8	25.9 ± 3.2	15.0 ± 8.6	0.5 ± 0.6	0.7 ± 0.8	155.1 ± 34.7	40.1 ± 5.4	1.2 ± 0.3
4 (40)	24.8 ± 2.4	26.1 ± 3.6	17.7 ± 11.7	0.2 ± 0.3	0.4 ± 0.3	153.5 ± 54.8	38.3 ± 3.5	1.3 ± 0.4
5 (64)	24.1 ± 2.4	26.7 ± 3.9	14.9 ± 9.5	0.4 ± 0.5	0.5 ± 0.6	178.5 ± 29.8	45.5 ± 6.9	1.2 ± 0.3
6 (72)	24.6 ± 1.9	25.3 ± 4.7	15.5 ± 8.6	0.2 ± 0.4	0.5 ± 0.6	183.4 ± 33.3	40.1 ± 6.5	1.4 ± 0.3
7 (69)	25.3 ± 2.4	27.3 ± 3.2	20.5 ± 10.6	0.1 ± 0.2	0.3 ± 0.4	160.6 ± 28.4	43.0 ± 8.1	1.5 ± 0.4
8 (50)	25.0 ± 2.1	26.8 ± 2.6	18.2 ± 9.7	0.1 ± 0.2	0.3 ± 0.7	175.5 ± 28.2	42.4 ± 7.6	1.4 ± 0.3
9 (38)	24.0 ± 1.7	27.0 ± 2.3	12.6 ± 6.2	0.1 ± 0.2	0.3 ± 0.5	175.9 ± 40.3	40.9 ± 7.2	1.4 ± 0.3
10 (37)	23.0 ± 1.7	24.8 ± 3.0	10.0 ± 6.4	0.1 ± 0.2	0.8 ± 0.8	129.4 ± 18.4	51.5 ± 3.2	1.2 ± 0.2
11 (25)	25.0 ± 1.9	27.2 ± 3.5	16.7 ± 8.0	0.3 ± 0.4	0.4 ± 0.5	179.0 ± 31.4	40.2 ± 6.0	1.4 ± 0.4
12 (20)	23.2 ± 1.6	28.0 ± 5.0	10.0 ± 5.6	0.4 ± 0.5	0.4 ± 0.7	154.6 ± 26.0	39.1 ± 3.7	1.0 ± 0.3
13 (31)	25.4 ± 2.4	26.7 ± 2.8	18.9 ± 9.0	0.4 ± 0.5	0.6 ± 0.7	175.1 ± 30.6	42.8 ± 6.8	1.4 ± 0.4
14 (20)	23.4 ± 1.5	26.4 ± 2.3	12.2 ± 5.6	0.1 ± 0.2	0.5 ± 0.8	162.5 ± 25.6	44.0 ± 6.9	1.3 ± 0.3

(n) = Progeny number; AFD, Average Fiber Diameter; CVAFD, Coefficient of Variation of AFD; F30, percentage of fiber with diameter over 30 μm; KEMP, percentage of kemp fiber; CONT, percentage of Continuous Medullated Fibers; SL, Staple Length; ACF, Average Curvature of Fiber; GFW, Greasy Fleece Weight. [1] = fleece samples taken at 4 month of age; [2] = fleece samples taken at 11 month of age. – = data not available.

progenies. A panel of 85 informative microsatellite markers distributed over 21 autosomes was used. The interval between the markers was on average 17.1 cM and the estimated genome coverage was 1328 cM, corresponding to 51% of the 21 autosomes (Table 2).

Nineteen QTL related to fleece traits were found in goat chromosomes (CHI) 1, 2, 5, 13 and 19. Detailed information and the localisation of chromosomal regions affecting the fleece traits are provided in Table 3 and Figure 1.

Evidence for putative QTL on different chromosomes was the following: on CHI1 four QTL affecting F30[1], GFW (distal region), CVAFD[1] and CONT[2] (central region) were located. On CHI2 five putative QTL for SL[2], CVAFD[1], ACF[1], CVAFD[2] and ACF[2] were found. Six QTL affecting fleece traits were found on CHI5: three QTL affecting AFD[1], F30[1], KEMP[1] (central region), two QTL for AFD[2], KEMP[2] (distal region) and one QTL for GFW (proximal region) on CHI5. Evidence for a QTL affecting CVAFD[1] was detected on CHI13. Finally, three putative QTL affecting CVAFD[1], SL[1] and GFW were detected on the central region on CHI19.

The size of the QTL effect ranged from 0.6 to 2.9 phenotypic standard deviations for different traits and families (Table 3), and the number of informative bucks ranged from 1 to 4 out of 14.

In all cases, the confidence intervals of QTL location estimated on five goat chromosomes (CHI1, CHI2, CHI5, CHI13 and CHI19) were on average 30 cM (11 cM for SL[1] on CHI19 and for KEMP[2] on CHI5 to 76 cM for CVAFD[1] on CHI2).

Discussion

We found several QTL affecting AFD[1] and AFD[2] (CHI5), CVAFD[1] (CHI1, CHI2, CHI13 and CHI19), CVAFD[2]

Table 2. Goat genome coverage by chromosome.

CHI	No. of markers	Coverage[1] (cM)	Markers (distance, cM)[2]
1	9	124	ILSTS004 (16), BM4307 (32), INRA011 (18), BM1312 (30), LSCV06 (16), CSSM32 (34), CSSM19 (7), BM3205 (7), MAF046
2	7	167	INRA40 (31), ILSTS030 (34), ILSTS082 (11), LSCV24 (34), LSCV37 (31), IDVGA64 (26), OarFCB011
3	2	38	McM58 (37), CSSM54
4	4	38	BMS1788 (19), McM218 (70), LSCV15 (20), OarHH35
5	5	75	OarFCB005 (15), LSCV25 (18), BMS1248 (21), ILSTS034 (21), BM2830
6	4	58	OarAE101 (19), BM0143 (18), BM4621 (21), BM0415
8	4	60	INRA129 (30), McM064 (45), HEL04 (30), CSSM47
9	5	77	INRA127 (6), BM2504 (38), TGLA073 (18), BM4208 (15), INRA144
10	3	38	TGLA272 (12), TGLA378 (25), TGLA102
11	3	28	INRA177 (28), ILSTS049 (78), ILSTS045
12	4	61	BMS0712 (35), BM6404 (26), INRA005 (8), OarVH117
13	2	32	ILSTS059 (32), IL2RA
14	3	83	CSSM66 (46), BM0302 (37), BM2934
15	3	74	INRA224 (40), LSCV05 (34), TGLA075
17	2	34	OarVH098 (34), ILSTS058
18	3	50	HAUT14 (30), SCRD232 (20), INRA210
19	10	97	BMS0745 (20), BMS1920 (8), IDVGA46 (9), LSCV36 (8), BP20 (4), MAF48 (4), OarFCB193 (11), SRCRSP06 (8), McM210 (25), MAP2
20	3	56	TGLA304 (31), INRA036 (25), ILSTS072
23	4	52	OarCP73 (21), BM1258 (19), OLA-DRB (12), OarHH56
25	2	40	BM4005 (19), BP28
27	3	46	LSCV41 (11), INRAMTT183 (35), OarJMP58
Total	85	1328	

Number of markers used and markers name by chromosome used.
[1] = Coverage in cM taken account markers intervals.
[2] = The first marker is the closest to the centromere and between brackets the distance in cM between markers.

(CHI2), F30[1] (CHI1 and CHI5), GFW (CHI1, CHI5 and CHI19), SL[1] (CHI19), SL[2] (CHI2), ACF[1] and ACF[2] (CHI2), CONT[2] (CHI1) and KEMP[1] and KEMP[2] (CHI5). Compared with other livestock species, there is very limited published literature on QTL identification in goat populations. Recently, Abadi *et al.* (2009) reported putative QTL affecting cashmere yield on three candidate regions previously reported by Cano *et al.* (2007). Several reports of linkage between genes and QTL with wool production traits are available for sheep (Parsons *et al.*, 1994; Rogers *et al.*, 1994; Allain *et al.*, 1998, 2006; Beh *et al.*, 2001; Ponz *et al.*, 2001; Purvis and Franklin, 2005; Bidinost *et al.*, 2008). Because of the homology between sheep and goat maps (Crawford *et al.*, 1995; Maddox, 2005), putative QTL affecting fleece traits found in the Angora goat on CHI1, CHI5 and CHI19 could be related to the keratin-associated protein (KAP) and keratin (*KRT*) gene family as pointed out by McLaren *et al.* (1997). In sheep, on chromosome 1 (OAR1), OAR3 and OAR11 several high glycine–tyrosine keratin-associated proteins (KAP6.1, KAP7, KAP8, KAP1 and KAP3) and keratin genes (*KRT1, KRT2*, *KRT2.13* and *KRT2.10*) were mapped by McLaren *et al.* (1997). Moreover, in sheep, a linkage between high glycine–tyrosine keratin gene loci and wool fibre diameter was previously demonstrated (Parsons *et al.*, 1994).

Four keratin family genes (*KRT8* and *KRT1B)* have been assigned to chromosome 5 in cattle (Fries *et al.*, 1991), and one of these genes (*KRT*) was assigned to chromosome 5 in the goat (Schibler *et al.*, 1998; Pinton *et al.*, 2000).

As mentioned above, the coincident results reported by Cano *et al.* (2007) and Abadi *et al.* (2009) and the QTL found in other species, such as the *KRT* and *KAP* genes family, could be the best candidates for the associated QTL on goat chromosomes 1, 5 and 19.

With the proposal to shorten the chromosomal regions, we have increased the number of kids by family on previous steps to fine mapping where the QTL were detected.

Implications

Ten chromosomal regions involved in mohair production on CHI1, CHI2, CHI5, CHI13 and CHI19 were identified and confirmed in a population of Angora goats. The data described in this report open up the opportunity for an in-depth search for a specific genome section and to characterise the variability involved in economic traits in Angora goats and other fleece goat breeds.

The development and application of fine mapping methodologies have been progressing in experimental and commercial livestock populations. Fine mapping will shorten the size of the candidate chromosomal regions harbouring the QTL detected in this study.

After fine mapping and identification of causative mutations in candidate genes, these QTL will have the potential to achieve additional genetic and economic gains by incorporating marker-assisted selection into breeding programmes.

Table 3. Putative QTL significant at the $P < 0.05$ and $P < 0.01$ chromosome level for traits by chromosome.

CHI	Trait	Informative families.	Closest markers.	Position (cM)	QTL effect (SE)	Effect/SDph	*F*-statistic
1	CVAFD[1]	4	LSCV06	104	3.5 (1.5) µm	1.3	2.4[3]
1	F30[1]	5/11	MAF046	176	4.5 (2.3)/9.9 (3.9)%	0.6/1.3	2.5[3]
1	GFW	4	MAF046	160	3.5 (1.5) kg	1.9	3.0[3]
1	CONT[2]	10/12	LSCV06	104	1.2 (0.6)/0.8 (0.4)%	2.4/1.6	2.7[3]
2	CVAFD[1]	2/8	LSCV24	72	2.3 (0.9)/2.7 (1.4) µm	0.8/0.9	2.6[3]
2	CVAFD[2]	3/4/6	LSCV37	100	6.4 (2.8)/6.7 (3.2)/7.4 (1.9) µm	2.0/2.1/2.3	2.5[3]
2	SL[2]	4/11	INRA40	12	73.5 (22.5)/88.3 (36.3) mm	2.3/2.7	2.3[3]
2	ACF[1]	7/11	ILSTS082	60	2.5 (1.1)/5.4 (2.1)%	0.9/1.9	2.7[3]
2	ACF[2]	4/9/11/12	LSCV37	104	8.9 (4.0)/7.3 (3.5)/11.1 (5.7)/11.1 (5.6) ^{0}/mm	2.3/1.9/2.9/2.9	2.2[3]
5	AFD[1]	3	BMS1248	40	1.5 (0.7) µm	0.9	3.0[3]
5	AFD[2]	6/7	ILSTS034	52	2.8 (1.1)/2.2 (0.9) µm	1.6/1.2	2.7[3]
5	F30[1]	3	BMS1248	36	7.3 (3.1)%	0.9	2.6[3]
5	GFW	3/4/6	OarFCB005	8	0.4 (0.2)/0.5 (0.3)/0.3 (0.1) kg	1.5/2.0/1.0	3.8[3]
5	KEMP[1]	7/8	BMS1248	32	0.8 (0.3)/1.2 (0.4)%	1.1/1.7	3.6[4]
5	KEMP[2]	6/12/13	BM3830	76	0.4 (0.2)/0.5 (0.2)/0.4 (0.2)%	1.2/1.4/1.3	3.0[3]
13	CVAFD[1]	2	IL2RA	32	0.8 (0.3) µm	1.1	2.6[3]
19	SL[1]	3/8/10	IDVGA46	28	13.0 (6.2)/13.2 (6.3)/15.8 (6.4) mm	1.1/1.1/1.3	2.1[3]
19	CVAFD[1]	3/4	MAF48	49	2.4 (1.1)/2.8 (1.2) µm	0.9/1.1	2.3[3]
19	GFW	7	MAF48	50	0.4 (0.1) kg	1.4	2.7[3]

Informative families, closest markers, position in cM, allele substitution effect (standard error), QTL effect relative to phenotypic standard deviation and estimated significance levels (*F*-statistic).
[1] = fleece samples taken at 4 month of age.
[2] = fleece samples taken at 11 month of age.
[3] = *F*-statistic significant at 5% level.
[4] = *F*-statistic significant at 1% level.

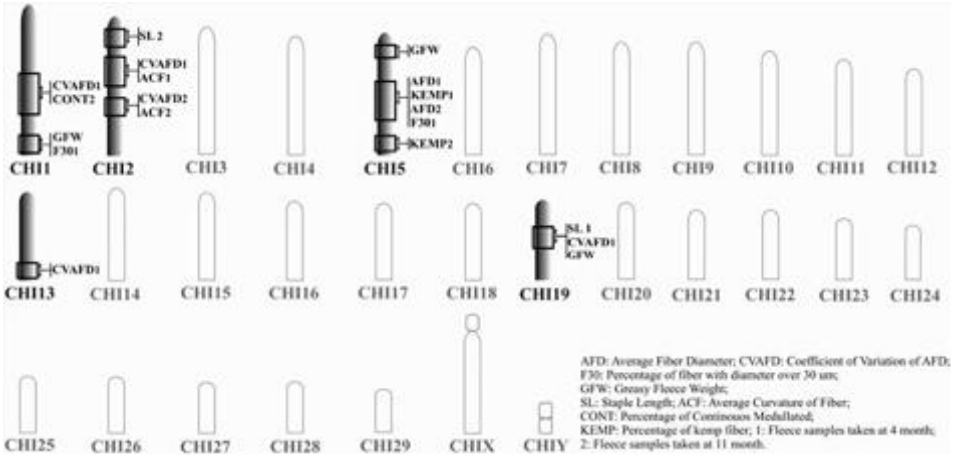

Figure 1. The chromosomal regions affecting fleece traits in Angora goats. The rectangles on the ideogram show the localisation of the chromosomal regions affecting fleece traits.

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

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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*

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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.

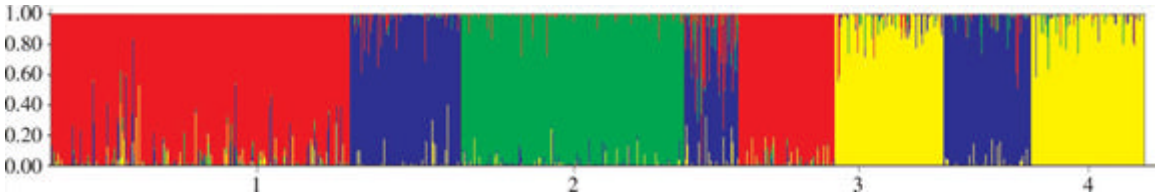

Figure 1. A summary plot of the estimates of *Q*. Each individual is represented by a single vertical line broken into *K* coloured segments, with lengths proportional to each of the four inferred clusters. The numbers (1–4) correspond to the herds.

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.

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The mission of the Animal Genetic Resources Information Bulletin (AGRI) is the promotion of information on the better use of animal genetic resources of interest to food and agriculture production, under the Global Strategy for the Management of Farm Animal Genetic Resources. All aspects of the characterization, conservation and utilization of these resources are included, in accordance with the Convention on Biological Diversity. AGRI will highlight information on the genetic, phenotypic and economic surveying and comparative description, use, development and maintenance of animal genetic resources; and on the development of operational strategies and procedures which enable their more cost-effective management. In doing this AGRI will give special attention to contributions dealing with breeds and procedures capable of contributing to the sustainable intensification of the world's medium to low input production environments (agro-ecosystems), which account for the substantial majority of the land area involved in livestock production; the total production of food and agriculture from livestock; and of our remaining farm animal genetic resources.

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The following types of articles are published in AGRI.

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Manuscripts prepared in English, French or Spanish with an English summary and another summary in either French or Spanish, should be submitted to AGRI Editor, AGAP, FAO, Viale delle Terme di Caracalla, 00100 Rome, Italy. Additionally the manuscript must be sent as a WinWord Electronic Mail attachment to agri-bulletin@fao.org. Photographs, coloured or black and white, and figures must be always sent by mail.

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Figures including titles and legends should be preceded and succeeded by two blank lines. Figure number and title are written, below the figure, in italics (12) and end with a dot. The term figures includes photos, line drawings, maps, diagrams etc.

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- Exemple dans le cas d'une référence sur une revue: Köhler-Rollefson, I. 1992. The camel breeds of India in social and historical perspective. Animal Genetic Resources Information 10, 53–64.
- Lorsqu'il s'agit de plus d'un auteur: Matos, C.A.P., D.L. Thomas, D. Gianola, R.J. Tempelman & L.D. Young. 1997. Genetic analysis of discrete reproductive traits in sheep using linear and nonnlinear models: 1. Estimation of genetic parameters 75, 76–87.
- Dans le cas d'un livre ou d'une publication ad hoc, par example un rapport, une thèse, etc.: Cockrill, W.R. (Ed.). 1994. The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp. 993.
- S'il s'agit d'un acte d'une réunion: Hammond, K. 1996. FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.), Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4–13.
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Merci pour votre collaboration

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Reglas y normas editoriales

El objetivo del Boletín de Información sobre Recursos Genéticos Animales (AGRI) es la divulgación de la información sobre una mejor gestión de los recursos genéticos animales de interés para la producción alimentaria y agrícola, siguiendo la Estrategia Mundial para la Gestión de los Recursos Genéticos de los Animales Domésticos. Todos los aspectos referidos a la caracterización, la conservación y el uso de estos recursos serán tomados en consideración, de acuerdo con el Convenio sobre la diversidad biológica.

AGRI publicará información sobre genética, encuestas fenotípicas y económicas y descripciones comparativas, uso, desarrollo y conservación de los recursos genéticos animales, así como sobre el desarrollo de estrategias operacionales y normas que permitan una gestión más eficaz de la relación costo/eficacia. Por ello, AGRI prestará especial atención a las contribuciones referidas a razas y normas capaces de contribuir a la intensificación sostenible de los medios (agroecosistemas) con ingresos medios y bajos en el mundo, que comprenden casi la mayor parte de las tierras dedicadas a la producción ganadera; la producción total de alimentos y agricultura provenientes de la ganadería; y el resto de los recursos genéticos de animales domésticos.

Los puntos de vista expresados en los artículos publicados en AGRI son solamente las opiniones de los autores y, por tanto, no reflejan necesariamente la opinión de las instituciones para las cuales trabajan dichos autores, de la FAO o de los editores.

La oportunidad o no de publicar un artículo en AGRI será juzgada por los editores y revisores.

Publicación electrónica

Además de su publicación impresa, la versión íntegra de AGRI se encuentra disponible electrónicamente en Internet, en el sitio: www.fao.org/dad-is/

Tipos de artículos

Serán publicados en AGRI los siguientes tipos de artículos:

Artículos sobre investigación

Se tomarán en consideración para su publicación en AGRI los estudios sobre la caracterización, conservación y uso de los recursos genéticos de los animales domésticos (AnGR) con una buena descripción del entorno. Se agradecerá el envío de fotografías de calidad que presenten a las razas en cuestión en su ambiente natural de producción.

Artículos de revisión

Se podrán tomar en consideración ocasionalmente aquellos artículos que presenten una revisión de los agroecosistemas, a nivel nacional, regional o mundial, con el desarrollo de uno o más aspectos referidos a la gestión de los recursos genéticos animales, incluidas las revisiones sobre el estado actual de las distintas áreas de AnGR.

Artículos específicos

Se solicitarán puntualmente artículos sobre temas específicos para ediciones especiales.

Otro material para publicación

Incluye la revisión de libros, noticias y notas referidas a reuniones importantes, cursos de formación y principales eventos nacionales, regionales e internacionales, así como conclusiones y recomendaciones relacionadas con los objetivos de estos principales eventos. Se invita a los lectores a enviar este tipo de material a los editores.

Guía para los autores

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Los artículos se presentarán en inglés, francés o español, junto con un resumen en inglés y su traducción en francés o español, y se enviarán al editor de AGRI, AGAP, FAO, Viale delle Terme di Caracalla, 00153 Roma, Italia. El artículo deberá ser enviado en versión WinWord en fichero adjunto por correo electrónico a *agri-bulletin@fao.org*. Las fotografías, color o en blanco y negro, se enviarán siempre por correo normal.

Los manuscritos se presentarán con doble espacio y con el número correspondiente a cada línea en el margen izquierdo. Todas las páginas serán numeradas, incluidas las de las referencias bibliográficas, cuadros, etc. El autor recibirá una notificación sobre la recepción de su documento.

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En la primera página del manuscrito se indicará el título abreviado del artículo, títulos y nombres de los autores, instituciones, direcciones completas (incluido código postal y número de teléfono); así como otros medios de contacto tales como fax, correo electrónico, etc. del autor principal. El título abreviado no deberá sobrepasar los 45 caracteres más los espacios correspondientes, y aparecerá en la parte

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Títulos

Los títulos de cada sección, por ejemplo Resumen, Introducción, etc., serán alineados a la izquierda. Dejar dos líneas en blanco entre las notas de pie de página con las direcciones y el Resumen y entre el título Resumen y el texto que sigue. El resumen no deberá exceder de 200 palabras. Deberá ser un resumen objetivo que describa brevemente los procesos y logros obtenidos, y no una presentación de cómo se ha llevado a cabo el estudio y una descripción genérica de los resultados. Dejar una línea en blanco entre el final del texto del resumen y las palabras clave, que se escribirán en cursiva así como el titulo Palabras clave. No deberán ser más de seis y no deberán contener "y" o "&". Todos los títulos principales de capítulo (14 regular) y subcapítulo (12 regular) serán en negrita e irán precedidos y seguidos de una línea en blanco. El texto correspondiente empezará sin sangrado. Un título dentro de un subcapítulo se escribirá en cursiva e irá seguido de un punto con a continuación el texto correspondiente.

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Los cuadros y las figuras se incluirán al final del texto siguiendo el orden de cita dentro del mismo. Las fotografías no serán devueltas a sus autores.

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- En el caso de un libro o de una publicación ad hoc, por ejemplo informes, tesis, etc.: Cockrill, W.R. (Ed.). 1994. The Husbandry and Health of the Domestic Buffalo. FAO, Rome, Italy, pp. 993.
- Cuando se trate de un artículo dentro de las actas de una reunión: Hammond, K. 1996. FAO's programme for the management of farm animal genetic resources. In C. Devendra (Ed.), Proceedings of IGA/FAO Round Table on the Global Management of Small Ruminant Genetic Resources, Beijing, May 1996, FAO, Bangkok, Thailand, 4–13.
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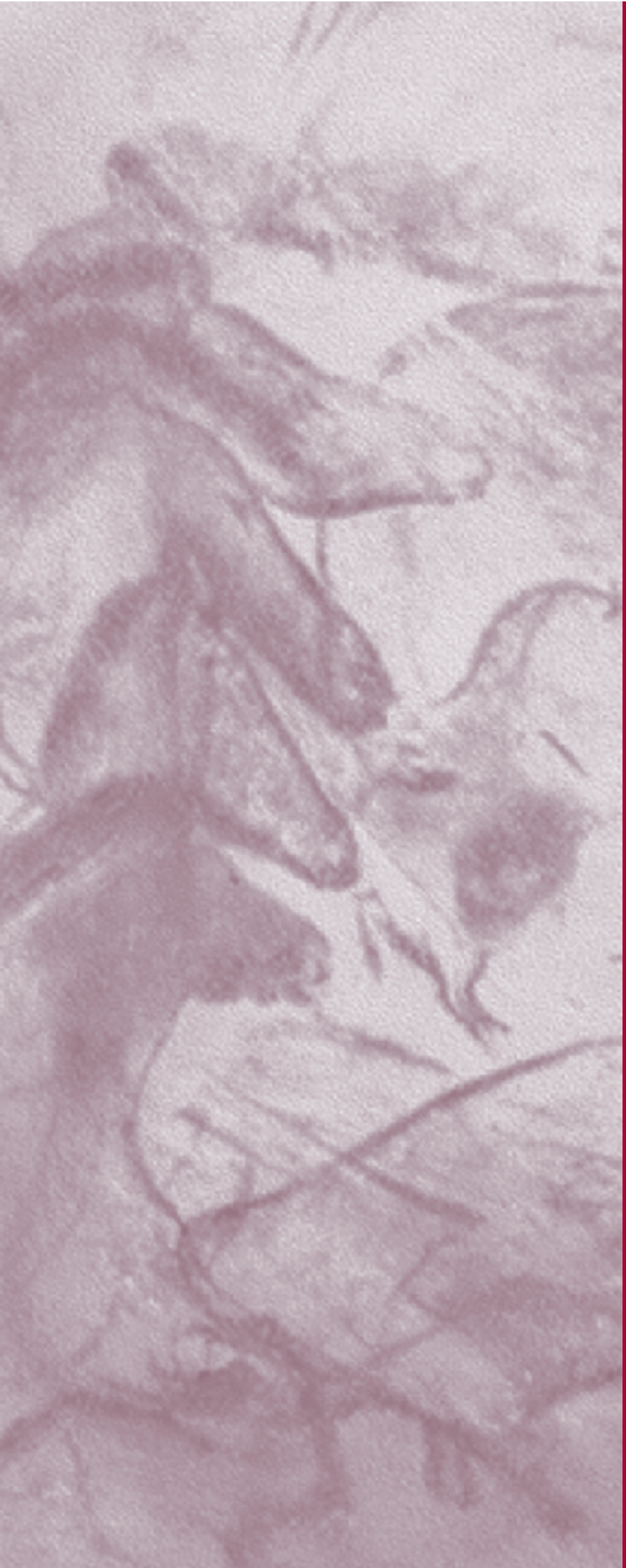
Gracias por su colaboración



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