

PRODUCTION AND REPRODUCTION PERFORMANCE OF THREE SOUTH AFRICAN ANGORA GOAT CYP17 GENOTYPES

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INTRODUCTION

South African Angora goats are known for their inability to cope with stress, especially during severe cold, wet and windy weather (Wentzel et al., 1979; Fourie, 1984). Previous research has shown that the Angora goat is unable to produce sufficient cortisol (the adrenal steroid hormone released in response to physiological stress) in response to cold stress (Van Rensburg, 1971; Herselman & Pieterse, 1992; Herselman & Van Loggerenberg, 1995; Engelbrecht et al., 2000; Engelbrecht & Swart, 2000). A single enzyme, cytochrome P450 17 α -hydroxylase/17,20 lyase (CYP17), was implicated as the probable cause of the problem (Storbeck et al., 2008). Two CYP17 genes have been identified within the South African Angora population, namely ACS- (GenBank accession no. EF524063) and CYP17 ACS+ (GenBank accession no. EF524064) (Storbeck et al., 2007). The two CYP17 genes express enzymes with significantly different activities (Slabbert, 2003; Storbeck et al., 2007; Storbeck et al., 2008; Storbeck et al., 2009). CYP17 isoforms have also been associated with different physiological cortisol responses in Merino sheep (Hough et al., 2010; Hough, 2012; Qui, 2015).

Three unique genotypes (named H_e, H_u and H_o) were subsequently identified. The H_o genotype has only one CYP17 gene, namely ACS-. The H_e genotype has both CYP17 genes (ACS+ and ACS-) at two different loci. Crossing H_o and H_e goats has been shown to yield an intermediate genotype, H_u, which receives both ACS- and ACS+ from the H_e parent, but only ACS- from the H_o parent (Storbeck et al., 2008). Thus all animals will have an ACS- gene, but the H_o genotype lacks an ACS+ gene. A schematic presentation of the two genes of CYP17 in the Angora goat, yielding three genotypes, is presented in Figure 1.

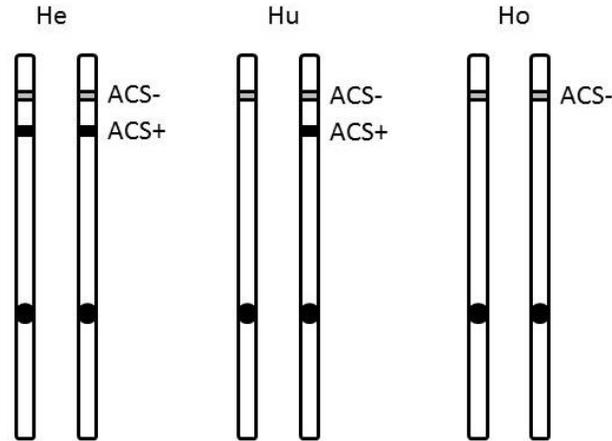


Figure 1. Schematic presentation of the two genes of CYP17 in the Angora goat, giving rise to three genotypes

An insulin-induced stress experiment confirmed that there was a significant difference in the ability of the three different genotypes to produce cortisol in response to physiological stress (Storbeck et al., 2008; Hough et al., 2010). The H_e genotype was the best cortisol producer during the insulin-induced stress test, with the H_o genotype producing the least cortisol. Subsequent to the insulin-induced stress test, a simulated cold stress test was performed at the Grootfontein Agricultural Development Institute (GADI) (Swart, 2012). While the H_o genotype again produced the least cortisol during the cold stress test, it was the rectal temperature of the H_u genotype that dropped significantly more than that of the other two genotypes. The H_e genotype was the best performer in both the insulin-induced and cold stress tests and therefore represents the hardiest genotype.

In addition to being important in cortisol production, the CYP17 enzyme is vital for the production of estrogens (female sex hormones) and androgens (male sex hormones) (Payne & Hales, 2004). The effect of the CYP17 genotypes on the reproductive fitness of Angora ewes was thus investigated (Swart, 2012, 2013). The results indicated that the H_o genotype is a poor reproducer; 62.5% of the H_o group was poor reproducers, while the H_u and H_e groups contained 35% and 42% poor reproducers respectively. Poor reproducers were defined as ewes weaning fewer kids than they had kidding opportunities in the flock. However, a larger sample group needs to be investigated before final recommendations can be made to the industry.

This study formed part of a bigger project which investigated the possibility of breeding hardier Angora goats without negatively affecting the reproductive fitness of the goats or decreasing the quality of mohair that South Africa is known for. Data gathered to date suggest that the H_e genotype is the hardiest and should be selected for. However, information of the relative production and reproduction

performance of the three genotypes is lacking. The aim of this study was therefore to evaluate growth, mohair production and reproduction of the three Angora goat CYP17 genotypes to ultimately be able to make recommendations to the industry as to the way forward regarding implementation of selection practices incorporating the CYP17 genotype.

MATERIAL AND METHODS

Experimental resources

Resources from the GADI-Biobank, including blood samples and phenotypic data were used for this study. An assessment of the available Angora ewes and their reproduction and production data in the GADI-Biobank was performed. Samples from 480 ewes with reproduction, body weight and hair data from three flocks participating in the Angora Biobank were included in the study. For each flock, ewes with good, average and poor reproductive performance, and having recorded body weight and fleece data, were selected for genotyping of the CYP17 locus. The average number of kids born per ewe mated in the three flocks were 99%, 72% and 122% for Flocks 1, 2 and 3 respectively (Snyman, 2010). The corresponding number of kids weaned per ewe mated were 78%, 58% and 105%. Adult body weights of the ewes in the respective flocks were 37.0 kg, 33.4 kg and 44.5 kg. Blood samples from the identified ewes were obtained from the GADI-Biobank.

Experimental procedures

Genomic DNA was isolated from the blood samples and genotyping was carried out using an ARMS-qPCR (amplification refractory mutation system qPCR) assay at the University of Stellenbosch. Genotypes of 466 ewes were available for inclusion in the study.

The following production and reproduction data were obtained from the Angora Biobank database and analysed with suitable models:

- Reproductive performance of ewes
- Body weight of ewes before mating
- Fleece weight, fibre diameter, style and character recorded during the winter shearing of the adult ewes
- Body weight and fleece data recorded at younger ages.

Body weight, fleece and reproduction data recorded for Flock 1 from 2000 to 2015, Flock 2 from 2000 to 2014 and Flock 3 from 2000 to 2010 were available for analyses. Body weight data included birth weight, weaning weight, 8-month, 12-month and 16-month body weight, as well as body weight recorded annually on the ewe flock before mating. Fleece data included fleece weight and fibre diameter recorded at the second and third shearings at 12 and 18 months of age respectively. Fleece weight, fibre diameter, style and character were also recorded annually on the ewe flocks during the winter shearing.

The PROC GLM procedure of SAS (2009) was used to determine the effect of genotype on body weights and fleece traits at the different ages.

Individual reproduction records included information on whether the ewe kidded or not, whether the ewe aborted or not, number of kids born, stillborn kids, kids that died soon after birth, kids reared by a foster mother, kids reared as orphans, number of kids weaned and total weight of kids weaned. Total lifetime reproductive performance in the flock for the ewes genotyped was calculated for number of kids born, number of kids weaned and total weight of kids weaned. The PROC GLM procedure of SAS (2009) was used to analyse the effect of genotype on individual reproductive performance, as well as flock lifetime reproductive performance. The CHISQ procedure of SAS (2009) was used to determine if there were any differences among the three genotypes in whether the ewe kidded or not, whether the ewe aborted or not, number of kids born, kids reared by a foster mother, kids reared as orphans and number of kids weaned.

RESULTS

The distribution of the animals across the CYP17 genotypes for the pooled data and for the three flocks are summarised in Table 1. The highest percentage animals had the H_u genotype in all flocks, as well as in the pooled data. H_o was the least represented, except in Flock 2, where H_o and H_e were evenly represented.

Table 1. Number (%) of animals per genotype in the dataset and in the different flocks

Genotype	Pooled	Flock 1	Flock 2	Flock 3
H _e	171 (36.7%)	132 (41.5%)	6 (16.7%)	33 (29.5%)
H _u	240 (51.5%)	153 (48.1%)	24 (66.6%)	63 (56.2%)
H _o	55 (11.8%)	33 (10.4%)	6 (16.7%)	16 (14.3%)
Total	466	318	36	112

Body weight from birth until adult age across the three genotypes is presented in Table 2. Animals of the H_u genotype were heavier from weaning age onwards, although this difference in body weight was only significant at 8 months of age and in the adult ewes. No differences were observed between the H_e and H_o animals.

Table 2. Body weight of animals across three genotypes from birth until adult age

Trait	H _e	H _u	H _o
Birth weight (kg)	2.92 ± 0.11	2.90 ± 0.11	2.87 ± 0.11
Weaning weight (kg)	15.7 ± 0.6	16.0 ± 0.6	15.9 ± 0.7
8-month body weight (kg)	19.8 ± 0.7	20.4 ^b ± 0.7	19.3 ^a ± 0.8
12-month body weight (kg)	22.3 ± 0.9	22.5 ± 0.8	22.4 ± 0.9
16-month body weight (kg)	26.5 ± 0.9	27.2 ± 0.9	26.3 ± 1.0
Adult ewe body weight (kg)	40.1 ^a ± 0.4	40.9 ^b ± 0.3	39.8 ^a ± 0.4

^{a,b} Values with different superscripts differ significantly ($P < 0.05$)

Fleece traits from second shearing until adult age across the three genotypes is presented in Table 3. No differences were evident at the second or third shearings. Adult ewes of the H_e genotype (1.35 kg) produced heavier ($P < 0.05$) fleeces than both the H_u (1.27 kg) and H_o (1.24 kg) genotypes. Fibre diameter of the fleeces of the H_o ewes (33.0 µm) was higher ($P < 0.05$) than that of the fleeces of the H_e ewes (32.2 µm). The fleeces of the H_o ewes had the best style.

Table 3. Fleece traits of animals across three genotypes from second shearing until adult age

Trait	H _e	H _u	H _o
Fleece weight – 2 nd shearing (kg)	1.29 ± 0.14	1.23 ± 0.13	1.22 ± 0.14
Fibre diameter – 2 nd shearing (µm)	26.3 ± 0.7	26.5 ± 0.7	26.3 ± 0.7
Fleece weight – 3 rd shearing (kg)	1.35 ± 0.06	1.33 ± 0.05	1.34 ± 0.06
Fibre diameter – 3 rd shearing (µm)	28.2 ± 0.5	28.4 ± 0.5	28.6 ± 0.6
Adult fleece weight – winter shearing (kg)	1.35 ^a ± 0.03	1.27 ^b ± 0.02	1.24 ^b ± 0.03
Adult fibre diameter – winter shearing (µm)	32.2 ^a ± 0.3	32.7 ± 0.2	33.0 ^b ± 0.3
Style of fleece – winter shearing	2.97 ± 0.04	2.92 ^b ± 0.04	3.04 ^a ± 0.07
Character of fleece – winter shearing	3.01 ± 0.04	2.98 ± 0.04	2.93 ± 0.06

^{a,b} Values with different superscripts differ significantly ($P < 0.05$)

Reproductive performance of ewes across the three genotypes is presented in Table 4. No significant differences were recorded in reproductive performance among the genotypes. The H_o had the lowest and the H_e the highest number of kids born and weaned per year. H_u ewes had the best lifetime flock reproductive performance.

Table 4. Reproduction of ewes across three genotypes

Trait	H _e	H _u	H _o
From individual reproduction records			
Total weight of kids weaned / year (kg)	18.3 ± 1.0	18.2 ± 0.8	18.1 ± 1.1
Number of kids born / year	1.07 ± 0.05	1.06 ± 0.04	1.03 ± 0.06
Number of kids weaned / year	0.93 ± 0.06	0.90 ± 0.04	0.89 ± 0.06
From lifetime flock reproduction			
Number of kidding opportunities	4.64	4.23	4.44
Total weight of kid weaned / lifetime (kg)	68.3 ± 4.4	72.1 ± 2.8	67.42 ± 4.9
Number of kids born / lifetime	4.71 ± 0.22	4.72 ± 0.14	4.39 ± 0.25
Number of kids weaned / lifetime	3.77 ± 0.24	3.83 ± 0.15	3.58 ± 0.26

Number of kids born in the different flocks in terms of percentage of ewes of each genotype which gave birth to either 0, 1, 2 or 3 kids is summarised in Table 5.

Table 5. Number of kids born in the different flocks across three genotypes

Flock / Number of lambs born	H _e	H _u	H _o
	Percentage of ewes of a specific genotype that had x number of lambs		
Flock 1 (P=0.131)			
0	12.93	11.16	7.09
1	66.20	71.19	68.79
2	19.47	17.04	23.40
3	1.40	0.60	0.71
Flock 2 (P=0.142)			
0	26.67	29.41	51.52
1	70.00	68.07	48.48
2	3.33	2.52	0.0
Flock 3 (P=0.060)			
0	8.25	3.85	0.0
1	49.48	61.54	59.68
2	42.27	34.62	40.32
Pooled (P=0.142)			
0	12.87	11.82	11.44
1	64.24	68.79	63.56
2	21.72	18.99	24.58
3	1.17	0.40	0.42

For each flock, within each genotype, the percentage of ewes for all number of kids born categories adds up to 100%. No significant trend was observed in Flock 1. In Flock 2 approximately 20 to 25% more H_o ewes did not give birth to any kids, compared to the H_u and H_e genotypes, while approximately

20% fewer H_o ewes gave birth to 1 kid. In Flock 3 there were no H_o ewes that did not produce a kid. Looking at the pooled data, there was no difference among the genotypes in terms of percentage of ewes of each genotype which gave birth to either 0, 1, 2 or 3 kids.

Number of kids weaned in the different flocks in terms of percentage of ewes of each genotype which weaned either 0, 1, 2 or 3 kids is summarised in Table 6. There was no significant trend observed in Flock 1, and ewes were spread evenly among genotypes in terms of number of kids weaned category. In Flock 2 more H_o ewes did not wean a kid compared to the H_c and H_u genotypes. Furthermore, fewer H_o ewes weaned 1 kid and none weaned 2 kids. In Flock 3 fewer H_o ewes weaned 0 kids, while no definite trend was observed among genotype for ewes weaning either 1 or 2 kids. As was the case with number of kids born, again there was no difference in the pooled data among the genotypes in terms of percentage of ewes of each genotype which weaned 0, 1, 2 or 3 kids.

Table 6. Number of kids weaned in the different flocks across three genotypes

Flock / Number of lambs weaned	H _c	H _u	H _o
	Percentage of ewes of a specific genotype that weaned x number of lambs		
Flock 1 (P=0.655)			
0	24.61	22.62	20.57
1	63.40	65.91	68.09
2	11.99	11.16	11.35
3	0.0	0.30	0.0
Flock 2 (P=0.377)			
0	50.00	47.90	66.67
1	46.67	49.58	33.33
2	3.33	2.52	0.0
Flock 3 (P=0.131)			
0	13.40	17.79	6.45
1	51.55	56.25	59.68
2	35.05	25.96	33.87
Pooled (P=0.772)			
0	24.19	24.65	23.31
1	61.25	61.92	61.02
2	14.56	13.23	15.68
3	0.0	0.20	0.0

The occurrence of ewes that did not kid and ewes that aborted in the different flocks across the three genotypes is summarised in Table 7. For these calculations, ewes that did not kid included ewes that aborted. No definite trend could be observed across the flocks. In Flock 1, no differences were recorded among genotypes, while in Flock 2, significantly more H_o ewes did not kid than ewes of the other genotypes. In Flock 3, there were significantly more H_c ewes that did not kid, while all the H_o ewes

kidded. In the pooled data, no significant differences among genotypes were recorded. As far as abortions are concerned, no significant differences were observed among the genotypes, although the H_u ewes had the most abortions in Flocks 2 and 3 and in the pooled data.

Table 7. Occurrence of ewes that did not kid or aborted in the different flocks across three genotypes

Flock	H_e	H_u	H_o
	Percentage of ewes of a specific genotype that did not kid		
Flock 1 (<i>P</i> =0.133)	12.93	11.16	7.09
Flock 2 (<i>P</i> =0.042)	26.67	29.41	51.52
Flock 3 (<i>P</i> =0.039)	8.25	3.85	0.0
Pooled (<i>P</i> =0.745)	12.87	11.82	11.44
	Percentage of ewes of a specific genotype that aborted		
Flock 1 (<i>P</i> =0.838)	2.18	1.96	1.42
Flock 2 (<i>P</i> =0.951)	10.00	10.92	9.09
Flock 3 (<i>P</i> =0.491)	1.03	1.92	0.0
Pooled (<i>P</i> =0.578)	2.34	3.03	2.12

The occurrence of kids being fostered or reared as orphans in the different flocks across the three genotypes is summarised in Table 8. The highest percentage of kids that had to be fostered was born to H_o ewes in Flock 1. Most kids that had to be reared as orphans were also born to H_o ewes in Flock 1. All orphans in Flock 3 were born to H_e ewes.

Table 8. Occurrence of kids being fostered or reared as orphans across three genotypes

Flock	H_e	H_u	H_o
	Percentage of ewes of a specific genotype that had kids being fostered		
Flock 1 (<i>P</i> =0.042)	2.34	0.75	2.84
	Percentage of ewes of a specific genotype that had kids being reared as orphans		
Flock 1 (<i>P</i> =0.661)	3.43	2.87	4.26
Flock 3 (<i>P</i> =0.248)	1.03	0.0	0.0
Pooled (<i>P</i> =0.343)	2.99	1.92	2.54

DISCUSSION

The distribution of animals across the three CYP17 genotypes of 36.7% for H_e, 51.5% for H_u and 11.8% for H_o is in accordance with that of Angora veld rams genotyped with the same genotyping method in

2013 (Swart, 2013). In the latter study, 38.0% rams had a H_c, 46.4% a H_u and 15.6% a H_o genotype. The current distribution differs somewhat from earlier genotyping using a different genotyping method, where 42.9% H_c, 40.6% H_u and 16.5% H_o animals were observed (Storbeck et al., 2011). However, this previous method could not always accurately distinguish between H_c and H_u genotypes. An 80% correlation between the two genotyping methods was found (Swart, 2011).

In this study, animals of the H_u genotype were heavier from weaning age onwards, although this difference in body weight was only significant at 8 months of age and in the adult ewes. No differences were observed between the H_c and H_o animals. These results are in accordance with preliminary results found for the fine hair goats kept at the Jansenville Experimental Station born between 2000 and 2008 which included 117 H_c, 119 H_u and 62 H_o animals. No significant difference in body weight was observed among the genotypes for these ewes genotyped with the earlier method (Swart, 2010; Storbeck et al., 2011).

Adult ewes of the H_c genotype (1.35 kg) produced heavier ($P < 0.05$) fleeces than both the H_u (1.27 kg) and H_o (1.24 kg) genotypes in the current study. Fibre diameter of the fleeces of the H_o ewes (33.0 μm) was higher than that of the fleeces of the H_c ewes (32.2 μm ; $P < 0.05$) and the H_u ewes (32.7 μm ; $P > 0.05$). The H_c ewes thus produced the heaviest fleeces with the lowest fibre diameter. In the earlier study on the fine hair ewes, no significant differences in any of the fleece traits were observed among the genotypes (Swart, 2010; Storbeck et al., 2011).

No significant differences were recorded in reproductive performance among the genotypes, although the H_o ewes had the lowest (1.03 and 0.89) and the H_c ewes the highest (1.07 and 0.93) number of kids born and weaned per year respectively. In a preliminary study 98 ewes of Flock 1 were genotyped with the same genotyping method used in the current study. In this earlier study 62.5% of the H_o ewes were poor reproducers, while the H_u and H_c groups had 35% and 42% poor producers respectively. Ewes were classified as poor reproducers when they weaned fewer kids than they had kidding opportunities. However, only eight ewes with H_o genotypes were identified in the sample group and there was no significant difference between the H_o and other genotypes (Swart, 2012). Hough (2012) also reported that reproduction of Merino sheep seemed to be unaffected by the CYP17 genotype.

CONCLUSIONS

The CYP17 genotype plays a role in the stress coping ability of the animal via cortisol production in the adrenal cortex. The H_c CYP17 genotype was previously identified as the hardest genotype pertaining to stress coping ability in the Angora goat. From the results of this study no evidence could be found that selection for any of the three genotypes would adversely affect any growth, mohair production or reproduction function of Angora ewes. CYP17 genotype also had no observable effect on

the reproductive fitness of rams, as measured by testosterone production. As far as mohair production is concerned, the adult H_c ewes produced the heaviest fleeces with the finest fibre diameter. Furthermore, although not significant, the H_e ewes produced the highest number of kids born and weaned per year among the three genotypes.

For breeders interested in incorporating the CYP17 genotype into their selection strategy, it is recommended that all H_o genotype rams could be culled as a first step. Preferably only H_c sires should be used. As the H_u genotype is in abundance in most of the flocks, it would be unfeasible to cull possible H_u sires with desirable production characteristics. These sires should, however, only be mated to H_c genotype ewes, as these matings would only yield H_c and H_u genotype offspring. Mating of H_u sires to H_o ewes would yield H_o and H_u progeny, while a mating between a H_u sire and H_u ewes will yield H_o, H_u and H_c progeny. It is not possible to get rid of the ACS- gene, as all the animals possess this gene. An effort can, however, be made to decrease the number of animals that do not have the ACS+ gene (the H_o genotype), thereby increasing the frequency of the ACS+ gene in the population.

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