Sheep & Goat Research Journal
Volume 31, 2016 - October

Genetic Parameters for Internal Parasite Resistance, Reproduction, and Growth Traits in a Closed Line of Kiko × Boer Goats Divergently Selected for Internal Parasite Resistance[1]

C.L. Thomas[2,3], W.R. Lamberson[3], R.L. Weaber[4], L.S. Wilbers[2], T. Wuliji[2], J.D. Caldwell[2], and B.C. Shanks[1,2]

[2] *Lincoln University, Department of Agriculture and Environmental Sciences, Jefferson City, Mo. 65101*

[3] *University of Missouri, Division of Animal Sciences, Columbia, MO 65211*

[4] *Kansas State University, Animal Sciences and Industry, Manhattan, KS 66506*

[1] *Corresponding author: Dr. Bruce Shanks, 110 Small Animal Research Facility, Department of Agriculture and Environmental Sciences, Lincoln University, Jefferson City, MO 65101. Phone 573-681-5382; Fax: 573-681-5411. Email:shanksb@lincolnu.edu.*
Lincoln University Cooperative Research Manuscript #20150045.
The research in this paper was funded through the National Institute for Food and Agriculture of the United States Department of Agriculture, Accession No. 224326.

Summary

Prevalence of gastrointestinal nematodes is a major challenge for goat producers. One approach to combating internal parasites is to utilize the host animal's natural or acquired resistance to parasites in a selection program. Therefore, our objective was to estimate genetic parameters for parasite resistance, reproduction, and growth traits in a closed line of Kiko (K) × Boer (B) goats divergently selected for internal parasite resistance. Beginning in 2011, 146 mixed-age (1-yr-old to 6-yr-old) B does were assigned to one of two selection lines: a high line (HL) selected for high resistance to internal parasites and a low line (LL) selected for low resistance to internal parasites. Unrelated K bucks, purchased on the basis of parasite resistance, were exposed to each corresponding doe line. Resulting F_1 doe progeny were selected based on parasite resistance and were then backcrossed within line to K bucks to produce F_2 ¾ K × ¼ B progeny. Fecal egg count (FEC), blood packed cell volume (PCV), and FAMACHA© scores were measured monthly to evaluate impact of *Haemonchus contortus* parasite load. Genetic parameters were estimated with linear mixed models using restricted maximum-likelihood procedures. Heritability estimates for FEC, PCV, and FAMACHA© score were 0.13, 0.06, and 0.11, respectively and estimates for litter size, birth weight, and weaning weight were 0.23, 0.18, and 0.17, respectively. The genetic correlation between FEC and FAMACHA© was 0.46, while genetic correlations between FEC and PCV and FAMACHA© and PCV were 0.00 and -0.09, respectively. Results indicate that parasite resistance may be lowly heritable, regardless of parasite indicator trait measured, suggesting that selection progress would be possible, yet slow.

Key words: Genetic Correlation, Goat, Heritability, Parasite, Resistance

Introduction

In recent years, goats have become increasingly popular as an alternative livestock enterprise. However, goats are more susceptible to internal parasites than any other type of livestock (Vagenas et al., 2002; Schoenian, 2003). Arguably, parasitism is the most serious economic constraint affecting goat production in the United States.

The parasitic nematode of most concern for goat producers is *Haemonchus contortus* (Hendrix and Robinson, 2014), which traditionally has been controlled through commercial anthelmintic treatments. However, there has been increasing concern about the development of anthelmintic resistance in parasite populations (Terrill et al., 2001; Howell et al., 2008). Alternatives to commercial anthelmintics, such as herbal remedies, mineral supplements, and condensed tannins are being used; and rotational stocking or mixed-grazing systems have been developed. However, even if effective, these alternatives require intensive inputs and efforts that are not always conducive to all operations.

One approach is to utilize the host animal's natural immunity in a selection program to increase the level of parasite resistance in a herd. Genetic variability of parasite resistance within sheep flocks has been utilized and manipulated by selection in numerous research projects, especially in Australia and New Zealand (for review, see Windom, 1996). In goats, there is promising evidence that parasite resistance is under genetic control as well, but the number of studies is limited, especially from the United States (Wildeus and Zajac, 2005). Without research-based guidance on parasite resistance, much of the selection emphasis of goat producers in the central United States has been directed toward production traits, with little regard given to parasite resistance.

Our objective was to estimate genetic parameters for parasite resistance, reproduction, and growth traits in a closed line of Kiko × Boer goats divergently selected for internal parasite resistance.

Materials and Methods

Foundation Herd Establishment

In fall 2011, a divergent selection program for parasite resistance in goats was initiated at the Lincoln University George Washington Carver Farm located in Jefferson City, Missouri. All experimental procedures were reviewed and approved by the Institutional Animal Care and Use Committee (approval # 1410) at Lincoln University prior to initiation of the project. The experiment began with 146 mixed-age (1-yr-old to 6-yr-old) Boer and high-percentage Boer does (B) that were assigned to one of two divergent selection lines: a high line (HL; n = 74) selected for high resistance to internal parasites and a low line (LL; n = 72) selected for low resistance to internal parasites. The B does were not previously selected for internal parasite resistance; however, all available parasite-related data collected were used to calculate Expected Progeny Differences (EPD) to rank and sort does into each corresponding line. Expected Progeny Differences were computed prior to each selection point using a repeated records model via ASREML (described later; Version 4; VSN International, Hemel Hempstead, UK). Unrelated Kiko (K) bucks (n = 12) were purchased from individual producers on the basis of internal parasite resistance (six high and six low), as indicated by mean fecal egg count (FEC) collected and summarized by unbiased buck performance tests in Oklahoma and Maryland. After this, lines were closed and all selection was from within line. Kiko bucks were exposed to each corresponding doe line in separate breeding pens beginning in December, 2011 to produce F_1 K × B progeny. Breeding between K bucks and B does continued in 2012 and 2013; however, natural death loss and removal of non-pregnant B does from the experiment reduced the number of B does each year (Table 1).

Selected Animals

Each year from 2012 to 2014, F_1K × B doe progeny were selected (described in detail below) prior to the breeding season based on parasite resistance as determined by FEC EPD. Selected F_1 K × B HL and LL does were then backcrossed within line to original foundation HL and LL K bucks, respectively, to produce F_2 ¾K × ¼B progeny. Care was taken to avoid mating F_1 K × B does to related K bucks. Selected F_1 K × B HL and LL does remained in the herd for the duration of the project; however, death loss and disposal of non-pregnant does from the experiment reduced numbers each year (Table 1).

Selection and Parasite Sampling Procedures

First generation K × B HL and LL does were selected each fall of their birth year, prior to the breeding season, based on FEC EPD. Multiple FEC measurements were taken in an effort to improve accuracy of selection decisions because of environ-

Table 1. Description of the data analyzed.

Pedigree		Total no.		
	No. of sires	85		
	No. of dams	253		
	No. of paternal grand sires	31		
	No. of maternal grand sires	34		
	No. of paternal grand dams	50		
	No. of maternal grand dams	105		
			Treatment[a]	
Foundational herd		Total no.	HL	LL
	No. of Boer does	146	74	72
	No. of Kiko bucks	12	6	6
Bred (exposed)	2011	146	52	57
	2012	142	70	72
	2013	79	40	39
Progeny born[b]	2012 (F_1)	123	66	57
	2013 (F_1)	176	75	101
	2013 (F_2)	19	10	9
	2014 (F_1)	90	48	42
	2014 (F_2)	41	20	21

[a] Treatment: HL = high line (high resistance to internal parasites); LL = low line (low resistance to internal parasites).
[b] Progeny born: F_1 = Kiko × Boer; F_2 = ¾ Kiko × ¼ Boer.

mental conditions associated with traits such as FEC (Falconer and Mackay, 1996). Fecal egg counts, packed cell volume (PCV), and FAMACHA© scores were measured monthly on all animals, beginning at weaning in August until just prior to selection and breeding in December. Approximately 2 g of feces were collected from the rectum to estimate FEC using the modified McMaster's technique (Whitlock, 1948) with the precision of each egg counted representing 50 eggs per g of wet feces. Approximately 2 mL of blood were collected via jugular venipuncture using 18 gauge needles attached to evacuated-sample collection tubes containing heparin to estimate PCV. The PCV was subsequently determined by the micro-hematocrit centrifuge method using a HemataSTAT® II Centrifuge (Separation Technology, Inc., Sanford, Fla.). A FAMACHA© score for each animal was recorded as 1 (red, non-anemic), 2 (red-pink, non-anemic), 3 (pink, mild-anemic), 4 (pink-white, anemic), or 5 (white, severely anemic; Kaplan et al., 2004). Selection was based on EPD calculated from FEC data taken on a monthly basis. In the event that two of the following three criteria: a FEC of over 2,000 eggs per g (Machen et al., 1988), a FAMACHA© score of 4 or more, or PCV of 21 or less were recorded, that animal was immediately treated with commercial anthelmintics according to label recommendations (Valbazen® Suspension; Zoetis Inc., Kalamazoo, Mich. or Cydectin©; Boehringer Ingelheim, Inc., St. Joseph, Mo., or a combination). In treated cases, animals were selected on the basis of the number of doses administered rather than FEC data. Thus, selected HL individuals were those that were treated the fewest times or had the lowest FEC EPD, and for LL, selected individuals were those that were treated the most times or had the highest FEC EPD. No other criteria were used for selection with the exception of removal of non-pregnant does. For F_1 K × B does, selected individuals represented the most parasite resistant 80 percent from the HL and the least parasite resistant 80 percent from the LL.

Animal Management

All does (except F_1 and F_2 doelings after weaning) were managed as one group throughout the year, except at breeding. Breeding occurred once a year beginning in December by natural service in single-sire mating pens. Equal numbers of randomly selected does from each line were assigned to unrelated bucks of the same line. The breeding season lasted for 63 d, annually. During the breeding season, does were allowed access to pasture composed predominately of endophyte-infected tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh] and were hand fed a 14-percent crude protein corn-grain, soybean-meal, oat-grain-based supplement at NRC (2006) recommended levels. Does also had *ad libitum* access to water, trace minerals, and medium-quality grass hay composed predominately of endophyte-infected tall fescue if pasture was limited. Pregnancy status was determined within 45 d post-breeding by a trained technician using ultrasound equipment.

Does were wintered on pasture composed predominately of endophyte-infected tall fescue and medium-quality endophyte-infected tall fescue hay when pasture was limited and supplementation with a 14-percent crude protein corn-grain, soybean-meal, oat-grain-based diet continued at NRC (2006) recommended levels until it was increased 6 wk prior to kidding. Just prior to kidding in May, does were moved to large pens with indoor and outdoor access and observed at approximately 0700 and 1900 daily. Kids were ear-tagged, litter size (LS) was recorded, and birth weight (BWT) was measured within 24 h of birth. Starting at two wk of age, kids were allowed access to an 18-percent crude protein corn-grain, soybean-meal, oat-grain-based creep feed, offered until weaning at approximately 90 d of age. Kids were vaccinated according to label recommendations approximately 30 d pre-weaning for *Clostridium Perfringens* Types C and D and *Tetanus Toxoid* (Bar-vac© CD/T; Boehringer Ingelheim, Inc., St. Joseph, Mo.). At weaning, kids were re-vaccinated, sorted by sex, and weaning weights (WWT) were recorded. Until breeding, F_1 and F_2 doelings were moved to separate endophyte-infected tall fescue-based paddocks and were offered a 14-percent crude protein corn-grain, soybean-meal, oat-grain-based supplement at NRC (2006) recommended levels. All F_1 bucklings were removed from the study and all F_2 bucklings were kept separate on endophyte-infected tall fescue-based paddocks with additional corn grain-soybean meal-oat grain based diet supplementation (NRC, 2006) provided.

Statistical Analysis

A pedigree describing the ancestral lineage of the population was utilized for genetic evaluation procedures. The pedigree file included 85 sires, 253 dams, 31 paternal grand sires, 34 maternal grand sires, 50 paternal grand dams, and 105 maternal grand dams (Table 1). Heritabilities and genetic correlations were estimated for parasitological measurements, reproductive, and growth traits using ASREML Version 4 (VSN International, Hemel Hempstead, UK).

Parasitological Measurements

A trivariate, repeated-records animal model was used to calculate EPD and estimate genetic parameters for FEC, PCV, and FAMACHA© score on 686 animals and included fixed effects of contemporary group, age at observation, sex, and heterozygosity (100 percent for F_1 and 50 percent for F_2). Contemporary group was defined for each observation as age, generation (F_1 or F_2), and animals that had the same anthelmintic treatment scheme based on time and number of doses administered. Additive genetic and residual (co)variances for each trait and linear functions thereof, including heritabilities and genetic correlations, were computed.

In matrix notation the mixed model with repeated records equations can be expressed as follows:

$$\mathbf{y = Xb + Za + Zp + e}$$

where **y** is the vector of the observations, **b** is the vector of fixed effects, **a** is the vector of additive genetic effects, **p** is the vector of permanent environmental effects and **e** is the vector of residual effects. The matrix **X** is the incidence matrix for the fixed effects and **Z** is the incidence matrix relating observations to animals. Each animal has an additive genetic as well as a permanent environmental effect; hence both effects have the same design matrix. The three random effects have the following distribution:

$$\text{var}\begin{bmatrix} a \\ p \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2 a & 0 & 0 \\ 0 & \sigma^2 c & 0 \\ 0 & 0 & I^2\sigma_e \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix} G = \begin{bmatrix} A\sigma^2 a & 0 \\ 0 & I^2\sigma_e \end{bmatrix}$$

where **A** is the numerator relationship matrix among animals, **I** is the appropriate identity matrix, σ_a^2 is the direct-additive-genetic variance, and σ_c^2 is the variance due to permanent environmental effects. In this model, permanent environmental effects for different animals are uncorrelated, and within an animal there is no correlation between its additive and its permanent environmental effect. The total phenotypic variance is the sum of the three variance components. The mixed-model equation for a model with repeated records is:

$$\begin{bmatrix} X'X & X'Z & X'Z \\ Z'X & Z'Z + \lambda A^{-1} & Z'Z \\ Z'X & Z'Z & Z'Z + \gamma I \end{bmatrix} \begin{bmatrix} b \\ a \\ p \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ Z'y \end{bmatrix}$$

where now $\lambda = \sigma^2 e / \sigma^2 a$ and $\gamma = \sigma^2 e / \sigma^2 c$.

Reproductive Traits

Litter size was recorded for 458 animals and was analyzed using a single-trait analysis. The model for this analysis included additive direct animal and fixed effects of LS, contemporary group, and heterozygosity. Data were pre-adjusted to an adult doe basis using previously developed industry adjustments (Table 2). For this study, adjustments were derived from data collected at Texas A&M-San Angelo, the American Boer Goat Association (San Angelo, Texas), and Virginia Tech University-Blacksburg with adjustment factors developed similar to those researchers involved with the National Sheep Improvement Program (Notter et al., 2005).

In matrix notation the single-trait, mixed-model equation for analyses of LS can be expressed as follows:

$$\mathbf{y = Xb + Za + e}$$

where **y** is the vector of reproductive trait observations, **b** is the vector of unknown fixed effects, **a** is the vector of direct-genetic effects with associated incidence matrices **X** and **Z**, respectively, and **e** is a vector of random-residual effects. The mean vector is **E(y) = Xb** and

$$\text{var}\begin{bmatrix} a \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2 a & 0 \\ 0 & I\sigma^2 e \end{bmatrix}$$

where **A** is the numerator relationship matrix among animals, **I** is the appropriate identity matrix, and $\sigma^2 a$ and $\sigma^2 e$ are variances due to direct genetic and residual effects, respectively.

Growth Traits

Birth weights on 458 and WWT on 232 animals were recorded. Birth weight and WWT were used in a maternal-effects-model analysis because the dam has influence on the performance of her offspring over and above that of her additive genetic contribution. In this instance, maternal effects are strictly environmental for the offspring, but can have both genetic and environmental components (Willham, 1972). Any record with a missing or invalid birth date, weaning date, doe birth date, sire identification, or doe identification was omitted from the data set. Correct dates were necessary to calculate adjusted BWT and WWT and to ensure that contemporary groups were formed properly. If weaning age was not between 90 d to 120 d, then the record was removed.

Table 2. Multiplicative industry factors used to adjust litter size for effects of age of dam.

Age of dam	Industry adjustment factors[a]
1	1.48
2	1.17
3	1.05
4	1.01
5	1.00
6	1.00
7	1.02
8	1.05
9+	1.13

[a] Multiplicative factors used to adjust litter size for effects of age of dam presented by Notter et al. (2005).

Multiplicative factors derived from data collected at Texas A&M-San Angelo, the American Boer Goat Association (San Angelo, TX), and Virginia Tech University-Blacksburg (Notter et al., 2005) were used to adjust BWT and WWT for non-genetic factors of kid sex, type of birth (for BWT) or birth and rearing (for WWT), and age of dam (Table 3). In the data set, mean BWT and WWT weight prior to adjustment were 2.94 kg and 13.07 kg, respectively. After adjustments, mean adjusted BWT (BWT_{adj}) and adjusted WWT (WWT_{adj}) were 3.27 kg and 13.27 kg, respectively. Weaning weight was pre-adjusted for age of kid at weaning using the following formula:

$$90\text{ d }WWT_{adj} = (((\text{actual WWT} - \text{actual BWT})/\text{weaning age}) * 90) + \text{BWT}$$

The maternal effects model used to analyze BWT and WWT can be represented as follows:

$$\mathbf{y = Xb + Z_1a + Z_2m + e}$$

In this model the direct genetic and maternal genetic effects are considered: where **y** is the vector of observations, **b** is a vector of fixed effects, **a** is a vector of additive-genetic effects, **m** is a vector of maternal genetic effects and **e** is a vector of residual effects. **X** is the incidence matrix for the fixed effects and $\mathbf{Z_1}$ and $\mathbf{Z_2}$ are incidence matrices relating observations to random animal (additive genetic) and dam (maternal genetic), respectively. The random effects had the following distribution:

Table 3. Multiplicative industry factors used to adjust birth and weaning weights for non-genetic effects.

		Industry adjustment factors[a]	
Effects	Level	Birth weight[b]	Weaning weight[b]
Kids sex	Buck	0.91	0.90
	Doe	1.00	1.00
	Wether		0.97
Type of birth-rearing	1-1	1.00	1.00
	1-2		1.14
	2-1		1.04
	2-2	1.13	1.18
	3-1		1.08
	3-2		1.23
	3-3	1.27	1.27
Age of dam	1	1.27	1.10
	2	1.07	1.09
	3-7	1.00	1.00
	8+	1.05	1.00

[a] Actual birth weights and age-adjusted (to 90 d) weaning weights are multiplied by the factor shown to correct for non-genetic effects of kid sex, type of birth (for birth weight) or birth and rearing (for weaning weight), and age of dam. Birth weights were adjusted only for type of birth. This table was adopted from Notter et al. (2005).
[b] Multiplicative factors for birth weight and weaning weight by Notter et al. (2005).

$$\text{var}\begin{bmatrix} a \\ m \\ e \end{bmatrix} = \begin{bmatrix} A\sigma^2 a_2 & A\sigma a_2 m & 0 \\ A\sigma^2 am & A\sigma^2 m & 0 \\ 0 & 0 & I\sigma^2 e \end{bmatrix} = \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix}$$

$$G = \begin{bmatrix} A\sigma^2 a_2 & A\sigma a_2 m \\ A\sigma^2 am & A\sigma^2 m \end{bmatrix} = G_0 \times A$$

where G_0 is a 2 by 2 matrix: $\begin{bmatrix} \sigma^2 a_2 & \sigma a_2 m \\ \sigma^2 am & \sigma^2 m \end{bmatrix}$ and $\times$ **A** is a direct product.

Further, $\sigma^2 a$ is a direct genetic variance, $\sigma^2 m$ is the maternal genetic variance, σam is the covariance between direct and maternal genetic effects, and $\sigma^2 e$ is the error variance. The model shows that both random effects have a covariance structure depending on the genetic relationships. Related dams have related maternal effects, and there is a correlation between dam's direct additive genetic effects and her maternal genetic effects. The total phenotypic variance is equal to:

$$\sigma^2 p = \sigma^2 a + \sigma^2 m + \sigma^2 am + \sigma^2 e.$$

The mixed model equations are:

$$\begin{bmatrix} X'X & X'Z_1 & X'Z_2 \\ Z_1'X & Z_1'Z_1 + \alpha_{11}A^{-1} & Z_1'Z_2 + \alpha_{12}A^{-1} \\ Z_2'X & Z_2'Z_1 + \alpha_{21}A^{-1} & Z_2'Z_2 + \alpha_{22}A^{-1} \end{bmatrix} \begin{bmatrix} b \\ u \\ m \end{bmatrix} = \begin{bmatrix} X'y \\ Z_1'y \\ Z_2'y \end{bmatrix}$$

where $\begin{bmatrix} \alpha_{11} & \alpha_{12} \\ \alpha_{21} & \alpha_{22} \end{bmatrix} = G_0^{-1}\sigma^2 e.$

Results

Parasitological Measurements

Descriptive statistics for parasitological traits are shown in Table 4. Mean FEC, PCV, and FAMACHA© scores were 1,591, 27, and 3, respectively. Heritability estimates for FEC, PCV, and FAMACHA© are presented in Table 5. The heritability estimate for FEC was 0.13, which was similar to estimates of 0.13 reported by Baker et al. (2001) in 4.5-mo-old and 8-mo-old Galla and Small East African goats, 0.14 by Mandonnet et al. (2001) in 4-mo-old Creole goats, 0.18 by Gunia et al. (2011) in Creole goats, 0.05 in New Zealand involving Saanen milk goats by Morris et al. (1997), 0.02 in Australia with Angora goats by Bolormaa et al. (2009) and 0.05 and 0.13 (depending on the model used) in India with Barbari goats by Mandal and Sharma (2008). Findings from this study were lower than the 0.32 FEC heritability estimate by Vagenas et al. (2002) in Scottish feral goats and crosses, and the 0.20 FEC heritability at 82 d of age and 0.33 FEC at 10 mo of age in a population of Creole goats (Mandonnet et al., 2001). Overall, FEC is a lowly heritable trait in goats.

The heritability estimate for PVC was 0.06 (Table 5). Our estimate is somewhat lower than the heritability estimate reported by Baker et al. (2001) of 0.18 in Galla and Small East African goats and by Gunia et al. (2011), who reported a heritability estimate of 0.13 for PCV in Creole goats. Our heritability estimate for FAMACHA© score was 0.11 (Table 5), which was lower than the estimate of 0.55 for FAMACHA© score in Merinos reported by Van Wyk and Bath (2002). No heritability estimates for FAMACHA© score in goats were found in the literature.

Reproductive Traits

Number of records and descriptive statistics for adjusted LS (LS_{adj}) are shown in Table 6. The heritability estimate for LS_{adj} was higher (h^2 = 0.23; Table 7) than previous reported estimates including: 0.10 in Boer goats reported by Notter et al. (2005), using the same multiplicative factors applied in this study to adjust for LS, 0.12 in Boer goats (Zhang et al., 2009), 0.09-0.12 in Polish goats (Bagnicka and Lukaszewicz, 2000), 0.11-0.18 in dairy goats (Bagnicka et al., 2007), and 0.18 and 0.11 in Creole goats reported by Menendez-Buxadera et al. (2004) and Gunia et al. (2011), respectively.

Growth Traits

Number of records and descriptive statistics for BWT and WWT are shown in Table 6. Multiplicative factors were used to

Table 4. Summary statistics for parasitological measurements.

Trait[a]	No. of records	Mean	Minimum	Maximum	Standard deviation
FEC	3,826	1,591	50	23,350	2,433.0
PCV	3,872	27	10	41	8.3
FAMACHA© score[b]	3,875	3	1	5	0.9

[a] Parasitological measurements: FEC = fecal egg count; PCV = packed cell volume.
[b] FAMACHA© scores range from 1-5 with: 1 - red, non-anemic; 2 - red-pink, non-anemic; 3 - pink, mild-anemic; 4 - pink-white, anemic; 5 - white, severely anemic (Kaplan et al., 2004).

Table 5. Direct (h_d^2) heritability estimates for FEC, PCV, and FAMACHA© score.

Trait[a]	h_d^2
FEC	0.13 ± 0.07
PCV	0.06 ± 0.04
FAMACHA© score[b]	0.11 ± 0.08

[a] Parasitological measurements: FEC = fecal egg count; PCV = packed cell volume.
[b] FAMACHA© scores range from 1-5 with: 1 - red, non-anemic; 2 - red-pink, non-anemic; 3 - pink, mild-anemic; 4 - pink-white, anemic; 5 - white, severely anemic (Kaplan et al., 2004).

adjust BWT and WWT for non-genetic factors of kid sex, type of birth (for BWT) or birth and rearing (for WWT), and age of dam and resulted in heritability estimates for BWT_{adj} and maternal BWT_{adj} of 0.18 and 0.26, respectively (Table 7). Heritability estimates from this study were similar to heritability estimates of 0.15 for direct BWT and 0.10 for maternal BWT in Boer goats, in which the same adjustments factors were applied (Notter et al., 2005), 0.19 for direct BWT (using a smaller sample size and fitting an animal model ignoring parity of dam and interactions among the effect factors) in Boer goats (Zhang et al., 2008), 0.17 for direct BWT in Boer goats (Zhang et al., 2009), 0.16 for direct BWT in Boer goats (Schoeman et al., 1997), and 0.18 for direct BWT in Emirati goats (Al-Shorepy et al., 2002).

Heritability estimates for 90 d WWT_{adj} and maternal WWT_{adj} (pre-adjusted for non-genetic effects) were 0.17 and 0.04, respectively (Table 7). Zhang et al. (2009), analyzing Boer goats, reported an estimate of direct genetic heritability for 90 d WWT of 0.22, which was similar to the estimate found in our study. In a study with Boer goats, Schoeman et al. (1997) found similar results (h^2 = 0.18) for direct WWT in herds that occupied two different locations in Africa. Higher estimates were found by Supakorn and Pralomkarn (2012), who utilized three different goat breeds (Boer, Thai Native, and Saanen) and reported direct heritabilities of 0.26 to 0.36 (depending on the model used) for WWT at 150 d to 155 d of age. In another experiment with Emirati goats weaned at 2 mo, Al-Shorepy et al. (2002) reported a WWT heritability estimate of 0.32.

Genetic Correlations

Parasitological measurements

Estimated genetic correlations among FEC, PCV, and FAMACHA© scores are presented in Table 8. Genetic correlations between FEC and PCV and between FAMACHA© scores and PCV were slight (r = 0.00 and r = -0.09, respectively), while the genetic correlation between FEC and FAMACHA© was large and positive (r = 0.46). In contrast to current findings, Baker et al. (2001) with Galla and Small East African goats and Gunia et al. (2011) with Creole goats indicated that the average genetic correlation between FEC and PCV was -0.53 and -0.21, respectively. Genetic correlations between the various parasitological measurements were scarce in the literature for goats.

Table 6. Summary statistics for litter size, birth weight, and weaning weight after pre-adjustment using industry standard adjustment factors.

Trait[a]	No. of records	Mean	Minimum	Maximum	Standard deviation
LS_{adj}[b]	458	1.6	1.0	4.2	1.00
BWT_{adj}, kg[c]	458	3.3	1.5	5.4	0.63
WWT_{adj}, kg[c]	232	13.3	5.4	25.6	3.72

[a] Performance trait: LS_{adj} = adjusted litter size; BWT_{adj} = adjusted birth weight; WWT_{adj} = adjusted weaning weights.
[b] Multiplicative factors were used to adjust litter size for effects of age of dam.
[c] Actual birth weights and age-adjusted (to 90 d) weaning weights were corrected for non-genetic effects of kid sex, type of birth (for birth weight) or birth and rearing (for weaning weight) and age of dam. Birth weights were adjusted only for type of birth.

Table 7. Direct (h_d^2) and maternal (h_m^2) heritability estimates for performance traits from analysis that used data pre–adjusted using industry standard multiplicative adjustment factors.

Trait[a]	h_d^2	h_m^2
LS_{adj}[b]	0.23 ± 0.15	
BWT_{adj}[c]	0.18 ± 0.52	0.26 ± 2.10
WWT_{adj}[c]	0.17 ± 0.10	0.04 ± 0.02

[a] Performance trait: LS_{adj} = adjusted litter size; BWT_{adj} = adjusted birth weight; WWT_{adj} = adjusted weaning weights.
[b] Multiplicative factors were used to adjust litter size for effects of age of dam.
[c] Actual birth weights and age-adjusted (to 90 d) weaning weights were corrected for non-genetic effects of kid sex, type of birth (for birth weight) or birth and rearing (for weaning weight), and age of dam. Birth weights were adjusted only for type of birth.

Table 8. Genetic correlations (r) among FEC, PCV, and FAMACHA© score.

Parasitological measurement[a]	r
FEC – PCV	0.00 ± 7.71
FEC – FAM[b]	0.46 ± 0.11
FAM[b] – PCV	-0.09 ± 0.04

[a] Parasitological measurements: FEC = fecal egg count; PCV = packed cell volume; FAM = FAMACHA© score.
[b] FAMACHA© scores range from 1-5 with: 1 - red, non-anemic; 2 - red-pink, non-anemic; 3 - pink, mild-anemic; 4 - pink-white, anemic; 5 - white, severely anemic (Kaplan et al., 2004).

Growth traits

The genetic correlation between direct BWT and direct WWT was positive (0.24; data not shown). The American Boer Goat Association reported a genetic correlation of 0.50 between BWT and WWT (Notter et al., 2005). The positive genetic correlation between BWT and WWT suggests that selection for increased WWT can lead to increased BWT in goat kids.

Conclusion

Results of this study indicate that parasite resistance may be lowly heritable, regardless of parasite indicator traits measured. Heritability estimates for parasite related measurements in the current study were similar to previous estimates reported in literature and suggested that selection progress may be possible, but slow.

When heritability estimates were calculated for reproductive and growth traits using a model to estimate non-genetic fixed effects for kid sex, birth/rearing type, and age of dam from the data, our results were lower than reported estimates. However, if data was pre-adjusted for these factors using industry standard adjustments, heritability estimates for both reproductive and growth traits were in the range of previously reported literature. These results emphasize the importance of properly adjusting records before making selection and breeding decisions.

Because *H. contortus* has a short lifecycle and extreme prolificacy, control in goats typically is a major management challenge. Selection for parasite resistance in goats may be a sustainable way to control this internal parasite and limit reliance on commercial anthelmintics.

Literature Cited

Al-Shorepy, S. A., G. A. Alhadrami, and K. Abdulwahab. 2002. Genetic and phenotypic parameters for early growth traits in Emirati goat. Small Rumin. Res. 45:217–223.

Bagnicka, E. and M. Lukaszewicz. 2000. Reproduction traits and their heritability in Polish goats. Pr. Mater. Zoot. 56:121–128.

Bagnicka, E., E. Wallin, M. Łukaszewicz, and T. Ådnøy. 2007. Heritability for reproduction traits in Polish and Norwegian populations of dairy goat. Small Rumin. Res. 68:256–262.

Baker, R. L., J. O. Audho, E. O. Aduda, and W. Thorpe. 2001. Genetic resistance to gastro-intestinal nematode parasites in Galla and Small East African goats in the sub-humid tropics. Anim. Sci. 73:61–70.

Bolormaa, S., M. Olayemi, J. H. J. van der Werf, N. Baillie, F. Le Jambre, A. Ruvinsky, and S. W. Walkden-Brown. 2009. Estimates of genetic and phenotypic parameters for production, haematological and gastrointestinal nematode-associated traits in Australian Angora goats. Anim. Prod. Sci. 50:25–36.

Falconer, D. S. and T. F. C. Mackay. 1996. Heritability. Introduction to Quantitative Genetics. Pearson Education Ltd., Essex, England. pp. 160–183.

Gunia, M., F. Phocas, R. Arquet, G. Alexandre, and N. Mandonnet. 2011. Genetic parameters for body weight, reproduction, and parasite resistance traits in the Creole goat. J. Anim. Sci. 89:3443-3451.

Hendrix, C. M. and E. D. Robinson. 2014. Diagnostic parasitology for veterinary technicians. 4th ed. Elsevier Health Sciences, St. Louis, MO.

Howell, S. B., J. M. Burke, J. E. Miller, T. H. Terrill, E. Valencia, M. J. Williams, L. H. Williamson, A. M. Zajac, and R. M. Kaplan. 2008. Prevalence of anthelmintic resistance on sheep and goat farms in the southeastern United States. J. American Vet. Med. Assoc. 233(12):1913–1919.

Kaplan, R. M., J. M. Burke, T. H. Terrill, J. E. Miller, W. R. Getz, S. Mobini, E. Valencia, M. J. Williams, L. H. Williamson, M. Larsen, and A. F. Vatta. 2004. Validation of the FAMACHA© eye color chart for detecting clinical anemia in sheep and goats on farms in the southern United States. Vet. Parisitol. 123:105-120.

Mandal, A. and D. K. Sharma. 2008. Inheritance of faecal nematode egg count in Barbari goats following natural *Haemonchus contortus* infection. Vet. Parasitol. 155:89–94.

Machen, R., F. Craddock, T. Craig, and T. Fuchs. 1988. A *Haeomonchus contortus* management plan for sheep and goats in Texas. http://animalscience.tamu.edu/ansc/publications/sheeppubs/L5095-haemonchus.pdf (Accessed 23 July 2016.)

Mandonnet, N., G. Aumont, J. Fleury, R. Arquet, H. Varo, L. Gruner, J. Bouix, and J. V. Khang. 2001. Assessment of genetic variability of resistance to gastrointestinal nematode parasites in Creole goats in the humid subtropics. J. Anim. Sci. 79:1706–1712.

Menéndez-Buxadera, A., G. Alexandre, and N. Mandonnet. 2004. Discussion on the importance, definition and genetic components of the number of animals born in the litter with particular emphasis on small ruminants in tropical conditions. Small Rumin. Res. 54:1–11.

Morris, C. A., M. Wheeler, B. C. Hosking, T. G. Watson, A. P. Hurford, B. J. Foote, and J. F. Foote. 1997. Genetic parameters for milk yield and faecal nematode egg count in Saanen does. N. Z. J. Agric. Res. 40:523–528.

National Research Council. 2006. Nutrient Requirements of Goats. National Academy Press, Washington DC.

Notter, D., B. Vanimisetti, and L. Kuehn. 2005. The 2005 American Boer Goat National Evaluation. BGIN Notebook. No. 3.

Schoeman, S. J., J. F. Els, and M. M. van Niekerk. 1997. Variance components of early growth traits in the Boer goat. Small Rumin. Res. 26:15–20.

Schoenian, S. 2003. Integrated Parasite Management (IPM) in Small Ruminants. http://WWTw.sheepandgoat.com/articles/IPM.html. (Accessed 28 January 2015).

Supakorn, C. and W. Pralomkarn. 2012. Genetic parameter estimates for weaning weight and Kleiber ratio in goats. Songklanakarin J. Sci. Technol. 34:165–172.

Terill, T. R. Kaplan, M. Larsen, O. Samples, J. Miller, and S. Gelaye S. 2001. Anthelmintic resistance on goat farms in Georgia: efficacy of anthelmintics against gastrointestinal nematodes in two selected goat herds. Vet Parasitol. 97:261–268.

Vagenas, D., F. Jackson, A. J. F. Russel, M. Merchant, I. A. Wright, and S. C. Bishop. 2002. Genetic control of resistance to gastro-intestinal parasites in crossbred cashmere-producing goats: Responses to selection, genetic parameters, and relationships with production traits. Anim Sci. 74:199–208.

Van Wyk, J. A. and G. F. Bath. 2002. The system for managing *Haemonchosis* in sheep and goats by clinically identifying individual animals for treatment. Vet. Res. 33:509–529.

Whitlock, H. V. 1948. Some modifications of the McMaster helminth egg-counting technique apparatus. J. Counc. Sci. Ind. Res. 21:177–180.

Wildeus, S. and A. M. Zajac. 2005. Gastrointestinal parasitism in hair sheep and meat goat breeds grazing naturally infected pasture. Sheep Goat Res. J. 20:42–46.

Willham, R. L. 1972. The role of maternal effects in animal breeding: III. Biometrical aspects of maternal effects in animals. J. Anim. Sci. 35:1288-1293.

Windom, R. G. 1996. Genetic control of resistance to helminths in sheep. Vet. Immunol. Immunopathol. 45:245–254.

Zhang, C. Y., L. G .Yang, and Z. Shen. 2008. Variance components and genetic parameters for weight and size at birth in the Boer goat. Livest. Sci. 115:73–79.

Zhang, C.Y., Y. Zhang, D. Q. Xu, X. Li, J. Su, and L. G. Yang. 2009. Genetic and phenotypic parameter estimates for growth traits in Boer goat. Livest. Sci. 124:66–71.

