SELECTION FOR PARASITE RESISTANCE IN KIKO × BOER GOATS

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Master of Science

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by

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SELECTION FOR PARASITE RESISTANCE
IN KIKO X BOER GOATS

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a candidate for the degree of master of science,

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“I can do all things through Christ who strengthens me” (Philippians 4:13)

“What then shall we say in response to these things? If God is for us, who can be against us?” (Romans 8:31)

“I have set the Lord always before me. Because he is at my right hand, I will not be shaken” (Psalms 16:8)

“Trust in the Lord with all your heart and lean not on your own understanding.” (Proverbs 3:5)

Prayer and work conquer all!

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CHAPTER 1

INTRODUCTION

Goat numbers are on the rise in the United States (Kaplan, 2004). This is partly due to increasing numbers of ethnic groups and immigrants who readily consume goat meat (Solaiman, 2007). Yet, producers are unable to meet current demand (Solaiman, 2007). Perhaps the largest challenge for goat producers and the most important economic and health constraint affecting productivity is gastrointestinal nematode infection (Jackson et al., 2012; Preston et al., 2014). Parasitism causes significant production losses and animal mortality (Aboelhadid et al., 2013) and goats are more susceptible to internal parasites than any other farmed ruminant (Waller, 1997; Vagenas et al., 2002; Schoenian, 2003; Jackson et al., 2012).

Extensive use of anthelmintic chemicals in order to control gastrointestinal nematode infections has inevitably led to the emergence of parasite populations that are resistant (Jackson and Coop, 2000). To date, anthelmintic resistance has been recorded in many of the common parasites of goats and sheep (Jackson, 1993; Jackson et al., 2012). Goats have had a long established link with anthelmintic resistance, and many of the earliest cases of multiple resistances were reported in goats (Watson and Hosking, 1990;

Jackson et al., 1992; Varady et al., 1993; Chartier et al., 1998; Jackson and Coop, 2000; Terrill et al., 2001; Paraud et al., 2009).

Even though numerous nematodes exist in goat populations, *Haemonchus contortus* is of most concern to producers (Jackson et al., 2012). *H. contortus* is one of the most prevalent and pathogenic parasites infesting the abomasum of ruminants irrespective of age, gender, and breed (Kuchai et al., 2012). In Missouri, as well as much of United States, goats are naturally exposed to favorable environmental conditions that accommodate the development as well as survival of parasites. Furthermore, *H. contortus* has the ability to lay dormant in the abomasum of its host during the winter season (Hepworth et al., 2006).

The escalation of anthelmintic resistance in small ruminant husbandry and the increased demand for chemical-free meat and milk products has led to alternative approaches to sustainably manage gastrointestinal nematode infections. Among them is utilization of the host animal's natural or acquired immunity in a selection program to increase the level of parasite resistance in a herd. Through superior genetics, some animals are much more resistant or resilient to parasite infections and can survive parasite levels without showing any symptoms, while another animal may be killed by the same level of infestation (Hepworth et al., 2006). Some investigators suggest that genetic variation exists within species (Rohrer et al., 1991; Patterson et al., 1996; Mandonnet et al., 2001), and there is promising evidence that parasite resistance is under genetic control, but published studies are limited (Wildeus and Zajac, 2005; Gunia et al., 2011).

The overall aim of this research was to investigate the genetic variability in resistance to gastrointestinal nematode parasites in divergently selected Kiko (K) x Boer (B) goat progeny. Boer are the most popular meat goat breed in the United States (APHIS-USDA, 2005) and are an efficient breed indigenous to South Africa (Casey and Van Niekerk, 1988), whereas, Kikos are a composite breed from New Zealand that are primarily known for their hardiness and ability to resist parasites. The specific objectives of this study were to estimate genetic parameters for parasite resistance, reproduction, growth, and carcass traits in a closed line of Kiko x Boer goats divergently selected for parasite resistance.

CHAPTER 2

LITERATURE REVIEW

Introduction

The objective of this review is to summarize the scientific knowledge regarding parasite resistance and its impact on the meat goat industry in North America. This will be achieved by first discussing parasite resistance and describing *Haemonchus contortus* as the main parasite of concern. Then, the lifecycle of *H. contortus* and anthelmintic resistance will be highlighted. Indicator traits for parasite resistance such as fecal egg count (FEC), packed cell volume (PCV), and the FAMACHA© eye color chart system will be discussed. Additionally, heritabilities of reproductive traits, growth traits, carcass traits, and parasitological measurements will be reviewed. Genetic correlations among the various parasitological measurements will also be included. Finally, characteristics and differences between Boer and Kiko breeds for parasite resistance will be discussed.

Parasite resistance

Parasite resistance has been defined by Bishop and Morris (2007) as both the hosts' ability to modulate the pathogen or parasitic lifecycle and also the hosts' resistance to consequences of infection from the disease (parasites). Similarly, Gray (1995) defines parasite resistance as ability of a host to reduce the number of parasites that establish, reproduce, or survive. Parasite resistance is a term that is often confounded with parasite resilience. Resilience describes the ability of animals to maintain performance in the face of a disease challenge, that is, to resist anemia irrespective of fecal egg count of blood-sucking parasites (Bishop and Morris, 2007; Burke and Miller, 2008; Saddiqi et al., 2012). Resistance is the ability to control parasite infections by suppressing their establishment, controlling their number, and regulating their life cycle (Gunia et al., 2013). In short, resistance is the ability to suppress the establishment or the growth of worm infection while resilience is the capability of an animal to maintain acceptable health/performance under a worm challenge, mainly blood-sucking parasites like *H. contortus* (Albers et al., 1987).

Haemonchus contortus

H. contortus is found throughout the world and is one of the most prevalent and pathogenic parasites infesting the stomach of ruminants, irrespective of age, gender, and breed of the host, leading to tremendous loss in variety of ways (Kuchai et al., 2012). *H. contortus* is also known as the barber pole worm and a variety of other names such as stomach worm and wire worm. *H. contortus* is a major clinical problem for goats

(Machen et al., 1998; Chaudary et al., 2007; Yacob et al., 2009). Common signs of *H. contortus* infestation include anemia, low packed cell volume (PCV), diarrhea, dehydration, and peripheral internal fluid accumulation (Miller et al., 1998; Yacob et al., 2009). Also, infested goats can display signs of lower growth rates, markedly reduced reproductive performance, and higher rates of illness and death(Leite-Browning, 2006). Consequently, *H. contortus* may account for greatly reduced profits in a goat operation (Miller et al., 1998).

***Haemonchus contortus* life cycle**

Goats are born without *H. contortus*; however, they become infested with the worm when they start grazing (Leite-Browning, 2006). As shown in Figure 1 (Page 9), the cycle begins when the larvae in the infective L3 stage of development are ingested while kids are grazing and travel to the abomasum of the host (Leite-Browning, 2006). Once in the abomasum larvae can follow one of two different paths. The L3 larvae can burrow into the internal layer of the goat's abomasum where they develop to a L4, or pre–adult larvae. Alternatively, L3 larvae can go into hypobiosis (Machen et al., 1998; Vanimisetti, 2003).

Hypobiosis is a period of dormancy that occurs when the environment is not suitable to the lifecycle of these parasites (Whittier et al., 1988;Miller, 2004; Hepworth et al., 2006). During this time, L4 stage larvae hibernate in glands in the abomasum without developing further or causing any problems to the host (Leite-Browning, 2006). They

remain metabolically inactive in the host until there are favorable conditions for them to resume development and then begin to lay eggs (Miller, 2004).

When an L3 stage larva enters the abomasum, provided that the environmental conditions are favorable, they will molt into L4 and then into L5, the adult form (Hepworth et al., 2006). Adult worms, found in the abomasum where they feed on blood, are normally anywhere from 10 to 30 mm in length (Machen et al., 1998). Adult females are very prolific and are able to deposit from 5,000 to 10,000 eggs per d, which are passed through goat feces to pasture (Machen et al., 1998; Miller, 2004; Hepworth et al., 2006; Leite-Browning, 2006). This is one of the main reasons why *H. contortus* is so difficult to control and so dangerous to sheep and goats. Eggs hatch either in soil or water. When the soil is warm and moist, eggs in the fecal pellet will hatch into L1 larvae (first stage juveniles). The L1 larvae then develop and move through stages L2 and L3 (Vanimisetti, 2003). Once the larvae enter the L3 stage, the infective stage, they emerge from the fecal pellet and climb up onto blades of plants where they wait to be ingested by a grazing animal, thus completing the lifecycle (Leite-Browning, 2006). Large numbers of juvenile parasite worms (L3) may accumulate on heavily grazed pastures (Machen et al., 1998).

Hepworth et al. (2006) reported that after a goat has ingested L3 larvae, the worm will burrow into the mucosal (internal layer) of the stomach, nourishing on red blood cells of goats, which can be life-threatening. The life cycle (egg to mature adult) is 17 to 21 d (Hepworth et al., 2006). Warm, moist soil surface conditions favor propagation, while hot, dry, or extremely cold conditions are detrimental to larvae survival. The L3 larvae can survive on pasture for up to 90 d in the summer and up to 180 d in the fall or

winter. *H. contortus* larvae thrive in temperatures ranging from 21° to 27° C, where there is an average of approximately 5 cm of rainfall per mo (Machen et al., 1998). Extremely hot or dry environments will cause egg laying to stop, but larvae can survive temperatures below 0° C (Machen et al., 1998).

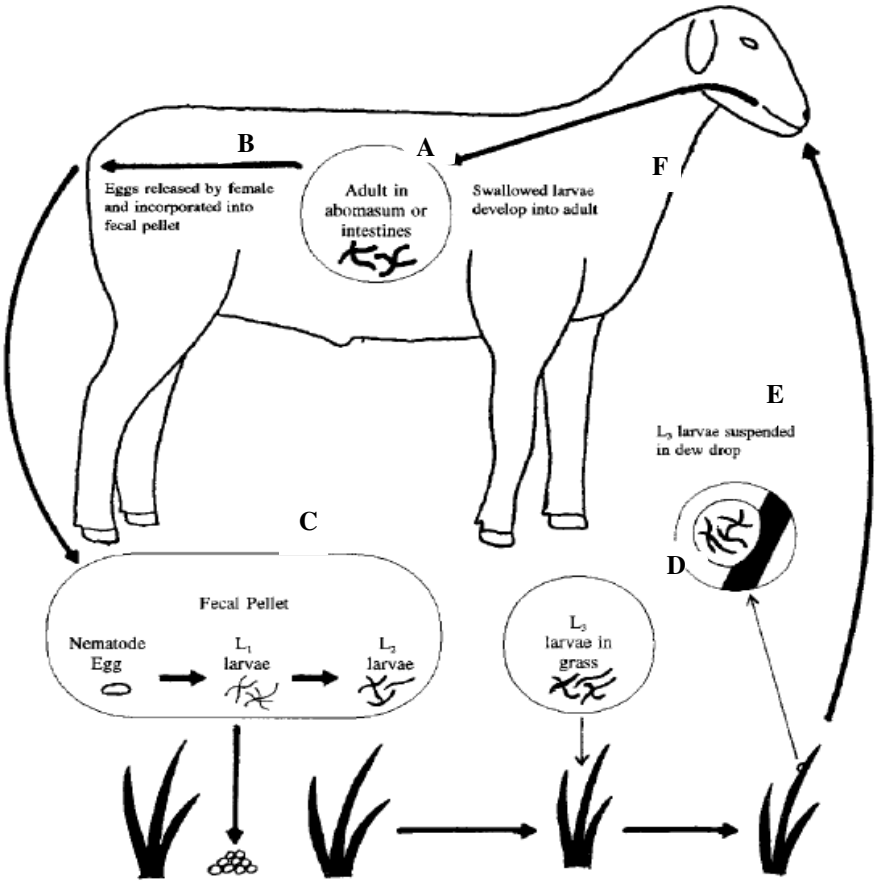

Figure 1.Life cycle of *Haemonchus contortus*.

A - Adult worms in abomasum or intestines.

B - Eggs released by female worm and incorporated into fecal pellet.

C - Egg to L1 larvae to L2 larvae.

D - L3 larvae in grass.

E - L3 larvae suspended in dew drop.

F - Swallowed larvae develop into adults (Machen et al., 1998).

Anthelmintic resistance

Anthelmintics are drugs that either kill egg laying adults or kill larvae before they become adults and become capable of laying eggs (Hepworth et al., 2006). However, prevention and control of parasites that infect sheep and goats are becoming increasingly difficult due to overuse, and in some instances, improper use of the available anthelmintic dewormers, which results in increasing resistance by parasites to common anthelmintics (Shalaby, 2013). For one, there are just a few anthelmintics that are approved for use in small ruminants by the FDA (Hepworth et al., 2006). Secondly, parasites have built up resistance to many of the available anthelmintics (Uhlinger et al., 1988; Craig and Miller, 1990; Uhlinger et al., 1992; Miller and Barras, 1994; Miller and Craig, 1996;Zajac and Gipson, 2000; Kaplan, 2004; Hepworth et al., 2006; Shalaby, 2013). Anthelmintic resistance occurs when a drug is being improperly or overly used and parasites develop a tolerance to the drug, making it no longer effective in killing them. Resistance makes it very difficult to effectively control *H. contortus* because it lowers the number of options available to treat the parasite, especially since resistance to one drug often means that a parasite will be resistant to all drugs in that compound class (Hepworth et al., 2006; Shalaby, 2013).

Resistance is one of the main reasons why parasites, *H. contortus* in particular, are a large problem for small ruminant producers (Hepworth et al., 2006). Since anthelmintic resistance is so prevalent, some producers deworm only some of the animals in the herd, focusing mainly on the animals that are more heavily burdened by parasites. By only deworming a small portion of the herd, there is a population of worms that are left untreated. This slows the rate of resistance since a proportion of the worms in the

population are still susceptible to anthelmintics. By maintaining this sensitive worm population, the anthelmintic resistant genes are diluted among the population, and resistance is slowed down (Kaplan, 2004; Hepworth et al., 2006). Another option is selection for parasite resistance. Various parasitological measurements can be utilized to select the animals that need to be treated or to select resistant animals for breeding stock.

Parasitological measurements

Internal parasite level in goats cannot be measured directly; rather, indicator traits such as weight gain (loss), fecal egg counts (FEC), packed cell volume (PCV), and level of FAMACHA©, which can be readily quantified, can be used as selection traits in a breeding program. Thus, effective management of internal parasites cannot often be accomplished by using only one management factor; rather a combination of factors can produce the most effective defense against internal parasites. With the recent increase of anthelmintic resistance in *H. contortus*, using results from FEC, PCV, and the FAMACHA© eye color chart system to evaluate the parasite load of an animal, allows producers to be able to use a selective treatment approach or toselect animals that are resistant.

Fecal egg count

Parasite infestation can be indicated by fecal egg count (FEC). Fecal egg count is an estimate of the number of adult worms present in the goat's stomach. Fecal egg count

is an indirect measure of a host's worm burden and aids in evaluating the number of parasite eggs excreted per gram of feces (Saddiqi et al., 2012). Specifically for *H. contortus*, FEC also serves as an indicator of seasonal changes in level of infection (Miller, 2004). Trends in FECs over time can be seen, thus reflecting the relative direction of infection (Saddiqi et al., 2012). Beh and Maddox (1996), citing other studies, acknowledged that FEC are simple, repeatable, and represent the standard method for assessing the level of parasite burden in an animal. Among phenotypic parameters, FEC is the most reliable, practical, and frequently used indicator to assess the host resistance/tolerance potential against gastrointestinal nematodes (Gray, 1991; Woolaston, 1992; Kemper et al., 2009; Saddiqi et al., 2012).

A common method for determining FECs in goats is the Modified McMaster technique (Mines, 1977; Shulaw, 2012). Even though this procedure can be done in various ways, the basic method entails using a weighed sample of fecal material. After weighing the fecal sample, it is diluted using a solution that causes eggs to float, and then the mixture is placed in a specialized slide made for counting eggs (Cringoli et al., 2004). Counting of *H. contortus* parasite eggs is done under a microscope (Figure 2), which gives an estimate of the number of eggs in a specific amount of feces from an animal, which is expressed as eggs per gram (epg) of feces (Machen et al., 1998; Shulaw, 2012).

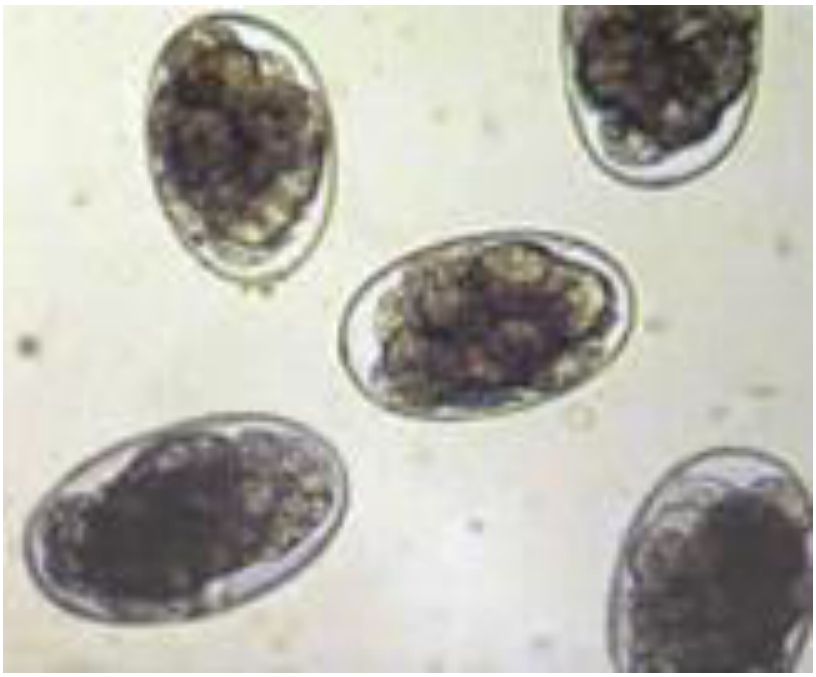

Figure 2.*Haemonchus contortus* parasite eggs found in sheep and goat feces as seen under a microscope (Hepworth et al., 2006).

Fecal egg counts of goats on pasture range from nearly zero up to several thousand in some individuals (Machen et al., 1998). Fecal egg counts above a threshold value of 2,000 epg of feces are generally accepted as indicative of a heavily parasitized animal (Fernandez, 2012). Eggs shed from goats with high FECs contaminate the environment and are ingested by the rest of the herd, increasing the total parasite population (Hepworth et al., 2006). However, FECs alone should not be used as a stand-alone diagnostic tool to determine the severity of parasite infection (Hepworth et al., 2006; Shulaw, 2012; Saddiqi et al., 2012).

Packed cell volume

Anemia, which can be determined by packed cell volume (PCV), or hematocrit, is another important clinical sign of parasite infection (Saddiqi et al., 2012). Packed cell volume is the percentage of blood that is red blood cells and is usually above 30% in goats (Miller, 2004). When PCV drops below 20%, symptoms of anemia usually start to appear (Miller, 2004). *H. contortus* can consume up to 10% of an animal's total blood volume in a day (Hepworth et al., 2006). Packed cell volume is determined by centrifuging blood in a capillary tube (Figure 3), which packs the cells and facilitates measuring its percentage (Goat Diagnostic Methods, 2014).

Gauly and Erhardt (2001) and Saddiqi et al. (2012) both agreed that hematocrit is a useful indicator of blood-sucking parasites, such as *H. contortus*, which is the dominant species. *H. contortus* can affect an animal's ability to maintain erythropoiesis, which is the ability to produce red blood cells. Therefore, *H. contortus* can lead to substantial acute blood loss and death. Low values for PCV are thus commonly associated with high FEC due to adult parasites' sucking of copious amounts of blood from the abomasum (Baker et al., 2003; Saddiqi et al., 2010a; Saddiqi et al., 2010b; Saddiqi et al., 2012). However, similarly to FECs, PCV values should be used as a support for other response criteria, and not necessarily as a stand-alone diagnostic tool.

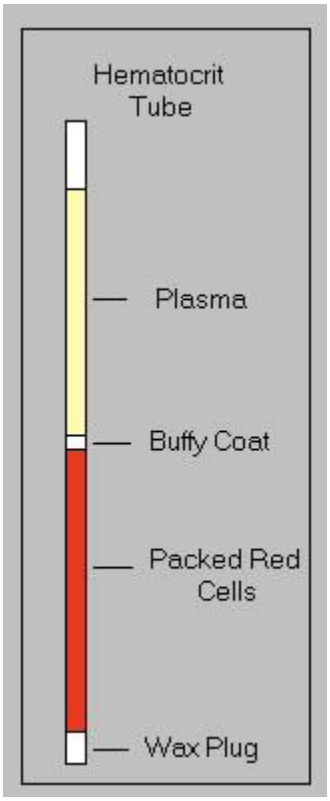

Figure 3.How packed cell volume appears inside a centrifuged blood tube (Hematocrit, 2013).

The FAMACHA© eye color chart system

Level of anemia can also be evaluated using the FAMACHA© eye color chart system (Figure 4). Anemia is most easily identified in small ruminants by the color of mucous membranes, particularly those in the lower eyelid, using the FAMACHA© eye color chart system. The FAMACHA© eye color chart system was originally developed in South Africa to help producers monitor and evaluate the level of anemia without having to rely on laboratory testing (van Wyk and Bath, 2002).

In this method, level of anemia can be easily evaluated by observing color of mucous membranes in areas with many capillaries that are close to the surface. For that reason, ocular mucous membranes (lower eyelid) of goats are examined and compared to a laminated color chart bearing the picture of sheep conjunctiva (Kaplan et al., 2004). The FAMACHA© eye color chart shows pictures of eyes at five different levels of anemia scaled from 1 to 5 as follows:

1 - Red, non-anemic;

2 - Red-pink, non-anemic;

3 - Pink, mild-anemic;

4 - Pink-white, anemic;

5 - White, severely anemic (Hepworth et al., 2006).

A normal animal will have healthy, red mucous membranes indicating no anemia is present and is therefore presumed to be free of dangerous levels of parasites, while an animal heavily burdened with *H. contortus* will exhibit light pink or white membranes

(Hepworth et al., 2006). Since anemia is the primary pathological effect from infection with *H. contortus*, this system can be an effective tool for identifying those animals that require treatment. Effectiveness of the FAMACHA© eye color chart system in goats has been extensively tested and validated by various studies done in different countries, including South Africa (Malan et al., 2001; Vatta et al., 2002), the United States (Kaplan et al., 2004; Burke et al., 2007), Germany (Moors and Gauly, 2009), and Switzerland (Scheuerle et al., 2010).

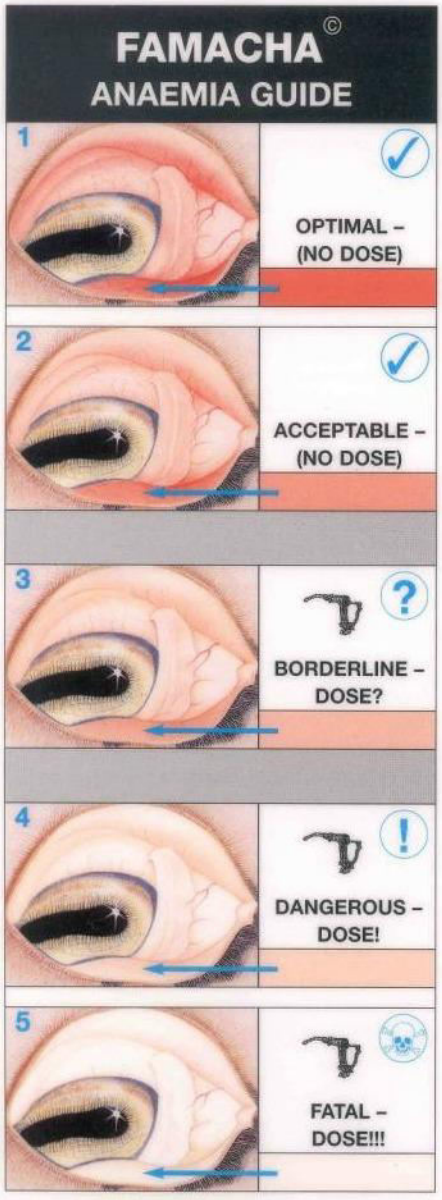

Figure 4.FAMACHA© eye color chart for visual screening of small ruminants with different levels of anemia due to *Haemonchus contortus.* Scores range from 1-5 with: 1 - red, non-anemic; 2 - red-pink, non-anemic; 3 - pink, mild-anemic; 4 - pink-white, anemic; 5 - white, severely anemic (Hepworth et al., 2006).

Heritabilities

The concept of heritability is of central importance in any modern breeding program. Heritability in its simplest term can be defined as an estimate of the degree to which differences between animals are repeated in their progeny (Jacquard, 1983). Knowledge of genetic parameters such as heritability and genetic correlations between traits are required to construct efficient selection indexes to make genetic improvement in traits via a selection program (Supakorn and Pralomkarn, 2012).

Heritabilities of reproductive traits

Due to various reasons, such as difficulty in accurately measuring reproductive performance at an early age and lack of large flocks, only a few genetic parameters for reproduction traits in goats have been reported (Bagnicka and Lukaszewicz, 2000; Menendez-Buxadera et al., 2004; Notter et al., 2005; Bagnicka et al., 2007; Zhang et al., 2009). However, heritability estimates of reproductive performance in ruminant livestock is generally assumed to be low (h^2 = 0.10; Casey and Webb, 2010)in species for which many estimates of heritability are available. In a study done by Zhang et al. (2009), direct heritability estimates for reproduction traits were low; with a heritability estimate of 0.12 for litter size at birth in Boer goats. Other reported estimates of heritability for litter size include:0.10 in Boer goats (Notter et al., (2005); 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 (Menendez-Buxadera et al., 2004) and 0.11 (Guniaet al., 2011) in Creole goats.

Heritabilities of growth traits

Portolano et al. (2002), Handford et al. (2006), and Zhang et al. (2009) suggested that body weights and growth rates pre-weaning are often considered as indicators of late growth and are of economic benefit in goats. However, there have been few heritability estimates reported for both early and late growth traits in goats. The mean direct heritability estimate in Boer goats for birth weight was 0.17 (Zhang et al., 2009). This was slightly lower than the previous birth weight heritability reported by Zhang et al. (2008) of 0.19, which had a smaller sample size and fitted an animal model ignoring parity of dam and interactions among the effect factors. A low estimate of heritability for birth weight (0.16) in Boer goats was also reported by Schoeman et al. (1997), who fitted a model ignoring parity of dam, birth season, and interaction effects. Notter et al. (2005) also reported heritability estimates of 0.15 for direct birth weight and 0.10 for maternal birth weight in Boer goats. Al-Shorepy et al. (2002) reported the heritability estimate for birth weight in Emirati goats to be 0.18.

Notter et al. (2005) reported heritability estimates of 0.10 for direct weaning weight and 0.06 for maternal weaning weight in Boer goats. Supakorn and Pralomkarn (2012), utilizing three different goat breeds (Boer, Thai Native, and Saanen) reported an average direct heritability of 0.26 to 0.36 for weaning weight at 150 to 155 d. Zhang et al. (2009), analyzing Boer goats, reported an estimate of direct genetic heritability for 90 d weaning weight of 0.22. In another study, also utilizing Boer goats, Schoeman et al. (1997) found the estimate of direct heritability for weaning weight to be 0.18 for herds that occupied two different locations in Africa. In Emirati goats weaned at 2 mo, Al-Shorepy et al. (2002) reported the heritability estimate for weaning weight to be 0.32.

Heritabilities of carcass traits

Compared to other livestock species, estimates of heritabilities for carcass traits in goat are limited. Meat production traits of goats have received relatively little scientific attention when compared to other ruminants. This may be due to the traditionally low economic significance of goats in developed countries (Warmington and Kirton, 1990). Despite the lack of scientific reports, heritabilities for carcass traits in goats would be presumed to be moderately to highly heritable, if equated to heritabilities reported for carcass traits in lambs. Ingham et al. (2007) reported estimates of 0.37 for hot carcass weight in crossbred lambs. Greeff et al. (2008) also reported a hot carcass weight heritability of 0.36 in Merino lambs. Mortimer et al. (2010) estimated heritability of hot carcass weight to be 0.35 in Australian sheep.

Only a few heritability estimates have been reported for shear force in lambs (Botkin et al., 1969; Karamichou et al., 2006; Cloete et al., 2008; Mortimer et al., 2010). Heritability of shear force was estimated to be 0.28 using records from the progeny of Rambouillet, Columbia and Corriedale sires (Botkin et al., 1969). This was lower than estimates of 0.39 found in Scottish Blackface lambs by Karamichou et al. (2006) and an estimate of 0.44 in South African terminal crossbred lambs reported by Cloete et al. (2008). In an Australian study utilizing Merino, Border Leicester x Merino, Terminal x Merino and Terminal x Border Leicester-Merino lambs, Mortimer et al. (2010) reportedmoderate to high heritabilities for meat quality measures for shear force (0.27 aged 1 d, 0.38 aged 5 d). Mortimer et al. (2014) reported the heritability for shear force of loin muscle in Merino and crossbred progeny of Merino to be moderate (0.27).

No reported heritability estimates for carcass traits in goats were discovered in the literature.

Heritabilities of parasitological parameters

As stated earlier, since parasite resistance cannot be measured directly, many studies have quantified within-breed heritabilities of FEC as the indicator of relative nematode level. Many more heritability estimates for parasite resistance have been reported for sheep than goats (Bishop and Morris, 2007). Several studies (Eady et al., 1996; Morris et al., 1997; Morris et al., 2000; Bishop et al., 2004; Gruner et al., 2004) reported that FEC is a moderately heritable trait in lambs, and one which responds to selection. Furthermore, Van Wyk and Bath (2002) reported the heritability estimate of FAMACHA© to be 0.55 in Merinos. Of the research that has been calculated on genetics of parasite resistance in goats, the bulk has been conducted in regions outside the United States.

Fecal egg count tends to be lowly heritable in kids and does (Woolaston et al., 1992; Morris et al., 1997; Mandonnet et al., 2001;Vagenas et al., 2002; Gunia et al., 2011). Nevertheless, Vagenas et al. (2002) showed that response to selection for decreased FEC can be achieved over a short time period. Vagenas et al. (2002) reported a mean FEC heritability of 0.32 in Scottish feral goats and crosses. Also, Mandonnet et al. (2001), in the French West Indies, estimated heritabilities for FEC of 0.20 at 82 d of age, 0.14 at 4 mo of age, and 0.33 at 10 mo of age in a population of Creole goats. Baker et al. (2001) reported heritability estimates of 0.18 and 0.13 for PCV and FEC,

respectively, taken at 4.5 and 8 mo of age in Galla and Small East African goats. Similarly,Gunia et al. (2011) reported heritability estimates of 0.13 and 0.18 for PCV and FEC, respectively in Creole goats.

In contrast, lower heritabilities for FEC were reported in a study conducted in Fiji (0.04 in young goats and 0.08 in adults; Woolaston et al., 1992), in New Zealand involving Saanen milk goats (FEC heritability of 0.05; Morris et al., 1997), in Australia with Angora goats (FEC heritability of 0.02 to 0.16; Bolormaa et al., 2009) and in India with Barbari goats (FEC heritability of 0.05 to 0.13 depending on the model used; Mandal and Sharma, 2008). Thus, selection for resistance and/or selection against susceptibility using a measurement such as FEC have been moderately successful.

Genetic correlations among parasite measurements

Kaplan et al. (2004) indicated that correlations between FEC and PCV, FEC and FAMACHA©eye scores, and PCV and FAMACHA©eye scores were all high and significant in a study including both sheep and goats. Scheuerle et al. (2010) and Kaplan et al. (2004) indicated that correlations between FEC and PCV and PCV and FAMACHA© eye scores were negative and significant, whileFEC and FAMACHA©eye scores were positive and significant in studies including both sheep and goats.Various other studies have verified the negative correlation of PCV and the FAMACHA© values (Kaplan et al., 2004; Burke et al., 2007; Riley and Van Wyk, 2009; Scheuerle et al., 2010). Also, it has been found in many studies that FEC is highly correlated with actual worm burden (McKenna, 1981; Eady, 1995; Stear et al., 1995).

Goat breeds utilized in the project

Boer

Boer goats are the most popular meat goat breed in the United States (USDA-APHIS, 2005). They are indigenous to South Africa where they were developed for meat production (large mature size and fast growth rate) from indigenous African and introduced European stock. Performance testing of Boer goats, which began in 1970, has had a large role in the development of the breed (Casey and Van Niekerk, 1988). Unequivocally, the Boer breed has made a large impact on the developing United States meat goat industry. Erasmus (2000) citing 'The Boer Goat, 1973', states that the attributes of the improved Boer may best be described by the following quotation: "Certainly one of the most hardy of small-stock breeds on earth, with a great ability of adaptation; it is therefore found in such a wide variety of climates and grazing conditions." This breed is capable of producing offspring with exceptional growth rates (Erasmus, 2000). Boer goats have a reputation for high fertility, averaging 98% of does bred under good management and nutrition (Campbell, 1984). Furthermore, the kids of Boer goat does are early breeders, reaching puberty at 6 mo of age (Casey and Van Niekerk, 1988).

Kiko

The Kiko breed was developed from selected New Zealand feral goat does bred to Nubian, Toggenberg, and Saanen bucks. Further crossbreeding, interbreeding, and selection pressure for survivability and growth rate was applied resulting in the Kiko

breed (Batten, 1987). Kikos were imported to the United States in the mid 90's. According to the American Kiko Goat Association®, primary characteristics of Kiko goats include: hardiness, the ability to resist parasites, and substantial weight gains (AKGA, 2015). The Kiko breed is also excellent for crossbreeding. Kids are born of average size but with considerable vigor and are fast growing. From birth to weaning, the Kiko displays a rate of growth at least equivalent of any other breed, but this is achieved without the management and feed inputs generally required for satisfactory meat production in other breeds (Solaiman et al., 2012).

Genetic differences for parasite resistance between breeds

As with any other species of animal, goats vary in their degree of susceptibility to *H.contortus* and other parasites. Some animals, by means of their genotypes, are much more resistant or resilient to parasitic infections and can survive parasite levels without showing any symptoms, while another animal may be killed by that same level of infestation (Hepworth et al., 2006).

Genetic differences in regard to nematode parasite resistance between individual goats (Woolaston et al., 1992; Morris et al., 1997; Baker et al., 2001; Mandonnet et al., 2001; Vagenas et al., 2002; Mandal and Sharma, 2008; Bolormaa et al., 2009;Gunia et al., 2011),and between different breeds including Galla and Small East African breeds in Kenya (Baker et al., 2001; Baker et al., 1998), Boer, Spanish, and Kiko breeds in Tennessee (Browning and Leite-Browning, 2011), Jamunapari and Barbari breeds in Mathura (Chauhan et al., 2003), Caninde, Bhuj, and Anglo-Nubian breeds in Brazil

(Costa et al., 2000), West African Dwarf and Red Sokoto breeds in Nigeria (Onyenwe et al., 2005), Thai Native and Anglo-Nubian breeds in Thailand (Pralomkarn et al., 1997), and Myotonic, Nubian, Pygmy, and Spanish breeds in Virginia (Wildeus and Zajac, 2005) have been observed in various studies. The strongest evidence for breed differences in goats comes from studies involving the Small East African breed, which generally emerges as being resistant when compared with other breeds (Bishop and Morris, 2007).

Evidence of differences between breeds of goats for parasite resistance, including Boer and Kiko breeds, are largely empirical in nature. Browning et al. (2006) did report greater mean FEC for Boer than Kiko does (521.7 versus 298.1) and indicated that a greater percentage of Boer does required unscheduled anthelmintic treatment (43.2 ± 4.0%) than Kiko does (9.8 ± 4.2%). Further studies by Pellerin and Browning (2012) showed that Boer does had low stayability and cumulative kid production rates compared with Kiko does.

Browning et al. (2014), in a crossbreeding study utilizing Boer, Kiko, and Spanish straight-bred does exposed to Boer, Kiko, and Spanish bucks, in a three breed diallel, assessed doe-kid performance on southeastern United States pastures. Results from this study showed that Kiko-influenced does were heavier than Spanish-influenced does. This corresponded to the heavier weights of straight-bred Kiko does compared with Spanish does reported earlier by Browning et al. (2011) and the significantly higher level of weaning weight heterosis between Boer and Kiko than for the Boer-Spanish cross (Browning and Leite-Browning, 2011). The higher values for litter weight, multi-

kid litters, and doe efficiency indicate that the Kiko influence is positive for reproductive output compared to the Spanish influence (Browning et al., 2014).

Conclusion

H. contortus is a major clinical issue for goats. With the life cycle of *H. contortus* being so short (17 to 21 d), paired with extreme prolificacy, it is extremely hard to control this parasite. Despite availability of anthelmintic dewormers, prevention of this parasite has become increasingly difficult. Both overuse and improper use of the available anthelmintic dewormers has led to increasing resistance by parasites. Indicator traits such as FEC, PCV, and FAMACHA© have proven useful in monitoring parasite levels in goats and are important criteria for a selection program based on parasite resistance.

In any breeding program the concept of heritability is of central importance. Heritability estimates of reproductive and growth traits in goats were found to be low to moderate in this review. No reports of heritabilities for carcass traits in goats were found in the literature. While many more heritability estimates for parasite resistance have been reported for sheep than goats, results show that parasite measurements are mostly lowly heritable in goats also. Reports for correlations between FEC and PCV, FEC and FAMACHA© eye scores, and PCV andFAMACHA© eye scores are all highly significant in goats.

The two goat breeds highlighted in this review include Boer and Kiko. Boer goats are the most popular meat goat breed in the United States and have made a large impact on the developing United States meat goat industry. The Kiko breed is excellent

for crossbreeding, is known for its hardiness, and ability to resist parasites as confirmed in the literature. Even though gastrointestinal parasitism is a primary impediment to goat well-being and productivity, opportunities may exist to improve goat performance under internal parasite challenges through better genetic management.

CHAPTER 3

GENETIC EVALUATION OF PARASITE RESISTANCE, REPRODUCTION, GROWTH, AND CARCASS TRAITS IN KIKO x BOER GOATS DIVERGENTLY SELECTED FOR PARASITE RESISTANCE

Abstract

Goat production has increased in the United States over the last three decades. However, the prevalence of gastrointestinal nematodes is a major challenge for goat producers as it is a leading cause of health issues and death loss. One feasible approach to combatting internal parasites is to select naturally immune goats. Therefore, the objectives of this study were to estimate genetic parameters for parasite resistance, reproduction, growth, and carcass traits in a closed line of Kiko x Boer goats divergently selected for parasite resistance. Beginning in December, 2011, 146 mixed-age Boer and high percentage Boer does (B) 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. All available parasite-related data collected were used to calculate Expected Progeny Differences (EPD) to rank and sort does into each corresponding line. Twelve unrelated Kiko (K) bucks were purchased on the basis of

parasite resistance (six high and six low), as indicated by mean fecal egg count (FEC). 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 each year from 2011 to 2013 to produce F_1 K x B progeny. The F_1 doe progeny from K x B matings were selectedprior to the breeding season based on parasite resistance as determined by FEC EPD. Selected F_1 K x B HL and LL does were then backcrossed within line to K bucks to produce F_2 ¾ K x ¼ B progeny.To evaluate parasite load, FEC, packed cell volume (PCV), and FAMACHA© scores were measured monthly on all animals from weaning up until breeding. Genetic parameters for parasite resistance, reproduction, growth, and carcass traits were estimated using ASREML procedures. Heritability estimates for FEC, PCV, and FAMACHA© score were 0.13, 0.06, and 0.11, respectively. Correlations between FEC and FAMACHA© were large and positive (r = 0.46), while correlations between FEC and PCV and FAMACHA© and PCV were slight (r = 0.00 and r = -0.09, respectively). Adjustment for kid sex, type of birth (for birth weight) type of rearing (for weaning weight), and age of dam (for litter size, birth, and weaning weight) were made on performance traits to correct for non-genetic effects and resulted in heritability estimates of 0.23 for litter size, 0.18 for birth weight, and 0.17 for weaning weight.Positive genetic correlations (r = 0.24) werefound between direct birth weight and weaning weight. Heritability estimatesfor final live weight was 0.58, and for hot carcass weight was 0.14; both loin eye area and shear force estimates were estimated to be outside the parameter space(1.00) because of insufficient records. Results of this study indicate that parasite resistance may be lowly heritable, regardless of parasite indicator traits measured, suggesting that selection progress would be possible, yet slow.

It appears that anthelmintic resistance issues in goats may be abated through genetic selection based on parasite resistance.

Introduction

In recent years goats have become increasingly popular with small landowners, in part because goats fit particularly well into forage-based production systems, especially in the central part of the country, including Missouri. The United States currently has approximately 2.3 million meat goats (USDA-NASS, 2014). Missouri ranks 4th in the nation with 84,200 head (USDA-NASS, 2014). This increased popularity can be attributed to goats' ability to efficiently and profitably convert low-value feedstuffs into meat, milk, and fiber products. Furthermore, goats can be useful for biological management practices by controlling noxious weeds and brush and minimizing fire hazards through fuel load reduction.

According to recent census statistics, the population of potential goat-consuming ethnicities (Asians, Hispanics, and Caribbean natives) is continuously increasing (U.S. Census Bureau, 2010). Moreover, demand for goat meat has consistently overwhelmed domestic supply in recent years (Solaiman, 2007). Overall, United States total goat meat imports during 2013 equaled 15,921 MT, a little more than 2012. During the final quarter of 2013 alone, United States goat meat imports equaled 3,704 MT. Australia was the leading supplier of goat meat to the United States with 97.4 percent of total imports(USDA-NASS, 2014).

Therefore, the future prospects of the goat industry appear bright. However, producers are unable to meet current demand partly because goats are more susceptible to internal parasites than any other types of livestock (Vagenas et al., 2002; Schoenian, 2003). In much of the United States, including Missouri and surrounding areas, goats are

managed under conditions which naturally expose them to gastrointestinal parasites (Vagenas et al., 2002). Parasite infections have a large impact on animal health and productivity. In severe cases, animal death may result. 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* (Barber pole worm), which is from the round worm family and lives in the stomach of these animals (Hendrix and Robinson, 2014). *H. contortus* is especially prevalent in warm and humid environments. Traditionally, *H. contortus* and other parasites have been chiefly controlled through commercial anthelmintic treatments. However, there has been increasing concern about the development of anthelmintic resistance in parasite populations (Jackson and Coop, 2000). In parallel, the demand for chemical-free milk and meat by consumers has led researchers to explore alternatives to commercial anthelmintics (Saddiqi et al., 2012). Other strategies for controlling parasites include multispecies grazing, rotational grazing, herbal remedies, mineral programs, and tannins, but even if effective, these alternatives require high management efforts that are not always conducive to low-input production operations.

One sustainable approach to the gastrointestinal parasite problem in goats is to utilize the host animal's natural or acquired immunity in a selection program to increase the level of parasite resistance in a herd. Saddiqi et al. (2012) suggested that to overcome the anthelmintic resistance dilemma and to market chemical-free high-value products, evaluation or breeding of genetically resistant/resilient livestock would be a feasible and practical strategy. The use of genetics to help combat infectious disease is not a novel concept; natural selection has produced resistance for millennia, and examples exist for

all domestic livestock species and for all types of infection (Bishop et al., 2002; Bishop and Stear, 2003). 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), and there is evidence that some North American breeds such as Florida Gulf Coast Native sheep and those originating from the Caribbean are more resistant to gastrointestinal parasite infection (Zajac, 1995).

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), because the bulk of the work has been conducted in foreign regions (Malan et al., 2001; Vatta et al., 2002; Moors and Gauly, 2009; Scheuerle et al., 2010; Gunia et al., 2011). Without research-based guidance on parasite resistance, much of the selection emphasis of goat producers in Missouri and surrounding states has been directed toward production traits, mainly growth-related measures, with little regard given to parasite resistance. Genetic selection of goats for improved parasite resistance would provide producers with an alternative for alleviating the negative effects of parasitism and reducing commercial anthelmintic dependence, and would be compatible with the modern trends towards sustainable agriculture.

Therefore, the objectives of this study were to estimate genetic parameters for parasite resistance, reproduction, growth, and carcass traits in a closed line of Kiko x Boer goats divergently selected for parasite resistance.

Material 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 (Project number 1410) at Lincoln University prior to initiation of the project. The experiment began with 146 mixed-age 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. Boer does were not previously selected for parasite resistance; however, all available parasite-related data collected was 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 (Version 4; VSN International, Hemel Hempstead, UK). Unrelated Kiko (K) bucks (n = 12) were purchased from individual producers on the basis of parasite resistance (six high and six low), as indicated by mean 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 x B progeny. Breeding between K bucks and B does continued in 2012 and 2013; however, death loss and disposal of non-pregnant B does from the experiment reduced the number of B does each year (Table 1).

Selected animals

Each year from 2012-2014, F_1 doe progeny from K x B matings were selected (described in detail later) prior to the breeding season based on parasite resistance as determined by FEC EPD. Selected F_1 K x B HL and LL does were then backcrossed within line to the original foundation HL and LL K bucks, respectively, to produce F_2 ¾ K x ¼ B progeny. Care was taken to avoid mating F_1 K x B does to related K bucks. Selected F_1 K x B HL and LL does remained in the herd for the duration of experiment; 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 x 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 environmental conditions associated with traits such as FEC (Falconer and Mackay, 1996). Fecal egg counts, packed cell volume, 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 gram of feces. Blood samples were collected via jugular venipuncture using evacuated sample collection tubes containing an anticoagulant and 18 gauge needles to estimate PCV. Packed cell volumes were subsequently

determined by the micro-hematocrit centrifuge method using a HemataSTAT® II Centrifuge (Separation Technology, Inc., Sanford, FL). FAMACHA© scores were recorded as 1 (red, non-anemic), 2 (red-pink, non-anemic), 3 (pink, mild-anemic), 4 (pink-white, anemic), or 5 (white, severely anemic; Hepworth et al., 2006). Selection was based on EPD calculated from the FEC data taken on a monthly basis. In the event that 2 of the following three criteria, a FEC of over 2,000 eggs per g, a FAMACHA© score of 4 or more, or PCV of 21 or less were recorded, that animal was immediately treated with commercial anthelmintic. In those cases, animals were selected on the basis of the number of times treated 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 does based on pregnancy status. For F_1 K x B does, selected individuals represented the most parasite resistant 80% from the HL and the least parasite resistant 80% from the LL.

Animal management

All does (except F_1 and F_2 doe kids after weaning) were managed as one group throughout the year, except at breeding. Breeding occurred once a year 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 tall-fescue and were supplemented with a corn-

soybean meal-oat based diet at NRC (2006) recommended levels. Does also had*ad libitum* access to water, trace minerals, and medium-quality hay if pasture was limited. Pregnancy status was determined via ultrasound by a trained technician within 45 d post breeding.

Does were wintered on pasture and/or mixed-grass hay, and supplementation 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 kidding pens with indoor and outdoor access and observed twice daily. After kidding, kids were ear-tagged, litter size (LS) was recorded, and kids were weighed within 24 h of birth. Starting at two wk of age, kids were allowed access to an 18% crude protein, corn-soybean meal-oat-based creep feed, fed until weaning at approximately 90 d of age. Typical health and vaccination protocols were followed at all times for does, bucks, and kids. At weaning, kids were sorted by sex, and F_1 and F_2 doe kids were moved to separate tall fescue-based paddocks with additional corn-soybean meal-oat based diet supplementation (NRC, 2006) provided. All F_2 buck kids were kept separate on tall fescue-based paddocks with additional corn-soybean meal-oat based diet supplementation (NRC, 2006) provided.

All F_1 buck kids were removed from the rest of the group at weaning and were confined in a small ruminant barn with full access to a self-fed high-concentrate feed, water, and mineral supplement. At approximately 27 kg, intact F_1 K × B buck kids (n = 28) were transported approximately 450 km from Lincoln University to the University of Arkansas abattoir. Goats were harvested after overnight lairage with hay and water. Final live weight (FLW) was measured prior to harvest. Immediately after harvest, hot

carcass weight (HCW) was measured and recorded. Loin eye area (LEA) was measured at 24 h postmortem by trained evaluators.

Following a 48 h chill period (1°C), the *longissimus muscle* (LM) was excised from each carcass, vacuum packaged, and stored frozen (-20°C) for shear force (SF) determination. Samples were removed from the freezer approximately 28 d after the LM was excised and thawed overnight at 1°C. Once samples were thawed, they were trimmed to only include the LM and placed on an electric countertop griddle set at 204°C. Samples were turned approximately every 2 min and cooked to an internal medium degree of doneness (71°C). Internal temperature was measured by a digital thermometer placed in the center of each sample. Following cooking, samples were cooled to room temperature (approximately 20°C), and 6 to 8 cores were removed parallel to the longitudinal orientation of the muscle fibers. Individual cores were sheared once using an Instron machine (Instron Corp., Canton, MA) with a Warner-Bratzler shear attachment. An average SF value was calculated and recorded for each sample.

Statistical analysis

A pedigree describing the ancestral lineage of the population was utilized in the genetic evaluation procedures. The pedigree file included 85 sires, 31 paternal grand sires, 34 maternal grand sires, 253 dams, 50 paternal grand dams and 105 maternal grand dams (Table 1). Heritabilities and genetic correlations were estimated for parasitological

measurements, reproductive, growth, and carcass traits using ASREML Version 4 (VSN International, Hemel Hempstead, UK).

Parasitological measurements

A trivariate repeated records animal model was used to 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 (50% K x 50% B or 75% K x 25% B). Contemporary group was defined for each observation as age, heterozygosity, and animals that had same anthelmintic treatment scheme. 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;

$$\text{var}\begin{pmatrix} a \\ p \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 & 0 \\ 0 & \sigma_c^2 & 0 \\ & & \end{pmatrix} = \begin{pmatrix} G & 0 \\ & \end{pmatrix} \quad G = \begin{pmatrix} A\sigma_a^2 & 0 \\ & \end{pmatrix}$$

$$e \quad 0 \quad 0 \quad I\sigma_e^2 \quad 0 \quad R \quad 0 \quad I\sigma_e^2$$

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 are:

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

Where now $\lambda = \sigma_e^2 / \sigma_a^2$ and $\gamma = \sigma_e^2 / \sigma_c^2$.

Reproductive traits

Litter size was recorded for 458 animals and was analyzed in a single trait analysis. The model for this analysis included additive direct animal and fixed effects of litter size, contemporary group, and heterozygosity. Two separate analyses were performed, first genetic parameters were calculated with unadjusted data and then data were adjusted to an adult doe basis using previously developed industry adjustments. Multiplicative factors used to adjust litter size for effects of age of dam are shown in Table 2. Adjustments were derived from data collected at Texas A&M-San Angelo, the

American Boer Goat Association, Virginia Tech University, and from adjustment factors developed from sheep by the National Sheep Improvement Program (Notter et al., 2005).

In matrix notation the single-trait mixed model equation for analyses of litter size 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 $\mathbf{E(y) = Xb}$ and

$$\text{var}\begin{pmatrix} a \\ e \end{pmatrix} = \begin{pmatrix} A\sigma_a^2 & 0 \\ 0 & I\sigma_e^2 \end{pmatrix}$$

where **A** is the numerator relationship matrix among animals, **I** is the appropriate identity matrix, and σ_a^2 and σ_e^2 are variances due to direct genetic and residual effects, respectively.

Growth traits

Birth weights (BW) on 458 and weaning weights (WW) on 232 animals were recorded. Birth weight and WW were used in a maternal effects model analysis. This was done since the mother has influence on the performance of her offspring over and above that of her additive genetic contribution. In this case, the maternal effects are strictly environmental for the offspring, but can have both genetic and environmental components. 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 BW and WW and to ensure that contemporary

groups were formed properly. If weaning age was not between 90 to 120 d, then the record was removed.

Similar to LS, adjustment factors for growth traits were derived from data collected at Texas A&M-San Angelo, the American Boer Goat Association, Virginia Tech University, and from adjustment factors developed from sheep by the National Sheep Improvement Program (Notter et al., 2005). The multiplicative factors used to adjust BW and WW for non-genetic effects as adapted from Notter et al. (2005) are presented in Table 3. Multiplicative factors were used to adjust BW and WW for nongenetic factors of kid sex, type of birth (for BW) or birth and rearing (for WW), and age of dam. In the data set, mean BW and WW weight prior to adjustment were 2.94 kg and 13.07 kg, respectively. After adjustments, mean adjusted BW (BW_{adj}) and adjusted WW (WW_{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:

$$WW_{adj} = (((AWW - BW)/WA) * 90) + BW,$$

where WW_{adj} is the adjusted 90 d WW, AWW is the actual WW, BW is the actual BW, and WA is the weaning age of the kid in d.

The maternal effects model used to analyze BW and WW 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:

$$\text{var}\begin{matrix} a \\ m \\ e \end{matrix} = \begin{matrix} A\sigma_a^2 & A\sigma_{am} & 0 \\ A\sigma_{am}^2 & A\sigma_m^2 & 0 \\ 0 & 0 & I\sigma_e^2 \end{matrix} = \begin{pmatrix} \mathrm{G} & 0 \\ 0 & \mathrm{R} \end{pmatrix}$$

$$\mathrm{G} = \begin{pmatrix} A\sigma_a^2 & A\sigma_{am} \\ A\sigma_{am}^2 & A\sigma_m^2 \end{pmatrix} = \mathrm{G}_0 \times \mathrm{A}$$

where $G_0$is a 2 by 2 matrix: $\begin{pmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am}^2 & \sigma_m^2 \end{pmatrix}$ and × **A** is a direct product.

Further σ_a^2 is a direct genetic variance, $\sigma_m^2$is the maternal genetic variance, $\sigma_{am}$is the covariance between direct and maternal genetic effects and $\sigma_e^2$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$\sigma_p^2 = \sigma_a^2 + \sigma_m^2 + \sigma_{am}^2 + \sigma_e^2$

The mixed model equations are:

$$\begin{pmatrix} \mathrm{X'\,X} & \mathrm{X'\,Z_1} & \mathrm{X'Z_2} \\ & & \end{pmatrix} \begin{pmatrix} \mathrm{b} \\ \end{pmatrix} \quad \begin{pmatrix} \mathrm{X'\,y} \\ \end{pmatrix}$$

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

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

Carcass traits

Carcass data were analyzed on 28 F_1 K x B intact male kids. Four carcass traits were evaluated in this study: FLW, HCW, LEA, and SF. Carcass traits were also analyzed with a multiple trait animal model and ASREML procedures to estimate genetic parameters. The fixed effects of contemporary group and covariates for the fractional contribution of heterozygosity, post-harvest treatment, and slaughter endpoint were included in the analyses. Pedigrees from single-record contemporary groups remained in the pedigree file; however, performance data did not contribute to the evaluation. Only factors that influenced the records significantly were fitted in animal models to estimate genetic parameters.

The multiple trait model used to analyze carcass traits (FLW, HCW, LEA, and SF) can be represented in its general form as follows:

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

however, with more traits the observation vector **y** is partitioned in parts for each trait. For each trait the mixed model looks like:

$$\mathbf{y_i = X_i b_i + Z_i u_i + e_i}.$$

where **y** represents the $\mathbf{n_i}$ observations for each trait where there are $\mathbf{p_i}$ fixed effects associated with trait **i** so that $\mathbf{X_i}$ is an $\mathbf{n_i}$ x $\mathbf{p_i}$ matrix and $\mathbf{b_i}$ is a $\mathbf{p_i}$ x 1 dimensional column vector. $\mathbf{X_i}$ and $\mathbf{Z_i}$ are incidence matrices for fixed effects and random effects for trait **i**, respectively.

The multiple trait model can be represented as follows:

$$\begin{pmatrix} y_1 \\ y_2 \end{pmatrix} = \begin{pmatrix} X_1 & 0 \\ 0 & X_2 \end{pmatrix} \begin{pmatrix} b_1 \\ b_2 \end{pmatrix} + \begin{pmatrix} Z_i & 0 \\ 0 & Z_2 \end{pmatrix} \begin{pmatrix} u_1 \\ u_2 \end{pmatrix} + \begin{pmatrix} e_1 \\ e_2 \end{pmatrix}$$

Results and Discussion

Parasitological measurements

In Table 4, mean, minimum, and maximum values for parasitological traits are shown along with standard deviations. 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 and 8 mo of age Galla and Small East African goats, 0.14 by Mandonnet et al. (2001) in 4 mo 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, it seems that FEC is lowly heritable in goats.

The heritability estimate for PVC was 0.06 (Table 5), which was 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© was 0.11 (Table 5), which was lower than the estimate of 0.55 for FAMACHA© in Merinos reported by Van Wyk and Bath (2002). No heritability estimates for FAMACHA© score in goats were found in the literature.

Performance traits

Reproductive traits

The mean, minimum, and maximum values of LS and adjusted LS (LS_{adj}) along with standard deviations are shown in Table 6. Heritability estimates for LS were first calculated without adjustment factors (Table 7), and then with adjustments (multiplicative factors used to adjust litter size for effects of age of dam; Table 8). The heritability estimate for LS_{adj} was higher (h^2= 0.23; Table 8) than the heritability estimate calculated before adjustments were made (h^2= 0.03; Table 7). Previous estimates of heritability for LS include: 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, mean, minimum, and maximum values for BW and WW along with standard deviations is shown in Table 6. Heritability estimates for growth traits were also calculated with and without adjustment factors (Tables 7 and 8). Multiplicative factors were used to adjust BW and WW for non-genetic factors of kid sex, type of birth (for BW) or birth and rearing (for WW), and age of dam. Prior to adjustment, heritability estimates for direct BW and maternal BW were 0.13 and 0.00, respectively (Table 7). After adjustments, heritability estimates for BW_{adj} and maternal BW_{adj} were 0.18 and 0.26, respectively (Table 8). Heritability estimates from this study were similar to heritability estimates of 0.15 for direct BW and 0.10 for maternal BW in Boer goats, in which the same adjustments factors were applied (Notter et al., 2005), 0.19 for direct BW (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 BW in Boer goats (Zhang et al., 2009), 0.16 for direct BW in Boer goats (Schoeman et al., 1997), and 0.18 for direct BW in Emirati goats (Al-Shorepy et al., 2002).

Before adjustments were made, heritability estimates for 90 d WW and maternal WW were 0.02 and 0.04, respectively (Table 7). However, after adjustments were made, heritability estimates for 90 d WW_{adj} and maternal WW_{adj} were 0.17 and 0.04, respectively (Table 8). Zhang et al. (2009), analyzing Boer goats, reported an estimate of

direct genetic heritability for 90 d WW of 0.22, which was similar to the estimate found in our study. In another study, also analyzing Boer goats, Schoeman et al. (1997) found similar results ($h^2 = 0.18$) for direct WW 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 for WW at 150 to 155 d. In another study done with Emirati goats weaned at 2 mo, Al-Shorepy et al. (2002) reported the heritability estimate for WW to be 0.32.

Carcass traits

In Table 9, number of records, mean, minimum, and maximum values for carcass traits are shown along with standard deviations. Heritability estimates for carcass traits are presented in Table 10. The heritability estimate for FLW was 0.58 and 0.14 for HCW. The heritability estimates for LEA and SF were estimated to be outside the parameter space (1.00) because of insufficient records. Compared to other livestock species, heritabilities for goat carcass traits reported in the literature are limited. Nonetheless, heritabilities for carcass traits in goats could be presumed to be moderately to highly heritable, if equated to heritabilities reported for carcass traits in lambs. Ingham et al. (2007) reported estimates of 0.37 for HCW in crossbred lambs, which was higher than the heritability estimate of 0.14 found in the present study, but similar to Greeff et al. (2008) who reported a HCW heritability of 0.36 in Merino lambs and Mortimer et al. (2010) who estimated the heritability of HCW to be 0.35 in Australian sheep. Mortimer et al. (2014) reported the heritability for SF of loin muscle in Merino and crossbred progeny of Merino to be moderate (0.27). The heritability of SF was estimated to be 0.28

using records from the progeny of Rambouillet, Columbia and Corriedale sires (Botkin et al., 1969). This was lower than estimates of 0.39 found in Scottish Blackface lambs by Karamichou et al. (2006) and an estimate of 0.44 in South African terminal crossbred lambs reported by Cloete et al. (2008). In an Australian study utilizing Merino, Border Leicester x Merino, Terminal x Merino and Terminal x Border Leicester-Merino lambs, Mortimer et al. (2010) reported moderate to high heritabilities for SF (0.27 aged 1 d, 0.38 aged 5 d).

Genetic correlations

Parasitological measurements

Estimated genetic correlations among the three parasitological parameters are presented in Table 11. Genetic correlations between FEC and PCV and between FAMACHA© scoresand 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, Scheuerle et al. (2010) and Kaplan et al. (2004) indicated that genetic correlations between FEC and PCV and PCV andFAMACHA© eye scores were negative and significant. Various other studies have verified the negative genetic correlation between PCV and FAMACHA© (Kaplan et al., 2004; Burke et al., 2007; Riley and Van Wyk, 2009; Scheuerle et al., 2010). However, similar to current finding genetic correlation between FEC and FAMACHA© eye scores were positive and significant in studies including both sheep and goats (Kaplan et al., 2004; Scheuerle et al., 2010).

Growth traits

Before adjustments were made, the genetic correlation between BW and WW was found to be -0.73. However, when the correlation was recalculated taking into account adjustment factors, the genetic correlation between direct BW and direct WW was positive (0.24). The American Boer Goat Association reported a genetic correlation of 0.50 between BW and WW (Notter et al., 2005). The positive genetic correlation between BW and WW suggests that selection for increased WW can lead to increased BW.

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 suggests that selection progress may be possible, but slow. Even though gastrointestinal parasitism impedes goat well-being and productivity, results from this study indicate that opportunities do exist to improve goat performance through genetic management.

Among the various performance traits evaluated, when heritability estimates were calculated for reproductive and growth traits before adjustments were made, numbers were lower than reported estimates. However, after adjustments were made, heritability estimates for both reproductive and growth traits were in the range of previously reported literature. No reports of heritabilities for carcass traits were found for goats in the

literature; however, heritability estimates obtained from this study showed that FLW was highly heritable and HCW was lowly heritable, but number of records was low. Heritability for LEA and SF were not estimable because of an insufficient number of records.

Even though *H. contortus* is a major clinical issue for goats due to its short lifecycle and extreme prolificacy, selection for parasite resistance may be a sustainable way to control this parasite and limit reliance on commercial anthelmintics.

Table 1. Summary statistics for pedigree file

Pedigree		Total no.		
	No. of paternal grand sires	31		
	No. of maternal grand sires	34		
	No. of paternal grand dams	50		
	No. of maternal grand dams	105		
	No. of sires	85		
	No. of dams	253		
			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
Progenyborn[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 parasite); LL= low line (low resistance to internal parasite).

[b]Progeny born: F_1 = Kiko x Boer; F2 = ¾ Kiko x ¼ Boer.

Table 2. Multiplicative factors used to adjust litter size for effects of age of dam[a]

Age of dam	Adjustment factors
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]This table was adopted from Notter et al. (2005).

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

		Adjustment factors[a]	
Effects	Level	Birth weight	Weaning weight
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 days) weaning weights are multiplied by the factor shown to correct for nongenetic 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).

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(Hepworth et al., 2006).

Table 5. Heritability estimates for FEC, PCV, and FAMACHA© score

Trait[a]	h_a^{2c}
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(Hepworth et al., 2006).
[c]h_a^2= direct heritability ± standard error.

Table 6. Summary statistics for litter size, birth weight, and weaning weight prior to adjustment and after adjustment

Trait[a]	No. of records	Mean	Minimum	Maximum	Standard deviation
LS	458	1.5	1.0	4.0	0.91
BW, kg	458	2.9	1.1	5.4	0.61
WW, kg	232	13.1	5.4	25.5	3.85
LS_{adj}[b]	458	1.6	1.0	4.2	1.00
BW_{adj}, kg[c]	458	3.3	1.5	5.4	0.63
$WW_{adj,}$ kg[c]	232	13.3	5.4	25.6	3.72

[a]Performance trait: LS = litter size; BW = birth weight; WW = weaning weight; LS_{adj} = adjusted litter size; BW_{adj} = adjusted birth weight; WW_{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 days) weaning weights were 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.

Table 7.Heritability estimates for performance traits before adjustment

Trait[a]	h_a^{2}[b]	h_m^{2}[c]
LS	0.03 ± 0.07	
BW	0.13 ± 0.11	0.00 ±0.00
WW	0.02 ± 0.01	0.04 ±0.07

[a]Performance trait: LS = litter size; BW = birth weight; WW = weaning weight.
[b]h_a^2 = direct heritability ± standard error.
[c]h_m^2 = maternal heritability ± standard error.

Table 8. Heritability estimates for performance traits after adjustment

Trait[a]	h_a^{2}[b]	h_m^{2}[c]
LS_{adj}[d]	0.23 ± 0.15	
BW_{adj}[e]	0.18 ± 0.52	0.26 ± 2.10
WW_{adj}[e]	0.17 ± 0.10	0.04 ± 0.02

[a]Performance trait: LS_{adj} = adjusted litter size; BW_{adj} = adjusted birth weight; WW_{adj} = adjusted weaning weights.
[b]h_a^2= direct heritability ± standard error.
[c]h_m^2 = maternal heritability ± standard error.
[d]Multiplicative factors were used to adjust litter size for effects of age of dam.
[e]Actual birth weights and age-adjusted (to 90 days) 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 9. Summary statistics for carcass traits of F_1 Kiko x Boer intact male kids

Trait[a]	No. of records	Mean	Minimum	Maximum	Standard deviation
FLW, kg	28	26.61	14.28	39.23	12.23
HCW, kg	28	9.10	3.17	15.42	4.99
LEA, cm^2	28	7.74	4.19	11.29	4.06
SF, kg	28	2.68	1.33	4.85	1.50

[a]Carcass traits: FLW = final live weight; HCW = hot carcass weight; LEA = loin eye area; SF = shear force.

Table 10. Heritability estimates for carcass traits of F_1 Kiko x Boer intact male kids

Trait[a]	h_a^{2}[b]
FLW	0.58 ± 0.56
HCW	0.14 ± 0.53
LEA[c]	1.00 ± 0.00
SF[c]	1.00 ± 0.00

[a]Carcass traits: FLW = final live weight; HCW = hot carcass weight; LEA = loin eye area; SF = shear force.
[b]h_a^2= direct heritability ± standard error.
[c]LEA and SF were estimated to be outside the parameter space because of insufficient records.

Table 11. Genetic correlations among FEC, PCV, and FAMACHA© score

Parasitological measurement[a]	Genetic correlation[c]
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©.
[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(Hepworth et al., 2006).
[c]Genetic correlation± standard error.

CHAPTER 4

GENERAL DISSCUSSION

Review of literature has identified a few possible challenges associated with the present study. It is of popular belief that, as the host population moves towards resistance, response for disease resistance will decrease because as a gene conferring disease resistance spreads through a herd, the incidence of infection declines, thus reducing the fitness advantage of carrying the resistance gene (Roy and Kirchner, 2000). Secondly, in theory with an environmental advantage of lowered pasture contamination (as a result of selected parasite resistant individuals), reduced parasite challenge for unselected (control) individuals or individuals selected for low resistance (in the case of divergent selection) could result. However, the aforementioned point is negated if both populations of goats are maintained in the same environment, i.e., together. Lastly, two different types of host response can potentially be targeted from selection decisions, one being resistance, defined as the ability of a host to suppress establishment and/or development of a parasitic infection, and the other being resilience or the ability of a host to maintain acceptable health and performance parameters while subjected to the parasitic challenge (Bisset et al., 2001). It is possible that animals that are very resilient to parasite

infection and that are genetically valuable in their ability to cope with a parasite load will not be selected because of lack of resistance to parasites.

A major issue concerning parasite resistance-related goat research is the limited number of studies, especially from the United States (Wildeus and Zajac, 2005) as the bulk of the work has been conducted in foreign regions (Malan et al., 2001; Vatta et al., 2002; Moors and Gauly, 2009; Scheuerle et al., 2010; Gunia et al., 2011). With vastly different climatic regions and/or production systems these other studies cannot always be extrapolated to domestic conditions. Consequentially, most of the selection emphasis of goat producers in Missouri and surrounding states has been directed toward production traits, mainly growth-related measures, with little regard given to parasite resistance. Therefore, it is imperative to conduct further studies centered on parasite resistance, especially in order for domestic production to match consumer demand.

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