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Effect of fecal egg count estimated breeding value on antibody production in Katahdin lambs

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**Effect of fecal egg count estimated breeding value on antibody production in
Katahdin lambs**

Kelsey Lynne Bentley

**Thesis submitted to the Davis College of Agriculture, Natural Resources and
Design at West Virginia University in partial fulfillment to the requirement
for the degree of**

Master of Science in Animal Physiology

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2021

Keywords: Antibody, *H. contortus*, Katahdin, Sheep

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ABSTRACT

Effect of fecal egg count estimated breeding value on antibody production in

Katahdin lambs

Kelsey L. Bentley

With current pressures to seek out genetic solutions to combat antimicrobial resistance, genetic resistance to the gastrointestinal nematode *Haemonchus contortus* may reduce need for prophylactic antibiotic use. The Katahdin breed has effectively utilized post-weaning fecal egg count estimated breeding value (PFEC EBV) to reduce parasitism within their flocks, but there still remains significant opportunity for selection within breed. In a previous study, Katahdin sheep sired by low PFEC sires had greater survivability to weaning than lambs sired by high PFEC rams and preweaning was caused by other diseases than parasitism. Those data lead to the hypothesis that selection for PFEC also selects for improved generalized immunity. Therefore, the aim of this study is to compare effects of a divergent mating scheme based upon PFEC on antibody production in purebred Katahdin lambs. All lambs were managed as one cohort with dams running alongside their lambs until approximately 105 days of age. During this time on pasture a natural infection was established, blood samples were taken weekly, and fecal samples were collected bi-weekly. Lamb PFEC corresponded to sire type validated the divergent mating scheme. Circulating IgG was measured using an ovine-specific enzyme-linked immunosorbent assay (ELISA). These data indicate that lambs selected for low PFEC have greater abundance of circulating IgG than high PFEC-EBV lambs (LoPFEC, 886.79 ug/mL and HiPFEC, 465.15 ug/mL $P < 0.001$). A sire by week comparison indicated that low PFEC lambs had greater magnitude of circulating IgG after booster vaccination, at week five ($P < 0.001$). Taken together these data indicate that PFEC values may be used as a predictor of immunological fitness outside the context of parasitic infections and has implications for use in selection towards individuals less prone to subclinical disease, therefore, limiting the need for antibiotic use.

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Chapter 1: Literature Review

Parasitism in Small Ruminants

A major source of economic loss in small ruminant production is the impact of gastrointestinal nematode (GIN) infection (Zajac, 2006). Animal loss due to GIN infection coupled with loss of anthelmintic efficacy has led producers to seek alternative control methods. In the eastern United States, a bloodsucking nematode *Haemonchus contortus* is the predominant GIN species (Zajac, 2006). *Haemonchus contortus* (*H. contortus*) infection is characterized by chronic wasting, severe anemia and hypoproteinemia (loss of 200–600 mL blood/day), decreased wool production, poor carcass quality, submandibular edema (bottle jaw), and even death of infected animals (Ehsan et al., 2020). In 2015, the USDA National Animal Health Monitoring Survey (NAHMS) reported that 9.2% of nonpredator death loss was attributed to internal parasitism (USDA: NAHMS 2015). It was estimated that the annual economic losses caused by *H. contortus* to the livestock industry accounted for \$30–300 million globally (Emery et al., 2016).

Haemonchus contortus is a member of the Trichostrongylidae family. Other nematodes included within this family are *Ostertagia*, *Cooperia*, and *Trichostrongylus* (Zajac, 2006). Parasitic nematodes in this family have a similar direct life cycle with a total time of 21 days to develop from egg to adult worm. The lifecycle begins with adult female worms producing eggs which are shed within host feces. Once eggs are released from the host into the environment they develop into larvae within 24 hours and proceed through three stages of larval development (L1, L2, & L3). Once larvae reach the final stage of development (L3) they now have the capability to infect the host. The infective L3 larvae reside within water droplets on blades of grass and move about until host ingestion. After ingestion, L3 larvae will migrate through the other chambers of

the ruminant stomach to finally reside within the abomasum. The infective L3 larvae will then shed their cuticle and become L4 or preadult larvae and within 48 hours reach their final adult form. At this point the adult worms will pierce the abomasal walls and be sustained by feeding on the blood of their host. They will sexually reproduce, and the female worm will begin to produce eggs beginning the cycle again (Zajac and Garza, 2020).

Gastrointestinal nematode populations generally follow a yearly biphasic rise and fall on the pasture. Larvae available to grazing animals in the spring are either those that survived the winter on pasture, and will only survive if their energy stores last, or are progeny of hypobiotic larvae which have resumed development within the host (Eysker, 1997). The second population will be the offspring of GIN acquired in spring during the wet season (Craig, 1993). Host susceptibility and weather conditions will determine the level of larvae which are available. For small ruminants, more individuals will be susceptible in the spring being either naive lambs or lactating ewes, making it critical to protect these susceptible groups during this time.

The successful avoidance of haemonchosis relies on the early recognition of risk, periodic monitoring of *H. contortus* burdens, and preventative programs which include grazing management and nonchemical measures, in addition to anthelmintic treatments (Besier et al., 2016). The chronic form of haemonchosis is related to smaller but sustained burdens of *H. contortus*, seen as weight loss or poor weight gain, general ill thrift and anemia in some individuals (Dunn, 1978). Frequent and inappropriate use of anthelmintic within small ruminants has led to failure in effectiveness culminating in resistant species of worms. Research has demonstrated that *Haemonchus contortus* now has resistance to all major drug classes, including benzimidazoles, imidazothiazoles and macrocyclic lactones (Kotze and Prichard, 2016).

Genetic selection of animals with greater natural resistance to nematodes is a key component of integrated pasture management strategies, and currently relies heavily on diagnostic indicators. New laboratory tools based on molecular technologies will further improve both the diagnosis and management of *H. contortus* infections (Besier et al., 2016). Previous research has concluded that it is possible to select for resistance to worm infection in sheep, with the Rylington Merino line experiencing an annual genetic gain for estimated breeding value worm egg count of 2.7% (Karlsson et al., 2006).

However, conventional methods of identifying superior individuals, such as fecal worm egg counts (FECs) or hematocrit determinations, are expensive or logistically difficult, and therefore impractical for many producers, especially those in remote areas (Riley and Van Wyk, 2009). Visible signs of anemia have been implemented as a simple diagnostic indicator through the development of the FAMACHA™ system in South African Merinos, which involves color assessment in ocular conjunctival membranes. Small ruminants are evaluated by this test based upon the redness/whiteness of the lower ocular mucous membrane. Depending on mucous membrane color, a score between 1 and 5 is given to assess severity of the anemia. Animals that fall into categories 1 and 2 are considered healthy and do not require intervention. However, Kaplan et al. (2004) recommends that those individuals which score a 3 or higher should be treated. Selecting animals to be dewormed based on level of anemia allows for lower treatment cost as well as reducing rate of anthelmintic resistance development. When properly implemented, FAMACHA™ scoring may be used to identify animals that are consistently under heavy worm burden and can then be used as a tool to aid in culling decisions in effort to improve overall flock genetic resistance, only in the context of *H. contortus* infection. However, further

studies are required to determine optimal strategies for incorporating FAMACHA-based selective treatment protocols into integrated nematode control programs (Kaplan et al., 2004).

Katahdin Sheep

In the late 1950s, Michael Piel of Maine set out to develop a variety of sheep that would combine “the hair coat, prolificacy, and hardiness of the Virgin Island sheep with the meat conformation and rate of growth of wool breeds” (Breed Origin & History – KHSI). After crossing “African Hair Sheep” imported from St. Croix with a traditional wool breed like Southdown, Tunis, Hampshire, and Suffolk he created the type of sheep he was looking for (Breed Origin & History – KHSI). This new breed was named ‘Katahdin’ and has since expanded in popularity across the southeastern United States. The Katahdin breed is currently the fastest growing breed association registered through the National Sheep Improvement Program (NSIP) with 7,345 lambs registered in 2020-2021 (NSIP Database, 2021). However, significant variability exists for post weaning fecal egg count (PW FEC) estimated breeding value (EBV) within the Katahdin breed, providing continued opportunity for selection.

The traditional metric used to evaluate parasitic burdens and identify individuals which are susceptible and resistant to parasitic infections has been FEC. While FEC is an important diagnostic tool, feasibility of collecting and processing samples has been a longstanding issue posed by producers. The EBV’s for WFEC and PFEC are expressed as a percent reduction and evaluates an animal’s genetic merit for parasite resistance based on worm egg counts taken at weaning (WFEC) or post weaning (PFEC) (Pal and Chakravarty, 2020). Currently WFEC is measured between 45-90 days of age and is reported to range from -100.22 – 960.21 (NSIP Search- Katahdin). Whereas, PFEC is taken any time after 90 days and is reported to range from

-104.27 – 2035.33 (NSIP Search- Katahdin). These ranges reveal tremendous variation in parasite resistance exists among Katahdin sheep.

While specific immune mechanisms driving parasite-resistance are unclear there is, however, a clear genetic component to parasite resistance within the Katahdin breed and breeding strategies can be implemented to exploit these opportunities. Heritability for FEC in the Katahdin range from 0.18 for WFEC to 0.23 for PFEC displaying promise for genetic selection towards reduced FEC (Ngere et al., 2018). Selection for reduced FEC has proven effective in Australian Merino lines in Southern Brazil, with researchers seeing that selection for low FEC lambs improved genetic progress in reducing *H. contortus* infection (Benavides et al., 2016). So, it can be concluded that selection for improved parasite resistance using Katahdin FEC EBV is obtainable.

Immune Response

The St. Croix breed has the unique ability to inhibit worm establishment, thereby, lowering FEC and by doing so are used as a model for exploring parasite resistance. It is this ability that has prompted researchers to use this breed as a model of full host protective immunity (Gamble and Zajac, 1992). Resistance of the St. Croix to gastrointestinal nematodes like *H. contortus* is a result of coevolution of the host; with the hot and humid climate on a Caribbean island called St. Croix. The equatorial environment is ideal for conditions required for the cultivation of *H. contortus* year-round (Vanimisetti et al., 2004). This constant exposure to parasites made it crucial for these sheep to illicit an enhanced response to early larval infection. The response to early infection has been characterized as a more rapid Th2 response among infected St. Croix sheep as opposed to traditional wool breeds (Bowdridge et al., 2015). These data were confirmed in another experiment where there was increased expression of IL-12 in

white faced cross lambs (susceptible) compared to the St. Croix (resistant) indicating a Th1 polarization rather than a Th2 response (MacKinnon et al., 2015). This lack of immunocompetence in tandem with delayed recognition of parasitic infection allows for a greater likelihood of worm establishment in traditional wool breeds (Bowdridge et al., 2015).

It is certain that parasite resistance is immune mediated, and that underlying innate immune responses are critical for clearance of helminth infections. The ability of STC to recognize *H. contortus* L3 antigen and promote an early response is critical to preventing adult worm establishment. The mechanisms underlying early development to immune responses to parasitic infections are poorly understood. However, it is clear the timing of these events greatly contributes to the ability of St. Croix sheep to evade and protect against *H. contortus* infection, despite the underpinning mechanisms being undiscovered. Therefore, it is essential to further clarify responses of immune cells to *H. contortus* in both parasite susceptible and resistant breeds of sheep. Parasite resistance is rooted in immunomodulation, this has been proven through studies in which host inflammatory response controls the extent of *H. contortus* infection. In this study Romney wethers were given an artificial infection of *H. contortus* and treated with dexamethasone. This resulted in increased worm burdens for groups treated with dexamethasone when compared to controls (Matthews et al., 1979).

Circulating blood eosinophilia is a hallmark of helminth infections. Representing less than 5% of blood leukocytes in healthy animals, tissue and blood eosinophils increase dramatically during worm infection (Dawkins et al., 1989). The type 2 cytokine IL-5 plays a central role in inducing activation and recruitment of eosinophils to sites of infection (Huang and Appleton, 2016). It has been reported that eosinophils are defensive effector cells downstream of Th2 activation (Huang and Appleton, 2016). With the ability to promote inflammation

eosinophils have cytotoxic effector capabilities that assist in helminth entrapment and destruction (Loktionov, 2019). Balic et al. (2006) suggest that the cytokine environment in the abomasal tissue may be an important factor for determining the activation of eosinophils for effective expulsion of *H. contortus*.

Neutrophils are also important during early infection acting as a first responder to cellular trauma. Early IL-4 activation is critical to Th2 differentiation and for the clearance of helminths, with IL-4 deficient mice showing impaired expulsion of parasites (Oeser et al., 2015). In the presence of larval antigen ovine neutrophils were able to produce IL-4 as early as 3 hours of antigen stimulation at a quantity sufficient enough to activate PBMC which produce additional amounts of IL-4 (Middleton et al., 2020). This in turn will allow for a more robust and rapid Type 2 response in the host and lead to improved parasite expulsion.

The cytokines IL-4 and IL-13 are required to activate a Th2 response associated with helminth infections (Bao and Reinhardt, 2015). The importance of CD4⁺ T cells has also been demonstrated in sheep during *H. contortus* infection (Gill et al., 1993). After depletion of CD4⁺ T cells in Gulf Coast Native sheep via anti-ovine CD4 monoclonal antibody fecal egg counts were significantly higher at days 21 and 28 after *H. contortus* infection (Peña et al., 2006). Adult worm establishment also increased in sheep with depleted CD4⁺ T cells (Peña et al., 2006). Delayed IL-4/ IL-13 expression in susceptible sheep (ex. Suffolk) reflects the poor immunomodulation to larval *H. contortus* and disseminates their susceptible phenotype (Jacobs et al., 2016).

In addition to activating the necessary Th2 response, CD4⁺ T lymphocytes can alternatively initiate B cell production, which create specific antibodies to antigen. Enteric parasites similar to *H. contortus*, can be affected by B cell production in Peyer's patches located

within the gut. This specific network of lymphoid tissues found within the gut contain specialized cells capable of presenting antigen to B cells found within germinal centers leading to reduced establishment.

Antibody production has been documented to play a crucial role in host defense against *H. contortus* (Watson et al., 2016). It has been demonstrated that parasite specific antibodies IgA, IgE and IgG act in concert with effector cells and are produced at a greater extent in sheep with active *H. contortus* infections (Meeusen et al., 2005). IgE is directly linked with allergic response and was found to increase abomasal mucosa production in sheep infected with the nematode *Trichostrongylus axei* (Shaw et al., 1997). Whereas, IgA initially has a rather delayed response to a primary infection. During secondary larval exposure a rapid influx of IgA occurs to produce an anamnestic response in St. Croix sheep as opposed to white faced influenced lambs (Bowdridge et al., 2015). However, when evaluating humoral response to adult worms, typically IgG is the primary antibody in serum but it is important to note that abomasum antibodies are more important than serum antibodies in the protection against gastroenteric nematodes (Alba-Hurtado and Muñoz-Guzmán, 2013).

Markers for Improved Immunity in Livestock

Genetic selection for improved disease resistance is an important strategy to combat infectious diseases in agriculture. Various genetic approaches are being assessed as possible methods to enhance disease resistance of livestock. One of the most viable options is immunogenic strategies making use of genetic markers associated with improved immune response. Mallard et al. (2011) have implemented high immune response technology (HIR) of Immunity+™ in dairy cattle seeking to decrease instance of mastitis among dairy herds. Understanding biological and genetic relationships within animal immunity may prove to be

crucial during periods of stress, and response to vaccination or disease challenge. The cost of disease to the agriculture industry is substantial and antibiotic treatments need to be used with caution among livestock to help reduce the emergence of antibiotic-resistant pathogens. Therefore, alternate approaches are required to improve animal health and well-being without the use of prophylactic antimicrobials.

Previous research in dairy cattle has used a breeding value for Somatic Cell Score (SCS) as an indicator of udder health. However, SCS is an indicator of mastitis and limited in its implications outside of mammary disease. To better interpret SCS, a SCC of 100 cells/ $\sim$ 1 converts to a score of 3, each one-unit increase (or decrease) in score is associated with a doubling (or halving) of cell count (Shook and Schutz, 1994). This scoring method has been used since 1983 at all Dairy Records Processing Centers in the US (Shook and Schutz, 1994). A low SCS indicates a low level or absence of infection throughout the lactation. The continuum of scores indicates degrees of mastitis that cows experience during a lactation. It was concluded that increases in SCS between lactations and between months within lactation are attributable to increases in clinical mastitis (Coffey et al., 1986).

Whereas, High Immune Response (HIR) focuses on broad-based disease resistance with the concept of prevention at the forefront (Mallard et al., 2011). High Immune Response technology isn't a simple process and requires a 15-day test period along with the associated costs. The HIR patented test protocol includes initial blood collection for ELISA and immunization with antigens in the neck. Followed by a subsequent collection of blood to evaluate antibody mediated immune response (AMIR). Accompanied with a skin thickness test and background skin measurements to evaluate cell mediated immune response (CMIR) at day fourteen and a final skin fold measurement 24-48 hours later (Ngere et al., 2018). While this

platform requires a lot of input, it appears that the feasibility is of little concern with focus groups of Ontario farms indicating that 75% of producers have significant interest in the technology (Wagter-Lesperance et al., 2012). Producers indicated that they felt this would be a useful platform to aid in culling, treatment, and breeding decisions. Recent interest has also been placed on adapting this test to fight against Bovine Respiratory Disease (BRD). BRD results in the death of some 53,000 beef cattle in Canada each year, an economic loss of more than \$100 million. In North America as a whole, the estimated annual cost of BRD as high as \$1 billion dollars/year (Translating High Immune Response (HIRTM) Genomics to Improve Beef Cattle Health and Welfare | Genome Canada).

To accomplish this goal of selection for improved immunity, genome-wide association studies have been performed to look at genetic linkages between antibody-mediated and cellular mediated immune response with genomic profiles in dairy cattle. These immune responses were classified as antibody-mediated (AMIR) or cellular mediated immune responses (CMIR) and found to be heritable to offspring (h^2). AMIR was evaluated by measuring serum antibody of IgG₁ to the specific test antigen by ELISA at Day 0, 14, 21 days after immunization (Thompson-Crispi et al., 2014). Candidate genes within 250,000 base pairs of significant SNPs were identified to determine biological pathways associated with AMIR and CMIR, and that there is significant variation in SNP profiles between high and low responders (Thompson-Crispi et al., 2014). The significant variation associated with these genetic pathways controlling immune response indicates that there is potential for breeding decisions to influence animal health. These data indicate that it may be possible to calculate a genomic breeding value from this data and drive selection towards decreased incidence of disease within the dairy industry.

Recent studies have focused on evaluating host defense mechanisms as indicators of specific and broad-based inherent disease resistance. This selection for improved immunity has subsequently shown that this breeding strategy may lead to enhanced production traits. A study conducted on Australian Holstein heifer calves showed that high antibody responders had greater average daily weight gain than their low counterparts (Aleri et al., 2015). This proves to be consistent across species with research studies noting that piglets from high responder sows consistently reached market weight (100 kg) an average of ten to twelve days before low responders (Mallard et al., 1998).

The ability to adequately cope with stress is directly related to individual fitness in non-domestic populations and to improved animal welfare within domestic livestock species. Coping refers to the individual's behavioral and physiological efforts to manage (reduce, minimize, master, or tolerate) the internal and external demands of a situation that is appraised as stressful, and taxing or exceeding the individual's resources (Koolhaas et al., 1999). Livestock are required to cope with demands of a production environment which is intensively managed there are very few features that the animal can subsequently manipulate or change (Wechsler, 1995). In livestock, proactive and reactive individuals are found to differ in the physiological and neuroendocrinological response to stress, which may have implications for their health status. Koolhaas et al. (1999), demonstrated that the nature of neuroendocrine stress response may modulate immune responses and individual susceptibility to disease. This was demonstrated in an experiment in which both socially dominant and submissive pigs were immune compromised (elevated numbers of neutrophils, decreased antibody production) compared with socially intermediate pigs and concluded that although dominance may afford the animal greater priority

to resources (like food and mates), it may have some immunosuppressing effects as well (Morrow-Tesch et al., 1994).

Selection for Reduced Subclinical Disease

Clostridium perfringens (*C. perfringens*) is associated with release of bacterial exotoxins that result in necrosis of the abomasa or intestinal mucosa (Simpson et al., 2018). *C. perfringens* comes in multiple subtypes however, type C and D are most common and vaccinated for within small ruminants (Tizard, 2021). However, in past years it was found that at the SWAREC in Glade Spring VA an emergence of Type A clostridial disease arose. Prior to vaccination for type A (YR1), significant non-predator lamb death loss was observed in High PFEC-sired lambs (Weaver, 2020). After vaccination for *C. perfringens* type A, death losses between High and Low FEC-sired lambs returned to a more acceptable level. However, even during times of immense pathogen load within the environment, losses from lambs sired by Low FEC rams were consistent (Weaver, 2020). With these data it is reasonable to hypothesize that the significant death losses observed among these divergent groups is not confined to the context of GIN infections. That the ability to develop adaptive immunity to helminths can in turn be a predictive indicator of overall immunological fitness to a variety of pathogens.

This culminates to the question, what is the future of antibiotic usage within the livestock? High-density type management strategies currently used in commercial animal agriculture is incredibly conducive to rapid dissemination of infectious agents. The USDA animal and plant health inspection service (APHIS) reported that 15% of beef calves that enter feedlots receive antibiotics for the treatment of clinical respiratory disease, but therapeutic antibiotic doses are also administered to 10% of apparently healthy calves to mitigate anticipated outbreaks of respiratory disease (Watson et al., 2016). The use of antibiotics in livestock

production is perceived as one of the main contributors towards the increase in antibiotic resistance leading consumers to call for “antibiotic free” livestock (Goddard et al., 2017). However, reducing use of antibiotics within livestock has come at a cost; the reemergence of subclinical disease and animal suffering. With Denmark being one of the first countries to ban the use of antimicrobials for growth promotion it was been observed that therapeutic drug use increased and no reduction of resistant zoonotic bacteria (Jensen and Hayes, 2014). With this in mind, it becomes crucial to seek out genetic solutions to select for individuals which are predisposed to better combat subclinical disease and will require less therapeutic drug intervention.

Chapter 2: Materials and Methods

Katahdin Breeding Scheme

In 2018, lambs were removed from pasture 22 days after weaning (June 26). A fecal sample was collected rectally, and all lambs were dewormed with levamisole hydrochloride (8 mg/kg, Agrilabs, Columbia, MO, USA). In the first year of the project (2018) registered Katahdin ewes (n=119) were randomly mated service sires. To better understand lamb parasitism and death losses around the time of weaning, in year two (2019), sample collection began at the time of first vaccination (45-60 days of age). Body weights, blood samples, and FAMACHA™ scores were collected weekly until July 9, 2019 (approximately 110 days of age). Fecal samples were collected on a biweekly basis. At this point, lambs were removed from pasture and treated with levamisole hydrochloride (8 mg/kg, Agrilabs). Foot scald was assessed weekly by visual evaluation of lameness and treated with gamithromycin (6 mg/kg, Merial) as needed. Lambs were given anthelmintic treatment at FAMACHA™ score ≥ 3 . Levamisole hydrochloride was the primary anthelmintic used. Data was taken from industry Katahdin flocks which provided data to the National Sheep Improvement Program (NSIP). Rams were mated with ewes at the Southwest Virginia Agricultural Research and Extension Center in Glade Springs, VA. The mating scheme for year two (2019) implemented eight sires randomly bred to registered Katahdin ewes (n=137). However, for year three of the project (2020), a divergent mating scheme was implemented in which low PFEC EBV rams (Low Sire 3, Low Sire 4, Low Sire 5) were selectively mated to ewes with a PFEC EBV of less than -50. Likewise, high PFEC EBV rams (High Sire 1, High Sire 3, High Sire 4) were selectively mated to ewes with a PFEC EBV of greater than +50 (Table 1.). Interbreeding was deterred during the entirety of the study with sibling mating being circumvented by the introduction of new genetics.

Katahdin Sheep Management

All sheep were managed by the Southwest Virginia Agricultural Research and Extension Center (AREC) in Glade Springs, VA. The timeline for lamb management and data collection is outlined in Figure 1. Ewes were divergently bred to sires based on their post-weaning fecal egg count (PFEC) estimated breeding values (EBV). Lambing is intensively managed within individual jugs before being moved out onto pasture. Progeny are managed as one cohort with lambs alongside their dams until weaning. Blood samples were taken weekly and fecal samples bi-weekly starting on May 20th, 2020 and ending on July 8th, 2020. Lambs were weaned on June 3rd, 2020 and left on pasture until the end of sample collection. Lambs were vaccinated for CD&T and Clostridium Type A on May 20th, 2020, and then given an additional booster vaccination three weeks following on June 10th, 2020. During this study, FAMACHA™ scoring was used to determine whether lambs required anthelmintic treatment (Kaplan et al., 2004; Riley et al., 2009). Any lambs with a score of 3 or higher were treated with Levamisole orally at a rate of 8mg/kg. If a lamb succumbed to illness and passed while on test the date and probable manner of death were recorded and that individual was removed from analysis.

Sire Estimated Breeding Values (EBV)

Sire EBV's were reported in Table 1. Across all years the difference in average PFEC EBV for low sires versus high sires were 365%. Differences in weight were negligible with low FEC sires and high FEC sires having similar lamb weaning weight (WWT) (+1.9 vs. +1.3 (kg)) and post weaning weight (PWWT) (+2.4 vs. +2.1 (kg)) averages. Within the USA Hair Index the difference between low FEC sire average and high FEC sire average was slight (1.65). Therefore, production traits reported appear to be similar among both groups apart from the divergent selection for PFEC reduction.

Fecal Analysis

Fecal samples were analyzed using a modified McMasters technique (Whitlock, 1948).

Two grams of feces were weighed out and added to 28 mL of flotation solution (Specific gravity =1.20) which is a saturated salt solution. The feces and solution are then mixed until the feces are thoroughly homogenized. Once fully integrated this solution is then passed through unfolded gauze to strain out the solids from the liquids. Immediately fill both chambers of the McMasters slide using a transfer pipette. Set aside the slide for at least 5 minutes to allow for eggs to float to the surface of the slide. All eggs inside the grid areas were counted in both chambers.

Total egg count: (chamber #1 + chamber #2) * 50 = eggs per gram (EPG)

This multiplication factor of 50 is specific to the ratio of feces (2 grams) to flotation solution (28 ml) described in this procedure. Each egg observed represents 50 eggs/gram, therefore, this procedure will not detect fewer than 50 eggs/gram, which is equivalent to observing one strongylid egg on the McMaster slide.

Blood collection

Blood was collected from lambs by jugular venipuncture into 10-mL in red top serum tubes and placed on ice while being transported back to West Virginia University. Samples were then centrifuged at 400 x g for 20 minutes at 4°C and serum was collected. Serum for each individual was then placed in pre-labeled microcentrifuge tubes. All samples were stored in a -80° C freezer until time of assay. Individual samples were then pooled together by sire (Low Sire 3, Low Sire 4, Low Sire 6, High Sire 1, High Sire 3, and High Sire 4) at each of the eight time points.

Sheep Specific IgG ELISA

96-well 4HBX microplates (Thermo Scientific, Waltham, MA, USA) were coated with 5 µg/mL of monoclonal anti-goat IgG capture antibody (Sigma-Aldrich Product No. G2904)

diluted in Carbonate-Bicarbonate Buffer 0.1 M pH 9.6 and incubated at 4°C overnight. The plate was warmed to room temperature and washed using a NUNC® 12 channel Immuno-wash five times with 1x PBS-Tween wash buffer. The blocking agent PBS-B (1% Bovine Serum Albumin - BSA) was added to each well at a volume of 200 µL per well and placed on a shaker for 30 minutes at room temperature (20-25°C). After this incubation, the plate was again washed five times with wash buffer and samples were applied at 100 µL per well. Samples were pooled together based upon sire and analyzed in triplicates across eight-time points. Neat serum was diluted to 1:7200 into PBS-B and IgG standards (Sigma-Aldrich) were serially diluted beginning at 1000 ng/mL. The plate was incubated on a plate shaker at room temperature for two hours and then washed five times with wash buffer. An HRP-conjugated antibody (Sigma-Aldrich) was added to the plate at a 1:10000 volume dilution in PBS-B and incubated for one hour at room temperature (20-25°C). The plate was then washed ten times with wash buffer before the addition of the TMB substrate kit. After a twenty-minute incubation at room temperature, a stop solution of 2M H₂SO₄ was added at 100 uL per well. The absorbance was then read at 450 nm in an plate spectrophotometer (BioTek Instruments, Winooski, VT, USA). The concentration of IgG was calculated using a standard curve with a detection range of 15.63 – 1,000 ng/mL. The coefficient of variation (CV) for inter and intra-assay was less than 11%. Raw absorbance values for samples and standards were adjusted for blank absorbance of each plate.

Shropshire Sample Analysis

In the fall of 2020 post-weaning blood and fecal samples were collected from Shropshire sheep (n=41). Blood samples were analyzed for total immunoglobulin-G (IgG) using a sheep-specific ELISA. Animal owner provided PFEC EBV for all lambs analyzed. Shropshire sheep were sorted into low (PFEC EBV < 0) and high (PFEC EBV > 0) groups based on fecal egg count (FEC), which were analyzed using the modified McMaster's method. Sheep were divided

into these subsets due to approximate equal distribution of individuals (Low n=19, High n=22). FEC data was log transformed [$\ln(\text{FEC}+100)$] to achieve normality. Descriptive statistics are reported in Table 3.

Polypay Sample Analysis

In the fall of 2020 post-weaning blood and fecal samples were collected from Polypay sheep (n=88). Blood samples were analyzed for total immunoglobulin-G (IgG) using a sheep-specific ELISA. Fecal data were analyzed using the modified McMaster's Method. Animal owner provided PFEC EBV for all lambs analyzed. Polypay sheep were sorted into three groups by PFEC EBV; Group A (< -50) Group B ($> -50, +50$), and Group C ($> +50$). Sheep were divided into these subsets with most individuals falling within group B (Group A n= 25, Group B n=54, Group C n=9). FEC data was log transformed [$\ln(\text{FEC}+100)$] to achieve normality. Descriptive statistics are reported in Table 3.

Texel Sample Analysis

In the fall of 2020 post-weaning blood and fecal samples were collected from Texel sheep (n=60). Blood samples were analyzed for total immunoglobulin-G (IgG) using a sheep-specific ELISA. Fecal data were analyzed using the modified McMaster's Method. Animal owner provided PFEC EBV for all lambs analyzed. Texel sheep were sorted into four groups by PFEC EBV; Group A (< -50) Group B ($> -1, -50$), Group C ($0 \leq, +50$) and Group D ($> +50$). The Texel sheep were subdivided into four subsets due to the approximate equal distribution of individuals (Group A n=17, Group B n=18, Group C n=17, Group D n=8) FEC data was log transformed [$\ln(\text{FEC}+100)$] to achieve normality. Descriptive statistics are reported in Table 3.

Statistical Analysis -Katahdin

To determine lamb FEC differences, data were analyzed using the General Linear Model (GLM) procedure of SAS (SAS institute, Cary, NC) with fixed effects of sire, time and sire X

time interactions. A log transformation was used on FEC data [$\ln(\text{FEC}+100)$] for normality. Means comparisons were performed on LS means of fixed affects or interactions, using the Bonferroni. Significance was determined when $P \leq 0.05$.

To evaluate lamb IgG differences, data were analyzed using the General Linear Model (GLM) procedure of SAS (SAS institute, Cary, NC) with fixed effects of sire, time and sire X time interactions. Means comparisons were performed on LS means of fixed affects or interactions, using the Bonferroni. Significance was determined when $P \leq 0.05$. High Sire 4 was removed from analysis after it was determined his lambs had lower than expected PFEC values.

Statistical Analysis -Shropshire / Polypay / Texel

Data were analyzed using Sigma Plot Software. A one-way ANOVA was utilized with fixed effects for PFEC EBV grouping was used to evaluate average IgG, FEC and PFEC differences. Means comparisons of interactions were analyzed using LS means and differences were detected using the Holm-Sidak test. A log transformation was used on FEC data [$\ln(\text{FEC}+100)$] for normality. Significance was determined when $P \leq 0.05$.

Chapter 3: Results

Survivability and Sire Effect YR2

In year one of the project, significant death loss occurred among lambs due to an outbreak of *Clostridium perfringens* Type A. Lambs sired by High PFEC sires had significantly more death loss than lambs sired by Low PFEC sires (29.9% vs. 10.6%, respectively; $P < 0.05$)

Figure 2. When management strategies were put into effect to reduce lamb death High PFEC sired lambs experienced less death loss during year two (11.5%) and year three (12.3%) when compared to year one. Across all three years non-predator death loss in Low PFEC lambs remain relatively consistent (Figure 2). Death loss among Low PFEC lambs reflect average losses to be anticipated within the management system down in Glade Springs, VA. Blood collection from lambs of different sire types within year 2 were used to determine if sire PFEC contribute to differences in antibody production in offspring. Lambs sired by Low PFEC rams had significantly greater absorbance than High PFEC rams (1.65 vs 1.42 respectively $P < 0.0001$) (Figure 3B). Average absorbance of lambs across week by sire type were not statistically significant (Figure 3A) ($P > 0.05$).

Katahdin Analysis

When grazing pastures lambs will naturally be exposed to parasites and become infected. Expectedly, Low PFEC lambs experienced lower average FEC (eggs/gram) than their High PFEC counterparts in YR3. This was exasperated after weaning when a significant disparity occurs with Low PFEC lambs having a lower FEC than High PFEC lambs,(455 vs 943 eggs/gram; respectively, $P < 0.0001$, Figure A). There was a significant interaction of sire type by week that occurred after weaning with Low PFEC lambs having significantly lower FEC (Figure 4C) ($P < 0.005$).

For YR3 of the project there was a significant effect of sire type, and thus lamb PFEC, on IgG concentration where low PFEC lambs had a greater IgG concentration than high PFEC lambs (886 vs 633 ug/mL) ($P < 0.005$) (Figure 5A). However, no significant sire by week interaction was observed ($P > 0.05$) (Figure 5B). Upon analysis of individual lamb PFEC it was found that High Sire 4 had multiple lambs with negative PFEC values. To be more exact 15 out of the 27 lambs he sired had a PFEC value of less than +50 (Table 2.). Therefore, he was subsequently considered an outlier and excluded from analysis. After removal of High Sire 4 from analysis differences were magnified with low PFEC lambs having significantly more average IgG (886 versus 465 (ug/mL), $P < 0.0001$) (Figure 5B). A significant sire by week interaction was observed whereas low PFEC lambs had a greater IgG concentration post booster vaccination (Figure 5D, $P < 0.0001$).

In general, the magnitude by which FEC and PFEC values are correlated is key to derive differences in antibody production. Furthermore, log transformed FEC values were correlated with PFEC EBV values across all individuals and found to describe a positive linear correlation among Katahdin lambs in this study ($R^2=0.27$, $P < 0.0001$) (Figure 6A). Low PFEC EBV lambs had greater correlation between log transformed FEC and PFEC EBV values than high PFEC EBV lambs ($R^2=0.38$ vs $R^2=0.28$ respectively, $P < 0.0001$) (Figures 6C and 6B).

Shropshire Analysis

Average FEC for Shropshire lambs with negative EBV's (Low, $0 > \text{EBV}$) was significantly lower than those with positive EBV's (High, $0 < \text{EBV}$) for PFEC FEC (1375 vs. 4810 (eggs/g), respectively, $P < 0.05$) (Figure 7A). There was a positive linear correlation found between actual FEC data and PFEC-EBV values ($R^2 = 0.668$, $P < 0.001$) (Figure 7C). Taken together this shows that selection of PFEC EBV contributes to reduction of *H. contortus*. In

contrast, when analysis of serum IgG were conducted no significant difference were observed between low EBV and high EBV grouping (87.97 vs. 62.43 (ug/mL), $P = 0.067$) (Figure 7D).

Polypay Analysis

Polypay sheep were sorted into three groups by PFEC EBV; Group A (< -50) Group B (> -50, +50), and Group C (> +50). Average FEC for Polypay lambs within EBV groupings (A, B, & C) were statistically significant (106.3, 213.5, 790.0 (eggs/g) respectively, $P < 0.05$) (Figure 8A). There was a positive linear correlation found between actual FEC data and PFEC-EBV values ($R^2 = 0.287$, $P < 0.001$) (Figure 8C). Taken together this shows that selection of PFEC-EBV contributes to reduction of *H. contortus*. In contrast, when analysis of serum IgG were conducted a significant difference were observed between Group A and Group C (86.19, 53.08 (ug/mL) respectively $P = 0.049$) (Figure 8D).

Texel Analysis

Texel sheep were sorted into four groups by PFEC EBV; Group A (< -50) Group B (> -1, -50), Group C ($0 \leq$, +50) and Group D (> +50). Average FEC for Texel lambs within EBV groupings (A, B, C, & D) were not statistically significant (4365, 4603, 4369, and 6581 (eggs/g) respectively, $P > 0.05$) (Figure 9A). There was no linear correlation found between actual FEC data and PFEC values ($R^2 = 0.01$, $P > 0.05$) (Figure 9C). When analysis of serum IgG were conducted, no significant difference was observed between groupings by EBV range (86.19, 71.23, 53.08 (ug/mL) respectively $P > 0.05$) (Figure 9D).

Chapter 4: Discussion

Parasitism is a significant hindrance to lamb production in pasture-based management along the eastern United States. The stress associated with weaning attributes to a successive rise in *H. contortus* infection on pasture and results in negative consequences such as anemia, hypoproteinemia, and ultimately can lead to death in severe cases (Zajac, 2006). When under immense parasite stress lambs are more likely to experience increased instance of pathology to other microorganisms due to their weakened immune state.

Non-predator death loss is an inevitable part of lamb production, but death loss percentages tend to more often affect lambs sired by high post-weaning fecal egg count (PFEC) estimated breeding value (EBV) rams. When the Virginia Tech southwest AREC station experienced a high pathogen load of clostridium type A, lamb crop death loss reached over 40% (Weaver, 2020). However, among the death loss percentages, the data indicated distinct differences segregated by sire PFEC EBV. Where high PFEC sired lambs had a death loss of 29.9% and low PFEC sired lambs had a death loss of 10.6% (Weaver, 2020). However, when management strategies were put in place to vaccinate the lambs for clostridium type A death loss for high PFEC sired lambs dropped to 11.5% and low PFEC sired lambs dropped to 7.8% (Weaver, 2020). These data indicate that high PFEC sired lambs were unable to appropriately respond to a pathogen to the same extent as low PFEC sired lambs unless they were supported with additional management strategies, like vaccination.

Nevertheless, the interaction of maternal impact had yet to be explored and a divergent mating scheme was put in place mating high PFEC EBV ewes to high PFEC EBV rams and low PFEC EBV ewes to low PFEC EBV rams. Under this new design, we observed that the high lamb crop experienced a 12.3% death loss whereas the low lamb crop had a 5.6% death loss. These results advance the concept that selection for low PFEC lambs can work to increase

efficiency in terms of live lambs weaned. It can be concluded that a death loss of around 10% is to be expected at the SWAREC in Glade Springs, VA due to environment (Weaver, 2020).

Off a natural, pasture-based parasitic infection, trends in FEC differences were predicted with high lambs having significantly higher average fecal egg counts than their low counterparts (2558 vs. 1313 eggs/g respectively). Low PFEC lambs are better adept at early recognition of *H. contortus* larvae resulting in reduced establishment and subsequent parasite expulsion. Yet, rooted within the ability to develop an adaptive immune response is a predictive indicator of overall host fitness. This protective immunity may extend out to a vast array of pathogens and not be confined to only parasitic infections. Moreover, these data support the use of PFEC EBV as a tool to improve upon death loss percentages allowing producers to in turn generate lambs less likely to require intervention during periods of intense pathogen load.

Translating this into Katahdin antibody production, low PFEC EBV selected lambs on average had higher levels of circulating IgG (762.6 ug/mL) than high PFEC EBV selected lambs (739.4 ug/mL). This numerically greater concentration of antibody confirms the implications of selection for low PFEC EBV lambs. When observing the interaction of average antibody concentrations across multiple timepoints, there was no significant interaction. However, it is important to observe that High Sire 4 had a PFEC average progeny value much lower than expected (PFEC +100) because of this he was removed from analysis. After which, low PFEC EBV lambs have consistently higher levels of circulating IgG following CD&T booster. This indicates that high PFEC EBV lambs do not respond with the same magnitude of antibody in response to vaccination. However, vast variance for antibody production occurs between -51 and +149 PFEC EBV, Figure 10 depicts these thresholds for antibody production based upon PFEC EBV value.

Increasing pressure is being placed on the agricultural industry to select individuals that will require fewer antimicrobial treatments. Thus, selection for disease resistance and lamb fitness in dual environments (both feedlot and pasture-based management) is vital and can have long-lasting impacts on efficiency. To accomplish this goal high immune response technology has been an effective tool at selecting individuals genetically predisposition to better handle environmental pressures caused by pathogens. From this research, PFEC EBV has the potential to be a valuable diagnostic tool as a central measure of immunity. To observe this trend across breeds, acquisition of samples from breeds that are unrelated to the Katahdin were utilized and included: Shropshire, Polypay, and Texel sheep. Within the Shropshire group, individuals with low FEC had a greater average IgG concentration (87.9 $\mu\text{g/mL}$) than those with high FEC (62.4 $\mu\text{g/mL}$) ($P>0.05$). In the Polypay group, sheep in PFEC EBV Group A had numerically higher IgG concentration (86.2 $\mu\text{g/mL}$) than sheep in Group B (71.2 $\mu\text{g/mL}$) and Group C (53.1 $\mu\text{g/mL}$) ($P>0.05$). While data in either breed were not significant, the trend observed across breeds indicate that sheep with a lower PFEC EBV have numerically greater circulating antibody. After investigating the correlation between PFEC EBV and actual FEC data for this methodology to hold true it is vital to see a highly correlated positive linear relationship between PFEC EBV and FEC.

When analyzing the Texel samples, the lack of NSIP data for this breed leads to poor accuracy between FEC data and predictive measures of PFEC EBV. This lack of linearity leads to variability in antibody production due to the immense inconsistency in terms of infection status which is independent of PFEC EBV groupings. In order for PFEC to be an effective tool within the Texel breed more fecal egg count data must be submitted to provide more validity to PFEC values.

Lamb death loss data paired with circulating levels of IgG justify the need for further exploration into the utilization of PFEC EBV. The immense registry for the Katahdin breed provides a unique opportunity for producers to implement genetic progress within their herd without having to endure the time and cost associated with traditional diagnostic measures. Further exploration needs to be placed on studying the thresholds of PFEC EBV in tandem with subsequent production traits to select for enhanced efficiency in lambs.

Table 1. Sire Summary for Year 1 (YR1), Year 2 (YR2) and Year 3, (YR3) mating's with estimated breeding values (EBV).

Sire ID ¹	YR1 Ewes ²	YR2 Ewes ²	YR3 Ewes ²	EBV ³				
				WWT (kg)	PWWT (kg)	WFEC (%)	PFEC (%)	Hair Index
Low Sire 1	30	17	-	2.8	4.3	16.6	-38.3	101.2
Low Sire 2	30	-	-	2.2	2.8	-2.93	-34.9	102.8
Low Sire 3	-	18	34	1.7	2.3	-74.9	-96.9	102.0
Low Sire 4	-	17	25	-0.4	-3.2	-93.6	-95.2	104.5
Low Sire 5	-	17	-	0.7	0.9	28.1	-49.7	103.6
Low Sire 6	-	-	30	4.2	7.2	-74.5	-43.6	111.9
Low FEC Average	60	69	89	1.9	2.4	-8.6	-59.8	104.3
High Sire 1	29	17	29	0.1	0.9	255	323	105.5
High Sire 2	30	-	-	1.6	3.2	65.4	142	105.5
High Sire 3	-	17	29	2.3	2.7	199	573	105.8
High Sire 4	-	17	33	1.2	2.7	168	254	109.9
High Sire 5	-	17	-	1.2	0.8	77.2	234	103.3
High FEC Average	59	68	91	1.3	2.1	153	305	106.0
Sum/Difference⁴	119	137	172	0.6	0.3	162	365	1.65

¹ Sire ID denotes grouping based on FEC EBV. Four sires were utilized for breeding in YR1. Three new sires along with a carryover sire were used in YR2. One new sire along with five carryover sires were utilized in YR3.

² Represents number of ewes mated to each sire for a given year

³ Estimated breeding values based on NSIP EBV values were accessed 06/29/2021; weaning weight (WWT), post-weaning weight (PWWT), weaning fecal egg count (WFEC), post-weaning fecal egg count (PFEC), USA Hair Index.

⁴ Sum/Difference of ewes in low and high FEC sire EBV.

Table 2. Progeny average PFEC EBV values by Sire (YR 3).

Sire ID ¹	Progeny AVG PFEC (%) ²	Range PFEC Progeny	Progeny with PFEC < +50	Total Number of Progeny	EBV ³	
					Sire PFEC EBV (%)	Sire Accuracy
Low Sire 3	-47.2	-99 : -67	31	31	-96.9	91
Low Sire 4	-84.9	-99 : -50	22	22	-95.2	95
Low Sire 6	-76.6	-91 : 12	30	30	-43.6	93
Low FEC Average	-69.6	-	-	-	-78.6	93
High Sire 1	107	31 : 360	3	20	323	88
High Sire 3	211	94 : 344	0	22	573	94
High Sire 4	100	-23 : 249	15	27	250	87
High FEC Average	139	-	-	-	382	90
⁴ Sum/Difference	209	-	-	152	461	3

¹Sire ID denotes grouping based on FEC EBV for YR3

² Estimated breeding values based on NSIP EBV values were accessed 07/11/2021; post-weaning fecal egg count (PFEC) for lambs were accessed and average together by sire, and sire PFEC EBV and accuracy were reported.

³EBV values were accessed 07/11/2021 using National Sheep Improvement Program (NSIP) searchable database.

⁴Sum/Difference of ewes in low and high FEC sire EBV.

Table 3. Shropshire, Polypay and Texel Descriptive Statistics

Breed	PFEC Grouping	n	PFEC Mean¹	PFEC Min¹	PFEC Max¹	FEC Mean (eggs/g)	IgG Mean (ug/mL)
Shropshire	-	41	+26	-69	+154	3302	73.65
	A (< 0)	18	-35	-69	-2	1375	87.97
	B (> 0)	23	+73	+5	+154	4810	62.43
Polypay	-	88	-13	-91	+107	250.6	73.21
	A (< -50)	25	-69	-91	-50	106.3	86.19
	B (-50 > +50)	54	-6	-46	+49	213.5	72.61
	C (> +50)	9	+78	+54	+107	790.0	53.08
Texel	-	60	-9.3	-88	+138	4744	4349
	A (< -50)	17	-69	-88	-52	4365	4113
	B (-50 < -1)	18	-29	-46	-7	4603	4548
	C (0 ≤ +50)	17	+21	0	+47	4369	4383
	D (> +50)	8	+99	+52	+138	6581	4329

¹Estimated breeding values based on NSIP EBV values reported by animal owners

Figure 1.

Figure 1. Lambing weaning and off pasture dates for YR 3. (2020) Weaning fecal egg count (WFEC) data was collected one week prior to weaning. Blood was collected weekly and FEC on a biweekly basis.

Figure 2.

Figure 2. Lamb Death Loss Across YR1, YR2, & YR3 Non-predator death loss excluding parasite losses was reported from seven days of age until the end of testing. (Means with different letters within year are significantly different at $P \leq 0.05$).

Figure 3.

Figure 3. Sire Effect on Lamb Circulating IgG (YR2) (A) Average IgG absorbance for low PFEC EBV sired lambs versus high PFEC EBV sired lambs for Year 2. (B) Average IgG absorbance for low PFEC EBV lambs versus high PFEC EBV lambs across seven weeks and a final timepoint at week twenty-three ($P > 0.05$) (The * denotes significance of $P \leq 0.0001$).

Figure 4.

Figure 4. Average FEC of Katahdin Lambs by Sire (A) Average FEC of lambs across week by sire type ($P < 0.001$). **(B)** Average FEC of high and low sires across weeks. All lambs were weaned on 6/10/2020. Means with * are significant ($P < 0.001$).

Figure 5.

Figure 5. Average IgG Katahdin lambs based upon EBV Type (A) Average IgG (ug/mL) of lambs across week by sire type ($P > 0.05$). (B) Average IgG (ug/mL) of lambs by sire type ($P < 0.05$). (C) Average IgG (ug/mL) of lambs across week by sire type with High Sire 4 removed ($P < 0.001$). (D) Average IgG (ug/mL) of lambs across week by sire type with High Sire 4 removed. Means with * are significant ($P < 0.001$). * indicates significance of sire by week ($P < 0.001$).

Figure 6.

Figure 6. Transformed FEC data vs. PFEC EBV's for Katahdin lambs (A) PFEC- EBV values linear correlation with log transformed FEC, $\ln(\text{FEC}+100)$ across all individuals (B) PFEC- EBV values for low sired lambs linear correlation with log transformed FEC, $\ln(\text{FEC}+100)$ (C) PFEC- EBV values for high sired lambs linear correlation with log transformed FEC, $\ln(\text{FEC}+100)$.

Figure 7.

Figure 7. Shropshire Average FEC and IgG Concentration (A) Lamb average fecal egg count (FEC) by estimated breeding value (EBV) grouping. (B) Lamb average post-weaning fecal egg count (PFEC) estimated breeding value (EBV). (C) Correlation between FEC and PFEC-EBV across all individuals (n=42). (D) Serum IgG (ug/mL) by estimated breeding value grouping ($P = 0.65$). Means with * are significant ($P < 0.001$).

Figure 8.

Figure 8. Polypay Average FEC and IgG Concentration (ug/mL) (A) Lamb average fecal egg count (FEC) by estimated breeding value (EBV) grouping. (B) Lamb average post-weaning fecal egg count (PFEC) estimated breeding value (EBV). (C) Correlation between FEC and PFEC-EBV across all individuals (n=91). (D) Serum IgG (ug/mL) by estimated breeding value grouping (EBV). Means with different letters are significant ($P < 0.001$).

Figure 9.

Figure 9. Texel Average FEC and IgG Concentration (ug/mL) (A) Lamb average fecal egg count (FEC) by estimated breeding value (EBV) grouping. (B) Lamb average post-weaning fecal egg count (PFEC) estimated breeding value (EBV). (C) Correlation between FEC and PFEC-EBV across all individuals (n=60). (D) Serum IgG (ug/mL) by estimated breeding value grouping (EBV). No significance reported due to lack of correlation between FEC and PFEC EBV data.

Figure 10.

Figure 10. Visual Representation of IgG production based upon PFEC EBV value.

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