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Teenu Thomas
Department of Animal Genetics and Breeding, College of Veterinary and Animal Sciences, Mannuthy, Kerala Veterinary and Animal Sciences University, Kerala, India

Marykutty Thomas
Department of Animal Genetics and Breeding, College of Veterinary and Animal Sciences, Mannuthy, Kerala Veterinary and Animal Sciences University, Kerala, India

TV Aravindakshan
Department of Animal Genetics and Breeding, College of Veterinary and Animal Sciences, Mannuthy, Kerala Veterinary and Animal Sciences University, Kerala, India

Bindya Liz Abraham
Department of Animal Genetics and Breeding, College of Veterinary and Animal Sciences, Pookode, Kerala Veterinary and Animal Sciences University, Kerala, India

K Syamala
Department of Veterinary Parasitology, College of Veterinary and Animal Sciences, Mannuthy, Kerala Veterinary and Animal Sciences University, Kerala, India

Corresponding Author:
Teenu Thomas
Department of Animal Genetics and Breeding, College of Veterinary and Animal Sciences, Mannuthy, Kerala Veterinary and Animal Sciences University, Kerala, India

Factors influencing gastro-intestinal parasitic infection in native goats of Kerala

Teenu Thomas, Marykutty Thomas, TV Aravindakshan, Bindya Liz Abraham and K Syamala

Abstract
Gastro-intestinal (GI) parasitism is a globally indexed animal health constrain. It can lead to weight loss, stunted growth and even death in extreme conditions. Parasitism is an important production limiting disease of small ruminants. There are numerous anthelminthics available in the field for the control of parasites. Because of the unscientific use, parasites have developed resistance towards these drugs. Finding alternatives for gastrointestinal parasite control remains an urgent area of ruminant health research. There are many factors that can influence the parasitic load in an animal like breed, farm management, climate, nutrition and so on. In the present study the effect of farm and breed on gastro-intestinal parasitism are analysed.

Keywords: Gastro-intestinal parasitism, breed, climate, anthelminthics

1. Introduction
Goats are highly robust creatures that can survive and reproduce in extremely high temperatures and low humidity with the least amount of available nutrition, they significantly contribute to human lifestyles in poor economies. 20th livestock census revealed presence of 148.88 million goats in India with an increase of 10.1% over the previous census and Kerala has got a goat population of 1.36 million animals. Kerala has two endemic breeds of goat Malabari and Attappady which have great phenotypic diversity. The Malabari goats, seen all over the state, are descendants of ancient crosses between native feral goats and Arab, Surti, and Mesopotamian goats (Thomas *et al*., 2021) [10]. Attappady Black breeds, which are mainly found in the Attappady hill region of the Palakkad district, are adapted to harsh temperatures and sparse resource availability. They are reared mainly for mutton (Saranya, 2022) [8].
The most significant illness threatening livestock production systems in developing nations, particularly small ruminant production systems, is gastrointestinal nematode parasitism. Infections with the strongyle Haemonchus contortus are particularly significant (Bishop, 2012) [4]. Breeding livestock for improved resistance to disease is an increasingly important selection goal (Kemper *et al*., 2013) [6]. The nematode infection is a moderately heritable trait (Crawford *et al*., 2006) [5]. When parasites survive treatment and pass on resistance-related genes, onto their progeny resistance develops. These genes become more prevalent with additional selection and reproduction among the general population. Resistance to anthelmintic medication classes develops one class at a time, it seems. Finally for a species to become resistant, parasites with resistance genes must endure treatment, continue to proliferate, and pass on genes to the following generations of host. (Sangster *et al*., 2018) [7].
The complicated trait of parasite resistance governed by many minor genes with small effects r ather than a limited number of key genes with large effects. The majority of breeding programs for parasite control are based on indicator traits (Kalaldeh *et al*., 2019) [2]. Performance (growth rate) under parasite challenge conditions, faecal egg count (FEC), and anaemia-related parameters are likely to be indicator traits (Bishop, 2016) [4]. The heritability of FEC varies between 0.22 and 0.63, indicating that selection for resistance or against susceptibility using this parameter can be useful (Alba-Hurtado, F. and Muñoz-Guzmán, M.A., 2013) [1]. Numerous risk factors, caused by the host and environment, are crucial in the development of gastro intestinal nematode infections. Environmental factors, which heavily influence the kind, incidence, and severity of many parasite diseases, include agro-ecological conditions, animal husbandry practises such housing systems, deworming intervals, and pasture management. Other risk variables that affect the development of gastrointestinal

parasitic infections include the host species, sex of the animal, age, body condition, breed, and genotype (Badaso and Addis, 2015) [3], as well as the kind of parasite and the density of the worm population (Tariq *et al*., 2010) [9]. In the present study the qualitative and quantitative analysis of the FEC was performed and association analysis of FEC was done with the factors like breed and farm to study their effect on FEC of native goats of Kerala.

2. Materials and Methods

2.1 Host resistance towards parasitism measured by FEC method in native goats of Kerala

Goat faecal samples were collected during rainy season in the month of July 2022. The samples were collected with gloved hand directly from the rectum of each animal. Faecal examination was done on the same day at department of parasitology laboratory. Faecal sample was examined qualitatively by direct microscopic examination for the parasitic ova. For the quantitative analysis, FEC was carried out. The FEC was determined using Modified McMaster's technique with McMaster counting chamber for quantitative analysis. This procedure is most effective for reducing debris but increases the time required to perform each test.

The procedure performed was, one gram of faecal material, mixed with 14ml of water (to yield a total volume of 15 ml) in a mortar with the help of a pestle. Strained it to remove the coarse particles through a sieve. Transferred the filtrate into a centrifuge tube which is then centrifuged at 3000 rpm for 2 minutes. Discarded the supernatant and then flotation (saturated sodium chloride) solution was added to partially fill the tube, shaken well to re-suspend the sediment. Additional flotation solution was added to fill the tube. Entire McMaster counting chamber was immediately filled with the sample mixture using a pasture pipette without any air bubbles. Kept the slide still for at least 10 minutes before examining to allow the floatation process to occur. Observed the chamber through 10X objective, focusing the grid lines. Strongyle eggs were counted in each lane of the three chambers. To determine the number of parasite eggs per gram of faeces (epg), average of the counts from the three chambers were calculated. Since one chamber of the McMaster counting chamber was calibrated to accommodate 0.15 ml of faecal mixture, the average egg per chamber was multiplied by 100 to get FEC in epg. The number of epg also calculated using the formula,

Eggs/g = [no eggs counted X (T/V)]/ F

T = total volume of faeces/flotation solution mixture,
V = volume of aliquot examined in slide, and
F = grams of faeces used.

The EPG was measured on two replicates of each faecal sample, and the average of the two replicates was used for analysis.

2.2 Statistical analysis done in available FEC data

Descriptive statistics of FEC were computed. The mathematical model used for association analysis included the fixed effects of different farms and breed. The FEC was not normally distributed and exhibited positive skewness. A logarithmic transformation [log10 (FEC+100)] was therefore applied before statistical analysis. Statistical inferences were made on transformed data and reverse-transformed least square means were presented. The linear mathematical model used was

$Y_{ijk} = \mu + A_i + B_{j+} e_{ijk}$ where,

Yijk was the observation of log10 (FEC+100), µ was overall population mean, Ai was the fixed effect of ith breed and Bj was the fixed effect of jth farm and e_{ijk} random residual error effect.

The complete statistical analysis was done in IBM SPSS Version 21.0. Post-hoc tests, Least Significant Difference (LSD) and Duncan's Multiple Range Tests (DMRT) were used to identify homogeneous subsets.

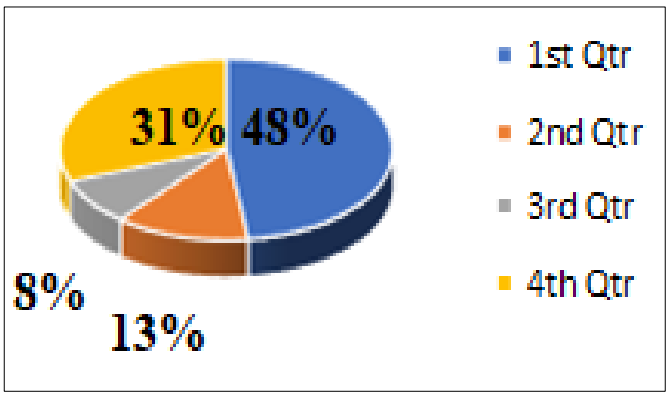
3. Results and Discussion

3.1 Qualitative Examination for GIN

On qualitative examination of faecal samples, 25.5 h of the goats under study were positive for strongyle ova, 8 percent were positive stronglyloides, 37.6 percent had coocidial oocyst and 4 percent were positive for moneizia ova. Results also showed that 5.2 percent had concurrent infection of strongyle and Strongyloides papillosus. In a study about gastro intestinal nematodiasis, reveals that there is a significant influence of season and host age on the prevalence of GIN infection in goats (Tariq *et al.*, 2009) [9]. These findings need to be taken into consideration while designing control strategies for the gastro-intestinal nematode infections of ruminants reared under the traditional husbandry system in temperate agro-climatic conditions.

3.2 Quantitative Analysis of Strongyle Ova

The FEC among Malabari goats was ranged from zero to 4933 with a mean S.E of 234.96±229.0265. The sampled goats were categorised into different groups according to FEC *viz*., lowly infected (FEC<500), mildly infected (FEC 500 to 1000), heavily infected (FEC 1000 to 1500) and very heavily infected (FEC>1500) and the results are shown in Figure 1. Quantitative egg counts must be quite stable and constant across brief time periods in order to be useful in determining the extent of a worm burden. The majority of animals (48%) were very lowly infected with FEC<500 and 31% percent had high FEC (>1500) and there was a well-defined over dispersion of nematode infection among Malabari goats of Kerala.



1st Qtr <500 2nd Qtr 500-1000 3rd Qtr 1000-1500 4th >1500

Fig 1: Frequency distribution (percent) of faecal egg count in Malabari goats

3.3 Association analysis of breed and farm with host parasitic resistance trait in Malabari goats

Faecal egg count (FEC), or the quantity of worm eggs in faeces, is an indicator for parasite burden but requires far less invasive sampling than other methods, making it the method of choice in most investigations (Bishop *et al*., 2016) [4]. The influences of breed and farm on FEC were analysed using General Linear Model (GLM) procedure. The mathematical model used for association analysis included the fixed effects of breed and farm. The FEC was not normally distributed. A logarithmic transformation [$\log_{10}$ (FEC+100)] was therefore made before statistical analysis. Statistical inferences were made on transformed data and reverse-transformed least square means are presented.

Results of analysis of variance for the effects of farm and breed on FEC in Malabari goats are shown in Table 1. There was a highly significant ($p \leq 0.01$) influence of farm and breed on FEC among native goats.

Table 1: Analysis of variance for the effects of farm and breed on FEC in native goats of Kerala

Source	Degrees of freedom	Mean squares	F value	p- value
Farm	3	10.582	198.037	<0.001**
Breed	1	1.04	19.455	<0.001**

Least square means (LSM) for the effect of genotypes of breed and farm type on FEC are given in Table 2. There was significant variation for FEC among goats based on breed and farm.

Table 2: Least square mean for the effects of genotypes of breed and farm on FEC in Malabari goats of Kerala

Factors	Number	FEC
Overall mean ± S.E.	176	234.96±229.0265
Farm		**
Mannampetta	18	108.643[a]
Puthur	30	121.898[a]
Thanur	29	154.881[b]
Mannuthy	99	1839.500[c]
Breed		**
Malabari	141	250.611[a]
Attappady	119	212.324[a]
MSE	0.042	

**Statistically significant at $p \leq 0.01$; NS- Statistically not significant; Least square means with different superscripts within factor differ significantly at $p \leq 0.05$ level

5. Conclusion

The present study reports the occurrence of significant association between farm and breed on FEC among native goats. The very few farmers have correct knowledge about important aspects of breeding, housing and deworming of goats. The farm management, nutritional status of animals, innate resistance which is a breed characteristic can be reasons for significant association.

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