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ANIMAL HUSBANDRY & VETERINARY SCIENCE | RESEARCH ARTICLE

Genetic resistance to natural coccidiosis infection in goats in a semi-arid region of India

P.K. Rout^{1*}, †S.C. Bishop², K.K. Chauhan¹ and S.K. Singh¹

Abstract: Coccidiosis is one of the major causes of kid mortality in tropical regions and causes significant loss to farmers by affecting growth and feed efficiency in the growing kid. The strategy to control the coccidiosis is mainly through drug usage and is not efficacious at present. Therefore, an alternative strategy is required to control the disease in goats. Increasing genetic resistance to coccidiosis may be an appropriate complementary control strategy. The purpose of this study was to analyse the genetic variation in severity of natural coccidiosis infections in kids in the semi-arid region. The observations were recorded in 227 kids of Barbari and Jamunapari goats. Barbari goats had higher mean faecal oocyst counts (FOC) than Jamunapari goats at 3 and 6 months of age. The heritability for FOC was 0.05 and 0.15 at 3 and 6 months of age, respectively. All phenotypic and environmental correlations between FOC and live weight traits were low and negative, indicating a tendency for more heavily infected kids in the flock to grow more slowly. Genetic correlations were largely similar, but had large standard errors. The results suggest that genetic resistance control strategy can potentially be useful for the better performance in the existing managerial condition.

Subjects: Bioscience; Biotechnology; Environment & Agriculture; Epidemiology

Keywords: goat; faecal oocyst count; genetic parameters; coccidiosis

ABOUT THE AUTHORS



P.K. Rout

Our group at Central Institute for Research on Goats works on enhancing goat productivity through selection. Breeding for enhancing production performance is one of the major objectives of our group; and we are using both production performance as well as molecular markers for precise selection decision. P.K. Rout is working on genetics of disease resistance in poultry and goats. As a part of our objectives, we also are carrying out our research on susceptibility pattern of goat in response to natural coccidiosis infection for sustainable goat production.

S.C. Bishop introduced epidemiological concepts into the field of disease genetics and successfully demonstrated the application of these concepts to several diseases in sheep, goat, cattle and fish. He made an outstanding contribution to our understanding of the impact of host genetics on infectious disease outcomes in farmed animals at the individual and population level and applied in farmer's field for enhancing productivity.

PUBLIC INTEREST STATEMENT

If we can complement genetics of disease resistance with traditional method of disease control, it will reduce the frequency of usage of drugs and anthelmintics for maintaining our food-producing animals in both intensive production systems as well as in farmer's field. This research is interesting for general reader as the introduction of genetic element into diseases control is an effective mean to reduce environmental pollution and drug residues in food produce from livestock. Again, this approach has the potential to limit the effects of disease and can increase the profitability of farmer and simultaneously address issues of sustainable livestock production.

1. Introduction

Coccidiosis an important enteric disease of goats and is observed in both intensive and extensive rearing conditions, in India and worldwide (Foreyt, 1990; Harper & Penzhorn, 1999; Rehman, Khan, Khan, & Ahmad, 2011). *Coccidia* infections are one of the major causes of kid mortality and they cause severe economic losses to goat production by affecting growth of kids during their early growth phase (Agyei, Odonkor, & Osei-Somuah, 2004; Faizal & Rajapakse, 2001; Radha, Jeyathilakan, Gomathinayagam, John, & Karunanidhi, 2004; Sharma & Singh, 1997; Vihan, Singh, & Singh, 1988). Coccidiosis is caused by infection with *Eimeria* species and it is host specific. Sixteen *Eimeria* species have been described from goats, worldwide (Smith & Sherman, 1994; Zajac & Conboy, 2006). The major coccidia species that were found in the semi-arid region of India were *Eimeria christenseni*, *Eimeria jochejevi*, *Eimeria ninakohlyakimovae* and *Eimeria arloingi* (Sharma, Agrawal, Mandal, Nigam, & Bhushan, 2009).

Chemical control of coccidiosis is not effective in livestock due to drug resistance and concerns about the drug residues in food chain and environment further limit drug use (Bishop & Morris, 2007; Chapman et al., 2013). We hypothesize that the use of genetic resistance in the host goat has the potential to limit the effects of disease and can increase the profitability of farmer and simultaneously address issues of sustainable livestock production. Genetic variability in resistance to coccidiosis has been extensively studied in chickens (Bacciu et al., 2014; Chapman et al., 2013; Clark & Blake, 2012; Pinard-Van Der Laan, Monvoisin, Pery, Hamet, & Thomas, 1998; Zhu et al., 2000) and sheep (Beraldi et al., 2007; Reeg et al., 2005), but less in other domestic livestock species (e.g. rabbits; de Rochambeau et al., 2006). The present study was designed to analyse genetic variation in natural coccidia infections in goats in the semi-arid region of India.

2. Materials and methods

2.1. Genetic stock and management

Measurements were recorded on Barbari and Jamunapari kids maintained at the Central Institute for Research on Goats (CIRG), Mathura, Uttar Pradesh, India. The Barbari goat is native to areas nearby to the CIRG; it is a medium size and dual-purpose breed and is known for its early sexual maturity and adaptability over a wide range of agro-climatic situations (Khan & Singh, 1995). Jamunapari goats were native to the Chakarnagar area of Etawah district, 150 km distant from Mathura. The Jamunapari goat is a milch breed with a large body size and high twinning rate (Rout et al., 2000). Barbari and Jamunapari breeds are well adapted to the climatic condition and the selective breeding is practiced in both breeds since last 25 years at CIRG (Rout et al., 2000).

The goats were maintained under a semi-intensive management system with 6–7 h of grazing and stall feeding with seasonally available green fodder *ad libitum*, supplemented with concentrate mixtures depending upon the status and age category of the animals. No rotational grazing was practised. Generally, animals were housed separately according to their ages, sex, physiological status and health status. Does were bred twice at each oestrus. Controlled breeding was practised with the does being bred during May–June and October–November followed by kidding in the months of October–November and March–April, respectively. Recording of birth weight, sex and type of kidding was carried out after kidding. Kids were weaned at the age of 3 months. The kids were stall-fed up to weaning and then allowed to graze nearby areas for very short periods, up to 6 months of age. The study area has semi-arid climate, rainfall is about 400 mm, and the mean temperature during study period varied from 6.0 to 24.3°C in winter and 27.5 to 42.4°C in summer.

2.2. Collection of samples

Parasitological data were collected on both the flocks over a period of one year following natural challenge, on 227 kids (115 males and 112 females). Faecal and blood samples were collected at the same time at 3 and 6 months of ages. Oocyst per gram was determined using the saturated salt flotation technique and quantified using the modified McMaster technique (MAFF, 1986) with each counted oocyst representing 200 eggs per gram of faeces. Packed cell volume (PCV) was estimated

by microhaematocrit centrifuge method and it is the percentage of total volume occupied by packed erythrocytes when a given known volume of whole blood is centrifuged for a constant period. Body weight was also recorded at birth and at 3 and 6 months of age, using an electronic balance (platform type; Avery India) of 120 kg capacity.

2.3. Data analysis

As faecal oocyst counts (FOC) were not normally distributed (they were right skewed), a set of logarithmic transformations were applied to FOC and the resulting transformed variables were tested for normality before analysis. The transformation $\log_e(\text{FOC} + 100)$ was found to be the most appropriate. All subsequent analyses of FOC were applied to the transformed data.

Traits analysed were (1) faecal oocyst count at 3 (FOC3) and 6 (FOC6) months, (2) packed cell volume at 3 (PCV3) and 6 (PCV6) months, (c) body weight at 3 (W3 M) and 6 (W6 M) months, and body weight gain from birth to 3 months of age (BWG 0–3 M) and from birth to 6 months of age (BWG 0–6 M). Preliminary analyses of data were performed using multiple regressions in the GENSTAT package (Lawes Agricultural Trust, 2005) to determine significant fixed effects and covariates for use in subsequent variance component estimation. Fixed effects for FOC, PCV, live body weight and body weight gain traits included season of kidding (September–March and April–October), sex (male or female), breed (Jamunapari and Barbari) and type of birth (single or multiple), and these were fitted in all variance component estimation analyses. The population comprised 227 progeny from 41 sires and 165 does and for the analyses, the pedigree was extended back up to three generations, obtaining a whole pedigree database of 1822 animals.

Estimates of variance and co-variance components were obtained using the ASReml program (Gilmour, Gogel, Cullis, Welham, & Thompson, 2002), initially fitting the univariate models. The following models were fitted:

$$\text{Model 1: } Y = Xb + Z_1 a + e$$

$$\text{Model 2: } Y = Xb + Z_1 a + Z_2 m + e$$

$$\text{Model 3: } Y = Xb + Z_1 a + Z_3 pe + e$$

where Y is the vector of observation on specific trait of the animal; b is the vector of fixed effect; a , m and pe are vectors of random effect describing additive genetic effect, maternal additive effect and permanent environment effect due to dam, respectively; X , Z_1 , Z_2 and Z_3 are the corresponding incidence matrices for b , a , m and pe , respectively.

Log-likelihood ratio tests were carried out to determine the most suitable model for each trait in the univariate analyses (Rout, Chauhan, Matika, & Bishop, 2011; Visscher, 2006). Subsequently, bivariate analyses were carried out using the animal model of best fit to estimate the genetic, phenotypic and environmental correlations between pairs of traits. These correlations were estimated using ASReml package.

3. Results and discussion

Summary statistics for Barbari and Jamunapari goats for each measured trait are presented in Table 1. Barbari goats had higher mean FOC than Jamunapari goats at both ages ($p < 0.05$); however higher maximum values were seen in Jamunapari goats at 3 months of age. Packed cell volume did not exhibit any definite trend over breed or age ($p > 0.05$). Jamunapari goats were heavier than Barbari goats at all the ages ($p < 0.05$). Jamunapari breed has been introduced at CIRG, Makhdoom that has same climatic condition as its native area and has adapted to the management system very well. Selective breeding is practiced for improving production performance in both breeds since last 25 years indicating that susceptibility pattern between breeds is not due to adaptability to new environmental condition and parasites.

Table 1. Summary statistics for FOC, packed cell volume and live weight for Barbari and Jamunapari goats at 3 and 6 months of age

Breed	Barbari		Jamunapari	
	3 month	6 month	3 month	6 month
Number of kids	135	135	92	92
Faecal oocyst count (FOC)				
Mean (ln(FOC))	7.13 ^a	6.47 ^b	6.90 ^{cab}	6.33 ^{ab}
SD	1.45	1.29	1.46	1.51
Maximum (ln(FOC))	10.34	10.15	10.62	9.74
Proportion of zero values	0.11	0.20	0.21	0.22
Packed cell volume (%)				
Mean	29.8 ^a	29.2 ^a	30.3 ^a	29.6 ^a
SD	2.33	1.85	1.68	1.56
Maximum	41.0	34.0	36.0	36.0
Body weight (kg)				
Mean	8.17 ^a	13.14 ^b	10.60 ^c	16.6 ^d
SD	1.75	2.72	2.04	3.23
Maximum	13.5	19.4	15.5	25.0

Note: Means with different superscripts are significantly different ($p < 0.05$).

In the genetic parameter estimation, log-likelihood ratio tests (results not shown) indicated that neither the permanent environment due to dam nor the maternal genetic effects improved the fitness of the model. Therefore, the heritabilities, which are presented in Table 2, were estimated by fitting only direct genetic effects. The heritability for FOC was low at 3 months and at 6 months of age. Heritabilities for body weight and body weight gain at different ages were moderate to high at the two ages, but PCV was not heritable in this data-set.

Phenotypic, genetic and environmental correlations between FOC, body weight and body weight gain at different ages are presented in Table 3. Genetic correlations involving FOC had very large standard errors, which limited their interpretive value. However, phenotypic and environmental correlations between FOC at 3 and 6 months of age were strong indicating that these two measurements are describing the same trait. Live weight at the two ages was also strongly correlated, at both the genetic and phenotypic levels, indicating that genetic control of these two measurements is also largely the same. All phenotypic and environmental correlations between FOC and live weight (or weight gain) traits were low and marginally negative, indicating a tendency for more heavily infected kids in the flock to grow more slowly.

Parasite resistance is complex and polygenic in nature, and genetic variation in host resistance is observed in all domestic species (Bishop & Morris, 2007; Bishop & Stear, 2003). The differential resistance pattern to coccidiosis infection was observed between poultry lines and between sires within a

Table 2. Heritabilities for faecal oocyst count, body weight, packed cell volume and body weight gain at 3 and 6 months of age

	FOC3	FOC6	BW3	BW6	PCV3	PCV6	BWG 0–3 M	BWG 0–6 M
h^2	0.05	0.15	0.61	0.43	0.00	0.00	0.61	0.37
SE	0.14	0.16	0.20	0.21	n/a	n/a	0.21	0.21

Notes: FOC3 and FOC6: Faecal oocyst counts at 3 and 6 months of age, respectively. BW3 and BW6: body weight at 3 and 6 months, respectively. PCV3 and PCV6: packed cell volume at 3 and 6 months of age, respectively. BWG 0–3 M and BWG 0–6 M: body weight gain between 0–3 and 0–6 months of age, respectively.

n/a: Not estimable during the analysis.

Table 3. Phenotypic (r_p), genetic (r_g) and environmental (r_e) correlations between faecal oocyst count, live weight and live weight gains at 3 and 6 months of age

	FOC3-FOC6	FOC3-BW3 M	FOC3-BWG 0–3 M	FOC6-BW6 M	FOC6-BWG 0–6 M	W3 M-W6 M
r_p	0.85(0.02)	-0.15 (0.07)	-0.15 (0.07)	-0.05 (0.07)	-0.04 (0.07)	0.70 (0.04)
r_g	0.82 (0.50)	-0.11 (0.78)	-0.22 (0.80)	0.38 (0.57)	0.35 (0.61)	0.87 (0.13)
r_e	0.87 (0.04)	-0.21 (0.21)	-0.19 (0.21)	-0.20 (0.19)	-0.17 (0.18)	0.57 (0.17)

Notes: FOC3 and FOC6: Faecal oocyst counts at 3 and 6 months of age, respectively. BW3 and BW6: body weight at 3 and 6 months, respectively. BWG 0–3 M and BWG 0–6 M: body weight gain between 0–3 and 0–6 months of age, respectively.

Values in parenthesis are standard errors.

random-bred line (Pinard-Van Der Laan et al., 1998). Similarly, goat genetic groups and herds exhibited significant difference to coccidiosis infection in different studies (Chhabra & Pandey, 1991; Ruiz et al., 2006). Experimental studies have also shown genetically determined variation in resistance against coccidiosis in rodents (Wakelin, Rose, Hesketh, Else, & Grecnis, 1993). Oocyst counts at 3 months of age were different between Jamunapari and Barbari goats, and breed difference has previously been observed between crossbred and indigenous breeds of South Africa (Harper & Penzhorn, 1999). The heritability of faecal oocyst count at 6 months of age (0.15), despite being thrice the heritability of FOC3 (0.05), is still considered low. Beraldi et al. (2007) reported that the heritabilities (SE) of strongyle faecal egg count and coccidia FOC in lambs were similar, being 0.26 ± 0.12 and 0.22 ± 0.21 , respectively; and the heritability for coccidian FOC ($h^2 = 0.06 \pm 0.03$) was very low in adult animal. In sheep, heritabilities of FOC were zero for days 17–40 and 41–60. However, the heritabilities in lamb were 0.79 ± 0.27 and 0.54 ± 0.18 after 3 months of age (Reeg et al., 2005).

In this data-set, the maternal genetic and permanent environmental effects were not significant. However, it is not clear whether this is because there is no effect, or simply because the data-set was too limited to estimate such effects. These data comprised only a single generation of goats and 62% of does had only a single progeny (mean number of kids per doe), giving very little opportunity to estimate these additional effects. Hence, a larger data-set would be required to resolve maternal effects on these traits.

Negative phenotypic and environmental correlations between body weight and oocyst excretion were slightly stronger at 3 months than at 6 months of age. A similar observation, i.e. a large impact in young animals, has been made on day 40 after birth in lambs, i.e. this is the final phase of heavy oocyst excretion and corresponds with the age when clinical coccidiosis is commonly observed in housed lambs (Gregory, Joyner, Catchpole, & Norton, 1980; Jungmann et al., 1973). Moreover, FOC at 3–6 months of age can be considered for selection experiment. However, the positive genetic correlation between FOC6 and W6 M indicates that host acquires resistance to infection after 6 months of age. Therefore, the faecal oocyst count during 3–6 months of age should be considered for genetic susceptibility analysis. These results suggest that selection to improve resistance to coccidiosis should also have the benefit of improving early growth in kids.

4. Conclusions

We have presented genetic parameters for coccidiosis resistance (FOC) as well as live weight in Indian goats naturally challenged with coccidiosis infection. Whilst the heritabilities for FOC at 3 and 6 months of age are generally low, they do indicate the potential for exploiting genetic variation between individuals. FOC at both 3 and 6 months of age is negatively phenotypically correlated with both live weight and live weight gain, therefore the faecal oocyst count between 3 and 6 months of age should be considered for genetic susceptibility analysis. However, before implementing these results in a breeding programme it would be necessary to first estimate more precise genetic parameters in a larger population.

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Competing interests

The authors declare no competing interest.

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