Small Ruminant Research 166 (2018) 7–11

Contents lists available at ScienceDirect

Small Ruminant Research

journal homepage: www.elsevier.com/locate/smallrumres

Resistance of sheep from different genetic groups to gastrointestinal nematodes in the state of São Paulo, Brazil

T.C. Gonçalves[a], M.M. Alencar[b], R. Giglioti[a,*], T.B. Bilhassi[a], H.N. Oliveira[a], M.D. Rabelo[b], S.N. Esteves[b], M.C.S. Oliveira[b]

[a] Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista Júlio de Mesquita Filho, Via de Acesso Prof. Paulo Donato Castellane, s/n, CEP 14884-900, Jaboticabal, SP, Brazil
[b] Embrapa Pecuária Sudeste (CPPSE), Rod. Washington Luiz, Km 234, CP 339, CEP 13560-970, São Carlos, SP, Brazil

ARTICLE INFO

Keywords:
Fecal egg counts
Sheep
Gastrointestinal parasites
Genetic groups
Susceptibility

ABSTRACT

Infections by gastrointestinal nematodes cause large losses to sheep breeders. In the study reported here, the resistance to gastrointestinal nematodes was analyzed in sheep of adapted and non-adapted breeds, maintained in naturally infected pastures. A total of 134 females from seven genetic groups were monitored during 20 months: Santa Inês (OSI), Dorper (ODO), Texel (OTX), Ile de France (OIF), and animals from crosses of Santa Inês ewes with Dorper (ODS), Texel (OTS) and Ile de France (OIS) rams. Blood samples were collected monthly to determine the packed cell volume (PCV), and feces were collected at the same time to count the eggs per gram (fecal egg counts = FEC) and identify the genera of the prevalent parasites. The statistical analyses of the data showed significant differences ($p < 0.05$) regarding the genetic group, collection month and interaction of month with the genetic group on the FEC. The correlation estimates between FEC and PCV were negative and significant ($p < 0.01$).The OTS genetic group presented the lowest mean of FEC value. Concerning the nematode genera, the greatest prevalence was observed for *Haemonchus* spp. (85.6%), followed by *Trichostrongylus* spp. (10.8%), *Oesophagostomum* spp. (2.9%) and *Cooperia* spp. (0.7%). The results obtained in this study show that the crossing of the Texel and Santa Inês breeds can be considered an alternative for sheep production in the Southeast region of Brazil due to the lower egg output by gastrointestinal nematodes.

1. Introduction

Infection by gastrointestinal nematodes (GINs) causes severe losses to sheep breeders in tropical and subtropical regions of the world (Perry et al., 2002; Emery et al., 2016). Parasites have a long history of co-existence with their hosts, but the equilibrium that existed between them was upset by the domestication of livestock, which occurred some 8,000–10,000 years ago and by the subsequent intensification of herding practices (Sargison, 2012; Karlsson and Greeff, 2012).

Infections by GINs reduce the productivity and cause mortality of young animals, but the most significant losses are provoked by sub-clinical infections (Eysker and Ploeger, 2000). Environmental factors such as temperature and humidity affect the survival of the free-living forms of GINs in pastures, where around 95% of the population of these parasites is concentrated (Bowman, 2003), and where occurs egg laying, hatching and development of larvae, and ingestion by the host animals (Stromberg, 1997; O'Connor et al., 2006). Since the climate conditions that prevail in most of Brazil favor the development of GINs, the systematic use of anthelmintics has become a common practice in small ruminant herds, leading to the dissemination of resistance to the majority of chemical substances in use (Veríssimo et al., 2012; Cintra et al., 2016). Besides inefficacy, growing concern over the presence of drug residues in the environment and foods of animal origin has stimulated studies to find more innocuous anthelmintics, such as copper and plants extracts (Torres-Acosta and Hoste, 2008), as well as vaccines (Matos et al., 2017). Besides these, the use of diets with high protein levels, selective treatments, confinement in stables to reduce contact with infective parasite forms, and selection of more resistant sheep are among the control strategies used (Zvinorova et al., 2016). Genetic variation for resistance to GINs can be observed between and within breeds, allowing the identification of specific genes that contribute to this variation (Stear and Murray, 1994).

In small ruminant production systems, adaptation to environmental conditions, such as heat tolerance and the ability to survive numerous endemic disease challenges is considered a critical factor (Bishop, 2012). With increasing demand for sheep in Brazil's Southeast region,

* Corresponding author at: Embrapa Pecuária Sudeste, Rodovia Washington Luiz, Km 234, CP 339, 13560-970, São Carlos, SP, Brazil.
E-mail address: gigliotirodrigo@gmail.com (R. Giglioti).

https://doi.org/10.1016/j.smallrumres.2018.07.003
Received 10 February 2018; Received in revised form 10 July 2018; Accepted 11 July 2018

methods to control of GINs have been studied, and the use of more resistant breeds is considered a viable alternative (Mugambi et al., 1997; Rocha et al., 2005; Amarante et al., 2009; McManus et al., 2009; Ngere et al., 2017). Analysis of faecal egg counts (FEC) has been used in many experiments to characterize the resistance to GINs of small ruminants, finding heritability levels ranging from 0.01 to 0.65 (Zvinorova et al., 2016). The strategy of using cross-breeding to exploit the complementarity and heterosis between diverse sheep breeds can be an alternative to obtain more resistant animals. Therefore, this experiment was designed aiming to investigate the resistance to GINs of Santa Inês sheep, a breed considered to be highly resistant to these parasites (Amarante et al., 2004), in comparison with the Dorper, Ile de France and Texel breeds and crosses of these breeds with Santa Inês breed. The data obtained can support the identification of more resistant genetic groups to be selected in southeastern Brazil.

2. Material and methods

2.1. Experimental area and animals

The study was carried out on the experimental farm of the Embrapa Southeast Stock Breeding research unit (Embrapa Pecuária Sudeste), located in the municipality of São Carlos, São Paulo state (latitude 22°01′S, longitude 47°53′W and 856 m above sea level). The climate in the region according to the Köppen scale is Cwa, characterized by relatively cool and dry winters and hot and rainy summers. The coolest period generally lasts from April to September. During 20 months (June 10, 2014 to January 11, 2016), 134 contemporaneous ewes of the genetic groups Santa Inês (OSI, n = 16), Dorper (ODO, n = 12), Texel (OTX, n = 13) and Ile de France (OIF, n = 8), along with crosses of ½ OSI + ½ ODO (ODS, n = 27), ½ OTX + ½ OSI (OTS, n = 29) and ½ OIF + ½ OSI (OIS, n = 29) were monitored monthly. The female sheep were separated from their mothers at weaning at three months of age, and were reared together in a pasture area covering 6.0 ha planted with Tanzania grass, divided into two modules of 3 ha each and subdivided into four paddocks with 0.75 ha each, with grazing for 10 days followed by rest for 30 days, at a stocking rate of 22 animals per hectare. In the summer, the pastures received nitrogen fertilization (150 kg of N/ha) and in the dry season the sheep were supplemented with corn silage. Water and mineral mixture were provided *ad libitum*. Monthy samples of feces were obtained to FEC and coprocultures and blood samples were used to measure the packed cell volume (PCV). To prevent mortality, the animals with FEC greater than or equal to 4000 and PCV lower than or equal to 21% were treated with a commercial anthelmintic – oral administration of a preparation based on levamisole chlorohydrate (Ripercol L, Fort Dodge) at a dose of 5 mg p/kg of body weight. All the experimental protocols were approved by the committee on the ethical use of animals for experimentation of Embrapa Pecuária Sudeste (PRT no. 03/2013).

2.2. Meteorological data

The data on average monthly temperature (°C) and total rainfall (mm) were obtained from the climatology station of Embrapa Southeast Stock Breeding research unit, for the purpose of characterizing the climate variations during the experimental period.

2.3. Collection and processing of the samples

The fecal samples were collected directly from the rectal ampulla of each animal in labeled plastic bags. The samples were used to determine the FEC according to the modified technique of McMaster (Ueno and Gonçalves, 1998) with sensitivity of 50 eggs/g $^{-1}$.

The eggs were counted under an optical microscope with 10X magnification.

To determine the nematode genera, coprocultures were prepared using 30 g of a pool of fecal samples collected from all animals of each genetic group, according to Roberts and O'Sullivan (1950). The infective larvae were identified according to Keith (1953), based on observation of 100 larvae, and the results were expressed as percentage of each genus found.

Simultaneously with the fecal samples, blood samples were obtained by puncture of the jugular vein and collection in tubes containing the anticoagulant EDTA. These samples were used to determine the packed cell volume (PCV) by the microhematocrit method. The values were expressed as percentage of red blood cells in the samples.

2.4. Statistical analysis

The FEC data were transformed into $\log_{10}$ (FEC + 1) to approximate the normal distribution. The FEC and PCV data were analyzed by mixed models that included repeated measures of the same animal. The fixed effects included in the model were genetic group and month by year of collection and their interactions, while the random effect was the animal within the genetic group. A variance and covariance matrix model with compound symmetry (CS) was used. This covariance structure was selected because it presented lower values in the Akaike's Information Criterion (AIC) and Bayesian Information Criterion (BIC) tests when compared to other structures such as the first order autoregressive or the unstructured covariance models. The repeatability was estimated as well as the residual correlations between FEC and PCV for each genetic group, using the same model, without month by year effect. The residuals were obtained by using the PROC MIXED option, and the Pearson correlation coefficients were calculated by the PROC CORR routine, in both cases using the SAS®. The Tukey test was used to compare the means of the genetic groups.

3. Results

3.1. Meteorological data

Fig. 1 shows the monthly variations of the total rainfall according to month and year of the experiment. The total rainfall levels varied from 0.6 mm in August 2014 to 520.6 mm in January 2016. The average monthly temperatures (data not shown in the graph) ranged from 17.4 °C in July 2014 to 24.6 °C in January 2015.

3.2. GIN infections

The statistical analyses revealed a significant effect ($p < 0.05$) of genetic group, collection month and interaction with the genetic group on the FEC counts. The lowest FEC average was observed for the OTS group, which differed from the other genetic groups ($p < 0.05$). The ODO group had the highest average FEC, but this did not differ significantly from OIF group ($p > 0.05$), which in turn did not differ from the other groups (Table 1). During the entire experimental period, the animals in the ODO group had the highest egg output, although a sharp decrease was observed in September 2015. The OSI group presented a large decline in the average FEC values in October 2015. The peak infection levels varied according to the genetic group, but in general occurred in September 2014, January and May 2015 and January 2016, which were months with the highest precipitation (Fig. 1).

The FEC counts during the experiment varied from zero to 17,000 (numbers not log-transformed). During the 20 months, 134 anthelmintic treatments were administered, according to the criteria established for the limits of FEC and PCV, of them 50 treatments in the ODO group, 31 in the ODS, 19 in the OIS, 14 in the OTX, 9 in the OIF, 7 in the OTS and 4 in the OSI.The repeatability values estimated for the different genetic groups (Table 1) indicate that under the conditions of this study, except for the OIF, OSI and OIS groups, which presented low values, all the others had moderate values. These moderate repeatability values estimated for the majority of the genetic groups indicate