8th World Congress on Genetics Applied to Livestock Production

Belo Horizonte,
August 13 to 18 , 2006

Book of abstracts

Communication 02-14

AN INVESTIGATION ON THE GENETIC RESISTANCE TO PARASITICAL FAUNA IN APPENNINICA SHEEP. G. Filippini[1], F. Aloisio[1] F. Cecchi[2], M. Biagetti[1], F. Macchioni[3], R. Ciampolini[2], G. Venditti[1], E. Ciani[2], E. Mazzanti[2] C. Sebastiani[1], D. Cianci[4]. [1]IZS UM, 06126 Perugia, Italy; [2]Dip. Prod. Anim., 56124 Pisa, Italy; [3]Dip. Pat. Anim., Profilassi Igiene Alim., 56124 Pisa, Italy; [4]Dip. Fis. Gen. Amb., 70124 Bari, Italy.

The study was conducted in a single herd of Appenninica sheep breed situated in Tuscany (Italy) from April to Novembre 2004 on 108 sheep with the aim to estimate the hereditary transmissibility of resistance. The samples were processed four times for coprological (*Coccidia*, gastro-intestinal *Strongylids* including *Nematodirus*, *Dicrocoelium* spp, *Moniezia*, *Strongyloides* and *Trichuris*) and haematological (PCV) examinations. The heritability coefficients were rather low but not different from values reported elsewhere, ranging from the value of zero (*Dicrocoelium, Strongyloides* and *Trichuris*) to 0.29 (*Coccidia*). On the contrary high repeatability values were observed ranging from 0.04 for *Trichuris* to 0.66 for *Strongylids*.

Communication 02-15

ASSOCIATION OF CSN3 AND CSN1S2 GENES WITH LITTER SIZE IN CHINESE XINONG SAANEN DAIRY GOAT. H. Chen[1,2*], X.Y. Lan[1*], C.Z. Lei[1], C.Y. Pan[1], R.F. Zhang[1], Y.D. Zhang[1], R.B. Li[1]. [1]College of Animal Science and Technology, Northwest A& F University, Shaanxi Key Laboratory of Agricultural Molecular Biology, Yangling, Shaanxi 712100, P. R. China. [2]Institute of Biotechnology, College of Life Science, Xuzhou Normal University, Xuzhou 221116, P. R. China. (* Corresponding Author: Tel: +86-029-87091379, E-mail: chenhong1212@263.net and lan342@126.com)

Xinong Saanen dairy goat breed in China who characterized by large body size, high milk yield, strong adaptation. However, few know that Xinong Saanen dairy goat is also one of breeds with high litter size, with a kidding rate of 200% (Zheng, 1988). High litter size contributes to goat production (meat and velvet). Hence, increase of litter size contributes to improve productivity in the goat industry. Research on litter size of Xinong Saanen goat is important to improve productivity of the goat industry and to get new knowledge on the...

Communication 02-16

LACTATION CURVE IN A HERD OF SAANEN GOATS: BAYESIAN APPROACH OF WOOD´S FUNCTION. J.S. Laranjo, T.M. Gonçalves, F.F. Silva, A.L.L. Costa, M.A. P. Rodriguez, G.F. Rebouças. FEDERAL UNIVERSITY OF LAVRAS, PO Box 3037, Lavras, MG, Brazil.

The objective of this study is to use Bayesian approach to fit the Wood´s model for milk yield of Saanen goats. Data were 127 first, 49 second and 19 third lactation records of Saanen goats, with respective average age at kidding of 17, 36 and 49 months. The posterior marginal were obtained by Gibbs Sampler and parameter functions were calculated from posteriori means of these parameters. The results showed differences in the curve indicating that animals in second lactation were the most persistent. The Bayesian method was implemented successfully and was efficient in the study of the different lactation curves. The behavior of the lactation curve for different lactation number depended on initial production, the rate of production until peak, peak milk yield and persistency of lactation.

A SEARCH FOR QTL . GOATS. D.L. Roldán*, J M.A. Poli. Instituto de G Argentina.

Most studies of QTL detec from aggregate data. There the scale and shape descri total of 208 goats were ge the CHI3, CHI6 and CHI patterns of Creole and cr detected in dairy cattle, u helpful tool for different s carrying specific alleles tha

MULTIBREED GENET STATES. E.J. Pollak. De 14853 U.S.A.

The first multiple breed g differences in the U.S. wa registry. Here we discuss analysis, experiences gai evaluations in the United S

ACROSS BREED SIRE WITH MULTIPLE MAI Cranfield. Centre for Ger Science, University of Gue Chain-wide economic ber calculated for combinatior area. Across breed age-cor characteristics and input r discounts was considered. any extent relative to a fixe discounts and those with d endpoints, and 0.71 for op sires in commercial beef pr

AN INVESTIGATION ON THE GENETIC RESISTANCE TO PARASITICAL FAUNA IN THE APPENNINICA SHEEP BREED

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INTRODUCTION

Appenninica is a local Italian sheep breed reared in Tuscany, Umbria and other regions of central and southern Apennine. In the past, it was considered a triple attitude breed (milk, wool and meat). Nowadays it is one of the most spread meat breeds, and it can supply also an important quantity of wool, though rather coarse.

Therefore, Appenninica plays a role of particular interest in the Italian production context, due to numerical and historical-cultural importance. This study was carried out in a single Appenninica herd from Tuscany to estimate heritability parameters of parasite resistance, as a preliminary step toward the search for possible associated molecular markers.

MATERIAL AND METHODS

Animals and sampling. A total of 108 subjects (54 daughter-mother pairs) were selected from a farm situated in Tuscany; records were collected 4 times in year 2004 (February, May, September and November) during a 9 months time. One faecal sample from each animal was collected each time; faecal samples were analyzed in order to determine EPG (Eggs Per Gram) or OPG (Oocyst Per Gram) using the McMaster technique, modified by Hansen and Perry (1994). Besides *Coccidia* and gastro-intestinal *Strongylids*, including *Nematodirus* sp., samples were also analyzed in order to evaluate the presence of *Dicrocoelium* sp, *Moniezia* spp, *Strongyloides* sp. and *Trichuris* sp. At the same time blood samples were also collected from animals to determine Packed Cell Volume (PCV); blood analyses were carried out directly in the field by means of micro-haematocrit equipment.

Statistical analyses. For the statistical analysis data regarding EPG and OPG were transformed to the natural logarithm according to the formula y = log (EPG/OPG+25) (Baker, 1997) to correct for heterogeneity of variance and to produce approximately normally distributed data. One-way analysis of variance was used to test the effect of season sample on the variables examined, while simple correlation was calculated in order to show the relationship between groups of parasites (JMP, 2002). Heritability coefficients of EPG, OPG and PCV were obtained using daughter-mother regression. The repeatability was tested with the method of intra-correlation-class using the above mixed linear model for repeated measures:

$$Y_{ijk} = \mu + \alpha_i + \tau_j + \varepsilon_{ijk}$$

where :Y_{ijk} = traits considered; μ = overall mean; α_i = random effect of the i^{th} subject; τ_j = fixed effect of the j^{th} sample (j = 1,.., 4); ε_{ijk} = residual error. All estimates of variance components for estimates of heritability were obtained with a derivate-free REML algorithm using Newton-Rapson method (Patterson and Thompson, 1974; Harville, 1977; Searle, 1971). All analyses were carried out using the statistical package JMP of the SAS Institute (2002).

RESULTS AND DISCUSSION

Differences between parasitical load in the four samples are shown in table 1. Most of the animals showed a medium level of infestation for *Coccidia*, with 46.95% of the samples falling in the class under 300 OPG, whereas lower levels of infestation were observed for all the other parasites (percentages of samples falling in the class under 300 OPG comprised between 89.57 and 99.42%; data no shown). The number of eggs per gram reaches its maximum in April, with the exception of *Strongyloides* for which the highest values are observed in November. Despite the high level of infestation observed in April, haematocrit values (PCV) remained within tolerable limits, with values always under or close to 30: such data are in agreement with the range of variability verified by the Commission of Study A.S.P.A. (1999). Significantly lower haematocrit values were found in autumnal samples ($P<0.05$).

Heritability coefficient for EPG regarding gastro-intestinal *Strongylids* resulted equal to 0.11 (Table 2), which is a low value compared to results obtained in previous studies (Nieto *et al.*, 2002; Nieuwoudt *et al.*, 2002; Vanimisetti *et al.*, 2002; Baker *et al.*, 1998) tough comparable with values reported on Italian breeds by Benvenuti *et al.* (2003) and Giuliotti *et al.* (2003). An heritability coefficient of 0.11 was also observed in *Moniezia* (UPG), while the highest value was observed in *Coccidia* (0.29 OPG). In the remaining groups of parasites, heritability coefficients resulted in almost null values, being probably biased by (probably due to) the general low degree of infestation in our population sample. Also the PCV heritability coefficient is rather low, though consistent with values reported on the Massese sheep breed by Giuliotti *et al.*,(2003) and Benvenuti *et al.* (2003), and on goat breeds by Hoste *et al.* (2001) and Olayemi *et al.* (2002). Repeatability coefficients showed markedly higher values than those observed for heritability coefficients, with the exception of the *Dicrocoelium* and *Trichuris* EPG parameter for which a coefficient close to zero was observed (0.05 and 0.04 respectively). The highest repeatability coefficient was observed for gastro-intestinal *Strongylids* (0.66), with a value higher than that observed by Giuliotti *et al.* (2003, 2005) on Massese and Zerasca ewes, but consistent with other values reported by Giuliotti et al. (2003), Hoste *et al.*, (2001), Stear *et al.* (1995, 2000), Doligalska *et al.* (1997) and Yvore *et al.* (1992). High values were observed also for *Coccidia* (0.62), and medium values for Moniezia (0.43) and *Strongyloides* (0.33).

PCV repeatability coefficient is rather high (0.47), showing a good incidence of the permanent factors on the total variability. Such result agrees with the value (0.44) reported by Bekele and Kasali (2002), whereas being lower than the value (0.53) reported by Vanimisetti *et al.* (2002), and than the values (0.58 and 0.59) reported, respectively, by Giuliotti *et al.* (2003) and by Benvenuti *et al* (2003). The analysis of correlations between groups of parasites for each sampling (data not reported for brevity) showed that gastro-intestinal *Strongylids* are always negatively and significantly correlated with *Coccidia*, with the exception of samples collected in November. Other significant and negative correlations are observed in the months of April and May between *Coccidia* and *Moniezia*, and also between *Coccidia* and *Dicrocoelium*; in contrast, a positive and significant correlation is observed between *Coccidia* and *Trichuris* in May. Concerning gastro-intestinal *Strongylids* we highlighted significant and positive correlations with *Dicrocoelium*, in April and May, with *Moniezia* and *Trichuris* in April, and with *Strongyloides* in November, while negative correlation was observed with *Trichuris* in September.

Table 1. Means of traits related to parasite load.

	April	May	September	November
Coccidia (OPG)	5731,07 A	246,48 B	255,80 B	656,12 B
Dicrocoelium (EPG)	17,42 a	15,89 a	7,32 b	8,32 b
Strongylids (EPG)	77,47 B	65,87 B	158,50 A	169,33 A
Moniezia (EPG)	20,27 ab	2,19 b	24,12 a	5,32 ab
Strongyloides (EPG)	24,10 ab	35,52 ab	11,27 b	51,00 a
Trichuris (EPG)	6,78 B	34,64 A	15,00 B	0,42 B
Nematodirus (EPG)	0,7	-	-	-
PCV (%)	30,55 a	30,69 a	29,58 b	29,07 b

Different symbols on the same row mean significant differences: P<0.01 (A, B); P<0.05 (a,b).

Table 2. Heritabilities and repeatabilities coefficients of traits related ton parasite load.

	Heritability		Repeatability		
Traits	h^2	SE	$\sigma^2_G + \sigma^2_{EP}$	σ^2_P	r
Coccidia	0.29	0.128	612.71	991.84	0.62
Dicrocoelium	0.00	0.041	28.42	448.4	0.05
Strongylids	0.11	0.061	295.70	448.84	0.66
Moniezia	0.11	0.057	44.03	102.13	0.43
Strongyloides	0.00	0.071	61.32	182.84	0.33
Trichuris	0.00	0.081	39.43	985.75	0.04
PCV	0.00	0.108	1688.13	3603.25	0.47

σ^2_G = Total genetic variance; σ^2_{EP} =Permanent envinronmental factors; σ^2_P = Phenotipical variance.

CONCLUSION

The findings from this research show that the level of infestation in the considered Appenninica population sample is generally weak for all parasites, made exception for *Coccidia*. The incidence of the permanent factors on the total variability supplied high values of the repeatability coefficient for most of the analyzed parasites; the heritability coefficient reaches medium-high values for *Coccidia*, gastro-intestinal *Strongylids* and *Moniezia*, but rather low values for the other parasites and for PCV. The most spread and harmful parasitic species (gastro-intestinal *Strongylids* and *Coccidia*) are characterized by interesting values of the repeatability and heritability coefficients that could allow genetic interventions, such as identification, by phenotypic evaluation, of the most resistant subjects and implementation of a supervised program of reproduction in order to enhance the individual resistance. In addition, a search for possible molecular markers associated with the quantitative trait could be performed, in order to assist and facilitate genetic selection practices.

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