8th World Congress on Genetics Applied to Livestock Production, August 13-18, 2006, Belo Horizonte, MG, Brasil

ESTIMATION OF GENETIC PARAMETERS AND GENETIC TRENDS FOR WOOL PRODUCTION AND QUALITY FOR THE URUGUAYAN MERINO

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INTRODUCTION

Between 1995 and 2000, the Association of the Uruguayan Merino Breeders of Uruguay (SCMAU) with the support of the Uruguayan Wool Secretarial (SUL) developed Central Progeny Centers (PTC). In these PTC, Uruguayan and Australian rams were genetically evaluated. The international wool market tendencies have shown the economical advantages of producing fine and superfine, where the Uruguayan Merino producers and their related institutes and associations decided to begin a national Project oriented to produce these high quality, differentiated and demanded products. Since 1998, SCMAU, SUL and the National Agriculture Research Institute (INIA) founded a Selection Nucleus at the "Glencoe" Experimental Unit (NFG) of INIA, as a part of the Fine Merino Project of Uruguay. The NFG was formed by 720 hoggets selected from the animals of 37 recognized stud breeders and sheep farmers with the intense use of frozen semen imported from Australia, chosen according to their performance at the Merino Sire Evaluation Scheme. Further, during 2001, in conjunction with the NFG and PTC, 7 key Merino Studs started with a pilot across flock genetic evaluation system, connected by reference rams. This was the pioneer seed for the implementation of the Merino National Genetic Evaluation In the 2002, other ten studs were incorporated to the genetic evaluation, resulting in a successful experience of technology adoption by the National Merino Stud Association. This year, the 4th National Genetic Evaluation was performed (progeny 2004). The purpose of this study is to present the first genetic parameter estimations for the Merino in Uruguay as well as the genetics trends realized for the National Merino Population compared with the NFG.

MATERIAL AND METHODS

Records and measurements. The *Asociación Rural del Uruguay* (ARU) provided pedigree information and SCMAU the performing data recorded at stud level. Five traits of economic importance for wool production and quality were recorded: Greasy Fleece (GFW), Clean Fleece Weight (CFW), Average Fibre Diameter (FD), Staple Length (SL) and Body Weight (BW) (aprox. 13-month old). The sampling and laboratory procedures and methodologies used are described by De Barbieri *et al.* (2005).

The data analysed had been recorded during the period 1995-2005. Several quality controls on performance records were carried out in order to exclude logical inconsistencies and biological improbabilities. Unlinked flocks, animals with unknown sires, contemporary groups with less than three observations or with less than two sires, trait values beyond three standard deviations of the contemporary group and animal with missing data for fibre diameter were deleted of the data set.

Estimation of genetic parameters: The genetic parameters for the five productive traits evaluated routinely in the National Genetic Evaluation System for the Merino Breed were estimated using a Restricted Maximum Likelihood - REML (Patterson & Thompson, 1971) by EM algorithm, as implemented in the computer program REMLF90 developed by Misztal & Tsurata (2001). For the estimation the following model was fitted:

 $y_{ijklm} = CG_i + BT_j + DA_k + age + a_l + e_{ijklm}$

where:

y_{iiklm} ...m-th performance record of animal l,

 CG_i ...fixed effect of the contemporary group i (flock-year-sex-management group) (142 levels),

 $BT_j \dots$ fixed effect of birth type j (2 levels),

 $DA_k \dots$ fixed effect of dam age k (4 levels),

age... age at measurement as a co-variable,

 a_1 ...random additive genetic effect of animal 1 (20,335 levels) and e_{ijklm} ...random residual.

Given that in the first 4 years (generations 1995-1998) date of birth and dam's identification and birth year were not recorded, an average age at shearing was fitted for these animals and all dams were fitted as age 4 (more than 3 years old).

Estimated Breeding Values (EBV) and Genetic trend: Breeding values were estimated by BLUP-Animal Model, using the computer program BLUPF90 developed by Misztal (2001), with solutions obtained by the sparse-matrix factorization package FSPAK90 (Misztal & Perez-Enciso, 1998). Genetic base was defined as animals born in 2002. Correlations between the EBV's of the last evaluation (2006), and BV's estimated with the proposed model with the new parameters were also computed. The routinely evaluation model was fitted only by the following contemporary group: flock-year-sex-management group-birth type and uses parameters from the literature.

RESULTS AND DISCUSSION

The original database included 14,849 records for FD. The amount of data diminished up to 13,497 after the mentioned quality control applied. The information is presented in Table 1.

Estimates of genetic and phenotypic parameters are shown in Table 2. Heritability values for GFW, CFW, SL and BW are similar to those reported in the literature (Fogarty, 1995; Safari *et al.* 2005). Conversely, heritability estimates for FD was slightly higher than found by Fogarty (1995) and Safari *et al.* (2005) for wool breeds (0.51 and 0.59, respectively). However, other authors found similar heritabilities to this work for FD (i.e Brown *et al.*, 2002 cited by Safari and Fogarty, 2003). Phenotypic and genetic correlations do not widely differ from average literature values (Safari *et al.*, 2005). The genetic correlation between FD and CFW was unfavorable (+0.12) but with a lower magnitude that the reported by Safari *et al.* (2005) (+0.28). Additionally, the genetic correlation value between FD and SL was much lower than that mentioned by Safari *et al.* (2005) (+0.08 vs. +0.19).

Traits	N°	Reduction (%) ¹	Mean	SD	Min	Max
GFW (Kg)	13,325	9.9	2.85	0.70	0.75	6.11
CFW(Kg)	12,965	9.8	2.16	0.53	0.60	4.73
FD (micron)	13,497	9.1	17.97	1.71	12.90	24.90
BW (Kg)	13,008	9.9	32.94	8.86	13.00	73.74
SL (cm)	12,419	10.0	7.89	1.57	3.00	14.50

Table 1. Descriptive statistics of production traits

¹Reduction of data after quality control applied.

Traits	GFW	CFW	FD	BW	SL
GFW	0.39	0.86	0.29	0.38	0.37
CFW	0.91	0.39	0.12	0.35	0.43
FD	0.25	0.16	0.67	0.17	0.08
BW	0.40	0.38	0.15	0.37	0.14
SL	0.29	0.34	0.12	0.17	0.48

Table 2. Genetic and phenotypic parameters for the Merino Breed¹

¹Heritabilities (in bold) on the diagonal, phenotypic and genetic correlations below and above the diagonal, respectively.

Estimated Breeding Values and Genetic trend: The estimated genetic parameters were used to estimate breeding values. Correlations between these EBVs and the EBVs from the last National Genetic Evaluation (2006) were very high: 0.94, 0.94, 0.98, 0.91 and 0.97 for GFW, CFW FD, BW and SL, respectively. Genetic trends for FD and CFW, comparing the different sources; the NFG (1999-2004) and National Merino Population (NFG included, 2001-2004; NMP) are presented in Figure 1. The evaluations of the genetic parameters of the NFG and NMP show a negative (favorable) trend for FD (-0.24 and -0.15 microns per year, which is equivalent to a -1.3 and -0.5% change per year, respectively). Genetic trends for CFW are - 0.01 and 0.02 Kg for the NFG and NMP, respectively. The tendencies observed in the NFG are in agreement with the breeding objective established when this Nucleus was set in 1998, having very important reductions in FD with slightly losses in CFW.

CONCLUSION

During the last 4 years, as a result of the implementation of the Fine Merino Project as well as the local commercial incentives to produce much finer wool, in general, there is an agreement in terms breeding objectives amongst Uruguayan Merino Stud Breeders to put more emphasis on decreasing FD, with increasing in BW and maintaining or increasing CFW. The genetic (co)variances and the genetic trends presented in this work clearly show that those breeding objectives highlighted can be achieved in commercial situation applying the technology offered by the main research bodies of the Uruguayan Sheep Industry. The collaboration between the breeders (SCMAU) and their institutions (INIA, SUL) provides the framework for having a successful National Genetic Evaluation Program, resulting in a very useful tools to produce fine and superfine wools in Uruguay, which are internationally highly demanded from the textile industry and costumers.



Figure 1. Genetic trends for FD and CFW for the NMP and NFG

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ACKNOWLEDGEMENTS

This work would not have been possible without the support of ARU and SCMAU.

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