

GENETIC PARAMETERS FOR REPRODUCTION IN INTENSIVELY AND EXTENSIVELY MANAGED DOHNE MERINO FLOCKS IN SOUTH AFRICA

S.W.P. Cloete¹, C.L. Nel¹, J.J. Olivier² and G.J. Delpont³

¹ Department of Animal Sciences, Stellenbosch University, Matieland, 7602 South Africa; ² Hillwood Village, Pinehurst, 7607 South Africa; ³Dohne Merino Breeders' Association, Stutterheim, 3083 South Africa

SUMMARY

The study used 61,974 ewe-year records of 26,254 ewes aged 20 months and older for number of lamb born per ewe lambing (NLB), number of lambs weaned per ewe lambing (NLW) and ewe rearing ability (ERA) obtained from intensively managed South African Dohne Merino flocks. Corresponding numbers for extensively managed flocks numbered respectively 14,067 and 5,181. Reproductive output of intensively managed flocks was higher at respectively 1.49 vs. 1.28 NLB and 1.32 vs. 1.19 NLW when compared to extensively managed flocks. In contrast, ERA was slightly lower at 0.894 vs. 0.932 in intensively managed flocks. Estimates of heritability in intensively managed flocks were 0.028 for NLB, 0.016 for NLW and 0.002 for ERA. Corresponding values in extensively managed flocks were respectively 0.066, 0.040 and 0.008. Genetic correlations of NLB with NLW and of NLW with ERA were positive, while genetic correlations of NLB with ERA were not significant. Genetic correlations between performance in intensive and extensive flocks, as derived from pedigree information, amounted to 0.999 for NLB, 0.840 for NLW and 0.595 for ERA. However, large SEs for the latter two correlations made it impossible to make firm recommendations. Further research is indicated.

INTRODUCTION

The South African Dohne Merino was developed from a cross between the Merino and the then German Merino, presently known as the South African Mutton Merino (Van Wyk *et al.* 2008). The Dohne Merino contributed approximately 28% of the weaning weight records to the National Small Stock database during 2010 to 2011 and has shown steady growth over the decade from 2003 to 2012 (Cloete *et al.* 2014). The breed has also been exported to other sheep producing countries, including Australia (Li *et al.* 2013). The genetics of yearling live weight and wool traits in Dohnes were studied by Van Wyk *et al.* (2008). However, the only account of genetic parameters for reproduction traits in the breed involved reproduction totaled over a number of lambing opportunities (Oliver and Cloete 2011).

The Dohne Merino breed is known to be farmed with under widely different conditions, ranging from extensive to very intensive (Jordaan 2013). The enhanced mating systems of intensive management complicate deriving genetic parameters for reproductive performance, since the observed phenotype could also depend on the environment at mating. Also, an alternative to the composite trait selection for reproduction by selecting for number of lambs weaned per mating in South Africa (see review by Brien *et al.* 2014) has been suggested by Bunter *et al.* (2020).

We thus studied the genetics of repeated reproduction records of South African Dohne Merinos. Knowledge of the managerial practices on individual farms allowed us to allocate specific flocks to either an intensive or extensive group. In the intensive group, routine management included the synchronisation of ewes, including the administration of fertility-enhancing drugs, followed by laparoscopic insemination and lambing under controlled conditions in lambing pens. The extensive group, on the other hand, were mated naturally on rangeland without any human intervention. The ewes lambing under the same conditions, and the daily recording of new births was the only human intervention at lambing.

MATERIALS AND METHODS

Traits, recordings and numbers: Data from registered Dohne Merino breeders were available to aid in the allocation of farms to the respective groups defined in the Introduction. Selection for reproduction in South African sheep at present hinges on analysis involving repeated records for number of lambs born (NLB) and number of lambs weaned (NLW) (Brien *et al.* 2014). Since many flocks do not provide complete mating lists to allow for the identification of barren ewes, these traits are expressed per ewe lambing for individual ewes available at lambing. This means that NLB equates to the definition used by Bunter *et al.* (2020) for litter size. Additional to NLB and NLW, ewe rearing ability (ERA) was constructed from the aforementioned traits, as described by Bunter *et al.* (2020). The latter trait is not considered in South African small stock selection at present. The intensive group was represented by 61,974 repeated records of 26,264 ewes lambing in 386 contemporary groups. Analyses on the extensive group used data of 14,067 repeated records of 5,181 ewes in 100 contemporary groups.

Statistical analyses: All data were analysed with ASReml4 (Gilmour *et al.* 2015). Contemporary group and ewe age in months were fitted to account for environmental differences among records. Ewe age was modelled as a fixed linear component as well as a cubic spline to account for random deviations from linearity. Random components included additive ewe effects as well as ewe permanent environmental effects. Initially, single-trait analyses were conducted within management groups, to define operational models for two-trait analyses to obtain genetic correlations among traits. Finally, the intensive and extensive datasets were merged to obtain genetic correlations of the expression of the traits in one environment with performance in the other environment. The pedigree file used in all analyses contained 44,145 individuals, 2,179 sires and 23,546 dams.

RESULTS AND DISCUSSION

Overall, means for the reproduction traits were higher in the intensively managed flocks than in the extensive flocks (Table 1). The exception was ERA which was somewhat better in the extensive grouping, but at a substantially lower birth rate. Derived coefficients of variation ranged from 24.5% for ERA in extensive flocks to 47.4% for NLW in intensive flocks. These estimates are broadly consistent with comparable figures reported in the extensive review by Safari *et al.* (2005) and by Cloete *et al.* (2017).

Table 1. Descriptive statistics, phenotypic variances (σ_p^2) and single-trait heritability (h^2) and repeatability (t) estimates for number of lambs born per ewe lambing (NLB), number of lambs weaned per ewe lambing (NLW) and ewe rearing ability (ERA) in intensively and extensively managed Dohne Merino flocks

Group and trait	Mean \pm SD	Range	σ_p^2	$h^2 \pm SE$	$t \pm SE$
<u>Intensive (n = 61974)</u>					
NLB	1.488 \pm 0.569	1 – 3	0.293	0.028 \pm 0.004	0.061 \pm 0.004
NLW	1.318 \pm 0.625	0 – 3	0.356	0.016 \pm 0.004	0.048 \pm 0.004
ERA	0.894 \pm 0.272	0 – 1	0.068	0.002 \pm 0.002	0.019 \pm 0.004
<u>Extensive (n = 14067)</u>					
NLB	1.282 \pm 0.486	1 – 3	0.201	0.066 \pm 0.012	0.095 \pm 0.009
NLW	1.185 \pm 0.508	0 – 3	0.236	0.040 \pm 0.010	0.064 \pm 0.009
ERA	0.932 \pm 0.229	0 – 1	0.052	0.008 \pm 0.006	0.019 \pm 0.009

NLB and NLW in intensively managed flocks increased to 48 months of age ($P < 0.05$; Figure 1). NLB subsequently remained similar but NLW declined from 60 to 84 months. Extensively managed flocks had an increased NLB and NLW up to 60 months, stabilised at 72 months and declined to 84 months. ERA increased from 24 to 36 months in extensively managed flocks and stabilised thereafter (Figure 1). In contrast, ewe age groups from 36 to 60 months had the best ERA in intensively managed flocks, with lower ($P < 0.05$) figures for 24-month-old ewes and those aged 72 months and older. Trends for NLB and NLW are generally similar with previous results for Dohne Merinos reported by Fourie and Heydenrych (1983).

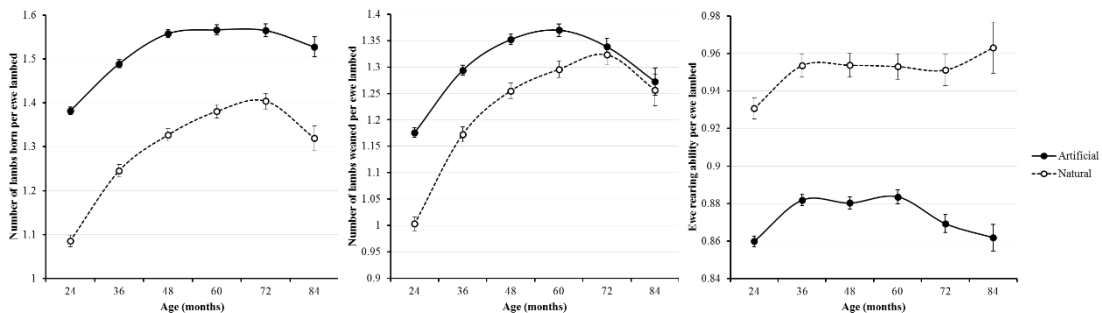


Figure 1. The effect of ewe age in months on the reproduction traits studied

Derived single-trait h^2 and repeatability estimates for NLB and NLW were significant in both management groups, although estimates in intensively managed flocks were somewhat lower ($P < 0.05$; Table 1). ERA was lowly heritable with a low repeatability estimate of around 0.02 in both groups. Recent results from Australian Merino industry (Bunter *et al.* 2020) and resource flocks (Dominik & Swan 2016; Cloete *et al.* 2017) supported a low h^2 for reproduction traits with estimates generally below 0.10 for NLB and NLW, and below 0.05 for ERA.

Phenotypic variance components from two-trait analyses in both intensively and extensively managed flocks in Table 2 were very close to single-trait values in Table 1. Estimates of h^2 were, however, slightly higher in intensive flocks than those in Table 1. In contrast, h^2 estimates of extensive flocks were only about half those in Table 1 for NLB and NLW ($P < 0.05$). Duplicate h^2 -estimates from different trait combinations were all within 0.001 from each other. Two-trait repeatability estimates were very close to the corresponding single-trait estimates, suggesting different repartitioning between h^2 and the animal permanent environment between management systems. Reasons for this result are not evident. In intensive flocks, genetic correlations were positive between NLB and NLW, negative in direction but not different from zero between NLB and ERA and positive between NLW and ERA (Table 2). The latter traits were uncorrelated in extensive flocks. Phenotypic correlations between NLB and NLW were positive in direction but smaller in magnitude than the corresponding genetic correlations. The negative phenotypic relationship between ERA and NLB (Table 2) reflected higher mortality rates of multiples, but the magnitude was low and in close agreement with previous estimates (Bunter *et al.* 2019; 2020).

Genetic correlations between the same trait expressed in either the intensive or extensive environment amounted to 0.999 ± 0.314 for NLB, 0.840 ± 0.459 for NLW and 0.575 ± 0.761 for ERA. The magnitude of these values suggested that NLB and NLW do not have to be considered as different traits. However, the SEs associated with these traits were high, and only the genetic correlation of unity for NLB reached a level of twice the corresponding SE. Genetic variances of small magnitude together with a low level of genetic connectedness between extensive or intensively managed flocks could contribute to the poor accuracy of these estimates. It is common for top ranking sires only to be used for laparoscopic artificial insemination, thus confounding management

groups by sire families. Genomic information could provide an alternative platform to link distant families in future studies, which could improve the accuracy of these estimates.

Table 2. Two-trait phenotypic variances (σ_p^2), heritability (h^2), repeatability (t) and correlation estimates for number of lambs born per ewe lambbed (NLB), number of lambs weaned per ewe lambbed (NLW) and ewe rearing ability (ERA)

Group and trait	Trait		
	NLB	NLW	ERA
<u>Intensive</u>			
σ_p^2	0.2932	0.3562	0.0683
NLB*	0.033 ± 0.005	0.741 ± 0.002	-0.078 ± 0.004
NLW*	0.865 ± 0.040	0.031 ± 0.005	0.560 ± 0.003
ERA*	-0.147 ± 0.140	0.364 ± 0.116	0.018 ± 0.005
T	0.061 ± 0.004	0.045 ± 0.004	0.020 ± 0.004
<u>Extensive</u>			
σ_p^2	0.2015	0.2362	0.0515
NLB*	0.030 ± 0.012	0.772 ± 0.004	-0.092 ± 0.009
NLW*	0.995 ± 0.110	0.017 ± 0.011	0.519 ± 0.006
ERA*	-0.196 ± 0.435	-0.019 ± 0.611	0.012 ± 0.011
T	0.095 ± 0.009	0.057 ± 0.008	0.020 ± 0.009

* Heritability estimates in bold on the diagonal, genetic correlations below and phenotypic correlations above the diagonal

CONCLUSIONS

This study indicated that reproductive traits in South Africa Dohne Merinos are lowly heritable, estimates for ERA not reaching significance in all instances. Repartitioning variances to h^2 and animal PE in two-trait analyses stood to reason in intensive flocks but the reason for the lower two-trait h^2 estimates for NLB and NLW in extensive flocks is difficult to explain. Genetic correlations for the same trait in the two environments were high in absolute values. However, interpretation was complicated by large SEs, suggesting the need for further research.

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