THE IMPORTANCE OF COMPLETE MATING, LAMBING AND WEANING DATA FOR THE ESTIMATION OF TOTAL WEIGHT OF LAMB WEANED BREEDING VALUES

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INTRODUCTION

It is a well-established fact that incomplete phenotypic or pedigree data will reduce the accuracy of BLUP models (Henderson, 1973), which will subsequently lead to bias in the estimated breeding values (EBV; Stock & Distl, 2010). Using these EBVs in selection programs will have a negative impact on the genetic gain of the population, which will subsequently result in the decrease of the profitability of the enterprise, making all the effort and time worthless (Casellas & Piedrafita, 2015; Id-Lahoucine & Casellas, 2017).

Several studies have highlighted the fact that missing phenotypic and pedigree data can be a serious problem for both developing (Nilforooshan et al., 2008) and developed (Harder et al. 2005; Sanders et al., 2006) countries. In studies on sheep and dairy cattle it was found that the lack of pedigree information resulted in the over estimation of heritabilities and EBVs for growth and lactation traits (Nilforooshan et al., 2008; Id-Lahoucine & Casellas, 2017).

Reproduction is the most important trait for small stock enterprises in South Africa to be considered during the selection of replacement rams and ewes (Wang & Dickerson, 1991; Olivier, 1999; Olivier, 2002; Fogarty et al., 2006), because of the effect that it will have on animals available for slaughter, as well as for selection. This fact therefore highlights the importance of the adult ewe flock and the subsequent selection for replacements ewes to be the dams of future generations. Accurate selection for reproduction is challenging because of the low heritability of these traits, as well as the fact that it is a sex limited trait that is expressed after selection was performed (Olivier et al., 1998). Furthermore, genetic progress could even further be hampered by incomplete and inaccurate reproduction data.

The lack of measurements for production traits is seen as a missing value in the estimation of EBV and will probably not have a big influence on the EBV of related animals (Olivier, 2016; Olivier, 2018). However, for reproduction traits, it is important to note that a ewe that did not lamb or wean a lamb should not be regarded as missing data and be excluded from the analysis. This information should be handled as zero values, which will contribute to the variation in these traits and improve the completeness of the data. The completeness of

reproduction data can be defined as all data with regard to ewes that weaned a lamb, ewes that lambed that did not wean a lamb and ewes that were mated but did not lamb.

According to Olivier (2019, J.J. Olivier, Pers. Comm., Bellville, 7530), participants of the National Small Stock Improvement Scheme have in the recent past failed to submit complete mating lists and in some instances lambing information, as only data of ewes that weaned at least one lamb were submitted. Omittance of this information is the major constraint to the usefulness of reproduction data. The aim of this study was therefore to quantify the effect of incomplete reproduction data and to confirm the importance of completeness of reproduction data.

MATERIALS AND METHODS

Data collected on the Grootfontein Merino stud (GMS) from 1968 to 2017 were used for this analysis. The GMS are kept at Grootfontein Agricultural Development Institute near Middelburg (31.4708° S; 25.0286° E), which lies on the eastern edge of the Karoo biome. Non-mountainous vegetation, which comprises 89% of the farm, is described as the Eastern Upper Karoo (Vegetation Type NKu 4) (Mucina et al., 2006). Mean annual rainfall is 373 mm (Du Toit & O'Connor, 2014). The stud was run under natural veld conditions and received strategic supplementary feeding. A detailed description of the management and selection of the stud was done by Nemutandani (2017).

The trait included in the analysis was total weight of lamb weaned per lambing opportunity (TWW). The complete dataset for reproduction traits of the GMS was used in this study, which included data from all the ewes that were born since 1968 in the stud. Subsets of the data were created by excluding or including the reproduction records of ewes. This was done to simulate different levels of data completeness. The first subset (TR – all mating, lambing and weaning data) included data from all the ewes that were mated, lambed or did not lamb and weaned or did not wean a lamb/s for each lambing opportunity. The second subset (TL – lambing and weaning data) included the data of the ewes that weaned at least one lamb of the litter, as well as the data of ewes that lambed but did not wean a lamb for each lambing opportunity. The third subset (TW – only weaning data) included only the data of the ewes that weaned at least one lamb of a litter of each lambing opportunity.

The Proc MEANS-procedure of SAS (SAS, 2016) was used to obtain the descriptive statistics of the datasets. The significance levels for the non-genetic fixed effects (Repeated records animal model: year of lambing and age of animal at lambing; single record animal model: year of birth) were obtained with the PDIFF-option under the Proc GLM-procedure of SAS (SAS, 2016). Only effects that had a significant effect ($P<0.01$) on a specific trait, were included in the final operational model.

The estimation of the genetic parameters for TWW of the three subsets, as well as the EBVs was done with the ASReml 4.0 program (Gilmour et al., 2014) by fitting a repeatability model. In order to quantify the effect of data completeness, the Spearman rank correlation under the PROC CORR-procedure of SAS (SAS, 2016) was used to estimate the correlations between the ranks of these EBVs for TWW of all three subsets.

Furthermore, lists were compiled of the Top 10% and Top 20% of the animals having the highest EBVs for TWW, estimated in the different data subsets. These lists were compiled for all animals in the pedigree file. The number and percentage of animals common to the different top lists were compared among the subsets.

The direct selection response for TWW for each subset was calculated using the following formula:

$$R = ih^2\delta_P$$

where; R is the direct selection response, i is the selection intensity, h^2 is the heritability and δ_P is the phenotypic standard deviation of the trait. For the purpose of this study, it was assumed that 5% males and 50% females were selected. The selection intensities for the males and females were taken from the Appendix Table A of Falconer and Mackay (1996). The selection intensities used in this study were calculated as the unweighted means of the selection intensities of males and females.

Correlated selection response among TWW of the three subsets, as well as body weight (BW) at performance testing age was calculated using the following formula:

$$CR_Y = ih_Xh_Yr_A\delta_{PY}$$

where; CR_Y is the correlated response in Y if selection is based on X, i is the selection intensity, h_X is the square-root of the heritability of X, h_Y is the square-root of the heritability of Y, r_A is the genetic correlation between X and Y and δ_{PY} is the phenotypic standard deviation of Y. BW was included for the correlated response calculations, because it can be used as an indirect selection criterion to increase TWW.

RESULTS AND DISCUSSION

The description of the data for the different subsets is summarised in Table 1. There was an increase in the number of lambs born (NLB) and number of lambs weaned (NLW) and total weight of lamb weaned with a decrease in completeness of the data. The increase in NLB, NLW and TWW between the TR and TL subsets were 29%, 28% and 28% respectively. The corresponding increase in NLW and TWW between TR and TW subsets was 51%. Similarly, there was an increase of 18% in NLW and TWW between the TL and TW subsets. These increases in the means of NLB, NLW and TWW are clearly linked to the exclusion of information of ewes that did not lamb or wean a lamb. An important part in the success of selection for reproduction is the

available variation in these traits. It is evident from Table 1 that there is a substantial decrease in the CVs of the traits as the completeness of the data decreases.

Table 1. Data description of different data subsets used for this analysis

Reproduction Data	Traits	Number of records	Mean	CV (%)
Subset 1 - TR Include: All mating, lambing and weaning data	Number of lambing opportunities	3866	3.34	48.09
	Number of lambs born	3866	1.2	45.27
	Number of lambs weaned	3866	0.92	58.03
	Total weight of lambed weaned (TWW1)	3866	24.52	58.09
Subset 2 - TL Include: All lambing and weaning data	Number of lambing opportunities	3565	2.93	49.91
	Number of lambs born	3565	1.55	25.43
	Number of lambs weaned	3565	1.18	42.45
	Total weight of lambed weaned (TWW2)	3565	31.28	41.83
Subset 3 - TW Include: All weaning data	Number of lambing opportunities	3340	2.72	51.27
	Number of lambs born	-	-	-
	Number of lambs weaned	3340	1.39	26.53
	Total weight of lambed weaned (TWW3)	3340	36.97	25.35

The repeatability (t), direct heritability (h^2_a) and animal permanent environmental effect (c^2_{pe}) for TWW ($\pm$ s.e.) of the respective subsets are summarised in Table 2. The heritabilities of TWW were low and ranged from 0.03 ± 0.01 to 0.06 ± 0.01 and these values increased with an increase in the completeness of the data. These values are in correspondence with values summarised in the literature (Safari et al., 2005; Olivier, 2014).

The estimates for c^2_{pe} were very low and ranged from 0.02 ± 0.01 to 0.04 ± 0.01 and are at the lower end of the range of 0.00 to 0.13 summarised by Olivier (2014). The repeatability estimates for the respective traits were low and ranged from 0.05 ± 0.01 to 0.10 ± 0.01. These estimates were slightly lower than the values summarised by Olivier (2014). The same trend in repeatability was observed as in h^2_a, with estimates increasing with an increase in the completeness in the data.

Table 2. Repeatability (t), direct heritability (h^2_a) and animal permanent environmental effect (c^2_{pe}) (± s.e.) for total weight of lamb weaned (TWW) of the respective subsets

Trait	h^2_a	c^2_{pe}	t
TR_TWW (Total reproduction)	0.06 ± 0.01	0.04 ± 0.01	0.10 ± 0.01
TL_TWW (Lambing data)	0.04 ± 0.01	0.03 ± 0.01	0.07 ± 0.01
TW_TWW (Weaning data)	0.03 ± 0.01	0.02 ± 0.01	0.05 ± 0.01

TR – All mating, lambing and weaning data; TL – Lambing and weaning data; TW – Weaning data

The range of repeatability model estimated breeding values (EBVs; Min-Max) for total weight of lamb weaned, as well as the average accuracies of the EBVs (Min-Max) for the respective subsets are summarised in Table 3. It is evident from Table 3 that the top end of the EBVs decreased with 2.15 kg as the variation in TWW decreased because of the exclusion (unavailability) of mating and lambing data. However, the lower boundary of the TWW EBVs increased substantially with 4.73 kg as the available variation decreased.

Table 3. The average of repeatability model estimated breeding values (EBVs; Min-Max) for total weight of lamb weaned (TWW), as well as the average accuracies of the EBVs (Min-Max) for the respective subsets

Trait	EBV	Accuracies
TR_TWW (Total reproduction)	0.54 (-8.92 to 9.53)	51.79 (23.33-67.23)
TL_TWW (Lambing data)	0.42 (-5.80 to 9.06)	47.96 (0.18-65.48)
TW_TWW3 (Weaning data)	0.23 (-4.19 to 7.38)	45.19 (0.13-64.14)

TR – All mating, lambing and weaning data; TL – Lambing and weaning data; TW – Weaning data

These changes in the upper and lower boundaries resulted in a 24% decrease in the EBV range between TR and TL, 59% between TR and TW and 28% between TL and TW. These changes suggest that EBVs of the better reproductive ewes will be affected negatively. However, the biggest concern is the fact that the EBVs of the ewes with poorer reproduction will increase. It is also evident that there was a decrease of 4% and 7% in the mean accuracies of TWW EBVs between TL and TR and between TW and TR respectively. The respective upper accuracy boundaries of TL and TW were 2% and 3% lower compared to TR. However, as with the EBVs, the changes in the lower accuracy boundaries of TR and TL from TW were much more substantial.

The Spearman rank correlations among the breeding values of TWW for the respective data subsets are summarised in Table 4. The Spearman rank correlation among TR, TL and TW ranged from 0.63 to 0.84. The unavailability of mating and lambing data will thus result in a major re-ranking of the ewes, especially when only weaning data are included.

Table 4. Spearman rank correlations among the total weight of lambed weaned EBVs of the different subsets

Trait	TL_TWW	TW_TWW
TR_TWW	0.84	0.63
TL_TWW		0.75

TR – All mating, lambing and weaning data; TL – Lambing and weaning data; TW – Weaning data

The number and proportion of common animals in the Top 10% and Top 20% lists when all animals in the pedigree were included are presented in Table 5 for TWW EBV estimated for TR, TL and TW. The highest percentage common animals in Table 5 were in the Top 20% lists between TR and TL, as well as between TL and TW, with just more than 70% common animals. The lowest percentage of common animals in both the Top 10% and Top 20% lists were 54.26% and 57.24% respectively, between TR and TW, which could be expected due to the difference in the level of completeness of the data. The proportion of common animals between TR and TL and TL and TW were 66.93% and 66.15% respectively in the Top 10% list. The differences in the proportion of common animals indicate that animals will be culled that could have increased the reproductive potential of the ewe flock. It also supports the notion that the Spearman rank correlations (Table 4) indicate that there will be substantial re-ranking of animals due to the difference in completeness of the data.

Table 5. The number and proportion of common animals in the Top 20% and Top 10% lists when all animals in the pedigree were included for total weight of lamb weaned (TWW) for the three subsets

Subsets	Top 10% list (n = 387)		Top 20% list (n = 774)	
	Number	%	Number	%
TR_TWW vs TL_TWW	259	66.93%	556	71.83%
TR_TWW vs TW_TWW	210	54.26%	443	57.24%
TL_TWW vs TW_TWW	256	66.15%	549	70.93%

TR – All mating, lambing and weaning data; TL – Lambing and weaning data; TW – Weaning data

The direct (on diagonal in bold) and correlated selection response (off diagonal) in TWW per generation for the subsets expressed in kilogram and as a percentage of the mean of TWW of each subset when selection is based on TWW or BW at performance testing age (± 14 months of age) are summarised in Table 6. Due to the favourable correlation between BW and reproduction (Safari et al., 2005; Olivier, 2014), BW is used as an indirect selection criterion for reproduction by many breeders. It was therefore included in the calculation of the selection responses for the respective subsets.

The direct response per generation to selection based on TWW were 1.60 kg, 0.95 kg and 0.51 kg for the TR, TL and TW subsets respectively. These responses present an improvement of 6.03%, 2.88% and 1.34% respectively that could be achieved per generation through direct selection. It is furthermore evident that there was an increase of 216% in the direct selection response that could have been achieved if complete and accurate reproduction data were recorded. The fact that BW has higher indirect selection responses in TWW compared to direct selection response can largely be attributed to the higher h^2_a of BW. However, the main constraint of using BW as the only selection objective is the unwanted increase in adult BW (Olivier, 2014).

Table 6. The direct (on diagonal in bold) and correlated selection response (off diagonal) in total weight of lamb weaned (TWW) per generation for the subsets expressed in kilogram and as a percentage of the mean of TWW of each subset

Trait under selection	Response in kg			Response as percentage of the means		
	TR_TWW	**TL_TWW**	**TW_TWW**	**TR_TWW**	**TL_TWW**	**TW_TWW**
Body weight	1.85	1.47	1.06	6.95	4.47	2.79
TR_TWW	**1.60**	1.16	0.72	**6.03**	3.53	1.89
TL_TWW	1.31	**0.95**	0.59	4.92	**2.88**	1.54
TW_TWW	1.13	0.82	**0.51**	4.26	2.50	**1.34**

TR – All mating, lambing and weaning data; TL – Lambing and weaning data; TW – Weaning data

The deviation of the selection responses of selection based on BW and TWW expressed as a percentage of the selection response obtained for selection based on TWW in each of the subsets is presented in Table 7. From Table 6 and 7 it is evident that indirect selection for BW would result in a 0.5 kg better selection response in the TL and TW subsets compared to direct selection for TWW. These differences between the indirect and direct selection responses in TL and TW are 55% and 108.78% respectively. Under these conditions of incomplete reproduction data, indirect selection on BW would be much more advantageous than direct selection.

Table 7. The deviation of the selection responses of selection based on body weight and total weight of lamb weaned (TWW) expressed as a percentage of the selection response obtained for selection based on TWW in each of the subsets

Trait under selection	TR_TWW (%)	TL_TWW (%)	TW_TWW (%)
Body weight	115.27%	155.00%	208.78%
TR_TWW	**100.00%**	122.46%	141.41%
TL_TWW	81.64%	**100.00%**	115.46%
TW_TWW	70.70%	86.59%	**100.00%**

TR – All mating, lambing and weaning data; TL – Lambing and weaning data; TW – Weaning data

CONCLUSIONS

It can be concluded from the results of this study that the completeness and accuracy in the collection of reproduction data will have a substantial impact on the improvement in total weight of lamb weaned per generation through selection. It is clear from the results that the omission of mating and lambing data will result in an increase of the mean of TWW, as well as a decrease in the variation available for selection. This decrease in the phenotypic variation was also reflected in the decrease of h^2_a, as well as the decrease in the EBV ranges.

Indirect selection for BW will be more advantageous as selection objective if the integrity of the reproduction data is questionable due a lack of completeness and accuracy. However, the small difference between the direct selection response in TWW and indirect response from BW for the TR subset, suggests that when all mating, lambing and weaning data were recorded, direct selection for TWW would be the most advantageous. It is therefore of the utmost importance that participants of the National Small Stock Improvement Scheme have to submit all relevant mating, lambing and weaning data for the evaluation of reproduction traits and the improvement of flock productivity.

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