

## ESTIMATING HERITABILITY OF SUBJECTIVELY ASSESSED OSTRICH LEATHER QUALITY TRAITS USING THRESHOLD MODELS

A. Engelbrecht<sup>1,2</sup>, S.W.P. Cloete<sup>1,3</sup>, K.L. Bunter<sup>4</sup> and J.B. van Wyk<sup>5</sup>

<sup>1</sup>Department of Animal Sciences, University of Stellenbosch, Matieland 7602, South Africa

<sup>2</sup>Institute for Animal Production, Oudtshoorn Research Farm, Oudtshoorn 6620, South Africa

<sup>3</sup>Institute for Animal Production, Elsenburg, Private Bag X1, Elsenburg 7607, South Africa

<sup>4</sup>Animal Genetics and Breeding Unit, University of New England, Armidale, NSW 2351, Australia

<sup>5</sup>Department of Animal, Wildlife and Grassland Sciences, University of the Free State, Bloemfontein 9300, South Africa

### SUMMARY

Several ostrich leather traits cannot be assessed objectively within the present industry structure. A subjective scoring system was devised to allow the assessment of several qualitative leather traits for the estimation of genetic parameters. Nodule size and shape, along with the presence of hair follicles and pitting damage were scored on linear scales from 1 to 9 on 1021 processed ostrich skins. The data were analysed together with live weight and skin size using threshold-linear animal models, with compression of categories where required. Heritability estimates were 0.44 for live weight, 0.33 for skin size, 0.46 for nodule size, 0.33 for nodule shape, 0.49 for hair follicles and 0.15 for pitting. The 95% highest posterior density confidence intervals for all variance components excluded zero. The quantitative slaughter traits were favourably related to nodule shape and nodule size, while the presence of hair follicles or pitting was not significantly related to the other traits on a genetic level. Sufficient genetic variation was demonstrated to allow sustained genetic progress for objective and subjectively assessed traits.

### INTRODUCTION

Ostrich leather is considered unique due to the feather follicles which gives it a distinctive nodulated appearance (Engelbrecht *et al.* 2009). The appearance of the nodules is consequently important when the value of ostrich leather is determined (Engelbrecht *et al.* 2005). Despite its importance, nodule traits are currently being assessed subjectively owing to a lack of practical objective evaluation methods (Cloete *et al.* 2006; Van Schalkwyk *et al.* 2005). The appearance and distribution of nodules, as well as the heritability of nodule size and density, varies between different locations on the skin (Cloete *et al.* 2006), making it difficult to accurately evaluate leather quality with objective methods.

Other aspects that influence the value of ostrich leather that are also being assessed subjectively are skin damage and skin defects. Skins are frequently downgraded due to pitting damage, defined as small superficial pits on the surface of the leather. This defect is clearly discernable on processed skins, and impairs the quality of the leather (Engelbrecht *et al.* 2009). An excessive occurrence of hair follicles among feather follicles is also considered a defect, resulting in skins being downgraded (Lunam and Weir 2006).

Slaughter age was previously shown to influence leather traits (Engelbrecht *et al.* 2005; Van Schalkwyk *et al.* 2005; Cloete *et al.* 2006). Van Schalkwyk (2008) later reported a significant interaction between age and weight for nodule traits, indicating that the effect of age and weight could not be partitioned accurately.

Cloete *et al.* (2008) recently demonstrated the genetic basis of most ostrich traits of economic importance, including slaughter and leather traits. Meyer *et al.* (2004) reported low heritabilities for nodule traits when measured with objective methods, while Engelbrecht *et al.* (2005) reported higher heritabilities for subjectively assessed nodule traits, analyzed with linear REML methods.

Improvement of these subjectively assessed leather traits through genetic selection was consequently further investigated. In order to better understand to what extent ostrich leather quality traits are heritable, linear-threshold models were used for data analysis in this study to properly account for the distribution and categorical nature of the data.

## **MATERIALS AND METHODS**

Pedigree records and processed skins were obtained from South African Black ostriches in the research flock maintained at the Oudtshoorn Research Farm, near Oudtshoorn in the Klein Karoo region of South Africa. The pedigree file contained 2577 records, the progeny of 300 sires and 282 dams. Processed crust skins from birds slaughtered between 1997 and 2007, aged 240 to 480 days (mean  $\pm$  s.d. = 367  $\pm$  55 days), were scored for nodule traits (nodule size and shape), and for the prevalence of hair follicles and pitting damage. Live weight at slaughter, slaughter age and crust skin size were available for most of the birds included in the investigation.

Average nodule size (NSZ) and nodule shape (NS) on skins were evaluated on linear scales of 1 to 9, with one indicating poor quality and 9 indicating excellent quality. Scoring for nodule size was standardized by establishing visual standards for each score. A representative skin was chosen for each score from one to nine based on the average size of the nodules on the skin. These skins served as standards against which each skin could be compared during scoring. For nodule shape, each score was defined in terms of the general shape of the nodules on the skin. Scores of 1 to 3 were used for skins with mostly poorly developed or elongated nodules, 4 to 6 for skins with relatively rounded nodules and 7 to 9 for skins with well-rounded nodules.

The overall occurrence of hair follicles (HF) and pitting (PIT) on skins were also evaluated on a scale of 1 to 9, with one indicating none and 9 indicating an excessive occurrence of the relevant defect on a skin. The scoring system was devised by Engelbrecht *et al.* (2005), and was applied by the first author throughout to exclude variation between scorers.

Linear-threshold animal model analyses were applied for the estimation of (co)variance components and genetic parameters. Analyses were performed using THRGIBBS1F90 software, which is suitable for the estimation of (co)variance components and genetic parameters in threshold-linear animal mixed models, and allows for any combination of categorical and continuous traits (Misztal *et al.* 2002). A single chain of 200,000 samples were run, with 40,000 samples being used as the burn-in period. The remaining 160,000 samples were retained for post-Gibbs analysis with the POSTGIBBSF90 graphical program (Misztal *et al.* 2002). Every 10<sup>th</sup> sample was saved and used to compute means (which were used as point estimates for parameters), posterior standard deviations and 95% highest posterior density (HPD) confidence intervals.

Fixed effects included in the analysis were contemporary group (n = 21) and gender (male and female). Slaughter age (240 to 480 days) was included as a linear covariate for all traits, while animal was added to the operational model as a single random effect. Preliminary analyses showed that thresholds could not be accurately discerned for all traits. The quality of threshold estimates depend on the number of records in categories, while too many categories (i.e. 9) tend to be similar to continuous traits and result in some thresholds having too little information (pers. comm. Ignacy Misztal). Due to the poor representation of certain categories (< 10 records), adjacent categories were merged to improve data distribution and the estimation of thresholds. Scores of 4 to 6 (average occurrence of pitting) and 7 to 9 (excessive occurrence of pitting) were pooled for pitting. After pooling adjacent categories based on the numbers of records per category, the number of categories entered in the final analyses amounted to five for pitting, six for nodule size and nodule shape (scores 1 and 2 pooled, and 7, 8 and 9 pooled), and seven for hair follicles (scores 7, 8 and 9 pooled).

Two sets of analyses were conducted: initially live weight (LW) and processed skin size (SSZ)

were analysed with each individual subjectively assessed skin trait in four three-trait analyses. A four-trait analysis involving all subjective traits was conducted subsequently.

## RESULTS AND DISCUSSION

Means ( $\pm$  s.d.) for LW ( $n = 1194$ ) and SSZ ( $n = 1451$ ) were  $92 \pm 17$  kg and  $137 \pm 14$  dm<sup>2</sup> respectively. The distribution of records for scored traits before merging is shown in Table 1. The distribution of scores ( $n = 1021$ ) for nodule traits and hair follicle prevalence did not deviate from normality, while scores for pitting were skewed and leptokurtic. Merging of pitting categories reduced skewness from 2.80 to 1.79 and kurtosis from 10.73 to 2.92. Pooling higher categories for pitting did not reduce the predominance of score 1, so pitting was absent for more than 50% of skins.

**Table 1. Number of records per category for scored ostrich skin traits**

Trait	Category								
	1	2	3	4	5	6	7	8	9
Nodule size	14	37	184	402	248	90	28	11	7
Nodule shape	14	75	233	333	232	101	30	3	0
Hair follicles	25	184	257	191	172	106	56	28	2
Pitting	648	271	49	31	9	8	3	1	1

Estimates of heritability ( $h^2$ ), trait variances, along with environmental and genetic correlations are provided in Table 2. Covariance ratios did not differ significantly between the different three-trait analyses, or between the three-trait analyses and the four-trait analysis when the relevant standard errors were compared (not presented). Estimates reported for the scored traits are from the four-trait analyses, while the estimates for LW and SSZ provided in Table 2 were averaged across the four three-trait analyses. The genetic variance components and ratios for all traits were significant, as reflected by the 95% highest posterior density (HPD) confidence limits excluding zero. The 95% HPD intervals for the genetic variance components were 47.2 to 105 for LW, 26.3 to 58.3 for SSZ, 0.27 to 0.86 for NSZ, 0.16 to 0.90 for NS, 0.24 to 0.73 for HF and 0.04 to 0.36 for PIT.

Estimates of  $h^2$  were moderate to high for all skin traits analysed, except for PIT, and were consistent across different sets of analyses. Estimates for NSZ, NS and HF were somewhat higher than previously reported by Engelbrecht *et al.* (2005) when data from a wider slaughter range were included in a linear model analysis (0.43 for NSZ, 0.20 for NS and 0.31 for HF). This could indicate that threshold analysis was more appropriate for estimation of parameters for subjectively scored skin traits. On the other hand, the use of more data from typical slaughter birds (narrower age range) could also have contributed to this result. In contrast,  $h^2$  of LW were similar to the previous estimate of 0.46, while  $h^2$  of SSZ was somewhat lower than the previous estimate of 0.47 (Engelbrecht *et al.* 2005).

The significant heritability estimate for pitting is somewhat surprising since pitting was previously thought to be related only to on-farm practices and environmental factors (Engelbrecht *et al.* 2009). It could, however, be an indication as to a parasitic origin of pitting damage, reflecting genetic differences in parasitic resistance.

The genetic correlation between live weight and skin size did not differ from unity, corresponding with previous studies conducted on the same resource population (Engelbrecht *et al.* 2005). Significant genetic correlations were also found between LW and NSZ, and between SSZ and NSZ or NS. The high correlation found between NSZ and NS confirmed previous results of Engelbrecht *et al.* (2005). It is noteworthy that genetic correlations of live weight and skin size with nodule traits were slightly lower in absolute terms when compared with the previous results

reported by Engelbrecht *et al.* (2005), who used a smaller data set with a wider range of slaughter ages and thus live weight and skin size. With more data at our disposal at present, it was possible to source sufficient records of animals with a more realistic slaughter age for this study. No other significant genetic correlations were found between the slaughter and skin traits investigated, although the standard errors were mostly so high that these estimates cannot be seen as conclusive.

**Table 2. Additive genetic ( $\sigma^2_a$ ) and environmental ( $\sigma^2_e$ ) variance components, along with heritabilities, genetic and environmental correlations ( $\pm$  s.e.), for ostrich slaughter traits**

	Trait					
	Live weight (LW)	Skin size (SSZ)	Nodule size score (NSZ)	Nodule shape score (NS)	Hair follicle score (HF)	Pitting score (PIT)
$\sigma^2$ (a)	75.92	42.29	0.56	0.53	0.48	0.20
$\sigma^2$ (e)	97.86	87.02	0.66	1.06	0.50	1.15
	Heritabilities (diagonal, bold), residual (above diagonal) and genetic (below diagonal) correlations					
LW	<b>0.44 <math>\pm</math> 0.09</b>	0.64 $\pm$ 0.08	0.40 $\pm$ 0.10	0.32 $\pm$ 0.19	0.12 $\pm$ 0.10	-0.22 $\pm$ 0.08
SSZ	0.98 $\pm$ 0.19	<b>0.32 <math>\pm</math> 0.07</b>	0.51 $\pm$ 0.10	0.49 $\pm$ 0.21	0.16 $\pm$ 0.08	-0.19 $\pm$ 0.07
NSZ	0.42 $\pm$ 0.16	0.49 $\pm$ 0.18	<b>0.46 <math>\pm</math> 0.12</b>	0.38 $\pm$ 0.12	0.26 $\pm$ 0.11	-0.26 $\pm$ 0.10
NS	0.32 $\pm$ 0.19	0.49 $\pm$ 0.21	0.78 $\pm$ 0.27	<b>0.33 <math>\pm</math> 0.12</b>	-0.07 $\pm$ 0.16	-0.12 $\pm$ 0.07
HF	-0.15 $\pm$ 0.16	-0.16 $\pm$ 0.08	0.04 $\pm$ 0.18	0.23 $\pm$ 0.20	<b>0.49 <math>\pm</math> 0.13</b>	0.03 $\pm$ 0.08
PIT	0.24 $\pm$ 0.21	0.25 $\pm$ 0.21	0.55 $\pm$ 0.32	0.32 $\pm$ 0.27	-0.24 $\pm$ 0.25	<b>0.15 <math>\pm</math> 0.06</b>

## CONCLUSIONS

Improvement of ostrich leather quality is important for continued profitability in the commercial industry. Accurate evaluation of skin quality and directed genetic selection for improved leather quality are therefore a prerequisite.

This study demonstrated that genetic variation exists for nodule traits and hair follicle prevalence to allow sustained genetic progress for these traits, should it be desired as part of the overall selection objective. In practice, selection decisions will depend on progeny test results, as nodule traits cannot be scored on live birds at present. Alternatively progress in traits like nodule shape and nodules size are or could be achieved through favourable genetic correlations with live weight and/or skin size, evaluated on an age constant basis.

## REFERENCES

- Cloete, S.W.P., Engelbrecht, A., Olivier, J.J. and Bunter, K.L. (2008) *Aust. J. Exp. Agric.* **48**:1247.
- Cloete, S.W.P., Van Schalkwyk, S.J., Engelbrecht, A. and Hoffman L.C. (2006) *S. Afr. J. Anim. Sci.* **36**:160.
- Engelbrecht, A., Cloete, S.W.P. and Van Wyk, J.B. (2005) *Proc. 3<sup>rd</sup> Int. Ratite Sci. Symp. & XII World Ostrich Congr.*, 121.
- Engelbrecht, A., Hoffman, L.C., Cloete, S.W.P. and Van Schalkwyk, S.J. (2009) *Anim. Prod. Sci.* **49**:549.
- Lunam, C.A. and Weir, K.A. (2006) RIRDC Pub No. 06/054, Canberra, Australia.
- Meyer, A., Cloete, S.W.P., van Wyk, J.B. and Van Schalkwyk, S.J. (2004) *S. Afr. J. Anim. Sci.* **34**:29.
- Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T. and Lee, D.H. (2002) *Proc. 7<sup>th</sup> World Congr. Gen. Appl. Livest. Prod.* **33**:743.
- Van Schalkwyk, S.J., Cloete, S.W.P., Hoffman, L.C. and Meyer, A. (2005) *S. Afr. J. Anim. Sci.* **35**:48.
- Van Schalkwyk, S.J. (2008) PhD Thesis, University of Stellenbosch, South Africa.