

Short Communication

Genetic variation in nodule size at different sites on the skins of slaughter ostriches

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Abstract

Nodule size is an important indicator of leather quality in the ostrich leather trade. The present study investigated genetic variation in nodule size at five sites on the skin, namely the neck, back, upper leg, flank and butt. Nodule size increased with an increased chronological age at all sites. Estimates of h^2 for nodule size ranged from 0.09 ± 0.07 on the flank region to 0.24 ± 0.10 on the upper leg region. Genetic correlations between nodule sizes measured at different sites were generally lower than expected, linked to high standard errors and mostly not significant. These preliminary results seem to suggest that nodule size on different locations of the skin is not necessarily the same genetic trait. Apart from the limitations evident from these results, the objective measurement of nodules on ostrich skins is tedious when done manually, with little prospect for automation. The number of nodules per dm^2 (nodule density) was considered within skin sites as an indirect criterion for the improvement of nodule size. However, genetic correlations between nodule density and nodule size were negative, variable in size and generally not significantly different from zero or unity. Based on these preliminary results, alternative strategies for the genetic improvement of ostrich skin nodule size should be considered.

Keywords: Genetic correlations, heritability, leather quality, nodule density

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Leather contributes markedly to the revenue of commercial ostrich farmers. Cloete *et al.* (1998) estimated that ostrich leather contributed approximately 70% to the total income obtained by ostrich farmers during the mid 1990's. This contribution has since declined, with ostrich meat becoming more popular. Leather is, however, still estimated to contribute more than 50% to the total income of ostrich producers, depending on the quality of the product (Hoffman, 2005).

Ostrich leather competes in the exotic leather market, and is marketed as a luxury product (Cooper, 2001; Adams & Revell, 2003). Despite its value, little is known about its physical properties and the influence of various factors thereon (Sales, 1999; Meyer, 2003). There is consensus that the size and general appearance of the nodules on ostrich skins contribute markedly to its value in the marketplace (Meyer *et al.*, 2004; Engelbrecht *et al.*, 2005; Van Schalkwyk *et al.*, 2005a). Previous studies have suggested genetic variation in qualitative nodule traits (Meyer *et al.*, 2004; Engelbrecht *et al.*, 2005), suggesting that it can be improved by selection. However, marked variation occurs in nodule parameters measured at different locations on the ostrich skin (Cloete *et al.*, 2004; Meyer *et al.*, 2004). The aim of the present study was therefore to extend the previous work of Meyer *et al.* (2004), by determining whether the heritability of nodule traits varies between locations on the ostrich skin.

Approximately 500 South African Black slaughter ostriches from the commercial ostrich population at the Oudtshoorn experimental farm were used. The background and origin of the population are well described in the literature (Van Schalkwyk *et al.*, 1996; Bunter & Cloete, 2004). The birds were slaughtered according to standard South African procedures (Van Schalkwyk *et al.*, 2005b). All the skins were processed to the chrome-crusted stage, using standard procedures (Meyer *et al.*, 2003a; b). Complete pedigree records (i.e. both sire and dam identities) were available for 439 of these ostriches, while sire identity only was known for a further 41 birds. These data were used to estimate genetic and environmental

parameters for two skin traits. For this purpose, average nodule size and density for each skin were determined at five localities of 1 dm² each, as described by Cloete *et al.* (2004). The localities were situated on the neck, mid-crown area, upper leg, lower flank and in the middle of the rear back area (subsequently referred to as the butt). The base diameter of 10 individual nodules within each site (chosen according to a predetermined grid) was measured with a Digimatic Caliper (Toolquip & Allied, P.O. Box 687, Goodwood 7459, South Africa) and the number of nodules was counted. An average value was subsequently derived from these measurements. The mean nodule diameter (subsequently referred to as nodule size) and density (nodules/dm²) were subsequently obtained for the respective localities on the skin. In preliminary analyses all nodules were also measured on the mid-crown and upper leg regions of 10 skins. Correlations of means derived from all measurements with means derived from 10 measurements were ≥ 0.89 . It was thus decided that means derived from 10 measurements were representative of the nodule size of specific skins.

In the previous study of Meyer *et al.* (2004), data were analysed across localities, using an unstructured repeatability model. However, this approach assumes equal means and variances for the traits (nodule size and nodule number) across localities. This was clearly not the case in the literature (Cloete *et al.*, 2004; Meyer *et al.*, 2004). The present study therefore estimated heritability for each location. Apart from random animal effects, year of slaughter was fitted as fixed and age at slaughter was fitted as a linear covariate. Initially single-trait animal models were fitted, using ASREML (Gilmour *et al.*, 1999). These analyses were followed with a multi-trait analysis involving nodule size at all five sites as different traits. This multi-trait analysis involving nodule size in the neck region failed to converge, and this location was excluded. Genetic and environmental correlations between nodule size at the respective sites were estimated from this analysis. Two-trait animal models involving nodule size and nodule number at each locality were fitted next, to obtain genetic correlations between these traits at the respective sites.

Traits were normally distributed in the majority of cases (Table 1). A significant deviation from normality in the case of nodule density on the upper leg was attributed to kurtosis rather than skewness. Interpretation of results was thus continued as motivated by Glass *et al.* (1972). Coefficients of variation (CV's) ranged from 17.9% to 25.2% in the case of nodule density, and from 11.7% to 13.7% in the case of nodule size. Corresponding CV's in the study of Meyer *et al.* (2004) were 33.4 for nodule density and 15.2 for nodule size, when measurements made at different locations were treated as the same trait. Means pertinent to each location were consistent with those available in the literature (Cloete *et al.*, 2004; Meyer *et al.*, 2004).

Table 1 Descriptive statistics for nodule density and nodule size measured on different locations on ostrich skins

Trait and Location	Number of skins	Mean \pm s.d.	Coefficient of variation	Skewness	Kurtosis	Range
Nodule density						
Neck	480	54.2 \pm 10.3	19.0	0.99	1.29	35 – 98
Mid crown	480	57.8 \pm 10.4	17.9	0.91	1.23	36 – 106
Upper leg	480	28.0 \pm 6.4	22.9	1.40	3.83	17 – 64
Lower flank	479	37.9 \pm 9.5	25.2	0.79	0.98	4 – 76
Butt	479	58.0 \pm 12.2	21.1	0.85	1.16	31 – 114
Nodule size						
Neck	480	3.24 \pm 0.45	13.7	0.29	-0.35	2.17 – 4.58
Mid crown	480	3.22 \pm 0.39	12.0	0.28	-0.11	2.32 – 4.51
Upper leg	480	3.71 \pm 0.49	13.1	0.21	-0.20	2.42 – 5.01
Lower flank	479	3.89 \pm 0.45	11.7	0.15	-0.41	2.73 – 5.03
Butt	479	3.93 \pm 0.48	12.3	0.03	-0.46	2.75 – 5.40

Nodule density decreased with an increased chronological age (as skin area and bodyweight increased – Cloete *et al.*, 2004) at all sites. Respective regressions (\pm s.e.) of nodule density on age (expressed per day) were -0.056 ± 0.009 at the neck, -0.066 ± 0.009 at the back, -0.0039 ± 0.006 at the upper leg, -0.079 ± 0.008

at the flank and -0.090 ± 0.010 at the butt. Nodule size, on the other hand, increased with an increased chronological age at all sites. Corresponding regressions (\pm s.e.) of nodule size on age (expressed as mm/day) were respectively 0.0031 ± 0.0004 , 0.0027 ± 0.0004 , 0.0036 ± 0.0005 , 0.0029 ± 0.0004 and 0.0041 ± 0.0004 at the five sites. It is generally accepted that nodule density decreases with slaughter age while nodule number increases (Cloete *et al.*, 2004; Meyer *et al.*, 2004). These results are therefore not surprising.

Estimates of heritability (h^2) ranged from zero to 0.22 for nodule density, with three estimates that were near 0.10 (Table 2). Only the h^2 estimate estimated for the mid crown locality was significant, i.e. more than twice the corresponding standard error. Four h^2 estimates for nodule size were approximately 0.10, while a higher estimate of 0.23 was found for the upper leg region. The latter estimate also reached significance ($P < 0.05$). It is notable that most estimates coincided with previous estimates of 0.10 for both traits when slightly fewer records were analysed across localities, using an unstructured repeatability model (Meyer *et al.*, 2004).

Table 2 Variance components and ratios for nodule size and nodule density, measured at five body locations on 480 slaughter ostriches (with: σ^2_a , the direct additive variance; σ^2_e , the residual variance; σ^2_p , the overall phenotypic variance)

Trait and locality	σ^2_a	σ^2_e	σ^2_p	$h^2 \pm$ s.e.
Nodule density				
Neck	4.44	60.77	65.21	0.07 ± 0.07
Mid crown	15.08	52.12	67.20	0.22 ± 0.09
Upper leg	0.09	29.68	29.77	0.00 ± 0.06
Lower flank	3.74	37.36	41.10	0.09 ± 0.07
Butt	7.46	70.67	78.12	0.10 ± 0.08
Nodule size				
Neck	0.0092	0.1189	0.1282	0.07 ± 0.08
Mid crown	0.0091	0.0820	0.0911	0.10 ± 0.08
Upper leg	0.0359	0.1231	0.1589	0.23 ± 0.10
Lower flank	0.0125	0.1181	0.1306	0.10 ± 0.07
Butt	0.0116	0.1031	0.1148	0.10 ± 0.08

Heritability estimates derived from the multi-trait analysis on nodule size (reported in Table 3) were within 0.01 of those derived from the initial single-trait analyses (see Table 2). Genetic correlations between nodule size measured at different sites were positive but differed from zero only between the mid crown and the butt, as well as between the upper leg and the lower flank. No significant differences from unity were found ($P > 0.05$), but several genetic correlations were below 0.50. The study therefore failed to prove conclusively if nodule size measured at the respective sites were the same trait, but some genetic correlations were lower than expected. It is conceded that studies of this nature would preferably involve > 1000 observations, but the labour involved in processing a skin manually proved to be too much to assess more skins. Two recorders working together could process one location on a skin in ~ 6 minutes, implying that it took at least a man-hour to process a single skin. It was attempted to automate the process using image analysis, a technology that was successfully applied to ostrich eggshell traits (Cloete Jr *et al.*, 2006). However, a lack of contrast on chrome-crusts as well as a lack of control over the shadows casted by the nodules complicated this endeavour. Correlations between nodule size derived from image analysis and those measured directly ranged from 0.12 to 0.59 for the respective localities.

When considering environmental correlations among nodule size for the respective sites, it was evident that these correlations were positive, moderate in size and significant ($P < 0.05$).

Correlations between nodule density and nodule size are presented in Table 4. Genetic correlations of nodule density with nodule size were negative and moderate to high in magnitude. However, the estimates were associated with large standard errors, and were significant only at the butt location ($P < 0.05$). The genetic correlation was unity in that case. Meyer *et al.* (2004) found a genetic correlation of -0.72 between

nodule density and nodule size in an unstructured repeatability model analysis across locations. This genetic correlation seemed to hold some promise with regard to indirect selection for nodule size on live birds. The outcome of the present study is less optimistic, suggesting that alternative approaches should be considered. Phenotypic and environmental correlations within locations were negative and significant ($P < 0.05$), and generally similar in sign and magnitude.

Table 3 (Co)variance ratios for nodule size measured at different sites on the ostrich skin, as derived from the multi-trait analysis. Heritability estimates are presented in bold figures on the diagonal, genetic correlations are above the diagonal and environmental correlations in italics below the diagonal

Location	Mid crown	Upper leg	Lower flank	Butt
Mid crown	0.11 ± 0.08	0.44 ± 0.33	0.48 ± 0.41	0.82 ± 0.26
Upper leg	<i>0.47 ± 0.04</i>	0.24 ± 0.10	0.81 ± 0.26	0.55 ± 0.30
Lower flank	<i>0.54 ± 0.03</i>	<i>0.55 ± 0.03</i>	0.09 ± 0.07	0.32 ± 0.48
Butt	<i>0.55 ± 0.03</i>	<i>0.41 ± 0.04</i>	<i>0.56 ± 0.03</i>	0.11 ± 0.09

Table 4 Genetic, phenotypic and environmental correlations between nodule density and nodule size at different locations on ostrich skins

Location	Genetic correlation	Phenotypic correlation	Environmental correlation
Neck	-0.68 ± 0.52	-0.37 ± 0.04	-0.35 ± 0.06
Mid crown	-0.51 ± 0.36	-0.25 ± 0.04	-0.21 ± 0.07
Upper leg	-0.46 ± 2.27	-0.24 ± 0.04	-0.25 ± 0.07
Lower flank	-0.72 ± 0.40	-0.28 ± 0.04	-0.23 ± 0.06
Butt	-1.00 ± 0.43	-0.23 ± 0.05	-0.15 ± 0.07

Some evidence of genetic variation in objectively measured nodule size of ostrich skins was obtained in this study. However, the derived h^2 estimates were generally lower than the estimated 0.31 obtained by Engelbrecht *et al.* (2005) for subjectively assessed nodule size. The latter study used a resource of sample skins on a structured 9-point scale to guide the assessor, with scores from 1-3 regarded as poor, 4-6 as average and 7-9 as good. The procedure of Engelbrecht *et al.* (2005) was much less time-consuming than the methods applied in the present study and it is therefore suggested that their procedure be used in future assessments of nodule size.

The issue of finding an indicator trait for nodule size on live birds remains unresolved. Genetic correlations with slaughter weight were favourable in the study of Engelbrecht *et al.* (2005). At 0.64, the genetic correlation was also of the same magnitude as those estimated for nodule density in the present study. Further work on this topic is therefore required.

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