

THE GENETIC ANALYSIS OF ADULT BIRD PERFORMANCE TOGETHER WITH SLAUGHTER TRAITS IN OSTRICHES

S.W.P. Cloete^{1,2}, A. Engelbrecht³, A.R. Gilmour⁴, M.F. Schou⁵, Z. Brand³ and C.K. Cornwallis⁵

¹Department of Animal Sciences, University of Stellenbosch, Stellenbosch, 7602 South Africa

²Directorate Animal Sciences: Elsenburg, Western Cape Department of Agriculture, Elsenburg, 7607 South Africa

³Directorate Animal Sciences: Oudtshoorn, Western Cape Department of Agriculture, Oudtshoorn, 6620 South Africa

⁴11 Holman Way, Orange, NSW, 2800 Australia

⁵Department of Biology, Lund University, Lund, Sweden

SUMMARY

Genetic analyses on economically important ostrich traits have currently only been done within trait complexes, such as breeding or slaughter traits. This study resolved the issue by investigating genetic correlations across the complexes of production traits in adult birds (i.e. egg and chick production as well as adult live weight) and slaughter traits in immature birds (slaughter weight, skin size, hair follicle score and nodule size score). All traits were heritable and variable indicating that responses to selection may be possible. Heritability estimates and genetic correlations within trait complexes were consistent with previously derived parameters. Two-trait analyses on single traits from each complex found generally negative genetic correlations of reproduction with slaughter weight and skin size, with the correlation between egg production and skin size being significant at -0.41. The genetic correlation between slaughter weight and adult weight was high and positive at 0.81, as expected when comparing the same trait measured at different life stages. Size dependent slaughter traits (skin size and nodule size) were also positively correlated to adult weight. These results are discussed in relation to ostrich production.

INTRODUCTION

Up to 70% of global commercial ostrich products originate from South Africa (Brand and Jordaan 2011). It is therefore not surprising that the literature on scientific ostrich breeding is also heavily dependent on studies of South African genetic resources (see Cloete *et al.* 2008b for a review). So far, most analyses have been conducted within trait complexes, e.g. live weight up to slaughter age (Bunter and Cloete 2004; Engelbrecht 2013), adult weight and reproduction (Cloete *et al.* 2008a), feather traits (Brand and Cloete 2015), chick survival (Wang *et al.* 2011) as well as slaughter traits (Engelbrecht 2013). As a result, little is known about the genetic correlations among traits of these trait complexes. This study therefore investigates genetic parameters for traits in the adult animal trait complex (Cloete *et al.* 2008a) and the slaughter bird trait complex (Engelbrecht 2013) and estimates genetic correlations between them.

MATERIALS AND METHODS

The study utilised data from the ostrich resource population maintained at the Oudtshoorn Research Farm of the Western Cape Department of Agriculture, which has been well-documented (Bunter and Cloete 2004; Cloete *et al.* 2008a; 2008b; Engelbrecht 2013). Only data of the South African Black strain on the farm were used. Data in the adult bird complex included repeated egg production, chick production (total egg and chick numbers over a breeding season) and adult live weight records, as described in detail by Cloete *et al.* (2008a). Data in the slaughter trait complex were slaughter weight and skin size, as well as the subjectively assessed traits of nodule size and hair follicle scores. All

these traits were reviewed by Engelbrecht *et al.* (2009) and subsequently assessed in a genetic analysis conducted by Engelbrecht (2013). The number of records used varied from 1079 for skin size to 6292 for adult weight (Table 1).

Genetic (co)variance components and ratios were derived from a three-trait repeatability model for adult birds and a four-trait animal model for slaughter traits in ASREML (Gilmour *et al.* 2016). For adult production traits, fixed effects included production year and animal age, sex for adult weight and the length of the breeding season in days as linear covariates for the reproduction traits. Year of hatch, sex and age at measurement were modelled for slaughter traits. Additive animal, animal permanent environment and service sire (for egg and chick production) were fitted as random for adult birds and additive animal for slaughter traits. Further analyses involved two-trait combinations of each slaughter trait with each adult bird trait, using parameters previously derived as priors. Animals with records were 1391 for adult weight, 678 females with reproduction records and 721 service sires mated to at least one female.

RESULTS AND DISCUSSION

The descriptive statistics reported in Table 1 were consistent with those of previous studies on adult birds (Cloete *et al.* 2008a) and slaughter birds (Engelbrecht 2013). Likewise, coefficients of variation were previously above 50% for reproduction traits, below 20% for live weight traits, below 10% for skin size and between 20 and 50% for subjective skin quality traits.

Table 1. Descriptive statistics for traits in the adult animal and slaughter animal trait complexes

Complex and trait	Number of observations	Mean	SD	CV	Range
<i>Adult traits at 5.4 (SD = 3.2) years:</i>					
Egg production (n)	3023	44.0	25.2	57.3	0 – 121
Chick production (n)	3023	21.0	17.5	83.3	0 – 90
Adult weight (kg)	6292	120.1	15.2	12.7	68 – 178
<i>Slaughter traits at 364 (SD = 71) days:</i>					
Slaughter weight (kg)	4085	92.4	17.1	18.5	40 – 148
Skin size (dm ²)	1079	140.8	9.3	6.6	104 – 170
Nodule size (n)	1749	4.49	1.22	27.2	1 – 9
Hair follicles (n)	1771	3.77	1.73	45.9	1 – 9

Heritability estimates from the three-trait model amounted to 0.16 for egg production, 0.11 for chick production and 0.37 for adult live weight (Table 2). Genetically, egg production and chick production were the same trait ($r_g = 0.99$), while the genetic correlations of reproduction traits with adult live weight were below 0.10 and not significant ($P > 0.05$).

Table 2. The observed phenotypic variance (σ_p^2) and (co)variance ratios for the traits in the adult animal complex. Significant ($P < 0.05$) correlations are denoted by an asterisk

Components and traits	Trait		
	Egg production	Chick production	Adult weight
σ_p^2	498.7	269.2	196.0
(Co)variance ratios: Heritability in bold on the diagonal, with genetic correlations below and phenotypic correlations above the diagonal (\pm standard error)			
Egg production (n)	0.16 \pm 0.04	0.74* \pm 0.01	0.06 \pm 0.03
Chick production (n)	0.99* \pm 0.03	0.11 \pm 0.04	0.04 \pm 0.03
Adult weight (kg)	-0.01 \pm 0.15	0.06 \pm 0.17	0.37 \pm 0.04

Animal permanent environmental effects ranged between 0.15 ± 0.04 for egg production and 0.30 ± 0.04 for adult weight (data not shown). Likewise, service sire effects amounted to 0.045 ± 0.011 for egg production and 0.046 ± 0.011 for chick production. These results were generally consistent with our previous study on the same resource population involving the same traits (Cloete *et al.* 2008a) as well as with results reviewed from the literature (Cloete *et al.* 2008b).

Heritability estimates from the four-trait model for slaughter traits were quite consistent in magnitude, ranging from 0.33 for skin size to 0.38 for slaughter weight (Table 3). Genetic correlations between slaughter weight, skin size and nodule size were positive, while those involving hair follicle score were variable in sign and not significant ($P > 0.05$). The heritability of slaughter weight compared well with those previously reported for live weight at an age close to the anticipated slaughter date (Bunter and Cloete 2004; Engelbrecht *et al.* 2009; 2011; 2013; Engelbrecht 2013). Genetic parameters involving skin size and subjectively assessed leather quality were also consistent with previous studies (Engelbrecht *et al.* 2009; Engelbrecht 2013).

Table 3. The observed phenotypic variance (σ_p^2) and (co)variance ratios for the traits in the slaughter animal complex. Significant ($P < 0.05$) correlations are denoted by an asterisk

Component and traits	Trait			
	Slaughter weight (kg)	Skin size (dm ²)	Nodule size score (n)	Hair follicle score (n)
σ_p^2	165.3	61.8	1.16	2.53
(Co)variance ratios: Heritability in bold on the diagonal, with genetic correlations below and phenotypic correlations above the diagonal				
Slaughter weight (kg)	0.38 ± 0.04	0.69* ± 0.02	0.33* ± 0.02	0.04 ± 0.03
Skin size (dm ²)	0.88* ± 0.05	0.33 ± 0.06	0.45* ± 0.03	0.03 ± 0.03
Nodule size score (n)	0.37* ± 0.10	0.55* ± 0.10	0.36 ± 0.06	0.14* ± 0.03
Hair follicle score (n)	0.06 ± 0.12	-0.17 ± 0.13	0.19 ± 0.13	0.37 ± 0.06

Genetic correlations of reproduction traits with slaughter weight and skin size were consistently negative in sign and mostly not significant ($P > 0.05$; Table 4). The exception was for the correlation of egg production with skin size which was more than double the corresponding standard error. If it is considered that growth is a key trait to ensure early slaughter and a reduced feed cost (Cloete *et al.* 2008b), these correlations are potentially unfavourable. On the other hand, it could be argued that the unbridled improvement of size could result in an increased maintenance need, as well as heavy animals that are difficult to handle, thereby compromising animal welfare and human occupational health and safety. Further research into the management of breeding programs, in light of these relationships, is therefore needed. Reproduction traits were not genetically correlated to the subjectively assessed skin quality traits. Genetic correlations of adult live weight with slaughter weight and skin size were positive and high. Adult live weight was positively related to nodule size but was uncorrelated with hair follicle score.

It was notable that some of the genetic and animal permanent environmental variation in the reproduction traits partitioned towards service sire. This was evident in analyses involving two-trait combinations of slaughter traits with adult reproduction traits, but most pronounced for analyses involving chick production. Heritability estimates and animal permanent environmental effects amounted to 0.09 to 0.18 respectively in these analyses, while service sires effects amounted to approximately 0.11. These results support our previous contention that the joint analysis of egg and chick production has assisted with the partitioning of additive, animal permanent environmental and service sire variances

for these traits (Cloete *et al.* 2008a). Analysing slaughter weight with adult weight also resulted in a slight repartitioning of variances in the latter trait and resulted in a heritability of 0.41 and an animal permanent environmental variance ratio of 0.27. Except for estimates for service sire variances for chick production, it was impossible to demonstrate significance ($P < 0.05$) for these repartitioned variances. Further research on this phenomenon as more data accrue is therefore also required.

Table 4. Genetic correlations of the traits in the slaughter animal complex with those in the adult animal complex. Significant ($P < 0.05$) correlations are denoted by an asterisk

Adult animal traits	Slaughter traits			
	Slaughter weight (kg)	Skin size (dm ²)	Nodule size score (n)	Hair follicle score (n)
Egg production (n)	-0.15 ± 0.15	-0.41 ± 0.20*	-0.10 ± 0.17	0.15 ± 0.17
Chick production (n)	-0.21 ± 0.18	-0.43 ± 0.24	0.05 ± 0.20	0.28 ± 0.18
Adult weight (kg)	0.81 ± 0.05*	0.65 ± 0.12*	0.31 ± 0.11*	0.11 ± 0.11

CONCLUSIONS AND RECOMMENDATIONS

This study confirmed that all traits in the slaughter and adult animal complexes were variable and heritable, as was also reported in previous studies. Genetic correlations within trait complexes were also consistent with previous results. Genetic correlations across trait complexes suggested that correlations of reproduction traits with quantitative slaughter traits were possibly unfavourable, although only significant for the estimate involving egg production and skin size. Further research on these correlations is needed. Live weight expressed in adult animals was genetically highly correlated with slaughter weight, as could be expected for the same trait recorded at different life stages. In line with this, previously determined size-dependent slaughter traits, namely skin size and nodule size score, were also genetically related to adult size. Given the profound effect of animal size on maintenance requirements in other species, it is important to update these results as data accrue to optimise the economic efficiency of selection strategies in ostriches. More accurate genetic correlations between trait complexes are needed for the design of breeding programmes to ensure a balanced breeding strategy for ostriches.

REFERENCES

- Brand T.S. and Jordaan J.W. (2011) *Appl. Anim. Husb. Rural Develop.* **4**: 1.
- Brand Z. and Cloete S.W.P. (2015) *S. Afr. J. Anim. Sci.* **45**: 20.
- Cloete S.W.P., Brand Z., Bunter K.L. and Malecki I.A. (2008a) *Austr. J. Exp. Agric.* **48**: 1314.
- Cloete S.W.P., Engelbrecht A., Olivier J.J. and Bunter K.L. (2008b) *Austr. J. Exp. Agric.* **48**: 1247.
- Engelbrecht A. (2013) PhD dissertation, Stellenbosch University, South Africa.
- Engelbrecht A., Cloete S.W.P., Bunter K.L. & van Wyk J.B. (2009) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **18**: 548.
- Engelbrecht A., Cloete S.W.P., Bunter K.L. and van Wyk J.B. (2011) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **19**: 183.
- Engelbrecht A., Cloete S.W.P., Bunter K.L., van Wyk J.B. and Hoffman L.C. (2013) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **20**: 381.
- Engelbrecht A., Hoffman L.C., Cloete S.W.P. and Van Schalkwyk, S.J. (2009) *Anim. Prod. Sci.* **49**: 549.
- Gilmour A.R., Gogel B.J., Cullis B.R., Welham S.J. and Thompson R. (2016) ASREML - User Guide Release 4.1. VSN International Ltd, Hemel Hempstead, HP11ES, UK.
- Wang M.D., Cloete S.W.P. and Dzama, K. (2011) *Proc. Assoc. Advmt. Anim. Breed. Genet.* **19**: 486.