GENETIC PARAMETERS FOR REPRODUCTION IN OSTRICHES

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SUMMARY

Between 1212 and 1487 hen-year reproduction records of a pair-bred ostrich flock were recorded from 1991 to 2003. These data were used to estimate (co)variances between reproduction traits. Egg (EP) and chick production (CP) were highly variable and moderately heritable ($h^2 > 0.25$). Hatched eggs as a percentage of EP (HATCH%) was lowly heritable ($h^2 = 0.05$), but depended strongly on the female permanent environment ($c^2 = 0.24$) and service sire ($ss^2 = 0.19$) effects. Average chick weight (ACW) was highly heritable ($h^2 = 0.71$) with a small contribution from the service sire ($ss^2 = 0.08$). Genetic correlations (r_a) between reproductive traits were generally favourable, and effectively unity between EP and CP. CP was unrelated genetically to ACW (r_a: -0.01). Correlations between service sire effects (r_{ss}) were low between HATCH% and EP but high with CP (r_{ss}: -0.01 vs 0.81).
Keywords: ostrich, egg production, chick production, heritability, genetic correlation

INTRODUCTION

The production of meat and leather is the major objective of commercial ostrich producers. However, the quantity of these products is determined by flock reproductive performance. There was an absolute scarcity of genetic parameter estimates until quite recently (Cloete *et al*., 1998). Progress has, however, been made with the estimation of genetic parameters for reproduction traits (see Bunter *et al*. 2001a; 2001b; Bunter 2002). In all of these studies it was impossible to accurately partition genetic, permanent environmental, service sire and paddock covariances, because of limited pedigree depth and many base parents with records. A degree of confounding between random effects, as well as a relatively small data set of less than 750 hen-year records also contributed. The present study aimed to re-estimate genetic parameters using additional data recorded subsequently, with an improved data structure.

MATERIAL AND METHODS

Data were obtained of a pair-bred ostrich resource flock at the Oudtshoorn Experimental Farm in the Klein Karoo region of South Africa for the 1991-2003 production seasons. The origin, management and husbandry of the flock were described by Van Schalkwyk *et al*. (1996) and Bunter (2002). During 2003, the number of breeding paddocks increased from 136 to 175. Females of the Zimbabwean Blue genotype (n = 21), without previous egg production records in the flock were introduced to some of these paddocks. South African Black females (with previous records in the flock) were used in the other paddocks, some with Zimbabwean Blue males as mates. Hen traits for this study are the interval from pairing off to the production of the first egg (time to lay – TTL), number of clutches produced (NCL), duration of lay (DUL), total egg production (EP), hatching percentage expressed relative to eggs produced (HATCH%), total chick production (CP), average

day-old chick weight (ACW) and total weight of day-old chicks produced per female (TCW). Between 1212 and 1487 hen-year records were analysed, representing 358 females mated to 375 service sires to form 530 unique combinations. Fixed effects included year (1991 to 2003), female age (2 to 21 years), dietary treatment (10 diets in 1998 and 1999 – Brand *et al*. 2003) as well as reproductive management treatments assessed during 2000 to 2002 (Lambrechts 2004). The number of days in production season (linear covariate) accounted for breeding seasons differing in length for experiments, or when animals were replaced within breeding seasons owing to death or incapacitation because of injury. Random effects were added to the operational model in sequence (using ASREML – Gilmour *et al*. 1999) to estimate parameters for the additive genetic effect of the female (h^2: all traits), the permanent environmental (c^2) effect of the female, the effect of the service sire (ss^2) of each female and the effect of their breeding paddock (pad^2). Log-Likelihood Ratios were used to distinguish between models fitting the data best. The full pedigree file was used, consisting of 1073 individuals, including 183 base animals. Pedigreed animals descended from 250 males and 251 females without known relationships. Uni-variate analyses were followed by bi-variate analyses involving all correlations between random factors appropriate to the specific trait combination.

RESULTS AND DISCUSSION

All reproduction traits were variable; coefficients of variation generally exceeded 50% (Table 1). The exception was ACW, with a coefficient of variation of ~10%. These results accorded with earlier studies (Deeming 1996; Bunter *et al*. 2001a; Bunter 2002; Cloete *et al*. 2004). Estimates of heritabilities (h^2) were mostly significant and moderate to high in magnitude (Table 1), the exceptions being NCL and HATCH%. Reported h^2 estimates for EP, CP and ACW were consistent with the earlier report of Cloete *et al*. (2004) and higher in absolute terms than those published by Bunter *et al*. (2001a), whereby the 2001 study was based on a smaller and less informative data set. In the case of TTL, Bunter *et al*. (2001a) reported estimates of 0.07 for h^2 and 0.11 for c^2. The summation of these figures corresponds well with the present h^2 estimate of 0.18. Bunter *et al*. (2001a) found no additive variation for NCL, which is consistent with the low h^2 estimate in the present study. Their h^2 estimate of 0.19 for DUL is comparable with the present estimate of 0.13.

Table 1 Means, standard deviations and variance ratios for reproduction traits of ostrich females (σ^2_p – phenotypic variation; h^2 – direct heritability; c^2 – permanent environment; ss^2 – service sire; pad^2 – breeding paddock)

Trait	Mean ± SD	σ^2_p	h^2 ± SE	c^2 ± SE	ss^2 ± SE	pad^2 ± SE
TTL (days)	41.7 ± 39.9	1241	0.18 ± 0.03	-	-	-
NCL (n)	6.13 ± 3.22	9.66	0.05 ± 0.04	0.06 ± 0.04	-	0.05 ± 0.02
DUL (days)	167 ± 65	3106	0.13 ± 0.03	-	-	-
EP (n)	44.7 ± 26.4	550	0.29 ± 0.04	-	0.07 ± 0.03	0.07 ± 0.02
HATCH%	46.4 ± 24.3	599	0.05 ± 0.05	0.24 ± 0.06	0.19 ± 0.04	-
CP (n)	22.1 ± 18.6	306	0.26 ± 0.12	0.26 ± 0.11	0.19 ± 0.07	0.07 ± 0.03
ACW (g)	862 ± 85	7883	0.71 ± 0.03	-	0.08 ± 0.02	0.03 ± 0.02
TCW (kg)	18.9 ± 16.6	239	0.25 ± 0.12	0.26 ± 0.01	0.21 ± 0.06	0.07 ± 0.03

- Excluded from the model in cases where effect was not significant

The present estimates of c² are consistent with those of Bunter *et al*. (2001a), except for TTL, EP and ACW where all the between female variation was partitioned to h² in the current data (Table 1). Previous studies found no significant ss² effect for EP (Bunter *et al*. 2001a; Cloete *et al*. 2004), compared to the present estimate of 0.07. Relatively small variance ratios may eventually become significant as the size of the data set increases. Variance ratios due to service sire effects were moderate for fertility traits: 0.19 for HATCH% in the present study. Previous ss² variance ratios for CP of 0.11 (Bunter *et al*. 2001a) and 0.09 (Cloete *et al*. 2004), increased to 0.19 in the present study. Significant pad² variances were below 0.10 throughout. The allocation of females without previous records to new breeding paddocks during 2003 may have contributed, by confounding additive genetic variation with variation attributable to breeding paddock characteristics.

Table 2 Derived correlations (± SE) between ostrich reproduction traits on the genetic, permanent environment, service sire, paddock and environmental levels (- Effect excluded)

Trait	Correlated trait	Genetic correlation	PE correlation	Service sire correlation	Paddock correlation	Residual correlation
TTL	NCL	-0.20 ± 0.24	-	-	-	-0.29 ± 0.03
	DUL	-0.70 ± 0.09	-	-	-	-0.56 ± 0.03
	EP	-0.57 ± 0.10	-	-	-	-0.46 ± 0.03
	HATCH%	-0.24 ± 0.23	-	-	-	-0.08 ± 0.04
	CP	-0.43 ± 0.13	-	-	-	-0.30 ± 0.03
	ACW	0.04 ± 0.11	-	-	-	-0.07 ± 0.04
	TCW	-0.43 ± 0.14	-	-	-	-0.27 ± 0.03
NCL	DUL	0.18 ± 0.27	-	-	-	0.51 ± 0.02
	EP	0.01 ± 0.25	-	-	0.80 ± 0.27	0.21 ± 0.03
	HATCH%	-0.62 ± 0.71	-	-	-0.33 ± 0.30	-0.05 ± 0.03
	CP	-0.25 ± 0.47	-0.12 ± 0.42	-	-0.74 ± 0.26	0.06 ± 0.03
	ACW	-0.18 ± 0.20	-	-	-0.63 ± 0.32	-0.05 ± 0.04
	TCW	-0.30 ± 0.49	-0.12 ± 0.40	-	-0.79 ± 0.25	0.04 ± 0.03
DUL	EP	0.93 ± 0.04	-	-	-	0.67 ± 0.02
	HATCH%	0.63 ± 0.23	-	-	-	0.11 ± 0.03
	CP	0.88 ± 0.08	-	-	-	0.44 ± 0.03
	ACW	-0.10 ± 0.13	-	-	-	-0.06 ± 0.04
	TCW	0.86 ± 0.09	-	-	-	0.41 ± 0.03
EP	HATCH%	0.99 ± 0.16	-	-0.01 ± 0.10	-	0.27 ± 0.03
	CP	1.03 ± 0.04	-	0.50 ± 0.19	1.06 ± 0.07	0.74 ± 0.01
	ACW	-0.13 ± 0.10	-	0.69 ± 0.26	-0.17 ± 0.30	0.13 ± 0.04
	TCW	1.01 ± 0.04	-	0.54 ± 0.18	1.12 ± 0.09	0.71 ± 0.02
HATCH%	CP	0.88 ± 0.13	0.86 ± 0.09	0.81 ± 0.08	-	0.74 ± 0.02
	ACW	0.39 ± 0.26	-	0.42 ± 0.75	-	0.07 ± 0.04
	TCW	0.93 ± 0.14	0.88 ± 0.09	0.75 ± 0.09	-	0.66 ± 0.02
CP	ACW	-0.01 ± 0.14	-	0.65 ± 0.22	-0.03 ± 0.32	0.17 ± 0.04
	TCW	1.01 ± 0.02	0.96 ± 0.02	0.98 ± 0.01	0.97 ± 0.02	0.95 ± 0.01
ACW	TCW	0.18 ± 0.14	-	0.75 ± 0.19	0.14 ± 0.30	0.23 ± 0.04

On a genetic level, TTL was negatively related to all the quantitative reproduction traits, viz. EP, CP and TCW, but independent of HATCH% and ACW (Table 2). The converse was true for DUL, of which genetic correlations with EP, CP, HATCH% and TCW were high and positive in sign. Corresponding estimates of correlations between c^2 effects reported by Bunter *et al*. (2001b) were similar in sign and magnitude. Genetic correlations involving NCL had relatively large standard errors, and were not significant. Genetic correlations indicate that EP and measures of chick output (CP and TCW) were essentially the same trait, as was also reported by Cloete *et al*. (2004). All correlations of HATCH% with measures of chick output were positive and high. The genetic correlations of EP and CP with ACW were negative in sign, but low and not significant. Previous estimates were low and positive in sign (Cloete *et al*. 2004). The low ss^2 effect on EP combined with the low ss^2 correlations for EP and CP indicates that these effects are not identical for each trait. High ss^2 correlations of HATCH% with CP and TCW confirm that the primary influence of service sires on CP is through their ability to fertilise the eggs produced by their mates. Except for correlations involving NCL (with a very low h^2), between pad^2 correlations followed genetic correlations as far as sign and magnitude are concerned. These results would support an argument that the significant paddock effects in this study could be related to an inability to partition additive genetic effects from variation between individual paddocks. The same reasoning may apply to the slightly higher than expected levels of PE and service sire variation observed in some instances.

CONCLUSIONS
The study confirmed genetic variation in several (TTL, DUL, EP, CP, ACW, TCW) ostrich reproduction traits. High repeatability estimates for EP and CP validate an earlier recommendation that selection on own performance would lead to current flock improvements (Bunter *et al*. 2001a). Further studies are required to investigate the relationships between repeated cycles of reproduction, to ascertain whether adequate genetic variation for accurate selection is present early in the reproductive life of an animal. Since parameter estimates to date have been obtained from a single resource flock, an urgent need exists for similar studies on other populations.

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