The Genetic and Phenotypic Relationship Between Feed Efficiency and Pendulous Crop in the Turkey (*Meleagris gallopavo)*

Owen W. Willems[1], Nico J. H. Buddiger[1,2] , Benjamin J. Wood[1,2] and Stephen P. Miller[1]
[1]Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, Ontario, Canada [2]Hybrid Turkeys, Kitchener, Ontario, Canada

ABSTRACT: This study used multiple-trait linear animal models to calculate the heritability, phenotypic and genetic correlations between pendulous crops (PCs), feed efficiency and body weight traits. Estimates for heritability were 0.15 and 0.11 for PCs in sire and dam lines, respectively. Genetic and phenotypic correlations in the dam line were close to zero between PCs and feed efficiency traits. Feed efficiency traits had low to moderate genetic correlations with PC in the sire line. Genetic correlations between PCs, feed intake and residual feed intake were -0.23 and -0.22, respectively. The correlations between PCs and feed efficiency traits show that PC should be included in the selection index whenever a feed efficiency trait is also included.
Keywords: turkey; feed efficiency; pendulous crop; genetics

Introduction

A pendulous crop (PC) in the turkey occurs when the striated muscle responsible for the movement of feed and water becomes non-functional. This causes the crop to become engorged as the affected animal will continue to eat and drink, but is no longer able to actively push feed into the gizzard. Fitness traits, including PCs are directly related to production, as affected animals are removed from the population at a loss (Wood, (2009)). In addition, PCs may become a concern from an animal welfare perspective as a bird may not be getting adequate access to feed and water due to the non-functional crop.

There are a number of reasons for the occurrence of PCs, both inherited and environmental (Asmundson and Hinshaw, (1938); Rigdon et al., (1961); Harper and Arscott, (1962); Roberson, (2003)). Environmental conditions that that have been linked to PCs have included diet changes, overheating in the brooder and inconsistent availability of both feed and water. The most likely scenario is that certain animals are genetically predisposed to the phenomenon and when reared in a specific environment along with a particular diet combination, the trait is expressed. Anecdotally, there is evidence to suggest that the more feed efficient strains of turkeys contain a higher percentage of PCs in the population and there may be a genetic correlation between feed efficiency and PC. In a recent analysis of PCs in the turkey, heritability estimates were 0.12 in both a sire and dam line, while the genetic correlation with 15-week body weight was 0.17 in the sire line and 0.09 in the dam line (Quinton et al., (2011)).

The objective of this study was to use a multiple-trait linear animal model to calculate heritability, alongside phenotypic and genetic correlations between PCs, feed efficiency and body weight traits. Genetic parameter estimates for PC may aid in the determination of optimal selection methods to decrease the occurrence in subsequent generations.

Materials and Methods

Population. Data was obtained for a sire line and a dam line from a turkey nucleus-breeding program. The sire line was selected for commercially important traits such as superior growth, feed efficiency, and meat traits. The dam line was selected for both commercial and reproductive traits. The lines were reared under conditions that resembled commercial production practices, including commercial management, ventilation, litter treatment, and housing densities.

Data collection and traits. Production data was compiled from birds hatched in 2005 to 2012. Throughout the growing period animals were culled from the population for PCs and recorded in the database. For the analysis, PCs were defined as a binary trait, where 0 = healthy and 1 = affected. For feed efficiency traits, birds were reared until 14 weeks of age in the general population then moved to individual pens (0.60 m wide, 0.85 m long, 0.82 m high). The feeding trial was conducted from approximately 14 to 19 weeks of age. Body weight was measured at the start of the trial (15 weeks of age) and at the end of the trial (19 weeks of age).

Significant differences in descriptive statistics were evaluated using a t-test (SAS 9.2). To determine residual feed intake (RFI), expected feed intake was calculated as a multiple regression with observed feed intake as the dependent variable (Model 1). To determine residual body weight gain (RG), expected body weight gain was calculated as a multiple regression with observed body weight gain as the dependent variable (Model 2).

$$\text{Model 1: } FI = \mu + b_1 MMW + b_2 WG + hatch + e$$

$$\text{Model 2: } WG = \mu + b_3 MMW + b_4 FI + hatch + e$$

In Models 1 and 2, *MMW* is the metabolic mid-weight:

$$MMW = \left(\frac{(start\ weight\ (kg) + end\ weight\ (kg))}{2} \right)^{0.75}$$

FI is feed intake over the test period, *WG* is body weight gain over the test period, μ is the intercept, b_1, b_2, b_3, and b_4

are partial regression coefficients, and e is the residual. The fixed contemporary group effect (*hatch*) was used to account for the common environmental effect that influenced birds hatched on the same date and managed in the same group. Regression coefficients from Models 1 and 2 were used to calculate RFI (Model 3) and RG (Model 4) respectively:

$$\text{Model 3: } RFI = FI - (\mu + \hat{b}_1 MMW + \hat{b}_2 WG)$$
$$\text{Model 4: } RG = WG - (\mu + \hat{b}_3 MMW + \hat{b}_4 WG)$$

Data analysis. Genetic parameters were estimated within each population by multiple-trait animal models using ASReml 3.0 (Gilmour et al., (2009)). Lines were analyzed separately. Results from preliminary univariate analyses were used as starting values for the subsequent multivariate analyses. The model for all traits was: *Trait = hatch + animal + e*, where *trait* is 15-week body weight, feed intake, FCR, RFI, RG. *Hatch* was as above, *animal* represents the random additive genetic effect, and e the residual random effect. The random effects were assumed to be normally distributed with a mean of zero.

Results and Discussion

Descriptive statistics. Table 1 shows the total number of observations and percentage of the population for each line affected with PC, as well as descriptive statistics for feed intake and FCR. The 2.27% rate of incidence for PC in the sire line was significantly higher than in the dam line, 1.52% ($p < 0.001$). Mean feed intake values obtained while on feed efficiency test were also significantly higher in the sire line, while the FCR was significantly lower (2.83 vs. 2.96). In a very early study, differences in PC expression were also seen between lines. A Bronze turkey and Bourbon Red turkey line, as well as their crosses were studied and the incidence of PCs in the Bourbon Reds were significantly lower than in the Bronze line (Asmundson and Hinshaw, (1938)). More recently, differences were also seen between sire and dam lines for rate of incidence of PC, where the sire line had 1.9% affected and the dam line 0.09% (Quinton et al., (2011)).

Table 1. Descriptive statistics for pendulous crop (PC), feed intake (FI) and feed conversion ratio (FCR)

Trait	Sire Line	Dam Line	P-value (t-Test)
PC			
n	283 639	253 358	
Affected (%)	2.27	1.52	< 0.001
FI			
Mean (kg)	18.20	14.23	< 0.001
SD	3.45	2.70	
FCR			
Mean (kg/kg)	2.83	2.96	< 0.001
SD	0.69	0.52	

Heritability estimates. Heritability estimates in both lines for body weight were slightly higher than earlier studies in the turkey (Quinton et al., (2011); Case et al., (2012)). Heritability estimates for feed intake, FCR, RFI and RG were similar to those results previously reported in the literature for turkey (Case et al., (2012); Willems et al., (2013)). There are few estimates for the heritability of PC in the literature, however, a recent study by Quinton et al. (2011) estimated heritability of PC to be 0.12 in both a sire and dam line in a study which investigated both survival and fitness traits in turkeys.

Genetic and phenotypic correlations. The correlations, both genetic and phenotypic in the dam line were close to zero between PC and feed intake, FCR, RFI and RG. A positive genetic correlation did exist between 15-week body weight and PC of 0.18. In the sire line, a genetic correlation of 0.16 was observed between 15-week body weight and PC. Unlike the dam line, feed efficiency traits in the sire line were found to have low to moderate genetic correlations with PC. The largest genetic correlations were between PC and feed intake (-0.23), and PC and RFI (-0.22).

Differences in the genetic correlations between PC and FE traits in the sire and dam lines gives insight into the rate of incidence in the two lines. As selection pressure in the sire line bears weight on feed efficiency traits, it may cause a correlated increase in the number of birds susceptible to PC. In the dam line, as the genetic correlations are close to zero, this is unlikely to be the case. Here it can be postulated that the natural rate of occurrence of PC in the dam line has remained unchanged over time. Differences in manifestations of PC dependent on line were also seen in previous experiments (Asmundson and Hinshaw, (1938); Harper and Arscott, (1962)). While disparities in PC incidence are likely multifactorial, given these and previous findings, it may be reasonable to infer that different lines of turkeys have differing genetic correlations between PC and production, feed efficiency, egg production, reproduction and fertility traits. These subtle differences in genetic correlations between PC and other traits may be the cause of divergent rates of incidence among lines in turkeys.

Conclusion

Pendulous crop can be an issue at the commercial level in the turkey industry, given less than ideal environmental circumstances. Genetic parameter estimates for both sire and dam lines provide the information necessary to make a breeding decision to incorporate PC into a selection index. Understanding the genetic correlation between PC and feed efficiency traits may shed some light on the steps necessary for the eradication of PCs in the turkey. Further investigation into the genetic correlation of PC with egg production, fertility, and reproductive traits is required to yield a greater understanding of this issue going forward.

Table 2. Additive genetic (σ^2_g), phenotypic (σ^2_p) variances and heritability (h^2) in a turkey sire and dam line for 15-week body weight (BW15), feed intake (FI), feed conversion ratio (FCR), residual feed intake (RFI), residual body weight gain (RG), and pendulous crop (PC), plus or minus standard error (SE)

Trait	σ^2_g	σ^2_p	$h^2 \pm$ SE
Sire line			
BW15	0.421	0.933	0.45 ± 0.01
FI	0.889	6.077	0.15 ± 0.01
FCR	0.030	0.377	0.08 ± 0.02
RFI	0.655	2.960	0.22 ± 0.03
RG	0.157	0.810	0.19 ± 0.03
PC	0.003	0.023	0.15 ± 0.00
Dam line			
BW15	0.239	0.494	0.48 ± 0.01
FI	0.467	2.634	0.18 ± 0.03
FCR	0.078	0.225	0.35 ± 0.04
RFI	0.398	1.550	0.26 ± 0.04
RG	0.112	0.404	0.28 ± 0.04
PC	0.002	0.015	0.11 ± 0.00

Table 3. Estimates of genetic (r_G) and phenotypic (r_P) correlations between pendulous crop (PC), 15-week body weight (BW15), feed intake (FI), feed conversion ratio (FCR), residual feed intake (RFI) and residual body weight gain (RG), plus or minus standard error (SE), in a turkey sire and dam line

Trait	PC $r_G \pm$ SE	PC $r_P \pm$ SE
Sire line		
BW15	0.16 ± 0.02	0.06 ± 0.00
FI	-0.23 ± 0.07	-0.21 ± 0.02
FCR	-0.12 ± 0.08	-0.14 ± 0.02
RFI	-0.22 ± 0.06	-0.32 ± 0.01
RG	0.08 ± 0.06	0.18 ± 0.02
Dam line		
BW15	0.18 ± 0.02	0.06 ± 0.00
FI	0.00 ± 0.08	-0.01 ± 0.02
FCR	0.05 ± 0.06	-0.06 ± 0.02
RFI	0.03 ± 0.07	-0.07 ± 0.02
RG	-0.05 ± 0.07	0.08 ± 0.02

Literature Cited

Asmundson, V. S., and W. R. Hinshaw. (1938). Poult. Sci. 17: 276-285.

Case, L. A., B. J. Wood, and S. P. Miller. (2012). Genet. Sel. Evol. 44: 2-6.

Gilmour, A. R., B. J. Gogel, B. R. Cullis et al. (2009). VSN International Ltd., Hemel Hempstead, UK: 1-267.

Harper, J. A., and G. H. Arscott. (1962). Poult. Sci. 41: 497-499.

Quinton, C. D., B. J. Wood, and S. P. Miller. (2011). Poult. Sci. 90: 2479-2486.

Rigdon, R. H., T. M. Ferguson, and J. R. Couch. (1961). Poult. Sci. 40: 766-771.

Roberson, K. D. (2003). Int. J. Poult. Sci 2: 389-393.

Willems, O. W., S. P. Miller, and B. J. Wood. (2013). Genet. Sel. Evol. 45: 26-34.

Wood, B. J. (2009). Can. J. Anim. Sci. 89: 201-213.