

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

Owen Willems, Nico Buddiger and Ben Wood

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 like PC's are directly related to production efficiency, as affected animals are removed from the population at a loss. In addition, PC's 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. Environmental conditions that have been linked to PC's 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 PC's in the population and there may be a genetic correlation between feed efficiency and PC's.

Hybrid Turkeys conducted a study with the objective to use a multiple-trait linear animal model to calculate heritability, alongside phenotypic and genetic correlations between PC's, feed efficiency and body weight traits. Genetic parameter estimates for PC's 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 PC's and recorded in the database. For feed efficiency traits, birds were reared until 14 weeks of age in the general population then moved to individual pens. 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).

Data analysis

Genetic parameters were estimated within each population by multiple-trait animal models using ASReml 3.0 with the lines analyzed separately. 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.

Results and Discussion

The incidence rate of PC in the sire line was higher than in the dam line. Mean feed intake values obtained while on feed efficiency test were also significantly higher in the sire line, while the FCR was significantly lower.

Differences in the genetic correlations between PCs and the feed efficiency 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.

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.

Table 1. Heritability estimates along with 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	$h^2 \pm SE$	PC $r_G \pm SE$	PC $r_P \pm SE$
Sire line			
BW15	0.45 ± 0.01	0.16 ± 0.02	0.06 ± 0.00
FI	0.15 ± 0.01	-0.23 ± 0.07	-0.21 ± 0.02
FCR	0.08 ± 0.02	-0.12 ± 0.08	-0.14 ± 0.02
RFI	0.22 ± 0.03	-0.22 ± 0.06	-0.32 ± 0.01
RG	0.19 ± 0.03	0.08 ± 0.06	0.18 ± 0.02
PC	0.15 ± 0.00	-	-
Dam line			
BW15	0.48 ± 0.01	0.18 ± 0.02	0.06 ± 0.00
FI	0.18 ± 0.03	0.00 ± 0.08	-0.01 ± 0.02
FCR	0.35 ± 0.04	0.05 ± 0.06	-0.06 ± 0.02
RFI	0.26 ± 0.04	0.03 ± 0.07	-0.07 ± 0.02
RG	0.28 ± 0.04	-0.05 ± 0.07	0.08 ± 0.02
PC	0.11 ± 0.00		

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.

For more information please visit https://asas.org/docs/default-source/wcgalp-proceedings-oral/120_paper_3657_manuscript_86_0.pdf?sfvrsn=2 or contact Dr. Ben Wood at ben.wood@hendrix-genetics.com