Genetic Properties of Feed Efficiency Parameters in Meat-Type Chickens

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Introduction

Feed cost constitute about 70% of the total cost of production, but the efficiency of feed utilization has not kept up the growth potential of today's broiler. Improvement in feed efficiency will reduce the amount of feed required for growth, production cost and the amount of nitrogenous waste (Zhang and Aggrey, 2003). Efficiency in feed intake (FI) is more difficult to quantify than growth, and as a result different measures of feed efficiency has been developed, each of which reflects different mathematical and biological aspects of efficiency. In broiler chickens, feed efficiency is usually expressed as the amount of feed consumed per body weight gain (BWG) referred to as feed conversion ratio (FCR). However, Chambers and Lin (1988) showed that a large proportion of the variation in FI and age constant FCR among broilers are due to body weight (BW) and efficiency of nutrient utilization. Also, variability in maintenance requirement, a major contributing factor to FI is not accounted in FCR. Koch *et al*. (1963) introduced the concept of residual feed intake (RFI) that accounts for both maintenance requirements and BWG.

Residual FI represents the amount of FI not accounted for by maintenance and BWG. Selection on RFI was proposed to improve feed efficiency because of its phenotypic independence of maintenance BW and BWG; however, Kennedy *et al*. (1993) showed that genetic variability in RFI is not independent of BW and BWG. Luiting (1990) also showed that feeding behavior, nutrient digestibility, maintenance requirements, and energy homeostasis and partitioning affect RFI in laying hens. Genetic variability in RFI has been investigated in beef (Arthur *et al*.; 2001), pigs (Mrode and Kennedy, 1993; Gilbert et al. 2007; Cai *et al*., 2008). To date, there are only a few studies on RFI in broilers with heritability ranging from 0.21-0.31 (Van Bebber and Mercer, 1994).

The aim of the current study was to estimate genetic parameters pertaining to RFI and FCR of growing broiler control population at two time periods and ascertain the genetic relationships among the parameters that contribute to feed efficiency.

Materials and Methods

Population and Animal Husbandry:

A pedigreed population was established from the Arkansas random bred population. Twenty-four males were pedigree mated to 72 females to produce 2,400 chicks in 8 hatches. Chicks were sexed at hatched and placed in pens with litter and fed a ration containing 225 g/kg protein, 52.8 g/kg fat, 25.3 g/kg fiber, 12.90 MJ ME/kg, 9.5 g/kg calcium (Ca), and 7.2 g/kg total phosphorus (P) (4.5 g/kg available P) until 18 d of age. Hereafter, they were fed 205 g/kg protein, 57.6 g/kg fat, 25.0 g/kg fiber, 13.20 MJ ME/kg, 9.0 g/kg Ca and 6.7 g/kg total P. (4.1 g/kg available P). At 28 d, birds were faster for 12 hours and transferred to individual metabolism cages until 42 days of age. Body weights were measured on days 28, 35 and 42. Feed intake was measured at day 28-35 and 35-42d. We calculated the metabolic body weight ($BW^{0.075}$) at day 28 and 35; feed intake at day 28-35 and 35-42, FCR and residual RFI at days 28-35 and 35-42. Experimental protocols were in accordance with the procedures of the University of Georgia institutional animal care and use committee.

Data editing and analytical algorithm:

After data editing, there were 2,289 with records and 104 parents with no records. The PROC MEANS (SAS, 1996) was used to obtain descriptive statistics of the data. Analyses were performed using the GIBBS2F90 program based on Markov Chain Monte Carlo approach. We assumed flat priors for systematic and random effects. The marginal posterior distribution of the trait of interest was obtained using Gibbs sampling. A single chain of 250,000-cycles length was generated. A burn-in period of 150,000 iterations was used as well as a 10-cycle lag to reduce autocorrelation among samples. A total of 10,000 samples were kept for post Gibbs analysis using the POSTGIBBSF90 program (with graph) (Misztal *et al*. 2002) to compute the posterior means (point estimate for traits), and the 95% highest posterior regions (HPD95%) of heritability and genetic correlations of the traits. Convergence was ascertained by employing the algorithm of Raftery and Lewis (1992).

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Results and Discussion

The means, standard deviation (SD) and heritability of traits studied are presented in Table 1. The heritability estimate of both FCR and RFI were higher than the estimate of Van Bebber and Mercer (1994) however, they were within the limits of published data on beef and pigs (Arthur *et al.*, 2001; Gilbert *et al.* 2007; Cai *et al.*, 2008).

Table 1: Means (SD) and posterior means of heritability (95% highest posterior density region intervals) of feed efficiency parameters in meat-type chickens

Trait	Means (SD)	Heritability
Metabolic body weight, 28d, g	158.64 (17.27)	0.45 (0.44-0.46)
Body weight gain, 28-35 d, g	364.66 (87.20)	0.51 (0.50-0.52)
Feed intake, 28-35 d, g	655.28 (130.38)	0.48 (0.48-0.49)
Feed conversion ratio, 28-35 d, g/g	1.84 (0.33)	0.49 (0.47-0.51)
Residual feed intake, 28-35 d, g	0.00 (79.07)	0.45 (0.45-0.46)
Metabolic body weight, 35d, g	206.74 (20.84)	0.49 (0.48-0.50)
Body weight gain, 35-42 d, g	455.58 (89.72)	0.48 (0.46-0.49)
Feed intake, 35-42 d, g	887.25 (146.35)	0.46 (0.46-0.48)
Feed conversion ratio, 35-42 d, g/g	1.99 (0.40)	0.41 (0.41-0.43)
Residual feed intake, 35-42 d, g	0.00 (82.11)	0.42 (0.42-0.43)

Genetic correlations among traits were obtained through a bivariate analysis and the results are presented in Table 2. The genetic interrelationships among the feed efficiency parameters are different at day 28-35 and day 35-42. The genetic correlation between RFI and metabolic BW was higher for day 35-42 than for day 28-35. The major difference between the two time periods was BWG. The lack of genetic correlation between RFI and BWG at day 35-42 was similar to that reported on cattle and pigs (Herd and Bishop, 2000; Arthur *et al*. 2001; Gilbert *et al.* 2007). However, Cai *et al*. (2008) also reported a positive genetic correlation between RFI and average daily again in a pig line selected for low RFI

Table 2: Posterior means of genetic correlations (95% highest regions intervals) of feed efficiency parameters in meat-type chickens

Trait	Genetic correlation with residual feed intake, 28-35 d	Genetic correlation with residual feed intake, 35-42 d
Metabolic body weight, 28d, g	0.29 (0.29-0.31)	
Body weight gain, 28-35 d, g	0.34 (0.33-0.35)	
Feed intake, 28-35 d, g	0.56 (0.55-0.57)	
Feed conversion ratio, 28-35 d, g/g	0.31 (0.30-0.31)	
Residual feed intake, 28-35 d, g		0.59 (0.58-0.59)
Metabolic body weight, 35d, g		0.45 (0.44-0.46)
Body weight gain, 35-42 d, g		0.06 (0.05-0.07)
Feed intake, 35-42 d, g		0.33 (0.33-0.34)
Feed conversion ratio, 35-42 d,g/g		0.84 (0.84-0.85)

In pigs RFI is negatively correlated to dressing percentage and positively correlated with backfat thickness (Gilbert *et al*. 2007). The body composition of broiler chickens at day28-35 is different from that of day35-42 therefore it is possible that the internal allocation of resources above maintenance into protein accretion and fat deposition could contribute towards the different inter-relationships between factors that affect RFI at these two time periods.

The genetic correlation between RFI and FCR was 0.31 at day28-35 compared to 0.84 at day 35-42. The genetic correlation among the FCRs was 0.55. This suggests that the nature of pleiotropic relationship between RFI and FCR may be dependent on age, and consequently the molecular factors that govern RFI and FCR may also depend on time of development, or the nature of resource allocation of FI above maintenance designated for protein accretion and fat deposition.

Conclusion

From the heritability estimate, selection for low RFI will improve feed efficiency despite the expected correlated response in reduced FI. However, there is a genetic dependency between RFI and BWG day 28-35. This dependency does not exit at day 35-42. Therefore, selection at day35-42 may be more attractive than day28-35. Collecting data for RFI studies can be daunting. Sample size and the stage of animal growth may also reflect the differences in literature reports on the genetic relationships among parameters affecting RFI. The weak genetic correlation between RFI and BWG at day 35-42 provides the independence of RFI on the level of production, thereby making it possible to study the physiological and nutrient digestibility mechanisms underlying RFI.

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