Association of SNPs with components of residual feed intake parameters in a meat-type chicken population

S. E. Aggrey[1], F. González-Cerón[1] and R. Rekaya[2]
[1]NutriGenomics Laboratory, Department of Poultry Science, University of Georgia, Athens, Georgia, USA, [2]Department of Animal and Dairy Science, University of Georgia, Athens, Georgia, USA

ABSTRACT: Feed efficiency (FE) is a compound trait and residual feed intake (RFI) has been the main biological measure of FE. RFI consists of two efficiencies that are indistinguishable. We have dissected RFI maintenance (RFI_M) and growth (RFI_G). The heritability of RFI_M and RFI_G are moderate but negatively correlated. Selecting on RFI_M will lead to smaller but efficient animals. Genetic gains in FE will be achieved by reductions in feed for maintenance. RFI_G is not an efficiency parameter and should not be used as a sole criterion for selection. The ability of the current method to estimate efficiency values for maintenance and gain provides geneticists with additional parameters to discriminate between animals with similar RFI_R. It also provides the flexibility to impose weights on RFI_M and RFI_G to meet a desired objective. RFI SNPs should be thoroughly evaluated because of the relationship between RFI_M and RFI_G.
Keywords: residual feed intake; SNPs; chickens

Introduction

For most producers in the broiler industry, feed utilization efficiency is usually expressed as feed conversion ratio (FCR), which by definition is the amount of feed required for a unit gain in body weight. Measuring FCR at a given age is relatively easy, but it is confounded with the maintenance requirement of birds of different sizes. Variability in the maintenance requirement, a major contributing factor to feed intake is not accounted for in calculating FCR. Feed conversion ratio is a ratio trait, and since the contributing factors of feed intake and body weight gain do not have similar statistical distributions, the ratio, i.e., FCR tends to have an asymmetric distribution. To ameliorate the deficiencies in FCR, Koch et al. (1963) introduced the concept of residual feed intake (RFI) that recognizes the differences in both maintenance requirement and weight gain. Residual feed intake is the remaining part of the feed intake that is not accounted for by the expected feed intake for maintenance and expected feed intake for weight gain. It is calculated by fitting a regression model of metabolic body weight and body weight gain on feed intake. Birds with negative RFI values by the regression equation eat less than expected and are considered as efficient and birds with positive RFI values are considered as inefficient. For over 60 years, RFI has been considered to be more "biological" than FCR, and several researchers have published work to explain its biological underpinnings (Zhang and Aggrey 2003; Herd et al. 2004; Richardson and Herd 2004; Herd and Arthur 2009; Aggrey et al. 2010; Boddicker et al. 2011). However, the RFI model developed by Koch et al. (1963) contains two efficiencies that are indistinguishable, i.e. efficiency of maintenance and efficiency of growth. In addition, the model ascribes the same efficiencies to each individual in the population, and as a result, two animals with the same RFI value are considered equally efficient. The current measure of RFI for growth is a combination of two efficiencies: (1) RFI maintenance (RFI_M) and (2) RFI gain (RFI_G), for which the biological bases may be different. The individual contribution of RFI_M and RFI_G towards RFI is unknown, their biological bases and interrelationship with other components of RFI are all unknown. Our objective was to decompose RFI into its component, and ascertain some physiological and SNP associations among the RFI components.

Materials and Methods

Population We used the Arkansas randombred broiler control population for this study. The animal husbandry and management used in the current study has been reported on by Aggrey et al. (2010). A pedigreed population composed of 24 sires and 72 dams was used to generate 2,289 chicks in 8 hatches with complete data. Body weight (BW) and feed intake (FI) measured at day 35 and 42 were used in the current analysis. Metabolic BW ($BW^{0.75}$) at day 35, FI at day 35 to 42, and FCR were calculated.

Approach The current method of estimating RFI (RFI_F) includes a residual term which is not due to an animal effect as the model uses average metabolic BW (MBW) and average BWG as adjustment parameters for each individual. This means that animals with BW greater than the population mean at the beginning of the feeding trial are intrinsically inefficient and are penalized. RFI_F has been estimated using a fixed regression model:

$$y_i = a_0 + a_1 MBW_i + a_2 BWG_i + e_i \quad [1]$$

where y_i is the FI for bird i, a_j is a fixed regression (j=0, 1, 2) and e_i is the error. The error term, e_i, is what is referred to as RFI_F which includes the sampling term that is not due to bird effect and consequently it is biased. We propose a new model that separates true RFI (RFI_R) from the residual terms, thus eliminating the bias present in the classical method and also separate the two components of RFI: metabolic efficiency (maintaining BW) and growth efficiency. The model in {1} can be written as: $y_i = a_0 + (a_1 + u_{1i})MBW_i + (a_2 + u_{2i})BWG_i + \varepsilon_i$ [2]

where a_j is the same as in model {1}, and u_{ji} (j=1,2) is bird j specific random regressions. Based in the model in [2], estimated RFI is calculated as:

$$RFI_i = \hat{u}_{1i} MBW_i + \hat{u}_{2i} BWG_i \quad [3]$$
$$RFI_i = RFI_{Mi} + RFI_{Gi}$$

where RFI_M and RFI_G are the MBW and BWG RFI's, respectively. The parameter u_1 represents the intrinsic efficiency of an animal for maintenance, and u_2, represents the intrinsic efficiency for growth.

When only one FI intake observation is collected per bird, no pedigree information between measured birds is available, and the residual and random regressions variance components are unknown, the model in [2] is not identifiable and u_{1i} and u_{2i} are not separable from each other or from the residual terms. In the current case, pedigree information between measured birds is available and hence the model is identifiable.

Both models in Equations 1 and 2 were implemented using a Bayesian approach via Gibbs sampler. Flat bounded priors were assumed for the fixed regressions and the residual variances. For the $\mathbf{u}_1$ and $\mathbf{u}_2$, the following prior was assumed:

$$p(\boldsymbol{u}_1, \boldsymbol{u}_2 | \boldsymbol{A}, G_0) \sim N(0, \boldsymbol{A} \otimes G_0)$$

Where **A** is the known additive relationship matrix and G_0 is a 2x2 matrix of genetic covariances.

Implementation via Gibbs sampler was straightforward for both models. All needed conditional distributions were in closed form, being normal for the position parameters (a_0, a_1, a_2, $\mathbf{u}_1$, and $\mathbf{u}_2$), scaled inverted Chi-square for σ_e^2 and σ_ε^2 with (n-2) degrees of freedom and scaled inverted Wishart for genetic (co)variance matrix. For model 1, a chain of 50,000 iterations was implemented with the first 10,000 rounds were discarded as burn-in period. RFI estimated under Equations 1 and 2 will be designated RFI_F and RFI_R, respectively.

Physiological parameters and SNP determination

We also studied the association of RFI parameters with SNPs and plasma hormone levels. We determined plasma triiodothyronine (T_3) and insulin-like growth factor-I (IGFI) levels at day 42, and perform correlation analysis between T_3 and IGFI, and RFI_M, RFI_G and RFI_R. We genotyped the population for several SNPs. From our association studies, we identified four SNP types (Table 2) in IGFI, NPY, AKR1 and PEPCK genes.

Results and Discussion

The heritability of the traditional method RFI_F and the current RFI_R was 0.13 and 0.35, respectively, an improvement of 260%. RFI_R is appealing because (1) it allows for efficiencies of MBW (u_1) and BWG (u_2) to be calculated for each individual and subsequently their separate RFI's (2) have the flexibility to include the relationship between RFI_M and RFI_G. Both RFI_M and RFI_G were moderately heritable (h^2~0.50) and can respond to selection, but the genetic correlation between RFI_M and RFI_G was highly negative (-0.95) indicating that these two efficiencies contribute in an opposing way towards RFI (Table 1). We have now dissected the "**black box**" of RFI and ascertained that RFI_M is the main contributing factor towards FE and that RFI_G is a feed inefficient factor. Selecting on RFI_M will decrease FI, but selecting on RFI_G will increase FI. The genetic antagonistic relationship between RFI_M and RFI_G is consistent with their relationships with MBW, BWG, FI and FCR (Table 2).

Table 1. Heritability (bold), residual (above diagonal) and genetic (below diagonal) of feed efficiency traits[1] in meat-type birds

	MBW	BWG	FCR	RFI_R	RFI_F	FI
MBW	**0.41**	0.18	0.04	-0.16	-0.05	0.27
BWG	*0.06*	**0.14**	-0.64	0.15	-0.01	0.49
FCR	*0.10*	*-0.55*	**0.10**	0.22	0.68	0.29
RFI_R	*-0.06*	*-0.02*	*0.27*	**0.35**	0.50	0.47
RFI_F	*-0.22*	*-0.09*	*0.48*	*0.40*	**0.13**	0.84
FI	*0.32*	*0.45*	*0.18*	*0.29*	*0.70*	**0.13**

[1]$MBW=BW^{0.7}5$; BWG=body weight gain; FCR=feed conversion ratio; RFI_F=residual feed intake (RFI) from fixed model; RFI_R=RFI from random model.

Table 2. Heritability (bold), residual (above diagonal) and genetic (below diagonal) of components of feed efficiency traits[1] in meat-type birds

	MBW	BWG	FCR	RFI_M	RFI_G	FI
MBW	**0.44**	0.15	0.04	-0.16	0.13	0.29
BWG	*0.18*	**0.10**	-0.69	-0.03	0.11	0.49
FCR	*0.35*	*-0.08*	**0.14**	0.27	-0.28	0.24
RFI_M	*0.23*	*0.23*	*0.64*	**0.49**	-0.97	0.30
RFI_G	*-0.24*	*-0.21*	*-0.64*	*-0.95*	**0.49**	-0.21
FI	*0.48*	*0.40*	*0.63*	*0.87*	*-0.86*	**0.22**

[1]$MBW=BW^{0.7}5$; BWG=body weight gain; FCR=feed conversion ratio; RFI_M=residual feed intake for maintenance; RFI_G=RFI for gain; FI=feed intake

Selecting on RFI_M will lead to smaller but efficient animals. Improvement in FE will be achieved by reducing FI for maintenance. RFI_G should not to be used as a sole criterion for selection. Despite the inefficient contribution of RFI_G towards RFI_R, to maintain growth in an improvement program, RFI_G can be used as part of the selection criterion. The biological (nutritional, physiological, molecular, etc) bases ascribed to RFI_R should be done with great caution and hesitation since RFI_R is a compound FE estimate with genetically negative correlated components. From our approach, we can now decipher the biological bases of RFI_M and RFI_G in order to devise innovative strategies for improvements.

Physiological and SNP associations: In the same population, plasma triiodothyronine (T_3) level was correlated ($r=0.10; P\leq 0.05$) with RFI_M but not RFI_G ($r=-0.03; P>0.54$) and IGFI level was correlated ($r=-0.11; P\leq 0.03$) with RFI_G and not with RFI_M ($r=0.06; P>0.18$). Correlation of plasma IGFI and RFI has been reported (Zhang and Aggrey, 2003; Herd et al. 2004; Richardson and Herd, 2004; Herd and Arthur, 2009; Boddicker et al. 2011; Aggrey et al. 2010), but we now show that plasma IGFI level is related to the inefficiency factor, and selection on IGFI may not have the expected response on FE as was observed from a selection on post-weaning plasma IGFI levels that had minimal effect on RFI in beef cattle (Lancaster et al. 2008). Without a comprehensive understanding of the genetic architecture of FE, improvement programs will achieve minimal expected outcomes. We have also identified four SNP types as shown

in Table 3. Marker type 1(IGFI) is significantly associated with RFI_R. This association is mainly due to RFI_M but not RFI_G. Selecting on such SNP type will lead to feed savings from animals with smaller maintenance requirement. Marker type 2 (NPY) was significantly associated with RFI_G, but not RFI_R. Since RFI_G is negatively correlated with FI, selecting on marker type 2 will increase growth and will not reduce FI. The NPY and AKR1 SNPs were not significantly associated with RFI_R, but with a component of RFI, and because of the negative correlation between RFI_M and RFI_G, the SNP effects cancel each other with respect to RFI_R. Improvements based on these two markers will likely lead to different outcomes in RFI_R, FI and growth. A major concern is that, as growth changes over the life of the birds the effects of the markers could cancel out. Marker type 3 affects both RFI_R components, but because these components are highly negatively correlated, their individual effects on RFI_R become non-significant, however, this marker type could be relevant in selection for feed efficiency depending on stage of growth and feed costs. Marker type 4 affects RFI_R, RFI_M and RFI_G, but the favorable genotype is the heterozygote and not a homozygote as in Types 1-3. Ascribing biological basis to RFI_R or selecting SNP to improve RFI should be done with detailed and careful analyses of efficiency components in order to achieve the expected result.

Table 3. SNP types and their association with components of residual feed intake in meat-type birds

Type	SNP	RFI_M	RFI_G	RFI_R
1	IGFI	$P \leq 0.01$	$P > 0.05$	$P \leq 0.05$
2	NPY	$P > 0.05$	$P < 0.03$	$P > 0.05$
3	AKR1	$P \leq 0.01$	$P < 0.01$	$P > 0.05$
4	PEPCKC	$P \leq 0.05$	$P < 0.05$	$P \leq 0.05$

Conclusion

The heritability of RFI_M and RFI_G are moderate but the highly antagonistic relationship suggests that these two efficiencies contribute in an opposing way towards RFI. As a result there should be caution in ascribing biological basis to RFI. Under the current methodology, a biological basis can be ascribed to RFI_M and RFI_G. This was confirmed by the relationship of the components of RFI with plasma hormone levels and also with types of SNPs. SNPs need to be vigorously evaluated prior to using them to aid any selection program. Selecting on RFI_M will lead to smaller but efficient animals. The genetic gains in feed efficiency will be achieved by reductions in feed required for maintenance. RFI_G is not an efficiency parameter and should not be used as a sole criterion for selection. The ability of the current method to estimate efficiency values for metabolic BW and BW gain provides geneticists with additional parameters to use to discriminate between animals with similar RFI_R. It also provides the flexibility to impose weights on RFI_M and RFI_G to meet a desired objective.

Literature Cited

Aggrey, S. E., Karnuah, A. B., Sebastian, B., and Anthony, N. B. (2010). Genet. Sel. Evol. 42: 25.

Boddicker, N., Gabler, N. K., Spurlock, M. E., Nettleton, D., and Dekkers, J. C. M. (2011). J. Animal Sci. 89: 40-51.

Herd, R. M., and Arthur, P. F. (2009). J. Anim. Sci. 87 (Suppl 14): E64-E71.

Herd, R. M., Oddy, V. H., and Richardson, E. C. (2004). Aust. J. Expt. Agric. 44: 423-430.

Koch, R.M., Swiger, L. A., Chambers, D., and Gregory, K. E. (1963). J. Anim. Sci. 22:486-494

Lancaster, P. A., Carsten, G. E., Ribeiro, F. R. B., Davis, M. E., Lyons, J. G., and Welsh, T. H. (2008). J. Anim. Sci. 86: 2862-2871.

Richardson, E. C., and R. M. Herd, R. M. (2004). Aust. J. Expt. Agric. 44: 431-440.

Zhang, W. and, Aggrey, S. E. (2003). World's Poult. Sci. J. 59: 328-339.