

Determination of Residual Feed Intake and Its Associations with Single Nucleotide Polymorphism in Chickens

XU Zhen-qiang¹, CHEN Jie¹, ZHANG Yan², JI Cong-liang², ZHANG De-xiang¹ and ZHANG Xi-quan¹

¹ Guangdong Provincial Key Lab of Agro-Animal Genomics and Molecular Breeding/Key Lab of Chicken Genetics, Breeding and Reproduction, Ministry of Agriculture/South China Agricultural University, Guangzhou 510642, P.R.China

² Wens Nanfang Poultry Breeding Co. Ltd., Yunfu 527400, P.R.China

Abstract

Marker assisted selection (MAS) for residual feed intake (RFI) is considered to be one of the powerful means to improve feed conversion efficiency, and therefore reduce production costs. To test the inner relationship among body compositions, growth traits and RFI, four models were proposed to assess the extensively explanatory variables accounting for partial variables in feed intake besides metabolic body weight and growth rate. As a result, the original model (Koch's model) had the lowest R^2 (80.78%) and the highest Bayesian information criterion (1 323.3) value among the four models. Moreover, the effects on RFI caused by single nucleotide polymorphisms (SNPs) were assessed in this study. Twelve SNPs from 7 candidate genes were genotyped in 2 Chinese native strains. rs14743490 of *RPLP2* gene showed suggestively significant association with initial body weight in both strains ($P < 0.10$). rs15047274 of *TAF15* was significantly associated with growth weight, final weight, and feed intake ($P < 0.05$) in N301 strain, in contrast, it was only suggestively significant associated with feed intake ($P < 0.10$) in N414 strain. rs15869967 was significantly associated with RFI in N414 strain but not in N301 strain. This study has identified potential genetic markers suitable for MAS in improving the above mentioned traits, but these associations need to be rectified in other larger populations in future.

Key words: RFI, model, SNPs, growth traits, association

INTRODUCTION

Feed intake (FI) and feed conversion play an essential role in individual's survival and selective competition. In the interim of modern poultry cultivation, feed cost accounts for approximately 70% in the total raising cost, especially in terms of meat-type broilers, it remains the paramount economic objective that should be improved. Feed conversion means that living beings convert the feed to the live weight, fundamentally transform energy into organism's

growth and development and maintenance requirement, which are dependent on internal environment and energy metabolism balance, including intake of feed, digestion or excretion. To date, several ratios have been successively proposed to assess feed conversion, such as relative growth rate (RGR), Kleiber ratio (KR), partial efficiency of growth (PEG), feed conversion rate (FCR) and that's what partly accounts for the endogenous function and external environmental elements concurrently exhibiting a degree of influence on feed conversion. The studies in FCR have concluded the great variation among different chicken

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XU Zhen-qiang, E-mail: zhenqiangxu@163.com; Correspondence ZHANG De-xiang, Tel: +86-20-85285759, Fax: +86-20-85280740, E-mail: zhangdexiang0001@sina.com

groups, and estimated that its heritability was low or moderate (Hess *et al.* 1941, 1948). Well chosen for FCR would improve feed conversion, however, the coefficient of correlation of these two traits were merely 0.22 (Pym and Nicholls 1979). Koch *et al.* (1963) have introduced the concept of residual feed intake (RFI_{koch}) that accounts for both maintenance requirements and growth. Representing the amount of FI not accounted for maintenance body weight and growth weight, and being regarded as an alternative measure of feed efficiency, RFI is the difference between an animal's actual feed intake and its expected intake based on its body weight and growth rate over a time period. Using models to estimate residual feed consumption had been put forward in laying hen, lamb and beef cattle (Luiting and Urff 1991; Knott *et al.* 2008; Montanholi *et al.* 2009). The optimal model suggested by Luiting and Urff (1991) in laying hens was defined as the regression residual from the optimum model of adjusted metabolic body weight, adjusted egg mass and gain weight (including an intercept) within short time periods and within diet. French sheep model including body compositions measured for calculating RFI was analogical, except that FI was adjusted for average dairy gain (ADG), body weight (BW), back fact and muscle depth at the 12th/13th ribs (Knott *et al.* 2008). RFI and associations of infrared thermography with efficiency and ultrasound traits have been processed in beef cattle through constructing novel models (Montanholi *et al.* 2009). Unequal R^2 engendered by diverse models could be explained by relative contribution of each trait to the total variation of RFI_{koch} . Obviously, this method might represent an important component to assess RFI. Given that body compositions differ in their importance for energy storage and growth traits differ in their importance for physical performance, the potential differences in the relationship between body compositions, growth traits and RFI should be considered.

The study of variations in candidate genes and gene expression underlying RFI was ubiquitous in livestock, but rare in poultry. A long-oligo microarray with 24 000 probes was applied to profile the liver transcriptome of 44 cattle selected for high or low RFI in cattle (Chen *et al.* 2011). Totally 161 unique

genes were identified as being differentially expressed, including members of the up-regulated genes in low-RFI individuals, most of which were involved in cellular growth and proliferation and activated by mitogen-activated protein kinases (MAPKs). SNPs in genes associated with growth rate, like *fat mass and obesity-associated (FTO)* and *transcription factor 7-like-2 (TCF7L2)*, have demonstrated significant associations with RFI in pigs (Fan *et al.* 2010). In chicken, merely a small amount of genes based on a few of literatures made contribution on feed efficiency in chicken, i.e., the genes connected with mitochondrial function and oxidative phosphorylation (Ojano-Dirain *et al.* 2007; Bottje and Carstens 2009; Kong *et al.* 2011). Quantitative trait locus (QTL) study showed that, a total of 16 QTLs distributed at 8 chromosomes (GGA1, GGA3, GGA4, GGA5, GGA7, GGA8, GGA9, GGA13) were relevant to RFI (de Koning *et al.* 2003, 2004; Parsanejad *et al.* 2004).

The goal of this study was fixed: 1) to test the usefulness and feasibility of body compositions and growth traits to explain FI variation by constructing models, and 2) to identify genetic markers associated with growth index and RFI.

RESULTS AND DISCUSSION

Four comparative models

The different models' idiographic information is presented in Table 1. It summarized the comparative regression equations, and pointed out respective and combined numerical values such as SD (standard deviation), minimum, maximum, R^2 and Bayesian information criterion. The simple way to code SD was altering the numbers of factors; the more factors added the smaller numerical values shown. However, impact factors adding to the equation resulted in the smallest R^2 (80.78%) and the highest Bayesian information criterion (BIC) (1 323.3) in the original model. Between the models where either shank length (SL) or shank width (SW) was fit, the determination of growth weight (GW) in FI was dominant (0.65 or 0.67, respectively), R^2 only increased a little bit than the original model (80.88 or 80.80%, respectively,

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