Online journal ISSN - 1676-5680
GMR Genetics and Molecular Research
EVOLUTION AND TECHNOLOGY

Genetic trends of abdominal fat content in a male broiler chicken line

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Genet. Mol. Res. 4 (4): 760-764 (2005)
Received December 9, 2004
Accepted April 29, 2005
Published December 15, 2005

ABSTRACT. Data of chickens from a broiler-breeding program were collected and used to determine the genetic trends of absolute and relative abdominal fat content. The genetic trends were estimated by the regression of trait genetic value averages on hatch-years. Genetic values from 32,485 individuals were used for regression analysis. The genetic trend estimate for absolute abdominal fat content was +0.39 g per year, indicating that abdominal fat deposition in the analyzed line, in absolute terms, tended to increase, making the existing excess fat deposition in the broilers even worse. However, the genetic trend of relative abdominal fat content was not significant, indicating that there is no increase on abdominal fat content when it is corrected for body weight.

Key words: Abdominal fat, Animal breeding, Broilers, Genetic value, Genetic trend

INTRODUCTION

Broiler production is the economic activity that has shown the greatest progress in Brazil in the last decades. This development has resulted mostly from the intense selection process conducted since first using cross-breeding in broilers. However, the intense selection for economic traits has led to an increased fat deposition in these animals, as described by Havenstein et al. (1994), who compared a typical 1957 broiler line to another from 1991. These authors verified an increase on fat deposition in broiler due to genetic selection for body weight.

The abdominal fat pad represents one of the main regions of fat deposition in chickens (Michelan Filho, 1986), and it seems to be directly related to total carcass fat (Becker et al., 1981).

Excessive fat is one of the main problems faced by the broiler industry nowadays, since it does not just reduce carcass yield and feed efficiency, but also cause rejection of the meat by the consumers (Kessler et al., 2000) and difficulties in processing (Chambers, 1990). As abdominal fat content seems to respond to selection according to Gaya (2003), it can be used as a selection criterion for decreasing fat content in broilers.

The study of genetic trends is an important factor for monitoring the selection process. It entails a graph representation of the changes observed on the genetic value averages of the studied species for a trait during selection (Ferraz and Eler, 2000). According to Costa et al. (2001), the knowledge of genetic trends allows the visualization of changes caused by selection in a trait, which permits analyzing the efficiency of the applied selection procedures and quantifying the genetic changes over time, besides allowing the correction of eventual mistakes in selection (Van Melis et al., 2001). Thus, the study of the genetic trends of abdominal fat content enables the evaluation and the orientation of selection applied over generations. Moreover, genetic trends in broilers are rarely presented in the literature, which emphasizes the importance of this study.

Therefore, the objective of the present study was to estimate the genetic trends of absolute and relative abdominal fat content in a male broiler line on hatch years.

MATERIALS AND METHODS

Data used on sibs of elite flock individuals were collected. Selection of elite flock had been made for composition of a male line. The use of carcass information from these sibs comprised a program named sib test, which aim was help choosing the best animals during the selection of the elite flock.

Pedigree chicks were housed by the Agroceres Ross M.G. de Aves S.A. at its facilities and raised as recommended by Agroceres Ross (2000). Type and composition of feeding were the same during the studied period.

The control of individual genealogy was made by hatch, using wingbands that contained a number and a corresponding bar code with all the necessary information for the identification of individuals.

At 42 days old, from November 2002 to July 2003, each flock of sibs was transported to the Experimental University of São Paulo Processing Plant, in Pirassununga, SP, Brazil. The birds were submitted to at least 10-h fasting, weighted and slaughtered. Data of broilers' body weight used as selection criteria as so as in the analyses were measured at the same age during all the studied period, at 42 days old. The identification of each animal and data collection were automatically recorded using portable terminals and bar code readers. After slaughter, the abdominal fat pad and the visceral organs were conditioned in plastic bags and stored at 0°C to be weighed two or three days later. Abdominal fat was considered to be the abdominal fat pad plus the gizzard fat. A software developed by Gaya et al. (2003) was used to collect and weigh the abdominal fat. The relative abdominal fat content was calculated as the division between the absolute abdominal fat content and broiler body weight at 42 days old and expressed in percentage.

The data were processed at the Animal Breeding Group of Basic Sciences Department of Animal Science and Food Engineering College of São Paulo University, in Pirassununga, SP, Brazil.

Extreme values, outliers, were identified by box-plot and removed from the dataset. The descriptive statistics were calculated by PROC MEANS of Statistical Analysis System, Version 8.2 (SAS Institute, 1999).

The genetic values were obtained by the restricted maximum likelihood method, using the animal model and the MTDFREML software (Boldman et al., 1993). Through this software, based on abdominal fat information from sib individuals, it was possible to determine the genetic values of these animals and of all their available parents. The numerator relationship matrix had 42,912 animals and the mathematic model used in the analysis was: $Y = Xb + Zu + e$, in which Y is the dependent variable vector; X is the incidence matrix for fixed effects; b is the fixed effect vector; Z is the incidence matrix for random effects; u is the genetic value random vector, and e is the residual effect vector, NID $(0, \sigma^2)$.

The fixed effects considered were flock, parents mating group and sex. These effects were evaluated by PROC GLM of Statistical Analysis System, Version 8.2 (SAS Institute, 1999), and found to be significant ($P < 0.05$) for absolute and relative abdominal fat content. The random effect considered was direct additive genetic effect.

Genetic trends of abdominal fat content were estimated by regression of the broiler average genetic values with respect to unit of time (hatch-year). The average genetic trend was given by regression coefficients. A total of 10,427 animals of the numerator relationship matrix did not have information about flock and hatch-year. Therefore, a total of 32,485 animals were used for establishing genetic trends, which were distributed over 3 hatch-years. The regression analyses were estimated by PROC REG of Statistical Analysis System,Version 8.2 (SAS Institute, 1999).

RESULTS

The descriptive statistics of absolute and relative abdominal fat content is presented in Table 1. The genetic trend of absolute abdominal fat content along the three hatch-years increased, where the average trend of +0.39 g/hatch-year ($P < 0.0001$) was found, even though the average genetic value of abdominal fat content was negative for the first hatch-year. For relative abdominal fat content, the estimated genetic trend was +0.0019 g/hatch-year, nonsignificant ($P = 0.3230$).

The graph of genetic trend of absolute abdominal fat content per hatch-years is shown in Figure 1.

Table 1. Number of observations (N), observed mean (MEAN), standard deviation (SD), coefficient of variation (CV), and minimum (MIN) and maximum (MAX) values of analyzed traits.

Abdominal fat content	N	MEAN	SD	CV (%)	MIN	MAX
Absolute (g)	6089	42.70	10.66	24.98	12.80	72.20
Relative (%)	6164	1.83	0.43	23.82	0.62	3.96

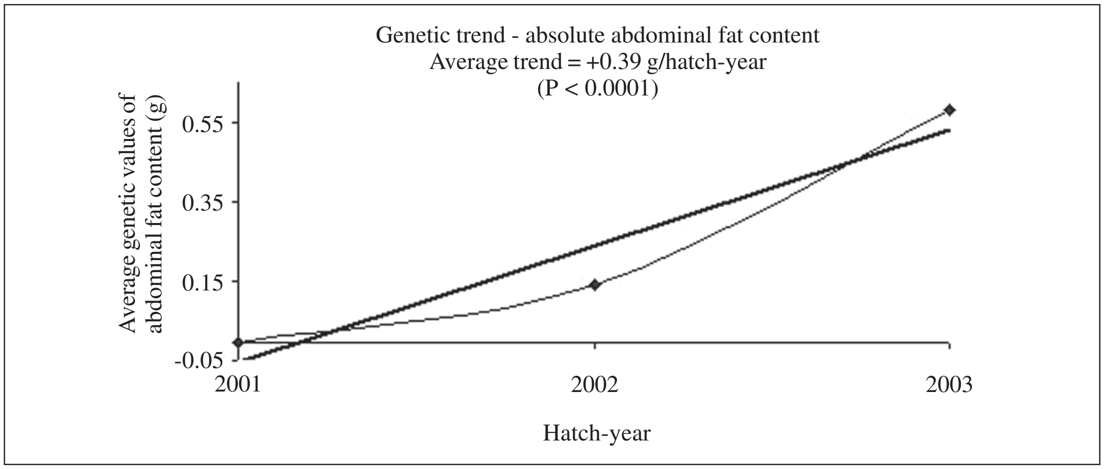

Figure 1. Genetic trend of absolute abdominal fat content per hatch-years estimated by regression analysis.

DISCUSSION

Based on the genetic trend of absolute abdominal fat content, fat deposition in the broiler line tended to increase during the selection process, maybe due to the high genetic correlations between body weight and abdominal fat content (Lin, 1981; Chambers, 1990; Gaya, 2003), since body weight is a selection criterion of the analyzed line. However, when in percentage of body weight, abdominal fat content does not seem to increase. It may be occurred because body weight was not included as a co-variate in the analyses of absolute abdominal fat content. The estimating of relative abdominal fat content allows that genetic values receive a correction for the effect of body weight. So, genetic values of relative abdominal fat content were exempt from possible correlated effects of body weight. According to Lin (1981), Leenstra (1986), Cartwright (1991), Havenstein et al. (1994), Kessler et al. (2000), and Rance et al. (2002), the selection criteria applied cause an increase in fat deposition in broilers, which was confirmed by the results of genetic trend of absolute abdominal fat content in the line examined here, in spite of the negative average genetic value obtained for this trait in one of the hatch years, which could be occurred due to selection criteria employed in broiler breeding program in this period. The evaluation of these criteria can elucidate the reason of this decline. We concluded that, although this line was not directly selected for absolute abdominal fat content, this trait increased almost 1% per hatch-year. In other words, the selection criteria used in this line induced to an unfavorable correlated response in absolute abdominal fat content.

If the use of these selection criteria continues, without any regard to controlling fat deposition in this line, the damages of excessive fat in the broilers could be aggravated even further with time.

As absolute abdominal fat content seems to respond to selection according to Gaya (2003), this could be used as a strategy for decreasing fat content in these animals.

ACKNOWLEDGMENTS

The authors are grateful to the Agroceres Ross Melhoramento Genético de Aves S.A. for the data provided and to FAPESP - the State of São Paulo Research Foundation - for scholarship grants.

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