

Genetic trends of absolute and relative heart weight in a male broiler line

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ABSTRACT. Data of chickens from a broiler-breeding program have been collected and used for determination of genetic trends of absolute and relative heart weight. The genetic trends have been estimated by regression of the genetic values of the traits over hatch-year. Genetic values of 42,912 individuals, obtained by restricted maximum likelihood, were used for regression analysis. The estimates of the genetic trends for absolute and relative heart weight were found to be -0.08 g and -0.004% per hatch-year, respectively. These trends show that heart weight in the line analyzed, in absolute and relative terms, has tended to decrease, which can make the metabolic disorders due to the reduction in heart weight in broilers even worse.

Key words: Animal breeding, Ascitic syndrome, Genetic value, Sudden death syndrome

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INTRODUCTION

Brazilian broiler aviculture has shown a large prominence in the world market, due to its important production and its performance in the exterior market for longer than 30 years. The broiler-breeding programs have been contributing greatly to the fast development of the broiler segment due to the selection strategies employed. Their usage has contributed to a higher supply and a reduction in the prices of the products. The search for increased broiler weight has been successfully accomplished, but this weight increase has been accompanied by the appearance of some metabolic disorders in the broilers, such as ascites and sudden death syndrome, where the development of these health problems has been related in most cases to the selection criteria adopted (Rauw et al., 1998; Rance et al., 2002).

Havenstein et al. (1994) and McEntee et al. (2002) compared non-selected broiler lines to male commercial lines, and they ascertained that the results of genetic selection for weight gain have led to a decrease in relative size of the heart, which can lead to the inability of this organ to appropriately supply tissue needs for oxygen, and consequently to the development of the above-mentioned disorders.

The weight modification that has been observed in broiler hearts has alerted investigators about the physiological problems such as ascitic syndrome and sudden death syndrome, which has generated a great economic loss in the poultry segment. Together, these two syndromes may be considered responsible for more than 30% of the total mortality occurring at poultry farms (Leeson, 1994).

A way for evaluating the method of selection that has been used is the study of genetic trend, which is related to the observed changes in the genetic value averages of the animals for a specific trait along the selection process (Ferraz and Eler, 2000). According to Costa et al. (2001), the study of the genetic trend allows the visualization of the changes due to the selection process, related to a specific trait over years. It is thereby possible to analyze the efficiency of the adopted selection procedures and to quantify the genetic change of the trait over time and to correct eventual errors related to selection strategies (Van Melis et al., 2001). Therefore, the study of the genetic trends of heart weight allows the guidance and the evaluation of the selection employed over generations. Since there is a certain lack of scientific understanding about this subject, studies related to this field become a must.

The objective of this study was to estimate the genetic trends of absolute and relative heart weight over hatch-years in a male broiler line.

MATERIAL AND METHODS

Data used on sibs of elite flock individuals were collected. Selection of elite flock had been carried out for creation of a male line. The use of carcass information from these sibs comprised a program named sib test, whose aim was to help choose the best animals during the selection of the elite flock.

Pedigree chicks were raised as recommended by Agroceres Ross (2000). Type and composition of feed were the same throughout the study period. The control of individual genealogy was performed by hatch, using wingbands that contained a number and a corresponding bar code with all the necessary information for the identification of individuals.

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At 42 days old, from November 2002 to July 2003, each flock of sibs was transported to the Experimental Processing Plant of the University of São Paulo, in Pirassununga, São Paulo, Brazil. The birds were submitted to at least 10 h of fasting, weighed and slaughtered. Data of broilers' body weight used as selection criteria as well as in the analyses were measured at the same age during the whole study 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 heart and other visceral organs were wrapped in plastic bags, stored at 0°C and weighed within 2 or 3 days. The software developed by Gaya et al. (2003) was used for collecting and weighing the hearts.

The dataset was processed in the Animal Breeding Group of the Basic Sciences Department of the Animal Science and Food Engineering College of São Paulo University, in Pirassununga, São Paulo, Brazil. The traits used in the analysis were absolute heart weight and relative heart weight, where the latter was calculated by dividing absolute heart weight by broiler body weight at 42 days old and expressed as a percentage. Extreme values of absolute and relative heart weight, defined as outliers, were identified by box-plot and removed from the dataset. The descriptive statistics were calculated by the PROC MEANS procedure from the SAS Institute (1999). The genetic values were obtained with the restricted maximum likelihood method, using the animal model and MTDFREML software (Boldman et al., 1993). With the use of this software, based on the information about heart weight from the individuals from the sib test, it was possible to estimate the genetic values of these animals as well as all their available relatives. 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 effects vector, NID (0, σ^2).

The fixed effects (vector *b*) considered were flock, parents mating group and sex. These effects were evaluated by PROC GLM from the SAS Institute (1999), and found to be significant (P < 0.05) for absolute and relative heart weight. The random effect (vector *u*) considered was direct additive genetic effect.

Genetic trends of absolute and relative heart weight were estimated by regression of the broiler average genetic values with respect to unit of time, hatch-year. Each hatch-year contains approximately two generations of broilers. The average genetic trend was given by regression coefficients. The regression analyses were estimated by PROC REG from the SAS Institute (1999).

RESULTS AND DISCUSSION

The descriptive statistics of absolute and relative heart weight are presented in Table 1. The genetic trends of these traits over hatch-years are presented in Table 2.

 Table 1. Number of observations (N), observed mean (Mean), standard deviation (SD), and coefficient of variation (CV) of the traits analyzed.

Heart weight	Ν	Mean	SD	CV (%)
Absolute (g)	6022	12.15	2.31	19.06
Relative (%)	6131	0.52	0.07	13.81

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Heart weight Absolute (g)	GVA		GT	SE
	2001 2002 2003	-0.09 -0.02 -0.11	-0.08 (P < 0.0001)	0.007
Relative (%)	2001 2002 2003	-0.004 -0.001 -0.006	-0.004 (P < 0.0001)	0.0003

Table 2. Genetic value averages (GVA), genetic trends (GT) and genetic trend standard errors (SE) of absolute and relative heart weight per hatch-year.

The regression coefficients for both functions were significant, considering the probability level of 1%. Over the three hatch-years studied, there was an average genetic trend of absolute heart weight of -0.08 g per hatch-year (P < 0.0001), presented in Figure 1, and an average genetic trend of relative heart weight of -0.004% per hatch-year (P < 0.0001), presented in Figure 2.



Figure 1. Genetic trend of absolute heart weight per hatch-year estimated by regression analysis.

The study of the genetic trends of absolute and relative heart weight shows that throughout the selection process, heart weight in the line analyzed tended to decrease. According to Havenstein et al. (1994), Rauw et al. (1998) and McEntee et al. (2002), the selection criteria adopted have been promoting the decrease in heart size, which was confirmed by the study of the genetic trends of absolute and relative heart weight in the line analyzed. This research shows that heart weight has shown a decrease of around 1% in absolute terms and 0.1%

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in relative terms, although the genetic correlation described by Gaya et al. (2006) between heart weight and body weight was high, since body weight is a selection criterion in the line analyzed. Thus, the selection criteria employed in these animals have led to an unfavorable correlated response regarding absolute and relative heart weight.



Figure 2. Genetic trend of relative heart weight per hatch-year estimated by regression analysis.

If the use of these selection criteria continues without any regard to controlling the decrease or even maintaining current heart sizes in broilers, the damages resulting from the reduction in heart size will be aggravated even further with time.

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