



## Genetic parameters for body weight, carcass chemical composition and yield in a broiler-layer cross developed for QTL mapping

Beatriz do Nascimento Nunes<sup>1</sup>, Salvador Boccaletti Ramos<sup>1</sup>, Rodrigo Pelicioni Savegnago<sup>1</sup>,  
Mônica Corrêa Ledur<sup>2</sup>, Kátia Nones<sup>3</sup>, Claudete Hara Klein<sup>1</sup> and Danísio Prado Munari<sup>1</sup>

<sup>1</sup>*Departamento de Ciências Exatas, Faculdade de Ciências Agrárias e Veterinárias,  
Universidade Estadual Paulista “Júlio de Mesquita Filho”, Jaboticabal, SP, Brazil.*

<sup>2</sup>*Empresa Brasileira de Pesquisa Agropecuária Suínos e Aves, Concórdia, SC, Brazil.*

<sup>3</sup>*Laboratório de Biotecnologia Animal, Escola Superior de Agricultura “Luiz de Queiroz,  
Universidade de São Paulo, Piracicaba, SP, Brazil.*

### Abstract

The objective of this study was to estimate genetic and phenotypic correlations of body weight at 6 weeks of age (BW6), as well as final carcass yield, and moisture, protein, fat and ash contents, using data from 3,422 F2 chickens originated from reciprocal cross between a broiler and a layer line. Variance components were estimated by the REML method, using animal models for evaluating random additive genetic and fixed contemporary group (sex, hatch and genetic group) effects. The heritability estimates ( $h^2$ ) for BW6, carcass yield and percentage of carcass moisture were  $0.31 \pm 0.07$ ,  $0.20 \pm 0.05$  and  $0.33 \pm 0.07$ , respectively. The  $h^2$  for the percentages of protein, fat and ash on a dry matter basis were  $0.48 \pm 0.09$ ,  $0.55 \pm 0.10$  and  $0.36 \pm 0.08$ , respectively. BW6 had a positive genetic correlation with fat percentage in the carcass, but a negative one with protein and ash contents. Carcass yield, thus, appears to have only low genetic association with carcass composition traits. The genetic correlations observed between traits, measured on a dry matter basis, indicated that selection for carcass protein content may favor higher ash content and a lower percentage of carcass fat.

*Key words:* broiler, carcass composition, genetic correlation.

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### Introduction

Great progress has been made in broiler production over the past few decades, and about 85 to 90% of the increase in productivity is attributed to genetics (Chambers, 1995). Broilers are mainly selected by certain performance traits, such as body-weight at marketing age. However, intense selection for rapid growth has been accompanied by negative consequences, including skeletal problems and increased carcass fat deposition (Burt, 2002). Even though difficult and costly (Ikeobi *et al.*, 2002; Lagarrigue *et al.*, 2006), phenotype-based selection methods for reducing fat deposition have improved carcass composition by reducing overall fatness. Though this has been in detriment of meat-quality (Nadaf *et al.*, 2007).

The identification of markers and genes that control phenotypic variation in quantitative traits remains a major challenge. Quantitative trait locus (QTL) mapping is a

method that has been used successfully to examine genetic contributions to certain quantitative traits, by correlating allelic variation in polymorphic genetic markers with trait variability (Tercic *et al.*, 2009). The identification of markers linked to genomic regions that regulate economically important traits could be useful in marker assisted selection. QTL mapping is the first stage in identifying chromosomal regions involved in the genetic control of traits that are economically important for the chicken industry. The genetic correlations between traits can provide information on how much genetic overlap exists between traits, and support QTL findings (Nones *et al.*, 2005).

The favorable progress in chicken performance is associated with an increase in fat deposition, possibly due to positive genetic correlations between body-weight and fat production traits (Zerehdaran *et al.*, 2004). According to Leenstra *et al.* (1986), the application of body weight as a selection criterion has favored chickens with larger appetites. These eat more than required for muscle development, growth and maintenance, whereby this excessive energy is accumulated in the form of fat (Lin, 1981; Leenstra *et al.*, 1986; Havenstein *et al.*, 1988).

Send correspondence to Danísio Prado Munari. Departamento de Ciências Exatas, Faculdade de Ciências Agrárias e Veterinárias, Universidade Estadual Paulista “Júlio de Mesquita Filho”, Via de Acesso Prof. Paulo Donato Castellane s/n, 14884-900 Jaboticabal, SP, Brazil. E-mail: danisio@fcav.unesp.br.

Carcass chemical composition traits, such as protein, fat and ash, are of great economic importance for the poultry segment, because they are directly related to the efficiency in meat production. Nevertheless, the evaluation of carcass chemical composition remains both difficult and costly. Genetic parameter estimates for these traits have been rarely reported, mostly due to the need for evaluating a large number of animals, so as to obtain reliable var-covariance component estimates. In this study we estimated genetic parameters for protein, fat, ash, and moisture in the carcass, as well as body-weight and carcass yield, in an F2 population designed to map quantitative trait loci (QTL) on a population of more than 3,000 chickens. This information, essential for a better understanding of the genetic architecture of carcass chemical composition in chickens, could possibly contribute to the development of new selection strategies in future broiler-breeding programs.

## Materials and Methods

### Experimental population

Two F2-chicken-resource populations (TCTC and CTCT) were developed at the Embrapa Swine and Poultry National Research Center, Brazil, by reciprocally crossing a broiler (TT) and layer (CC) lines, so as to produce populations with segregating QTL for performance and carcass traits. TT is a broiler male-line, with a genetic background of Cornish, Hampshire and White Plymouth Rock breeds, selected to improve body-weight, feed conversion, retail-cut yield, breast-weight, viability, fertility, hatchability, and reduced abdominal fat. CC is a pure White Leghorn line selected for egg production, egg-weight, feed conversion, hatchability, sexual maturity, fertility, viability, egg quality, and reduced body weight. When the F2 population was developed, the TT and CC lines involved had already undergone multi-trait selection for six and eight generations, respectively.

Seven TT males were mated to seven CC females to generate seven F1 TC families, totalizing about 50 chickens, and seven CC males were mated to seven TT females, giving rise to seven F1 CT families of about 50 chickens, as well. Seven TC males and 21 TC females, and seven CT males and 21 CT females (in both cases one male and three females from each full-sib family), were chosen at random to be parents of the F2 population. The F1 chickens chosen to generate the F2 population were reared as broiler-breeders. Each F1 male was mated to three non-related F1 females by artificial insemination to avoid inbreeding. Each F1 female produced around 100 F2 offspring in 17 hatches over eight months in 1999 and 2000, resulting in around 4,000 F2 individuals (half of each sex and each mating – CTCT and TCTC). Carcass-related traits were recorded for 3,422 (1,673 females and 1,749 males).

The F2 chickens, reared as broilers, received food and water *ad libitum*. A commercial broiler diet containing a

metabolizable energy concentration (ME) of 3,150 kcal/kg and 21% crude protein (1 to 21 days), 3,200 kcal ME/kg and 20% crude protein (22 to 35 days), and 3,200 kcal ME/kg and 18.5% crude protein (36 to 41 days) was provided.

### Description of traits

The body-weight of live chickens was recorded at 6 weeks of age (BW6). After slaughter, carcasses were stored at -4 °C for 6 h before dissection. Carcass-weight was measured after removing the feathers, feet, head, lungs, liver, kidneys, and gastrointestinal tract. Whole eviscerated carcasses were ground as frozen, homogenized and then returned to -20 °C until composition analysis. Carcass water, protein, fat and ash contents were measured by near-infrared reflectance spectroscopy (NIRS). Carcass chemical composition was measured in a 250 g sample (ground and homogenized) using a cell type Coarse in an NIR System 6500 (Silver Spring, MD, USA). Calibration curves for NIRS measurements were established based on chemical analyses of 100 carcasses from various crosses and lines, as described by Klein *et al.* (2003). Dry matter, protein, fat and ash contents were determined in compliance with the standards of the Association of Official Analytical Chemists (AOAC, 1995). Klein *et al.* (2003), on comparing laboratory results and NIRS estimates from 19 carcasses, obtained coefficients of 0.88, 0.96 and 0.95 for protein, fat and water, respectively. Carcass fat (ether extract), protein, ash content and moisture were estimated as percentages of sample-weight (250 g of ground and homogenized carcass). Thus, carcass fat content (in grams) was obtained by multiplying the percentage of fat in the sample by BW6. To avoid a possible undesirable effect of carcass water content, the fat, protein and ash contents were also expressed as dry matter (%), by dividing sample fat content by carcass dry-matter content (%) and multiplying by 100. These traits were reported as protein percentage of wet carcass (PPWC), fat percentage of wet carcass (FPWC), ash percentage of wet carcass (APWC), protein percentage of dry matter (PPDM), fat percentage of dry matter (FPDM), and ash percentage of dry matter (APDM).

### Statistical analysis

The normality of the residuals was verified for each trait, and records for which the standardized residual was higher than 3.5 or lower than -3.5 standard deviations were excluded. Least-squares analysis using the GLM procedure of SAS (SAS 9.1, SAS Institute, Cary, NC, USA) was used to define the fixed effects to be included in the mixed model. Animals of the same sex, hatch and genetic group (F2 TCTC and F2 CTCT) were considered, when contemplating fixed effects in the contemporary group (CG). These were found to be significant ( $p < 0.05$ ) for all traits.

The variance-covariance estimates and genetic parameters were obtained by the restricted-maximum-

likelihood method, using an animal model and MTHFREML software (Boldman *et al.*, 1995). The single- and two-trait animal models included the CG fixed-effect and random additive genetic and residual effects. The total number of animals in the numerator relationship matrix, including base animals, was 4,237.

## Results

Descriptive statistics for traits evaluated in the 3,422 F2 individuals in this study are listed in Table 1. Single-trait heritability estimates, as well as genetic and phenotypic correlations between the traits studied, are presented in Table 2. Heritability estimates obtained from two-trait analysis (results not shown) were very similar to those of single-trait analysis. For all the traits, excepting CY, PPWC and APWC, everything indicated the large proportion of phenotypic variance as being attributable to additive genetic effects.

The genetic association between BW6 and MP (Table 2) indicated that selection for higher live-weight would favor individuals with lower water accumulation in the carcass. In the case of BW6, and both protein and ash, results were moderate and inversely proportional, whereas the genetic association between BW6 and fat, although also moderate, directly proportional, regardless of whether measurements were of the percentage of wet carcass weight or dry matter.

A moderate genetic correlation was observed between CY and PPWC (Table 2), but not between CY and MP, FPWC, FPDM, PPDM, APWC or APDM. Thus, the genetic association of CY with others carcass components traits is expected to be low.

The genetic association between MP and PPWC and between MP and PPDM was high and directly proportional (Table 2). The same result was observed for ash content, with high and positive genetic correlation estimates be-

**Table 1** - Mean, standard deviation (SD), coefficient of variation (CV) and minimum and maximum values for performance, carcass and body composition traits.

Trait <sup>1</sup>	Mean	SD	CV (%)	Minimum	Maximum
BW6 (kg)	1.0	0.2	17.8	0.4	1.7
CY (%)	64.9	2.2	3.4	49.0	81.6
MP (%)	62.8	2.6	4.1	50.1	71.8
PPWC (%)	18.8	0.9	4.7	16.3	24.3
FPWC (%)	15.0	2.6	17.6	7.5	27.2
APWC (%)	2.7	0.3	12.1	1.6	4.6
PPDM (%)	50.7	3.1	6.2	40.3	64.2
FPDM (%)	40.0	4.8	12.1	24.5	56.9
APDM (%)	7.4	1.0	14.0	3.9	11.2

<sup>1</sup> BW6 = body weight at 6 weeks of age; CY = carcass yield; MP = moisture percentage in the carcass; PPWC = protein percentage in wet carcass; FPWC = fat percentage in wet carcass; APWC = ash percentage in wet carcass; PPDM = protein percentage in dry matter; FPDM = fat percentage in dry matter; APDM = ash percentage in dry matter.

**Table 2** - Heritability estimates (diagonal), genetic correlations (above the diagonal) and phenotypic correlations (below the diagonal) and their approximate standard errors (in parentheses) obtained for different carcass traits.

Trait <sup>1</sup>	BW6 (kg)	CY (%)	MP (%)	PPDM (%)	FPDM (%)	APDM (%)	PPWC (%)	FPWC (%)	APWC (%)
BW6 (kg)	0.31 (0.07)	0.22 (0.18)	-0.47 (0.15)	-0.45 (0.15)	0.46 (0.14)	-0.46 (0.15)	-0.34 (0.28)	0.45 (0.14)	-0.42 (0.17)
CY (%)	0.33 (0.02)	0.20 (0.05)	-0.09 (0.19)	-0.03 (0.19)	0.03 (0.19)	-0.10 (0.19)	0.55 (0.25)	0.04 (0.19)	-0.09 (0.20)
MP (%)	-0.33 (0.02)	-0.11 (0.02)	0.33 (0.07)	1.00 (0.004)	-0.99 (0.01)	0.97 (0.02)	0.83 (0.20)	-0.99 (0.004)	0.90 (0.06)
PPDM (%)	-0.37 (0.02)	-0.13 (0.02)	0.79 (0.01)	0.48 (0.09)	-0.99 (0.004)	0.96 (0.02)	0.87 (0.15)	-1.00 (0.003)	0.87 (0.06)
FPDM (%)	0.38 (0.07)	0.12 (0.02)	-0.73 (0.01)	-0.91 (0.01)	0.55 (0.10)	-0.97 (0.01)	-0.86 (0.15)	1.00 (0.001)	-0.91 (0.04)
APDM (%)	-0.33 (0.02)	-0.16 (0.02)	0.52 (0.02)	0.65 (0.01)	-0.78 (0.01)	0.36 (0.08)	0.73 (0.21)	-0.98 (0.01)	0.98 (0.01)
PPWC (%)	0.01 (0.02)	-0.002 (0.02)	-0.40 (0.02)	0.23 (0.02)	-0.20 (0.02)	0.14 (0.02)	0.02 (0.01)	-0.86 (0.16)	0.59 (0.24)
FPWC (%)	0.38 (0.02)	0.12 (0.02)	-0.88 (0.01)	-0.92 (0.01)	0.96 (0.005)	-0.74 (0.01)	0.00 (0.02)	0.53 (0.10)	-0.91 (0.05)
APWC (%)	-0.18 (0.02)	-0.12 (0.02)	0.04 (0.01)	0.30 (0.02)	-0.49 (0.02)	0.88 (0.01)	0.39 (0.02)	-0.37 (0.02)	0.15 (0.04)

<sup>1</sup> BW6 = body weight at 6 weeks of age; CY = carcass yield; MP = moisture percentage in the carcass; PPDM = protein percentage in dry matter; FPDM = fat percentage in dry matter; APDM = ash percentage in dry matter; PPWC = protein percentage in wet carcass; FPWC = fat percentage in wet carcass; APWC = ash percentage in wet carcass.

tween MP and APWC and between MP and APDM. In contrast, the genetic correlation estimates between MP and FPWC and between MP and FPDM were high and inversely proportional.

Genetic correlations between PPWC and PPDM, APWC and APDM, and FPWC and FPDM were high (Table 2), thereby indicating that measurements reported as the percentage of both dry matter and wet carcass weight, could be useful for evaluating the percentage of each trait in the carcass. However, when the breeding values for each trait, expressed as dry matter and wet weight, were plotted (Figure 1a, 1b and 1c for protein, fat and ash, respectively), a firm association was only observed between APWC and APDM (Figure 1b) and between FPWC and FPDM (Figure 1c).

The genetic association between protein with ash content was high and directly proportional, whereas the genetic correlation between protein with fat, and ash with fat were high but inversely proportional (Table 2). Selection for higher carcass protein content would favor individuals with lower fat content and higher ash content.

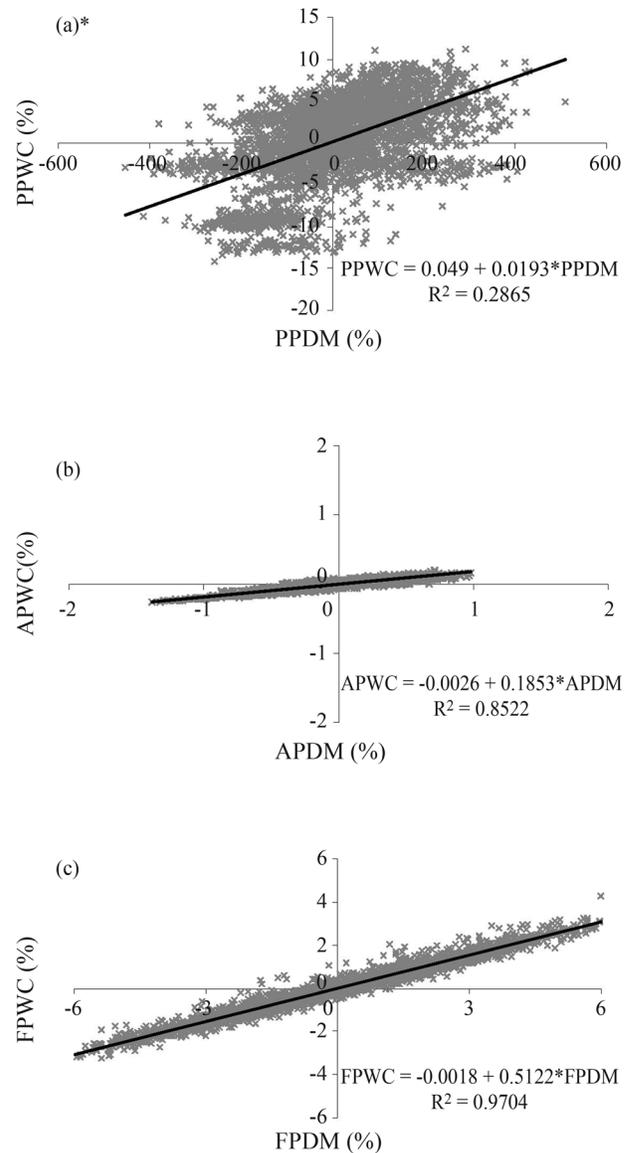
As observed for genetic correlations, the estimates of phenotypic correlations between PPDM and FPDM, as well as between FPDM and APDM were high in magnitude and negative in sign. Nevertheless, a high and positive phenotypic association was observed between PPDM and APDM.

Environmental correlation estimates were only important for MP and PPWC ( $-0.59 \pm 0.04$ ) and MP and APWC ( $-0.23 \pm 0.05$ ). These were similar in magnitude but opposite in signs to the genetic correlations observed between the same traits, this inverse response thereby indicating that inherent environmental associations should be taken into account during analysis.

## Discussion

The lower mean body-weight at 6 weeks (Table 1) was expected, when compared to the results reported for pure broiler lines, with means ranging from 1.7 to 2.3 kg (Schmidt *et al.*, 2003), and for chickens from a cross between a high-reproductive female line and a high-growth male line, as reported by Zerehdaran *et al.*, (2004), who studied live weights at 49 days of age (mean of  $2 \pm 0.3$  kg).

Although the mean for BW6 was low (Table 1), we emphasize that this is a broiler-layer cross developed for QTL mapping. Despite the possible inflation of genetic parameters for the traits studied (Table 2), through the use of such divergent lines, the aim was to estimate parameters for describing genetic associations between performance and carcass composition traits, as a means for understanding their genetic architecture, and not for selection. Furthermore, only few heritability estimates for these traits are reported in the literature.



**Figure 1** - Variation in breeding values for protein (a), ash (b) and fat content (c), expressed on a dry matter (PPDM, APDM and FPDM) and wet weight (PPWC, APWC and FPWC) basis. \*PPDM and PPWC were multiplied by 100.

The observed CY mean (Table 1) was similar to those reported by Schmidt *et al.* (2003) and Zerehdaran *et al.* (2004), which were 69.9% and 66.1%, respectively. In this study, means for MP, PPWC, FPWC and APWC were similar to those observed by Washburn *et al.* (1975) and Pesti and Bakalli (1997), ranging from 63.9 to 67.1% for MP,  $18.1 \pm 0.5\%$  for PPWC, 11.7% for FPWC, and from  $2.5 \pm 0.6\%$  to  $3.3 \pm 0.1\%$  for APWC. Means for PPDM, FPDM and APDM were close to those obtained by Chambers and Fortin (1984), which were  $50.4 \pm 0.7\%$ ,  $41.4 \pm 0.7\%$  and  $7.4 \pm 0.2\%$ , respectively. Perreault and Leeson (1992) obtained a higher mean ether extract percentage of  $47.7 \pm 0.7\%$  measured on a dry matter basis, at 43 days of age, when compared to our result for FPDM.

The findings herein compiled, when compared with the literature, indicated that the use of a light-weight layer line, in the reciprocal cross under study, in no way affected carcass yield, or carcass protein, fat, moisture and ash contents, expressed as percentages of wet carcass weight and dry matter. The general concordance of our results with those of others adds to their credibility.

Genetic correlations between BW6 and CY (Table 2) were low. Zerehdaran *et al.* (2004) reported a similar genetic correlation estimate between live weight at 7 weeks of age and CY. Siegel (1984) and Becker *et al.* (1984) reported a genetic association between live weight and carcass ether extract, similar in magnitude to that encountered herein between BW6 and carcass fat content.

Carcass composition (protein, fat and ash content) expressed on a dry matter basis would be more appropriate for studying selection based on heritability estimates than the same traits measured as the percentage of wet carcass weight, since higher heritability estimates were obtained when carcass composition traits were expressed as percentage of dry matter. Carcass composition on a dry matter basis is more precise, through not being influenced by the sample, whereas measurements expressed as wet carcass weight might be influenced by the amount of water. However, besides having been used to predict carcass fatness (Taylor and Shaffner, 1975; Verstrate *et al.*, 1980), percentages of carcass moisture may also be an effective means of accurately predicting percentages of carcass fat and protein content (Chambers and Fortin, 1984).

Similar heritability estimates, when compared to ours, were found by Le Bihan-Duval *et al.* (1999) (BW6  $0.42 \pm 0.02$ ) and Zerehdaran *et al.* (2004), (live-weight  $0.33 \pm 0.07$  and CY at 7 weeks  $0.41 \pm 0.07$ ). No heritability estimates were found in the literature for comparison with PPWC, PPDM, FPDM, FPWC, APDM and APWC data obtained herein.

Based on the heritability estimates found, in chickens, selection by the reduced amount of total fat (measured as the percentage of carcass dry matter or wet-carcass weight) would expectedly be effective in terms of genetic gain. Furthermore, the small magnitude of the standard errors of the heritability estimates is an indication of their reliability.

Selection for increased BW6 should result in a higher percentage of fat content and a lower one of protein and ash in the carcass. However, selection for CY would have little influence on carcass composition. The genetic correlations observed between the carcass-composition traits studied herein, indicate that selection by proteins may conduce to a higher percent of ash content and lower one of carcass-fat accumulation.

The moderate phenotypic correlation (Table 2) between BW6 and CY indicated that higher live-weights would not necessarily lead to higher CYs (Abram and Goodwin, 1977). Zerehdaran *et al.* (2004) reported phenotypic correlation estimates between live weight at 7 weeks

of age and CY of  $0.22 \pm 0.03$ , whereas Ávila *et al.* (1993), when studying 50-day-old chickens, found a phenotypic correlation of 0.35 between BW6 and CY, similar to that observed herein.

The phenotypic association between BW6 and MP (Table 2) indicated the possibility of a higher live-weight resulting in lower water accumulation in the carcass. Pesti and Bakalli (1997) reported the relationship between these traits to be -0.22.

An increase in BW6 will necessarily result in a higher percentage of fat content, and lower protein and ash contents in the carcass. With the exception of PPWC, the phenotypic associations between BW6 and carcass composition traits, here expressed as the percentage of wet carcass weight, were, in both direction and magnitude, similar to those reported by Chambers and Fortin (1984), who encountered phenotypic correlations between live weight (at 47 to 61 days of age) and PPWC, FPWC and APWC, of -0.18, 0.56 and -0.25, respectively. Siegel (1984) and Becker *et al.* (1984) reported a phenotypic association between live weight and ether extract in the carcass whose magnitude was similar to that found in the present study, between BW6 and fat content in the carcass. Furthermore, these correlations, as observed between BW6 and PPDM, FPDM and APDM were also similar to those noted by Chambers and Fortin (1984) between live weight and PPDM, FPDM and APDM of -0.47, 0.53 and -0.46, respectively.

Based on wet and dry matter, a negative phenotypic correlation between moisture and carcass lipid percent was estimated herein, as occurred with Silva *et al.* (2003) who obtained a highly negative estimate ( $r = -0.88$ ;  $p < 0.0001$ ) between the same two factors. Although the correlation between MP and PPWC was negative, this was high and positive between MP and PPDM and MP and APDM, although very low between MP and APWC. Chambers and Fortin (1984) reported phenotypic associations of 0.92 (protein and moisture) and 0.72 (ash and moisture), thus in agreement with the present results.

Chambers and Fortin (1984) reported phenotypic associations of -0.95 between protein and fat, -0.80 between fat and ash, and 0.74 between protein and ash, in carcass dry matter, thus in agreement with the present results. Although no linear relationship was observed between PPWC and FPWC, Washburn *et al.* (1975) and Chambers and Fortin (1984) obtained estimates of -0.46 and -0.70, respectively.

Although a positive phenotypic correlation was established between APWC and PPWC (Table 2), this was negative between APWC and FPWC. Similar results were reported by Chambers and Fortin (1984) with 0.42 between the former and -0.46 between the latter. In the present study, positive relationships were observed between FPWC and FPDM, PPWC and PPDM, and APWC and APDM,

thus indicating a directly proportional linear association between these traits.

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