Genetic Correlations For Breast Weight And Meat Quality Traits In A Male Broiler Line[*]

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Introduction

In the last years, broiler production in Brazil grew more than 40%, reaching over than 11 million tons in 2008 (Avisite (2010)). This development, in Brazil and worldwide, resulted not only from the number of producers and their size, but was mainly due to the intense selection process realized since the beginning of the use of crossbreeding in poultry production. However, the selection for economic traits may induce several changes in broiler meat quality, according to Dransfield and Sosnicki (1999), which has been recognized as one of the mainly factors to be considered by the poultry industry, since it represents damages to this industry, besides interfering directly in meat consumer's preference.

One of the major problems met by the processing industry is PSE meat, where the initials refer to the words pale, soft and exudative. The PSE phenomenon is prognosticated by changes in some meat quality traits, involving the degeneration of meat functional properties due to the fast glycolisis *post mortem*, accelerating the fall in muscle pH while the carcass temperature is still high (Molette *et al*. (2003)). The combination of both circumstances can lead to the denaturation of muscle proteins, which causes lower water retaining capacity, and consequently a paler and firmer meat at cooking.

It is, therefore, necessary to estimate the genetic correlations between meat quality traits and breast weight, usually used as selection criterion in broiler breeding programs, what may help to anticipate how selection practiced until now has affected meat quality. However, the measure of those traits is rather complex and implies to slaughter animals, so, genetic parameters for meat quality traits in broiler are rare in literature (Le Bihan Duval *et al*. (2001); Gaya (2006); Le Bihan Duval *et al*. (2008)).

Thus, the present study aimed to estimate the genetic correlation coefficients among breast weight, usually used as selection criterion in broiler breeding programs, and meat quality traits, in a single male broiler line.

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Material and methods

Data origin and collecting. In the current study the data of sibs from an elite flock which had undergone selection for development and carcass of a male line were used, and in which the breast weight is one of the main selection criterion. From May 2005 to March 2006, each group of sibs of selected animals with 44 d of age was transported to the Experimental Processing Plant of the University of São Paulo (Pirassununga, São Paulo, Brazil), to measure carcass and meat quality traits, in a total of 13 slaughters. The birds were submitted to a minimum of 10 h of feed withdrawal prior to slaughter. The transportation of the broilers to the processing plant lasted about 6 h. The voltage used for electric shock in the immobilization of the birds was 40 V, at 60 Hz and an average of 2 A per bird, for nine seconds. Bleeding of the birds lasted three minutes. Prior to feather removal, birds were immersed in water at 57ºC for two minutes. After slaughter, the carcasses were stored at 0-2ºC during 24 h and, then, deboned. Meat quality data from the sib test flock were all measured in the *Pectoralis major* muscle and collected as follows. ***pH Measures.*** Meat pH was measured at 15 min directly on carcass (pH_i), 6 h directly on carcass (pH_6), and 24 h on deboned and skinless breast (pH_f) after slaughter, in the cranial-ventral portion of the muscle, all using a digital pHmeter. After pH_i measurement, carcasses were submitted to pre-chilling by immersion in cold water at 10ºC for 10 min and afterward stored in cooling chambers (0-2ºC). Initial range of pH fall (R_i) was calculated as the difference between pH_i and pH_6. Final range of pH fall (R_f) was calculated as the difference between pH_i and pH_f. ***Color Parameters.*** These parameters were measured 24 h after slaughter using a portable colorimeter (HunterLab, Miniscan XE) and the L*, a* and b* scale from CIELab System. The measurements were recorded at three different points on the muscle, on the ventral surface of the sample, considering the mean of these three points as the determined value. ***Water losses.*** *Pectoralis major* samples were collected 24 h after slaughter and weighed, providing initial breast weight (W1). These samples were, then, stored in a in a plastic bag at 0-2ºC and reweighed after 24 h (W2). Other *pectoralis major* samples were collected 24 h after slaughter and weighed, providing another initial breast weight (W3), which were frozen at -18ºC, defrost at 4ºC and weighed (W4). These samples were baked in an electric oven until the internal temperature reached 72ºC, and weighed (W5). Drip, thawning and thawning-cooking losses (DL, TL, TCL) were calculated, in percentage, as: DL = (W1-W2)/W1; TL = (W3-W4)/W3; TCL = (W4-W5)/W4. ***Shear force.*** This trait was determined using the same samples as for thawing-cooking loss, which, after baking and cooled, were submitted to shear force analysis. Four parallelepipeds measuring 2 x 2 x 1 cm were removed from each sample, which were sheared by a Warner Bratzler blade. The mean of shear force for the four parallelepipeds was considered as sample shear force (SF), given in kg. Breast weight, without skin (BRT) was also registered after deboning.

Statistical analyses. The descriptive statistics were calculated by PROC MEANS of SAS software (SAS Institute (1999)). Genetic correlations were obtained by restricted maximum likelihood (REML) method using an animal model and VCE software (Groeneveld (1997)). The numerator relationship matrix had 107,154 animals. The following mathematic model was used: $y = Xb + Zu + e$, where y is the dependent variables vector; X is the fixed effects incidence matrix, associating elements from b to y; b is the fixed effects vector; Z is the random effects incidence matrix, associating elements from u to y; u is the random effect vector, considered as the direct additive genetic effect; and e is the residual effects vector. The random maternal genetic effect was also considered in the model for BRT. The fixed effects considered were the contemporaries groups for each analyzed trait. The significance of the effects for the traits studied was estimated by PROC GLM of SAS software (SAS Institute (1999)), and found to be significant ($P<0.05$). The effects used were hatch (52 levels) and sex (2 levels). Hatch effects were included in the contemporaries groups for all traits. Sex was included for all traits except pH_i, pH_f, R_i, R_f, a*, and b*.

Results and discussion

Descriptive statistics for all traits and genetic correlations estimates among meat quality traits and breast weight can be found in Table 1. BRT was mainly genetically and positively related to pH_i, R_f, and b* (rg 0.47 ± 0.138, 0.84±0.302 0.42±0.152, respectively). BRT was also genetically but negatively correlated to TCL (rg -0.42±0.119).

Direct selection for higher BRT would increase pH_i, as genetic correlation between these traits was moderate to high. This estimate disagree from Dransfield and Sosnicki (1999), which affirm that the selection for higher breast weight tends to reduce initial meat pH and consequently unleashes a greater PSE meat frequency. The selection for BRT could affect pH_i, otherwise would not influence pH_f which are nearly uncorrelated. In literature is also found that pH_f was not correlated with breast yield (Le Bihan Duval *et al*. (2001)). An expressive genetic association was found between BRT and R_f. So, the selection to higher BRT, despite of increasing pH_i, and consequently leading to a lower incidence of the PSE condition development, tends to increase pH fall in 24 h. The genetic association between BRT and R_i was less expressive than BRT and R_f.

BRT were uncorrelated with color parameters L* and a*, but BRT was moderately to high correlated with b*. Selection for BRT would therefore increase yellowness, but not redness or lightness of the meat. Then, the use of these selection criterion by industry would not affect the paleness of the meat, what is important mainly for the final consumer. The genetic correlation estimate found for BRT and L* was similar to that reported in literature between L* and breast yield (Le Bihan-Duval *et al*. (2001)), but different from other reports between L* and breast weight (Le Bihan-Duval *et al*. (2008)).

Direct selection for BRT could not affect DL, TL, and SF, since these traits are not expressively correlated. However, the direct selection for BRT could decrease TCL, since the genetic correlation between these traits is moderate and negative, what could suggest an improvement of water retention ability of the meat in this line due to the selection for BRT. A low genetic association between water losses of meat and breast yield in broiler is already reported (Le Bihan-Duval *et al*. (2001)). All these results diverged from Dransfield and Sosnicki (1999), in which the selection for higher breast weight tends to increase the incidence of PSE condition in broiler meat, and, consequently, the water losses of meat.

BRT presented favourable genetic associations with meat quality attributes, since the direct selection for this could increase pH_i, and reduce TCL.

Table 1: Descriptive statistics for meat quality traits and genetic correlations with BRT$^{\alpha}$

Traits	N	Mean	SD	CV	Min.	Max.	r_g
pH_i	938	6.12	0.19	3.02	5.64	6.62	0.47 ± 0.138
pH_f	2107	5.80	0.13	2.32	5.44	6.20	-0.05 ± 0.125
R_i	618	0.26	0.16	61.06	0.01	0.78	0.32 ± 0.162
R_f	777	0.32	0.15	46.05	0.01	0.59	0.84 ± 0.302
L*	2130	56.07	3.00	5.30	47.62	63.98	0.11 ± 0.084
a*	2116	5.35	1.10	20.59	2.26	8.54	0.07 ± 0.125
b*	2098	13.59	2.12	15.59	7.77	19.20	0.42 ± 0.152
DL (%)	2030	2.06	0.58	28.21	0.30	3.70	0.14 ± 0.221
TL (%)	2125	6.46	3.22	49.82	0.40	18.30	0.20 ± 0.129
TCL (%)	2122	21.26	4.17	19.62	8.80	32.60	-0.42 ± 0.119
SF (kg)	2113	1.21	0.41	33.94	0.30	2.50	0.08 ± 0.138
BRT (g)	15868	512.93	89.47	17.44	245.00	770.00	-

$^{\alpha}$Number of observations (N), observed mean (Mean), standard-deviation (SD), coefficient of variation (CV), minimum (MIN) and maximum (MAX) values, r_g = genetic correlation between meat quality trait and BRT (±SE).

Conclusion

Breast weight was denoted as a favourable carcass selection criterion for meat quality attributes in the analyzed line, since it could improve initial pH and thawing-cooking losses of meat. Therefore, the continuance of its use as selection criterion is recommended in the analyzed line.

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