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# Genetic parameters of meat technological quality traits in a grand-parental commercial line of turkey

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**Abstract** – Genetic parameters for meat quality traits and their relationships with body weight and breast development were estimated for a total of 420 male turkeys using REML. The birds were slaughtered in a commercial plant and the traits measured included pH at 20 min (pH<sub>20</sub>) and 24 h *post-mortem* (pHu) and colour of the breast and thigh meat. The heritabilities of the rate and the extent of the pH fall in the breast muscle were estimated at  $h^2 = 0.21 \pm 0.04$  and  $h^2 = 0.16 \pm 0.04$ , respectively. Heritabilities ranging from 0.10 to 0.32 were obtained for the colour indicators in the breast muscle. A marked negative genetic correlation ( $r_g = -0.80 \pm 0.10$ ) was found between pH<sub>20</sub> and lightness ( $L^*$ ) of breast meat, both traits corresponding to PSE indicators. The pH<sub>20</sub> in the thigh muscle had a moderate heritability ( $h^2 = 0.20 \pm 0.07$ ) and was partially genetically related to pH<sub>20</sub> in the breast muscle ( $r_g = 0.45 \pm 0.17$ ). Body weight and breast yield were positively correlated with both initial and ultimate pH and negatively with the lightness of breast meat.

**turkey / meat quality / pH / colour / genetic parameters**

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## 1. INTRODUCTION

Poultry meat production has been very dynamic over the last decade during which time it has been greatly diversified with a large increase in the volume of the joints and processed products. This success has been strongly related to the improvement in growth and carcass yield, with a significant increase in the breast muscle proportion. More recently, due to consumer preferences and the industry demands, improvement of the meat quality has become a more prevalent concern. As in pigs, the fall of *post-mortem* pH significantly affects the storage and processing quality of poultry meat. In particular, a low pH in the early stages of rigor onset when muscle temperature is still high leads to protein denaturation, responsible for a poor water-holding capacity, bad functional properties and a pale colour of the meat [7,14,21]. Although the underlying mechanisms have not yet been elucidated in poultry, these meat defects described in turkeys and chickens have been identified by analogy with pigs as the PSE (pale soft exudative) like syndrome [26]. Ultimate pH also modifies the technological properties of the meat, with a low pH being associated with a decreased water-holding capacity and a pale colour [2,3], and a high pH with a poor storage quality [1]. Meat quality is influenced by a large number of factors, including environmental conditions such as stress before slaughter but also genetics. The genetics of the meat quality has been widely studied in pigs leading to the application of selection methodology to improve meat quality. In this species, a significant polygenic determinism of several meat traits has been shown as well as a strong impact of a few major genes [24]: most notably, the halothane sensitivity gene [20] responsible for the PSE phenotype and the *RN* gene [18] responsible for the “acid meat” condition have been well defined. By contrast with pigs, the genetic determinism of meat quality in poultry is poorly defined. Interestingly, significant levels of heritability were obtained for several meat quality traits in chickens in a recent study reporting first estimates of genetic parameters [17]. However, this experiment was realised under highly controlled experimental conditions, which did elicit the expression of meat quality defects. Thus, the present study was aimed at estimating the genetic parameters of muscle *post-mortem* pH fall and of meat colour measured under commercial conditions. This genetic analysis was conducted in turkeys for which meat quality is an important issue because a large part of turkey production is consumed as further-processed products.

## 2. MATERIALS AND METHODS

### 2.1. Animals

A total of four hundred and twenty turkey toms, originating from a commercial grand-parental dam line (BUT Ltd., Chester, UK) were used for this

**Table I.** Composition of the diets distributed during the rearing period.

Composition (%)	0–4 weeks	4–8 weeks	8–16 weeks
Maize	0	25.82	18.86
Wheat	45	14.46	31.9
Rapeseed oil	5	5	6
Soyabean meal	36.9	26.6	15.56
Corn gluten meal	5.7	6	6
Spring peas	0	0	15
Calcium carbonate	1.03	0.98	1.01
Dicalcium phosphate	3.73	3.69	3.42
Sodium chloride	0.4	0.4	0.4
Trace minerals	0.1	0.1	0.1
Vitamins	0.5	0.5	0.5
DL-methionine	0.4	0.43	0.44
L-lysine	0.86	0.7	0.75
Anticoccidial	0.05	0.05	0.05
Tryptophan	0.04	0.05	0.1
Threonine	0.34	0.27	0
Characteristics (calculated)			
Metabolisable energy (MJ · kg <sup>-1</sup> )	12.06	12.60	13.22
Crude proteins (g · kg <sup>-1</sup> )	260	240	200
Lysine (g · kg <sup>-1</sup> )	19.20	17.10	14.70
Methionine + cystine (g · kg <sup>-1</sup> )	12.50	12.00	11.10
Calcium (g · kg <sup>-1</sup> )	13.90	13.30	12.60
Available phosphorus (g · kg <sup>-1</sup> )	7.80	7.40	7.10

genetic analysis. This line was in generation eight, after closing from a cross of two similar phenotypically female lines. It was normally maintained with 60 males and 480 females. The offspring used for the present study were the progeny of 30 sires and 118 dams. All these birds were reared under similar conditions in a conventional poultry house at the Inra Avian Research Centre of Nouzilly, France. Feed and water were provided *ad libitum* throughout the growth period, until sixteen weeks of age. Three successive different diets were distributed at different ages (Tab. I). The birds were individually weighed at the day before slaughter. After a transport of about 2 h, the birds were slaughtered in a commercial plant (LDC, Sablé-sur-Sarthe, France) following usual commercial practices.

## 2.2. Muscle sampling and meat trait measurements

The pH of the meat was recorded in both the breast in the *Pectoralis superficialis* (*PS*) muscle and the thigh in the *Ilio tibialis* (*IT*) muscle, at 20 min (pH<sub>20</sub>) and 24 h *post-mortem*. The first time of measurement estimated the rate of the pH fall and the second one the ultimate pH (pHu) of the meat. At 20 min *post-mortem*, 2 g of fresh muscle were immediately homogenised in 18 mL of 5 mM iodoacetate buffer and the pH of the homogenate was measured using a portable pH-meter combined with a glass electrode. This method was described as the reference method by Santé and Fernandez [22]. At 24 h *post-mortem*, pH was assessed by a more rapid method by inserting the probe in the muscle. This was permitted by the strong correlation obtained at 24 h *post-mortem* between the direct tissue measurement of pH and the reference method [22].

The colour of the meat was recorded at 24 h *post-mortem* on the *PS* and *IT* muscles using CR 300 Minolta colorimeters. The CIE  $L^*a^*b^*$  system was used, where  $L^*$  is the lightness of the meat,  $a^*$  the redness and  $b^*$  the yellowness. The chroma ( $C$ ) and Hue ( $H$ ) values were also calculated as  $C = \sqrt{(a^{*2} + b^{*2})}$  and  $H = \tan^{-1}(b^*/a^*)$ . Chroma is a measure of the colour intensity which increases when  $a^*$  and/or  $b^*$  increases. Hue indicates the degree of change of the colour from red (low values of  $H$ ) to yellow (high values of  $H$ ).

The weight of the two breast muscles was also recorded at 24 h *post-mortem*. Breast yield was estimated as the weight of the breast muscles divided by body weight before slaughter.

Basic statistics for the different traits were calculated using the UNIVARI-ATE procedure of SAS<sup>®</sup> [23]. Mean characteristics of the *PS* and *IT* muscles were compared by a *t*-test.

## 2.3. Estimation of the genetic parameters

Coefficients of heritability ( $h^2$ ) for the various meat traits as well as genetic correlation coefficients  $r_g$  and phenotypic correlation coefficients  $r_p$  were estimated. Genetic parameters were obtained by the REML (restricted maximum likelihood) methodology with VCE (version 4.2.5) software [12]. The model of analysis included the genetic effect of each animal, and for the colour measurements, the fixed effect of the colorimeter. Although the three colorimeters used for this experiment provided different mean colour values, the standard deviation for each measurement did not largely vary between instruments ( $L^*$ :  $49.3 \pm 2.1$ ,  $51.9 \pm 2.6$ ,  $48.2 \pm 2.7$ ;  $a^*$ :  $3.6 \pm 1.3$ ,  $2.4 \pm 1.2$ ,  $3.5 \pm 1.5$ ;  $b^*$ :  $4.1 \pm 1.3$ ,  $7.10 \pm 1.5$ ,  $4.4 \pm 1.5$  for the colour measurements in *PS* by colorimeter 1, 2 and 3, respectively). The fixed effect of the operator was thus introduced in the model to take into account this instrumental variation.

In order to increase the accuracy of the genetic parameter estimation, pedigree information to ancestors of the parents of the animals used for the study was also considered. This comprised a total of 44 sires and 67 dams for the generation hatched in 1999 and 48 dams for the generation hatched in 1998.

An initial global estimation of the genetic parameters of body weight, breast yield and the various breast meat characteristics was carried out. This failed to achieve convergence probably because of the high estimated genetic correlations between the  $C$  and  $H$  parameters and the  $a^*$  and  $b^*$  parameters. Two distinct analyses were therefore performed, the first analysis included body weight, breast yield, plus  $pH_{20}$ ,  $pHu$ ,  $L^*$ ,  $a^*$ ,  $b^*$  measured in the breast, while the second analysis included the same traits except that  $a^*$  and  $b^*$  were replaced by  $C$  and  $H$ . The estimated genetic parameters with their standard errors for body weight, breast yield,  $pH_{20}$ ,  $pHu$ ,  $L^*$ ,  $a^*$ ,  $b^*$  in the breast were obtained by the first analysis. In a second step, the estimated heritabilities for the  $C$  and  $H$  parameters in the breast and their genetic correlations with the other traits as well as the corresponding standard errors were obtained from the second analysis. Genetic correlations between  $a^*$ ,  $b^*$ ,  $C$  and  $H$  indicators in the breast were estimated by a specific multi-trait analysis of these four traits. The latter failed to achieve convergence and later did not provide standard errors of the estimates. As for the breast meat characteristics, the global analysis for the thigh meat characteristics failed to achieve convergence, so that two distinct analyses were carried out, the first one including  $pH_{20}$ ,  $pHu$ ,  $L^*$ ,  $a^*$ ,  $b^*$  parameters and the second one  $C$  and  $H$  parameters. Finally, a specific analysis of  $pH_{20}$  in both breast and thigh meat was performed to estimate the genetic correlation between the rates of pH fall for both muscles.

### 3. RESULTS

The basic statistics for meat traits as well as body weight (BW) and breast yield (BRY) are reported in Table II. A wide variation in pH and colour was observed in both  $PS$  and  $IT$  muscles. The rate and the extent of the pH fall were lower in  $IT$  than in  $PS$  ( $P < 0.001$ ). Lightness was higher in  $PS$  than in  $IT$  ( $P < 0.001$ ), whereas the Hue value indicated that breast meat was more yellow and less red than thigh meat ( $P < 0.001$ ). The estimated phenotypic correlations between the breast and thigh characteristics are presented in Table III. High positive correlations were observed between the two muscles for both the initial and the final pH of the meat (0.49 and 0.52, respectively), as well as the  $b^*$  and  $H$  colour indicators (0.57 and 0.60, respectively).

The genetic parameters as well as the phenotypic correlations for breast meat characteristics, BW and BRY are presented in Table IV. The REML procedure assumed the normal distribution of the traits, this condition being not fully satisfied for some of the meat traits (especially  $a^*$  in  $PS$  and  $pHu$  in  $PS$  and  $IT$ ).

**Table II.** Basic statistics for meat traits, body weight and breast yield in the data set used for the genetic analysis.

Trait	<i>n</i>	Mean ± SD	Range	Skewness	Kurtosis
Body weight (g)	420	11 648 ± 914	8090–14 150	−0.78	1.95
Breast yield (%)	420	15.9 ± 1.3	11.7–19.7	−0.54	0.60
<i>Pectoralis superficialis</i> muscle					
pH <sub>20</sub>	398	6.25 ± 0.22	5.72–6.90	−0.19	−0.61
pHu	414	5.90 ± 0.11	5.50–6.24	−0.51	0.83
Lightness ( <i>L</i> <sup>*</sup> )	417	49.7 ± 2.9	40.3–58.4	0.14	0.42
Redness ( <i>a</i> <sup>*</sup> )	418	3.2 ± 1.4	0–9.9	1.03	1.87
Yellowness ( <i>b</i> <sup>*</sup> )	416	5.1 ± 1.83	0.2–10.9	0.39	−0.32
Chroma ( <i>C</i> )	416	6.20 ± 1.79	1.02–13.8	0.47	0.34
Hue ( <i>H</i> )	415	0.99 ± 0.24	0.37–1.57	0.02	−0.52
<i>Ilio tibialis</i> muscle					
pH <sub>20</sub>	389	6.42 ± 0.12	6.05–6.77	−0.16	0.02
pHu	415	6.05 ± 0.13	5.56–6.48	−0.62	1.01
Lightness ( <i>L</i> <sup>*</sup> )	419	48.6 ± 2.6	39.9–58.7	0.18	0.83
Redness ( <i>a</i> <sup>*</sup> )	420	9.2 ± 1.4	4.7–13.4	0.00	0.49
Yellowness ( <i>b</i> <sup>*</sup> )	420	2.7 ± 1.88	−1.4–8.4	0.57	−0.36
Chroma ( <i>C</i> )	420	9.77 ± 1.55	4.71–14.98	−0.03	0.48
Hue ( <i>H</i> )	420	0.28 ± 0.18	−0.18–0.85	0.46	−0.36

pH<sub>20</sub>: pH at 20 min *post-mortem*; pHu: ultimate pH at 24 h *post-mortem*.

**Table III.** Phenotypic correlations ( $r_p$ ) between the *Pectoralis superficialis* (*PS*) and *Ilio tibialis* (*IL*) characteristics.

	pH <sub>20PS</sub>	pHu <sub>PS</sub>	<i>L</i> <sub>PS</sub> <sup>*</sup>	<i>a</i> <sub>PS</sub> <sup>*</sup>	<i>b</i> <sub>PS</sub> <sup>*</sup>	<i>C</i> <sub>PS</sub>	<i>H</i> <sub>PS</sub>
pH <sub>20IL</sub>	<b>0.49</b> <sup>1</sup>	0.17 <sup>2</sup>	−0.10 <sup>3</sup>	−0.10	0.05	0.00	0.12 <sup>3</sup>
pHu <sub>IL</sub>	0.05	<b>0.52</b> <sup>1</sup>	0.01	−0.06	−0.02	−0.05	0.02
<i>L</i> <sub>IL</sub> <sup>*</sup>	0.00	0.05	<b>0.27</b> <sup>1</sup>	−0.17 <sup>2</sup>	0.23 <sup>1</sup>	0.14 <sup>3</sup>	0.28 <sup>1</sup>
<i>a</i> <sub>IL</sub> <sup>*</sup>	0.00	−0.04	0.03	<b>0.00</b>	0.02	0.02	−0.02
<i>b</i> <sub>IL</sub> <sup>*</sup>	0.00	0.01	0.39 <sup>1</sup>	−0.35 <sup>1</sup>	<b>0.57</b> <sup>1</sup>	0.36 <sup>1</sup>	0.61 <sup>1</sup>
<i>C</i> <sub>IL</sub>	−0.01	−0.04	0.19 <sup>1</sup>	−0.13 <sup>3</sup>	0.25 <sup>1</sup>	<b>0.17</b> <sup>2</sup>	0.22 <sup>1</sup>
<i>H</i> <sub>IL</sub>	0.01	0.02	0.40 <sup>1</sup>	−0.35 <sup>1</sup>	0.57 <sup>1</sup>	0.36 <sup>1</sup>	<b>0.60</b> <sup>1</sup>

pH<sub>20</sub>: pH at 20 min *post-mortem*; pHu: ultimate pH at 24 h *post-mortem*; *L*<sup>\*</sup>: lightness; *a*<sup>\*</sup>: redness; *b*<sup>\*</sup>: yellowness; *C*: chroma; *H*: Hue. <sup>1</sup>*P* < 0.0001; <sup>2</sup>*P* < 0.001; <sup>3</sup>*P* < 0.05.  $r_p$  values without exponents are non significant.

**Table IV.** Heritabilities ( $h^2$ , on the diagonal in bold) and genetic correlations ( $r_g$ , above the diagonal) with their approximate standard errors as well as phenotypic correlations ( $r_p$ , below the diagonal) for meat traits measured in the *Pectoralis superficialis* muscle, body weight (BW) and breast yield (BRY).

	BW	BRY	pH <sub>20</sub>	pHu	L*	a*	b*	C	H
BW	<b>0.35 ± 0.05</b>	0.11 ± 0.10	0.55 ± 0.10	0.55 ± 0.11	-0.41 ± 0.19	0.13 ± 0.11	-0.49 ± 0.15	-0.39 ± 0.17	-0.29 ± 0.13
BRY	0.25 <sup>1</sup>	<b>0.32 ± 0.04</b>	0.62 ± 0.10	0.23 ± 0.14	-0.24 ± 0.17	-0.18 ± 0.12	-0.31 ± 0.13	-0.46 ± 0.16	-0.02 ± 0.11
pH <sub>20</sub>	0.21 <sup>1</sup>	0.07	<b>0.21 ± 0.04</b>	0.59 ± 0.10	-0.80 ± 0.10	-0.25 ± 0.11	-0.35 ± 0.20	-0.62 ± 0.18	0.04 ± 0.11
pHu	0.15 <sup>3</sup>	0.06	0.26 <sup>1</sup>	<b>0.16 ± 0.04</b>	-0.53 ± 0.19	0.08 ± 0.12	-0.15 ± 0.21	-0.14 ± 0.21	-0.10 ± 0.16
L*	0.06	0.17 <sup>2</sup>	-0.19 <sup>1</sup>	-0.17 <sup>2</sup>	<b>0.12 ± 0.04</b>	0.22 ± 0.13	0.54 ± 0.18	0.69 ± 0.17	0.11 ± 0.16
a*	-0.11 <sup>3</sup>	-0.13 <sup>3</sup>	-0.22 <sup>1</sup>	-0.08	-0.11 <sup>3</sup>	<b>0.21 ± 0.05</b>	-0.09 ± 0.20	0.59 (ne)	-0.86 (ne)
b*	0.12 <sup>3</sup>	0.11 <sup>3</sup>	0.01	-0.06	0.57 <sup>1</sup>	0.01	<b>0.14 ± 0.04</b>	0.70 (ne)	0.61 (ne)
C	0.05	0.03	-0.09	-0.09	0.47 <sup>1</sup>	0.44 <sup>1</sup>	0.89 <sup>1</sup>	<b>0.10 ± 0.04</b>	-0.13 ± 0.19
H	0.18 <sup>2</sup>	0.17 <sup>2</sup>	0.19 <sup>1</sup>	0.00	0.48 <sup>1</sup>	-0.70 <sup>1</sup>	0.67 <sup>1</sup>	0.27 <sup>1</sup>	<b>0.32 ± 0.07</b>

pH<sub>20</sub>: pH at 20 min *post-mortem*; pHu: ultimate pH at 24 h *post-mortem*; L\*: lightness; a\*: redness; b\*: yellowness; C: chroma; H: Hue. ne: non estimable. <sup>1</sup>  $P < 0.0001$ ; <sup>2</sup>  $P < 0.001$ ; <sup>3</sup>  $P < 0.05$ .  $r_p$  values without exponents are non significant.

However, since the deviations from normality were not so drastic and since REML is rather robust to non normality, it was preferred not to perform box-cox transformation for data whose biological interpretation is not obvious. The heritabilities for  $\text{pH}_{20}$  and  $\text{pHu}$  in *PS* muscle were estimated as  $0.21 \pm 0.04$  and  $0.16 \pm 0.04$ , respectively. Colour indicator heritabilities ranged from 0.12 to 0.32. The rate and the extent of the pH fall were significantly positively related, with a phenotypic correlation of 0.26 and a genetic correlation of  $0.59 \pm 0.10$ . The lightness of the breast meat was closely genetically related to the rate of the pH fall ( $-0.80 \pm 0.10$ ) and, to a lesser extent, to the ultimate pH ( $-0.53 \pm 0.19$ ). Phenotypic correlations were more moderate but still significant ( $-0.19$  and  $-0.17$  with  $\text{pH}_{20}$  and  $\text{pHu}$ , respectively). The redness and yellowness of the breast meat also appeared significantly genetically related to  $\text{pH}_{20}$ , with negative correlations of  $-0.25 \pm 0.11$  and  $-0.35 \pm 0.20$ , respectively. This resulted in a significant negative genetic correlation between  $\text{pH}_{20}$  and the *C* value of breast meat ( $-0.62 \pm 0.18$ ). By contrast, no significant genetic relationship was observed between the Hue value and the *post-mortem* pH fall in breast muscle. A significant positive genetic correlation between the lightness and the yellowness of breast meat was observed ( $0.54 \pm 0.18$ ). This is consistent both traits being related to the rate and the extent of the pH fall in a similar direction. Both BW and BRY showed positive genetic correlations, ranging from 0.23 to 0.62, with both initial and ultimate pH in breast muscle. The corresponding phenotypic correlations were low to moderate but still positive (from 0.06 to 0.21). The measures of BW and BRY were negatively genetically correlated to the  $L^*$ ,  $a^*$ ,  $b^*$  and *C* values.

An estimated heritability of  $0.20 \pm 0.07$  was found for  $\text{pH}_{20}$  in the thigh muscle. In addition, a significant positive genetic correlation was obtained between the value of  $\text{pH}_{20}$  in *PS* and *IT* muscles ( $0.45 \pm 0.17$ ). The remaining quality characteristics measured in the thigh had lower heritabilities when compared to the breast: 0.02 for  $\text{pHu}$ , 0.04 for  $L^*$ , 0.002 for  $a^*$ , 0.14 for  $b^*$ , 0.025 for *C* and 0.11 for *H*. Therefore, the genetic correlations between the thigh meat characteristics (data not shown) will not be discussed.

#### 4. DISCUSSION

A wide range of rate of pH fall was observed in the present study conducted under commercial slaughtering conditions. A significant proportion of the birds exhibited fast rates of pH fall. Further investigations confirmed that the breast meat produced by birds showing the fastest pH decline (16% of the population with  $\text{pH}_{20}$  below 6) was characterised by a significantly reduced processing yield and higher drip loss of commercially packed products [10]. This great variability in the  $\text{pH}_{20}$  values contrasted with the results of a previous study on birds of the same genetic type slaughtered under experimental conditions,

in which the  $\text{pH}_{20}$  in breast meat remained above 6 [9]. These results confirmed that stressful commercial conditions favour the incidence of PSE defects in poultry. They also showed that the environment chosen to record meat traits may strongly affect the results of the genetic analyses.

This study shows for the first time in poultry that the rate of *post-mortem* pH fall measured in commercial conditions is partly genetically determined. The estimated heritabilities for  $\text{pH}_{20}$  in *PS* and *IT* were similar to the mean value of 0.16 reported by Sellier [24] in pigs obtained by averaging the heritabilities of a large number of studies. Few studies have reported the heritability of the rate of pH fall in poultry. Indeed, only one estimate has been published by Le Bihan-Duval *et al.* [17] in chickens, using animals reared and killed under experimental conditions. The heritability of pH measured at 15 min *post-mortem* in the breast meat was then estimated at a high value (0.49), which could suggest different genetic determinisms according to the poultry species. It could also suggest a significant impact of the slaughter conditions on the rate of pH fall.

A significant positive genetic correlation was observed between the rate and the extent of the *post-mortem* pH fall in breast meat. This was a rather surprising result since it is usually assumed that these parameters are controlled by different mechanisms: the ultimate pH is mainly determined by the initial glycogen reserve of the muscle at the time of slaughter, while the rate of pH fall is determined by the rate of ATP hydrolysis at death in relation with muscle metabolism and stress response of the bird [26]. In pigs, the existence of separate mechanisms was supported by the results of several genetic studies showing poor to moderate genetic correlations between pH after slaughter and ultimate pH [8,15,25]. A very low genetic correlation was found in the chicken too [17]. Further investigations in poultry would be useful to elucidate the mechanisms underlying the relationship we observed in the present study, between the rate and the extent of *post-mortem* pH fall in the breast muscle.

The colour of breast meat appeared to be strongly influenced by the rate of pH fall, a more rapid decrease leading to a lighter meat of a more intense red and yellow colour. In addition, the lightness of breast meat would also be significantly genetically correlated to the ultimate pH of the muscle in accordance with a previous study in the chicken [17]. The strong negative genetic correlation between  $\text{pH}_{20}$  and  $L^*$  was a consistent result since both traits are potential indicators of PSE meat. Indeed, an abnormally low pH at an early *post-mortem* time when carcass temperature is still high leads to protein denaturation responsible for an increased light scattering [4]. This contrasted with the results of previous genetic studies, the first where F2 generation birds derived from crosses of fast and slow growing grand-parental turkey lines were used [27] and the second using a pure selected line of broilers [17]. In both studies, no genetic relationships were found between meat quality traits,

particularly light reflectance and pH at 20 min *post-mortem*. However, the range of observed pH values in these studies conducted under experimental conditions was much lower than that observed in commercial practice, which may have led to misleading estimates for genetic relationships [27]. The negative relationship observed in the present study between the rate of the pH fall and the redness of the breast meat was also supported by recent results in the turkey [10, 13], showing that birds exhibiting a rapid glycolysis have a significant redder breast meat. It is interesting to note that in former studies in the turkey, Froning *et al.* [11] and Ngoka *et al.* [19] also reported that rapid glycolysis due to struggle before death is associated with a significantly increased redness, partly due to an increased blood flow and thus myoglobin content in the breast muscles. Further studies are needed to confirm the biochemical basis of the relationship between the pH decline and the colour indicators since the latter could be potentially useful tools to detect rapid glycolysis.

In this study, pH<sub>u</sub> as well as  $L^*$  and  $a^*$  indicators exhibited very low heritabilities in the thigh muscle whereas significant levels were obtained in the breast muscle. Similar variations were also reported in pigs by Larzul *et al.* [16], with heritabilities close to zero for the colour parameters measured in a predominantly red muscle and moderate ones for the same parameters in intermediate or predominantly white muscles. It is possible that the low heritabilities we obtained for the quality indicators in the thigh reflected a higher impact of the environmental factors or alternatively, were simply related to the difficulty of measuring meat quality on a heterogeneous muscle such as the *IT* muscle. At first sight, these first results suggest that a selection based on the measurements of the colour or the ultimate pH could be beneficial to the breast meat quality but would be of a limited benefit to the thigh meat quality. However, since a significant positive genetic correlation was obtained between the rate of pH fall in the breast and thigh muscles, it is likely that selection against very fast rates of pH fall measured in the breast muscle would also have an impact on pH responses in the thigh muscle.

The genetic results obtained in this study indicate that the lowest pH values, either at 20 min or 24 h *post-mortem*, were genetically correlated with the lowest growth and muscle development performance. Further studies are necessary to understand the underlying mechanisms which explain this relationship. Could the lightest birds be more susceptible or reactive to pre-slaughter stress? In chickens, low genetic correlations were estimated between the measures of the pH decline and both body weight and breast yield of the birds [17]. This was consistent with the studies of Fernandez *et al.* [9] in turkeys and Berri *et al.* [5] in chickens which showed that processing meat quality was not reduced in heavy lines in comparison with slow-growing lines. These preliminary results suggest that poultry could differ from pigs, for which unfavourable genetic relationships between meat “quantity” and quality have often been reported.

However, according to the review of Sellier [24], the genetic correlations between the usual criteria of meat quality (pH, reflectance, water-holding capacity) and carcass lean to fat ratio are moderate (up to  $\pm 0.25$ ). Moreover, in this species, HAL and RN major genes appear to be strongly responsible for this antagonism [24], which is not observed in populations free of these genes. For example, De Vries *et al.* [8] found on seven halothane negative breeds that growth rate and carcass lean percentage were poorly related to pH, the water-holding capacity and colour of the meat. To the best of our knowledge, the existence of a mutation similar to that identified in the case of the “acid meat”  $RN^-$  allele has not been yet proven in poultry. Very recently, a mutation in the turkey *alpha-RyR* gene, the avian equivalent of the mammalian *RyR1* gene in which a mutation is at the origin of a higher sensitivity to the PSE defect in pork, has been reported (Chiang *et al.* [6]). The relationship between the transmission of this mutation and the level of turkey meat quality has to be investigated.

## 5. CONCLUSION

Our study showed for the first time in poultry that meat traits measured under commercial conditions are partially genetically determined. Selection could therefore be useful to improve meat quality in the turkey. However, this study revealed a wide range of heritabilities according to the type of muscle. Indeed, even though heritabilities of meat quality indicators were moderate in the breast muscle, they remained very low in the thigh muscle with the exception of the rate of pH fall. Further investigations are now required to increase the accuracy of the genetic parameter estimates by using both larger data sets and including new meat traits such as water-holding capacity, texture or sensory quality. On the contrary, as largely discussed in this paper, the choice of the environment used to record meat traits has to be carefully considered. When experimental conditions have been used in order to ensure consistency of measurements, they do not permit the expression of meat quality defects such as PSE meat. A direct assessment of the impact of imposing a specific stress on the genetic parameters of meat traits remains to be conducted. This would help to determine the optimal strategy to select meat quality. Molecular genetics could also constitute an interesting alternative approach to rapidly identify the favourable genotypes.

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