# FAT AND MUSCLE ALLOMETRIC GROWTH OF DIFFERENT PIG GENOTYPES EVALUATED *IN VIVO* WITH COMPUTED TOMOGRAPHY FROM 30 TO 120 KG

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**Abstract – Growth and allometric growth of fat and muscle depths and areas of pigs from 3 genotypes from 30 to 120 kg was studied. Pigs (n=45) were CT scanned and measurements taken from one image in the shoulder, one in the loin and one in the ham areas. No significant differences were found between genotypes in most of the measures probably due to the fact that animals were fed the same diet. Allometric coefficients were significantly lower than 1 except for lateral fat thickness at the level of the last rib, top fat thickness in the ham area and the area of the superior part of the ham. Fat thickness in the shoulder grows more slowly than in the loin and ham, and the area of the superior part of the ham grows more slowly than the area of the loin.**

**Keywords – subcutaneous fat depth, loin area, ham, shoulder**

## I. INTRODUCTION

The determination of the evolution of body composition of pigs is performed by a series of slaughters [1,2]. There are more sophisticated and normally higher cost techniques that also have been used for this purpose such as computer tomography (CT) which, if available, avoids the slaughtering of the pigs [3,4]. The knowledge of the evolution of different fat and muscle depths and areas is important to determine the growth of these characteristics. This information can be used to improve pork production by selecting animals according to some of these characteristics such as the reduction of the subcutaneous fat content [5], or the increase of the loin area. This is influenced by genotype, sex, body weight or age and feeding, among other factors [3,6,7].

The aim of the present work was to study, by means of computer tomography, the growth and allometric growth of fat and muscle depths and areas of pigs from 3 different genotypes from 30 to 120 kg.

## II. MATERIALS AND METHODS

The experiment was carried out with 15 gilts, 5 DUx(LDxLW), 5 PIx(LDxLW) and 5 LDxLW. The piglets were born in the same week. The animals were fed *ad libitum* on the same pelleted diet based on cereals and soya. The diet consisted of 3365 kcal/kg, 1.05% lysine and 18% crude protein.

The study covered a live weight range of 30 to 120 kg. The pigs were weighed weekly and when they were near the target weight (30, 70, 100 and 120 kg) were chosen for CT examination. A General Electric HiSpeed Zx/i located in IRTA-Monells (Catalonia, Spain) was used. Three cross-sectional images were taken. Instrumental settings were: 140 kV, 145 mA, matrix 512 x 512, axial 7 mm thickness for 30 kg weight and 10 mm thickness for the rest of the weights. The gilts were fasted for minimum 8 hours, weighed and anesthetised before scanning. After scanning, the animals were returned to the farm to continue with the experiment. When they reached 120 kg, they were slaughtered at the IRTA slaughterhouse after being previously stunned with $CO_2$ 90%.

CT image analysis was carried out by means of VisualPork program developed by Girona University and IRTA [8]. The parameters analyzed by the CT are described in Table 1. They were obtained from three different images: shoulder (cross section SS of Porcine Myology Atlas [9]) (Figure 1), last rib (Figure 2) and ham (cross section N of Porcine Myology Atlas [9]) (Figure 3).

Table 1 Parameters evaluated by CT and their description

| Figure | Parameter | Description |
|---|---|---|
| - | Live weight | Weight before scanning |
| 1 | Fat shoulder | Subcutaneous fat at the top |
| 2 | Top fat LR | Subcutaneous fat at the top |
| 2 | Max. loin width LR | Maximum width of the right loin |
| 2 | Lateral fat LR | Lateral fat |
| 2 | Loin area LR | Right loin area |
| 2 | Loin perimeter LR | Right loin perimeter |
| 3 | Superior ham area | Area of the superior part |
| 3 | Top fat ham | Subcutaneous fat at the top |
| 4 | Superior ham fat area | Area of the fat of the superior part |

All data were analysed using the MIXED procedure by SAS ® software (SAS Institute Inc, Cary, NC, USA). The model included genotype and target weight as fixed effects and the deviation of live weight within target group as covariate. Repeated measures within animal were also considered. Interaction was not included because it was not significant.
The following allometric equation was used to evaluate the growth rate of each parameter evaluated relative to live weight:

$$Y = a X^{b}$$

Where Y is the parameter evaluated, X is live weight, a is the intercept and b is the allometric growth coefficient relating to growth of Y to that of X. The allometric equation was fitted by linearizing the function as $\log_{10} Y = \log_{10} a + b \log_{10} X$ considering repeated measures within each animal.

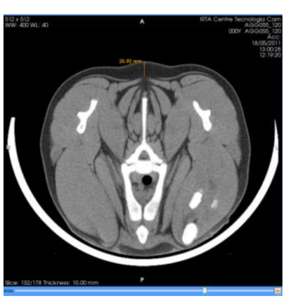

Figure 1. Axial image of the shoulder

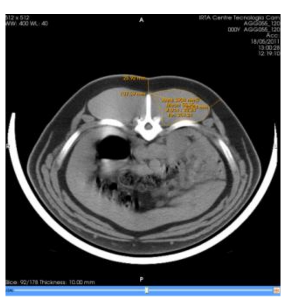

Figure 2. Axial image of the last rib

Figure 3. Axial image of the ham

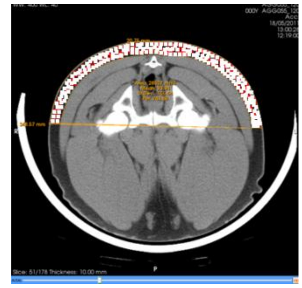

Figure 4. Fat area in the axial image of the ham.

## III. RESULTS AND DISCUSSION

No significant (P>0.05) differences were found between genotypes in any of the fat and muscle thicknesses evaluated (Table 2). The animals were fed the same diet and this diet could have been more adequate for one genotype than another and could have affected at the fat deposition. This could explain why crosses with PI presented similar fat thicknesses to crosses with DU when PI pigs were less fat than DU (Gispert et al., 2007). The loin area of animal PIx(LDxLW) was significantly (P<0.05) higher than that of LDxLW, DUx(LDxLW) being in between the two. In pure lines Gispert [6] found higher area for PI pigs compared with DU, LD or LW pigs. The area of the superior part of the ham image was significantly higher in animals PIx(LDxLW) and LDxLW compared with DUx(LDxLW). This indicates a higher conformation of PI crosses compared with DU ones.

Regarding the evolution of the different measures during growth, Table 2 shows that all of them increased between all the target weights studied. Only the area of the superior part of the ham was not significantly different (P>0.05) between 30 and 70 kg. This result makes sense due to the growth of the weight of the animal. However, this does not allow seeing whether this growth was similar in all the different depths, areas or perimeters evaluated. This can be understood by studying the allometric coefficients (Table 3). Regarding fat depths it is possible to see that the growth of fat thickness in the shoulder and at the top of the loin last rib image occurred relatively more slowly than body weight. Moreover this growth was much slower in the shoulder than in the loin. The growth of the lateral fat of the loin and the fat at the top of the ham image was faster than the other fat depths studied and similar (P>0.05) when compared to body weight increase. With respect to loin measurements (width and perimeter) no important differences were observed between them. Both of them grew much more slowly than body weight because they had an early maturity. The loin area grew faster than the superior ham area and both of them more slowly than body weight. However, the fat area in the superior fat of the ham grew at a rate similar to body weight and faster than the other areas studied.

## IV. CONCLUSION

It is possible not to find significant differences in fat and muscle depths and areas between genotypes if the diet is not adapted according to its growing potential. Fat thickness in the shoulder grows more slowly that of the loin and ham and the area of the superior part of the ham more slowly than the area of the loin.

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Table 2 Developmental change of the parameters studied depending of the genotype[1] and during the growth period[2].

| Parameter | LDxLW | PIx(LDxLW) | DUx(LDxLW) | 30 kg | 70 kg | 100 kg | 120 kg | RMSE |
|---|---|---|---|---|---|---|---|---|
| *Fat thickness* | | | | | | | | |
| Fat shoulder (mm) | 22.08 | 23.11 | 21.95 | 13.05[d] | 20.28[c] | 26.39[b] | 29.81[a] | 3.14 |
| Top fat LR (mm) | 16.79 | 19.10 | 18.23 | 7.52[d] | 16.07[c] | 22.35[b] | 26.21[a] | 3.02 |
| Lateral fat LR (mm) | 15.39 | 16.92 | 16.24 | 6.23[d] | 13.26[c] | 20.69[b] | 24.54[a] | 2.81 |
| Top fat ham (mm) | 12.08 | 14.26 | 12.95 | 5.57[d] | 9.97[c] | 16.11[b] | 20.75[a] | 2.97 |
| *Loin measures* | | | | | | | | |
| Max. loin width LR (mm) | 102.23 | 99.26 | 98.10 | 75.51[d] | 98.21[c] | 110.52[b] | 115.21[a] | 3.02 |
| Loin perimeter LR (mm) | 234.27 | 237.31 | 233.49 | 166.71[d] | 232.17[c] | 263.62[b] | 277.60[a] | 8.55 |
| *Areas* | | | | | | | | |
| Loin area LR ($cm^2$) | 34.50[b] | 37.73[a] | 35.38[ab] | 15.13[d] | 34.02[c] | 44.75[b] | 49.57[a] | 3.34 |
| Superior ham area ($cm^2$) | 313.65[a] | 322.31[a] | 293.49[b] | 245.43[c] | 260.70[c] | 343.70[b] | 389.44[a] | 19.91 |
| Superior ham fat area ($cm^2$) | 49.72 | 53.13 | 47.32 | 21.38[d] | 37.93[c] | 61.98[b] | 78.92[a] | 8.97 |

[1] Least squares means by genotype adjusted to live weight of 80.7 kg
[2] Different superscripts within genotype and effect (genotype or weight) indicate significant ($P<0.05$) differences.

Table 3 Estimated allometric growth functions relating the parameters studied to live weight[1]

| Parameter | log a | s.e | b | s.e | r | RMSE |
|---|---|---|---|---|---|---|
| *Fat thickness* | | | | | | |
| Fat shoulder (mm) | 0.24 | 0.06 | 0.58 | 0.03 | 0.92 | 0.06 |
| Top fat LR (mm) | -0.45 | 0.09 | 0.89 | 0.05 | 0.93 | 0.09 |
| Lateral fat LR (mm) | -0.65 | 0.08 | 0.97[2] | 0.04 | 0.94 | 0.08 |
| Top fat ham (mm) | -0.61 | 0.11 | 0.90[2] | 0.06 | 0.90 | 0.11 |
| *Loin measurements* | | | | | | |
| Max. loin length LR (mm) | 1.43 | 0.01 | 0.30 | 0.01 | 0.98 | 0.01 |
| Loin perimeter LR (mm) | 1.69 | 0.02 | 0.36 | 0.01 | 0.98 | 0.02 |
| *Areas* | | | | | | |
| Loin area LR ($cm^2$) | 1.93 | 0.05 | 0.86 | 0.03 | 0.97 | 0.05 |
| Superior ham area ($cm^2$) | 3.89 | 0.05 | 0.32 | 0.02 | 0.83 | 0.05 |
| Superior ham fat area ($cm^2$) | 1.94 | 0.09 | 0.92[2] | 0.05 | 0.92 | 0.09 |

[1] Allometric functions fitted by linearizing the functions as $\log_{10}Y=\log_{10}\cdot a+b\cdot\log_{10}X$
[2] b coefficients not significantly ($P>0.05$) different than 1
s.e.: standard error; r: correlation coefficient ; RMSE: Root mean square error