# Genetic analysis of pork bellies

Susanne Hermesch[1] and John O'Shea[2]

*[1]Animal Genetics and Breeding Unit, joint venture of the University of New England and NSW Department of Primary Industries, UNE, Armidale NSW 2351*
*[2]QAF Meat Industries, PO Box 78, Corowa, NSW, 2646*

## Pork bellies are an important cut of pork carcases

Pork bellies are one of the five major cuts from a pork carcase. In the Australian domestic market the belly portion of the middle has always been of great concern to manufacturers. The bacon rasher, as sold in the Australian market, requires a good meaty streak in the belly to be acceptable. The absence of this streak often leads to rejection and return of the product, and subsequent claims on the producer. The absence of a reasonable streak can also lead to watery pockets in the rasher and result in rejection by the consumer.

The composition of pork bellies is also of concern for a number of overseas markets. The belly is not used for bacon manufacture but sold in strips for use in stir-fry type meals in the Singapore market. In Korea the belly is used for barbeques as well as in soup and general cooking. The amount of fat is not an issue but there is still a requirement for a prominent meaty streak. In the Japanese market, the belly is used for the production of bacon and so the presence of a well-defined streak and a higher proportion of lean meat to fat are important.

In summary, the belly is a valuable cut of pig carcases with different markets having different requirements. In order to supply each market with the desired belly product it is necessary to be able to predict the composition of the belly and have a good understanding of the factors that influence belly composition.

It is the aim of this paper to describe a camera-based measurement system for the prediction of the fat percentage of pork bellies and to present genetic parameters for different characteristics of pork bellies.

## Predicting fat percentage of the belly

### 1. Procedure

The prediction equation for the fat percentage of the belly was developed at QAF Meat Industries. In order to achieve a more even distribution of fat percentage of the belly, 101 commercial bellies were pre-selected on subjective scores of fat and lean meat content of the belly. It was the aim to have as close as possible equal numbers in each subjective score of fat, and lean meat content of the belly. The subjective scoring was based on five fat and five lean meat classes. An experienced meat worker at QAF Meat Industries, who had shown in a previous trial to be better able to classify belly composition from digital images, performed the scoring.

Digital images of 101 commercial bellies were taken from the anterior side of the belly by mounting each belly on a rig in which the plane was elevated by 30° to the horizontal. In addition, the rig had been equipped with rulers along the bottom of the plane and along each side. These rulers were used to calibrate each picture during the image analysis. The commercial software package ImageProPlus™ was used for image analysis of the digital image of each belly and a number of area and length measurements of the belly were derived.

Bellies were string boned and minced after chilling for the determination of the reference fat percentage of the belly. The mince was then homogenised for the Near Infrared Spectroscopy (NIR) analyses to determine the fat percentage. Initially, soxthlet extraction was performed to calibrate the NIR analyses.

Multiple regression analyses were then performed to derive the belly characteristics, which together with fat depth at the P2 site, best predicted the fat percentage of the belly. It was the aim to derive a model that contained only a few parameters and at the same time explained a high amount of variation (high coefficient of determination). For a full description of the procedure see APL final report of project 1637 (Hermesch et al., 2004).

## 2. Prediction equation

The mean fat percentage of the belly was 20.09% with a standard deviation of 5.57%. The belly characteristics that were included in the final prediction equation were the intermuscular fat area (IMFA), the subcutaneous fat area (SFA) and the joint area of rib bone and rib muscles (BMA) (Figure 1 from Shaw and Rossetto, 2003). In addition, the prediction equation for fat percentage of the belly (FATPC) included the backfat depth at the P2 site recorded in the abattoir (Shaw and Rossetto, 2003):

$$\text{FATPC} = 13.689 + (0.484 \times \text{IMFA}) + (0.549 \times \text{P2}) - (0.226 \times \text{BMA}) + (0.271 \times \text{SFA}).$$

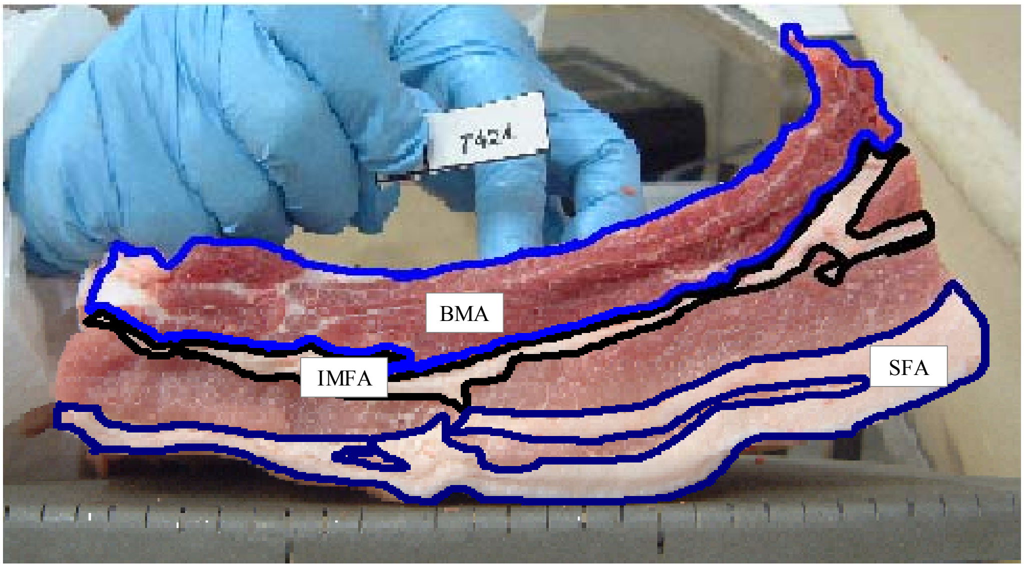

**Figure 1.** Definition of area measurements used in prediction equation for fat percentage of the belly (for abbreviations see text above).

Correlations between the three fat measurements included in the prediction equation and fat percentage of the belly were high ranging from 0.59 to 0.65 (Table 1). In comparison, the correlation between the joint area of rib bone and rib muscles and fat percentage of the belly was low (-0.13).

**Table 1.** Correlations between fat percentage of the belly and belly and carcase characteristics.

| Trait | Belly fat percentage |
|---|---|
| Hot standard carcase weight | 0.30 |
| Backfat at P2 site | 0.62 |
| Joint area of rib bone and rib muscles | -0.13 |
| Subcutaneous fat area | 0.59 |
| Intermuscular fat area | 0.65 |

## 3. Comparison with other studies

A direct comparison with other studies is often difficult because the composition of the belly used as a reference differs (i.e. lean meat percentage of the belly) or the study investigated a different cut (i.e. middle primal cut). Keeping this in mind, an Australian study and a number of German studies are mentioned for a comparison.

D'Souza and Mullan (2002) found that the P2 backfat measurement alone accounted for 60% of the variation in fat percentage of the middle primal cut. This equates to a higher correlation of 0.77 than the correlations between fat measurement and predicted fat percentage of the belly found in this study. The middle includes the fat area where the P2 backfat measurement is taken. This may have contributed to the higher correlation observed by D'Souza and Mullan (2002).

In Germany, a number of objective prediction equations for the lean meat content of the belly have been developed (Schmitten et al., 1986; Memmert et al., 1992; Tholen et al., 1998). Different measurement techniques including on-line AutoFom, linear carcase measurements and digital image analyses were recently evaluated by Tholen et al. (2003), using Magnetic Resonance imaging (MRI) (Baulein et al., 1998) as a reference method. The coefficients of determination ranged from 54 to 69% for digital imaging analysis of lean and fat areas recorded at the 13th and 14th rib's fat interface. These coefficients increased from 67 to 78% by using a combination of linear carcase measurements and digital imaging information. The coefficient of determination achieved in this study falls within this range.

## 4. Conclusions

Digital images of carcase surfaces can be easily taken in the boning room, provided that the surface of the cut is firm. This may not be achieved for carcases exhibiting pale, soft and exudative characteristics and carcases that have not been chilled.

Commercial software packages are readily available for the analysis of digital images providing a tool to derive a wide range of image characteristics.

The fat percentage of the belly was predicted from the backfat depth at the P2 site, intermuscular and subcutaneous fat areas as well as the joint area of rib bone and muscle. Area measurements were derived from images of the anterior side of the belly.

The prediction equation developed in this project needs to be confirmed for other populations given the large variation in belly composition that has been observed across projects.

## Genetic improvement of belly composition

### 1. Background

Currently, Australian breeding programs do not incorporate the composition of bellies in their selection decisions. Selection response in fat percentage of the belly might be achieved through indirect selection for reduced fatness in the whole carcase. However, this indirect response to selection depends on the magnitude of the genetic correlation between backfat, the trait currently used in breeding programs, and the fat percentage in the belly.

In Germany, the belly has always been evaluated as part of central testing procedures. Initially subjective evaluation of bellies was based on a five-point scale, with one representing fat bellies and five representing lean bellies. In 1981, this five-point scale was extended to a nine-point scale. Reference pictures were used as a basis for these subjective evaluations (see Littmann et al., 1994 for further details). Since the beginning of the 1990s the lean meat content of the belly has been incorporated into breeding programs and objective measurements of the lean meat percentage have been developed (Memmert et al., 1992). Since 1998, the prediction equations derived by Tholen et al. (1998) have been used and different methodologies of determining the lean meat percentage of the belly have been compared (Tholen et al. 2003).

### 2. Description of data

Belly characteristics were recorded between August 2001 and April 2003 on 2403 pigs from three commercial lines at QAF Meat Industries. The data set included entire males (N: 2026) and female pigs (N: 377). The majority of pigs (N: 1737) also had feed intake data available. The mean fat percentage of the belly was 18.8% with a coefficient of variation of 22% (Table 1). The intermuscular fat area had a substantially higher coefficient of variation of 48% in comparison to other belly characteristics. It was observed that the belly surface was sometimes distorted for very soft bellies, which mostly affected the intermuscular fat area.

Information about lifetime growth rate, backfat recorded at the P2 site and muscle depth between the third and fourth last ribs was available for approximately 35,000 animals. These animals consisted of pigs with belly information and their contemporaries recorded between January 2002 and July 2003. Juvenile insulin-like growth factor–1 (IGF-1) was recorded on approximately 50% of these animals (N~ 18,400). Feed intake data were recorded over a seven-week test period with electronic feeders for approximately 5500 pigs. The average live weight at the start of testing was 70kg. Pigs were restrictively fed on the basis of their starting weight, which ranged from 55 to 85kg. Colour (L-value of Minolta chromameter) and pH of the *longissimus dorsi* muscle were recorded 24 hours after slaughter (N~3800).

**Table 2.** Means and standard deviations along with coefficients of variation (CV%) for belly characteristics.

| **Trait** | **Abbreviation** | **n** | **Mean** | **SD** | **CV%** |
|---|---|---|---|---|---|
| Predicted fat percentage of the belly (%) | FATPC | 2331 | 24.8 | 5.55 | 22 |
| Area of bone and rib muscles ($cm^2$) | BMA | 2399 | 48.1 | 8.16 | 17 |
| Intermuscular fat area ($cm^2$) | IMFA | 2400 | 8.18 | 3.92 | 48 |
| Subcutaneous fat area ($cm^2$) | SFA | 2396 | 24.1 | 6.88 | 28 |
| Fat depth at P2 site (mm) | P2 | 2316 | 10.0 | 2.67 | 27 |

The pedigree file consisted of parents, grandparents and great-grandparents of animals with performance records including 5014 pigs in total. There were 512 sires, 3244 dams and 6544 litters.

### 3. Development of models

The SAS procedure GLM (SAS V6.12) was used to derive the fixed effect model for each trait. The effects that were analysed for belly characteristics included line, sex, feeding system and date of slaughter, along with the covariates of age of the animal at slaughter and live weight. These fixed effects explained 40 to 52% of the variation observed in belly characteristics (Table 3).

For juvenile IGF-1, the contemporary group consisted of the assay batch within date of bleeding. Sex of the animal, line and parity of the sow were fitted as further fixed effects. Age at bleeding was fitted as a linear covariable. The contemporary group for performance traits recorded on the live animal was based on the week of recording, the testing system (conventional pens vs. electronic feeders) and the sex of the animal (entire males vs. females). Line and parity of sow were further fixed effects. The weight of the animal at the end of test was fitted as a covariable for carcase and meat quality traits. Each week animals were slaughtered on the same day of the week, and day of the week of slaughter was part of the fixed effect model for meat quality traits.

**Table 3.** Coefficients of determination ($R^2$) and P-values for fitted fixed effects on belly characteristics.

| **Trait** | **$R^2$** | **Slaughter date** | **Line** | **Sex** | **Age at slaughter (linear)** | **Live weight (linear)** | **Live weight (quadratic)** |
|---|---|---|---|---|---|---|---|
| FATPC | .43 | .0001 | | .0001 | .0079 | .0001 | |
| BMA | .42 | .0001 | .0001 | .0582 | | .0001 | .0107 |
| IMFA | .48 | .0001 | .0001 | .0001 | | .0001 | |
| SFA | .52 | .0001 | | .0001 | .0180 | .0001 | |
| P2 | .40 | .0001 | .0016 | .0001 | .0081 | .0001 | |

The fixed effect model explained 15 to 20% of the variation in growth rate traits and feed conversion ratio. A larger proportion of the variation (27 to 40%) was accounted for by the fixed effect model for feed intake as well as backfat and muscle depth. In comparison, the model explained 32% of the variation for juvenile IGF-1. The main effects were contemporary group and line.

Variance components were estimated using ASREML (Gilmour et al., 1999) applying an animal model. Random effects included the animal effect as well as the litter effect. Heritabilities were estimated from univariate analyses and genetic correlations were obtained from bivariate analyses.

## 4. Heritability estimates

The fat percentage of the belly had a heritability estimate of 0.34 and an estimate of the litter effect of 0.05 (Table 4). The subcutaneous fat area had a similar heritability estimate. In comparison, heritability estimates for other belly characteristics were slightly lower ranging from 0.23 for intermuscular fat area to 0.26 for backfat at the P2 site measured in the abattoir. Litter effect estimates were low and not significantly different from zero due to the number of records available.

The heritability of 0.21 for juvenile IGF-1 with a litter effect of 0.11 is well in agreement with previous estimates of Australian populations as summarised by Bunter et al. (2002). Heritabilities for feed intake and feed conversion ratio were higher in this study (0.24 and 0.12 with litter effects of 0.11 and 0.08) in comparison to previous studies that were also based on data recorded under restricted feeding (Hermesch et al., 1999; Hermesch et al., 2002). In addition, the variance in feed conversion ratio was lower in comparison to previous studies. A number of quality control measures for data recording with the electronic feeders have been implemented (McSweeny, 2002) since these earlier studies, which may have contributed to these higher heritability estimates.

**Table 4.** Heritability and litter effect estimates ($h^2$ and $c^2$; with standard errors; se) and phenotypic variance (Vp) for belly characteristics, performance, carcase and meat quality traits.

| **Trait** | **Abbr.** | $h^2$ | **se** | $c^2$ | **se** | **Vp** |
|---|---|---|---|---|---|---|
| Predicted fat percentage of the belly | FATPC | .34 | .062 | .05 | .032 | 18.8 |
| Area of bone and rib muscles | BMA | .25 | .054 | .04 | .033 | 40.7 |
| Intermuscular fat area | IMFA | .23 | .055 | .05 | .033 | 8.48 |
| Subcutaneous fat area | SFA | .32 | .060 | .07 | .033 | 24.3 |
| Fat depth at P2 site | P2 | .26 | .057 | .03 | .033 | 4.50 |
| Juvenile insulin-like growth factor-1 | IGF1 | .21 | .019 | .11 | .008 | 814 |
| Lifetime growth rate | ADG | .30 | .018 | .08 | .005 | 4757 |
| Feed intake | FDINT | .24 | .038 | .08 | .021 | .037 |
| Feed conversion ratio | FCR | .12 | .031 | .11 | .02 | .137 |
| Backfat at P2 site, real time ultrasound | LF | .33 | .016 | .04 | .004 | 3.65 |
| Muscle depth, real time ultrasound | LMD | .23 | .014 | .02 | .004 | 22.0 |
| Colour of *m. longissimus dorsi* | CLD | .19 | .039 | .03 | .025 | 13.2 |
| pH of *m. longissimus dorsi*, recorded 24 hours after slaughter | PH24 | .21 | .038 | .03 | .025 | .022 |

The heritability estimates for backfat recorded on the live animal was slightly higher than the heritability of backfat recorded in the abattoir. Muscle depth recorded with real time ultrasound on the live animal had a heritability of 0.23. Higher heritability estimates for backfat and muscle depth measurements recorded with real time ultrasound in comparison to measurements taken with the Hennessy Chong machine in the abattoir were also found by Hermesch et al. (2000).

Both meat quality measurements had moderate heritabilities with estimates of 0.21 for colour (L-value of the Minolta chromameter) and 0.22 for pH recorded 24 hours after slaughter. However, pH recorded 24 hours after slaughter had a very low variance, which limits genetic progress that is possible in this trait.

## 5. Genetic correlations

**Belly characteristics**. All three individual fat measurements had high genetic correlations with the predicted fat percentage of the belly (range: 0.71 to 0.85; Table 5), which were slightly higher than the phenotypic correlations (range: 0.60 to 0.66). The genetic association between predicted fat percentage of the belly and joint area of rib bone and rib muscles was lower (genetic correlation; rg: -0.48).

**Table 5.** Genetic (first row, bold) and litter correlations (second row) under diagonal along with environmental (first row) and phenotypic correlations (second row) above diagonal between belly characteristics (r: correlation; se: standard error).

| **Trait** | **FATPC** | | **BMA** | | **IMFA** | | **SFA** | | **P2** | |
|---|---|---|---|---|---|---|---|---|---|---|
| | r | se | r | se | r | Se | r | se | r | se |
| FATPC | | | -.34 | .04 | .63 | .03 | .66 | .03 | .60 | .03 |
| | | | -.38 | .02 | .67 | .01 | .73 | .01 | .68 | .01 |
| BMA | **-.48** | **.12** | | | .18 | .04 | .15 | .05 | -.01 | .05 |
| | -.21 | .46 | | | .14 | .02 | .07 | .02 | -.07 | .02 |
| IMFA | **.71** | **.08** | **.03** | **.17** | | | .48 | .04 | .15 | .05 |
| | .99 | .22 | .07 | .47 | | | .50 | .02 | .29 | .02 |
| SFA | **.84** | **.05** | **-.09** | **.15** | **.56** | **.11** | | | .26 | .05 |
| | .87 | .16 | -.08 | .41 | .49 | .28 | | | .42 | .02 |
| P2 | **.85** | **.05** | **-.24** | **.14** | **.63** | **.10** | **.73** | **.09** | | |

For abbreviations see Table 4.

Bone and muscle area had no significant genetic correlations with the three fat measurements. Selection for reduced fatness levels through lower backfat at the P2 site for example will therefore not improve bone and muscle areas. Bone and muscle area was part of the prediction equation for fat percentage of the belly, which explains the stronger genetic association between the predicted fat percentage and bone and muscle area.

Genetic correlations between the three fat measurements were significantly different from one. These traits were therefore genetically different from each other.

**Belly characteristics and performance traits**. All belly characteristics describing fat level of the belly had similar genetic correlations with performance traits. The fat percentage of the belly, the intermuscular and subcutaneous fat area as well as the P2 backfat recorded in the abattoir had positive genetic correlations with juvenile IGF-1 concentration (range: 0.08 to 0.25), growth rate (range: 0.16 to 0.35) and feed intake (0.26 to 0.39) but had no genetic relationship with feed conversion ratio (Table 6).

Breeding programs use backfat recorded with realtime ultrasound at the P2 site for selection of leaner pigs. This backfat measurement is a genetically different trait than the fat percentage of the belly. In addition, live muscle depth had a low negative genetic correlation with fat percentage of the belly (rg: -0.16). However, live muscle depth had a significant genetic correlation (rg: 0.32) with the joint area of rib bone and rib muscle. Other genetic correlations between bone and muscle area and performance traits were not significantly different from zero.

**Table 6.** Genetic (rg) correlations with standard errors (se) between belly characteristics and performance traits.

| | FATPC | | BMA | | IMFA | | SFA | | P2 | |
|---|---|---|---|---|---|---|---|---|---|---|
| | rg | se | rg | se | rg | se | rg | se | rg | Se |
| IGF1 | .20 | .10 | .08 | .11 | .18 | .12 | .25 | .10 | .21 | .11 |
| ADG | .33 | .09 | -.11 | .11 | .35 | .10 | .29 | .09 | .16 | .10 |
| FDINT | .39 | .10 | -.17 | .12 | .32 | .12 | .26 | .11 | .31 | .12 |
| FCR | .01 | .13 | .06 | .14 | .04 | .15 | -.02 | .13 | .05 | .14 |
| LF | .80 | .05 | -.09 | .10 | .47 | .09 | .76 | .05 | .95 | .03 |
| LMD | -.16 | .08 | .27 | .09 | .04 | .09 | -.14 | .08 | -.05 | .09 |
| CLD | -.28 | .13 | .05 | .14 | -.16 | .15 | -.31 | .12 | -.21 | .14 |
| PH24 | .01 | .13 | -.01 | .14 | .03 | .14 | .02 | .12 | -.01 | .14 |

For abbreviations see Table 4.

The genetic correlation between intermuscular fat area and backfat recorded on the live animal was 0.47. In comparison, subcutaneous fat measurements taken on the carcase (SFA and P2) had larger genetic correlations with backfat measurements taken on the live animal (rg: 0.76 and 0.95). The magnitude of these genetic correlations support the concept that intermuscular fat area is genetically a different trait than subcutaneous fat, as indicated by Kouba et al. (1999). The authors discussed the relative development of subcutaneous, intermuscular and kidney fat and highlighted the fact that there have been very few studies on the development of intermuscular adipose tissue in pigs. They found that subcutaneous fat accounted for 60 to 70% of body fat while intermuscular fat accounted for 20 to 35% of body fat. Relative to other fat depots, intermuscular fat was more developed in genetically lean than in genetically fat pigs. This could be the result of the selection of pigs against subcutaneous fat only and selection for leanness has been less successful for reducing intermuscular fat.

## 6. Outlook

Genetic improvement of any trait is enhanced if it is possible to measure the trait of interest on a large number of animals, preferably on the live animal before selection. A method was presented that predicted the fat percentage of the belly from video image analyses of the belly. This measurement technique cannot be done routinely on the slaughter floor, which limits the number of animals that can be recorded for this trait. Further work should be directed towards the development of non-invasive measurement techniques that can be recorded routinely on selection candidates. For genetic improvement it would be ideal to have measurements on the live animal that have high relationships with the carcase measurement. Further work should make the best use of technologies available from overseas studies (i.e. Seifert et al., 2002; Sonnichsen et al., 2002).

Tholen et al. (2001) showed that carcase measurements taken with the fully automated classification system AutoFOM were highly heritable and recommended using these characteristics for the selection of AI-boars. However, heritabilities were lower for station tested purebred Pietrain boars and did not exceed 0.10. It was also observed in this project that very lean carcases had a reduced variation in fat percentage and that it was more difficult to take quality images of bellies from these lean carcases.

The prediction equation for fat percentage of the belly included a number of fat measurements and the area of bone and muscle under the rib. The joint area of rib bone and rib muscles had a lower heritability estimate than the different fat measurements. The joint rib bone and rib muscle area had no genetic relationship with fat measurements and a moderate genetic correlation with muscle depth recorded on the live animal. Overall, these results show that genetic improvement of specific muscles requires specific measurements for these traits. Further studies of the belly should include additional measurements of the lean meat area of the belly and should exclude bone areas.

The Australian payment system is based on hot carcase weight and backfat at the P2 site. The producer is not paid for any other differences in carcase composition. Therefore, belly composition does not have an economic value and is not part of the breeding objective at the moment. Payment systems may change in the future, especially in view of the need for Australian pork bellies to compete with imported products from Denmark. Future payment systems may take differences in carcase composition into account following the trend in Europe and North America.

## General conclusions

Genetic improvement of the predicted fat percentage of the belly and the joint area of bone and muscle, as well as intermuscular and subcutaneous fat areas is possible given their moderate heritability estimates and the variation observed for these traits.

Current breeding objectives are based on growth rate, backfat and feed conversion ratio. For this scenario, it is not worthwhile to include information about belly composition in selection decisions since belly characteristics can only be recorded on a limited number of animals after slaughter.

In the future, Australian payment systems may consider carcase and belly composition in more detail following the trend already observed in Europe and North America. Genetic parameters available from this project allow seedstock producers to incorporate belly composition in breeding decisions.

Breeders who wish to consider belly composition in their breeding program are able to incorporate characteristics of the belly into PIGBLUP. This setup requires only minor changes to the default parameters of PIGBLUP.

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# References

Baulain, U., M. Henning, E. Tholen, W. Wittmann and W. Peschke (1998). "Objektive Erfassung des Fleischanteils im Schweinebauch. 2. Mitteilung: Verwendung von Bildinformationen aus dem MR-Imaging." *Züchtungskunde* **70**: 205 - 212.

Bunter, K., S. Hermesch, B. G. Luxford, K. Lahti and E. Sutcliffe (2002). IGF-1 concentration measured in juvenile pigs provides information for breeding programs: a mini review. 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France.

D'Souza, D. and B. Mullan (2002). "Validation of a methodology to assess middle primal cuts in pig carcasses". APL Final report - project 1818

Gilmour, A. R., B. R. Cullis, S. J. Welham, and R. Thompson (1999). "NSW Agriculture Biometric Bulleting No. 3. ASReml Reference Manual." NSW Agriculture, Orange, NSW, Australia

Hermesch, S., B. G. Luxford and H.-U. Graser (1999). Genetic parameters for performance traits recorded under ad libitum and restricted feeding. Proc Assoc. Advmt Anim Breed Genet Vol 13. p. 142-145

Hermesch, S., B. G. Luxford and H.-U. Graser (2000). "Genetic parameters for lean meat yield, meat quality, reproduction and feed efficiency traits for Australian pigs. 1. Description of traits and heritability estimates." *Livestock Production Science* **65**: 239-248.

Hermesch, S., B. G. Luxford and H.-U. Graser (2002). Feeding level influences genetic parameters for performance traits in pigs. 7th World Congress on Genetics Applied to Livestock Production, Montpellier, France. Communication No. 03-34.

Hermesch, S., J. O'Shea and H. Grigg (2004). "Characterisation and improvement of belly composition". APL Final report - Project 1637.

Kouba, M., M. Bonneau and J. Noblet (1999). "Relative development of subcutaneous, intermuscular, and kidney fat in growing pigs with different body compositions." *Journal of Animal Science* **77**: 622-629.

Littmann, E. and W. Peschke (1994). "Zur Schätzung des Fleischanteils im Teilstück -Bauch- von LPA - Prüftieren." *Informationen und Hinweise der bayerischen Landesanstalt für Tierzucht* Gruber INFO 4/94: 5-9.

McSweeny, J. M. (2002). Genetic analysis of feed intake patterns and performance traits recorded in group-housed pigs. Masters Thesis; University of New England. Armidale.

Memmert, T., H. Jüngst, E. Tholen and F. Schmitten (1992). "Untersuchungen zur objektiven Bewertung des Teilstückes Bauch in der Fleischleistungsprüfung beim Schwein." *Züchtungskunde* **64**: 356-362.

SAS (1988). SAT/STAT User's Guide, Release 6.12 Edition, Cary, NC: SAS Institute Inc.

Schmitten, F., A. Klingelhoeller, K. H. Scheper, A. Festerling and H. Juengst (1986). "Einfluss des Mastendgewichtes auf die Fleischbeschaffenheit beim Schwein." *Züchtungskunde* **58**: 282-290.

Seifert, H., P. Zimmermann, G. Seifert and L. Kumpfert (2002). "Tissue differentiation of pork by way of ultrasonic measuring process - Method for an objective classification of belly quality." *Fleischwirtschaft*(82): 100-103.

Shaw, T. and J. Rosetto (2003). Belly fat determination using digital analysis. In: ‘Manipulating Pig Production IX, Ed. J. E. Paterson, Australasian Pig Science Association, p. 22.

Sonnichsen, M., A. Dobrowolski, R. Horeth and W. Branscheid (2002). "Commercial valuation of pig carcases by using Video Image Analysis." *Fleischwirtschaft* **82**: 98-101.

Tholen, E., U. Baulain, M. D. Henning and K. Schellander (2003). "Comparison of different methods to assess the composition of pig bellies in progeny testing." *Journal of Animal Science* **81**: 1177-1184.

Tholen, E., H. Brandt, H. Henne, F. J. Stork and K. Schellander (2001). "Genetic foundation of AutoFOM-traits." *Archiv für Tierzucht* **44**: 167-179.

Tholen, E., W. Peschke, U. Baulain and K. Schellander (1998). "Objektive Erfassung des Fleischanteils im Schweinebauch. 1. Mitteilung: Entwicklungen von Schätzgleichungen aus Schlachtkörpermaßen." *Züchtungskunde* **70**: 196-204.