# BIOLOGICAL GROWTH MODEL AS A NEW SELECTION STRATEGY FOR IMPROVEMENT OF FEED EFFICIENCY IN SWINE

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**Abstract.** Biological growth models are of increasing interest in animal breeding. One possible application is their use to optimise selection for feed intake capacity. For this to be achieved the input parameters of maximum protein deposition rate and minimum lipid to protein deposition ratio have to be known. Different methods can be used for measuring protein and lipid deposition rate on live animals (e.g. deuterium dilution technique, magnetic resonance tomography (MRT)) or on slaughter animals in a serial slaughter trial with the entire body chemically analysed. All these techniques are very expensive and can be obtained only in an experimental trial. Therefore, a trial that addresses these needs and also allows a comparison of the methods will be of great value. Correlation between protein or lipid deposition and indicator carcass cuts varied substantially during growth. The combinations of carcass cuts to predict protein and lipid deposition generally provided higher values. The number and kind of predicted variable varied during the growth, so it is necessary to measure protein also by direct methods.
**Keywords:** protein deposition, indicator cuts, biological growth model, selection, pig

# BIOLOGINIS AUGINIMO MODELIS, KAIP NAUJA SELEKCIJOS STRATEGIJA KIAULIŲ ŠĖRIMO EFEKTYVUMUI DIDINTI

**Santrauka.** Vis labiau domimasi biologiniais auginimo modeliais gyvulininkystėje. Vienas iš biologinio auginimo modelių yra selekcijos optimizavimas pagal pašarų suvartojimo pajėgumą. Taikant tokį biologinio auginimo modelį, turi būti žinomos didžiausios baltymų sąnaudų kiekio ir mažiausios lipidų sąnaudų pagal baltymus kiekio vertės. Baltymų ir lipidų sąnaudų kiekiui gyviems gyvuliams matuoti taikomi skirtingi metodai [pvz. deuterio atskiedimo technika, magnetinio rezonanso tomografija (MRT)]. Paskerstų gyvulių skerdenos visapusiškai chemiškai išanalizuojamos. Visi šie metodai yra labai brangūs ir gali būti atliekami tik eksperimento sąlygomis. Kontroliniai pjūviai baltymų ir lipidų sąnaudoms skirtingomis augimo stadijomis įvertinti kelia didelį susidomėjimą ir kartu tinka metodams palyginti. Koreliacija tarp baltymų arba riebalų atsidėjimo ir skerdenos puselių rodiklių labai įvairavo atskirais augimo periodais. Skerdenos puselių deriniai pagal numatomą baltymų ar riebalų atsidėjimo lygį buvo reikšmingesni. Kadangi numatomas skaičiaus ir rūšies kintamumas svyravo augimo metu, yra svarbu baltymų lygį nustatyti ir kitų metodų pagalba.
**Raktažodžiai:** baltymų atsidėjimas, skerdenos rodikliai, biologinis augimo modelis, selekcija, kiaulės.

**Introduction.** A successful simulation of the growth performance of a pig depends as much on a correct parameterisation of its genotype parameters as on a detailed description of its environment. These biological models can be used to optimise selection for feed intake, which may be based on the parameters of the protein deposition and the minimum lipid to protein deposition ratio (De Vries and Kanis, 1992). These parameters have to be known because they are critically important for the model. Therefore, the main objective of this study was the determination of protein and fat deposition at each stage of growth. In the present analysis, magnetic resonance tomography (MRT) and the deuterium oxide dilution technique were used to determine the protein and lipid deposition on live animal whereas chemical analysis of the entire body was carried out on slaughtered animals in a serial slaughter trial. All these techniques are very expensive and can be carried out only in an experimental trial of this kind. To reduce the costs of such a study, indicator cuts are of high interest. Indicator cuts, which are closely correlated with a protein and lipid mass, will make it possible to estimate protein and lipid deposition rate at a lower cost than alternatives. It is then possible to use the, Gompertz function to estimate the feed intake over the entire growth period, the maximum protein deposition rate and the minimum lipid to protein deposition ratio (Knap, 2000). Based on the estimated parameters of the Gompertz function selection to optimise feed intake curves can be one implication of the biological growth model.

**Research metods and conditions.**Data were obtained in a three generation full-sib design, which finally will be used to identify the genomic regulation of protein and lipid deposition rate. However, the first goal was to

determine protein, lipid and ash deposition during growth and its association with carcass characteristics. The base generation ($F_0$) consisted of 8 unrelated boars of a sire line and 32 unrelated sows of a dam line, which were mated to produce the $F_1$ generation. Animals not used to create the $F_2$ generation were tested on station to obtain protein, lipid and ash deposition at 15, 30, 60, 90, 120, 140 kg. Protein and lipid deposition was measured on all tested animals by deuterium dilution technique. As a reference method, chemical analysis of the entire body was used in a serial slaughter trial with 8 animals slaughtered at each of the 6 weight classes.

At slaughter the weights of the separate organs and intestinal tract were measured. Afterwards, these entrails were minced and two samples were taken from the material for the chemical analysis. One day later the left carcass side was dissected into ham, shoulder, loin, neck, belly and head. After weighing these carcass cuts, a fine dissection of each cut was executed. The weights from these parts were also taken. On the same day, the carcass cuts were separated into fractions meat/fat and bones. Both fractions were minced separately by the same procedure as for the entrails fraction. Two samples of each fraction were taken for chemical analysis. Each from the three fractions was analysed separately for its chemical composition. In order to be a representative each sample was autoclaved at 120°C and 2.3 bar for one hour and mixed afterwards with a blender. The samples were analysed using the methods of the VDLUFA (Naumann and Bassler, 1983). The samples were vacuum sublimated and thereafter dried in an oven at 65 °C until the weight was constant in order to determine the dry matter. Fat analysis was carried out with the official method (technique B) [Naumann and Bassler, 1983]. Based on the analysed chemical composition of each fraction and the weights the chemical body composition of the whole animal was determined.

MRT images were obtained on other 8 animals for weight classes 30 to 120 kg. In the present analysis the data of the chemical analysis and the MRT was used to estimate protein and lipid deposition, and their associations with carcass cuts were predicted using the weight of the main cuts of ham, shoulder, loin, belly and neck. Thereafter, each cut was dissected to obtain further information about its composition concerning lean meat, fat and bones. The data were analysed using SAS procedures, in particular the PROC NLIN Procedure for estimation of parameters of the Gompertz function. Body protein and lipid mass were related to the age (Tullis, 1981). The Gompertz function to estimate protein deposition was:

$$P = P_{\infty} \times e^{-e^{-B_{Gomp}} \times (age - t^*_P)}$$

and the Gompertz function to estimate lipid deposition was:

$$L = L_{\infty} \times e^{-e^{-B_{Gomp}} \times (age - t^*_L)}$$

where $P_{\infty}$ and $L_{\infty}$ are the asymptotic values that represent mature protein and lipid mass (kg), and $t^*_P$ and $t^*_L$ denote the x-coordinates of the points of inflection of the estimated P and L curves (in days). The multiple regression analysis to predict protein and fat mass using carcass cuts was accomplished with the PROC REG Procedure (SAS, 1992).

**The research results.** The correlations of protein or lipid mass of the carcass with carcass cuts are presented in Table 1. Protein and lipid mass was measured by chemical analysis. Some carcass cuts were closely correlated with the protein and fat mass but there was a change during the growth curve.

Whereas the weight of the entire ham was a good predictor for protein mass in pigs weighing 15 kg weight the associations at weight class 30 to 90 kg were only moderate. At the end of the measured growth period almost no correlation was found between these traits. In contrast, the weight of ham trimmed showed the highest correlations with protein mass at the beginning and at the end of the growth period. In the weight group of 140 kg highest associations to protein mass were obtained for the shoulder, shoulder trimmed, backfat and loin. Highest associations to predict lipid mass were found at early growth with ham, ham trimmed, shoulder, neck trimmed and loin trimmed. At the end of the test period, lipid mass was highly correlated with the abdominal fat and backfat. Over the total weight range, the correlation of ham trimmed with lipid mass changed from highly positive to negative. The results for some correlations between carcass quality traits and protein or lipid mass are represented in summary in Table 2. The highest association between protein mass and fat area, backfat thickness (BFT) or sidefat was estimated at 120 kg. The association of protein mass with fat area, BFT or sidefat differed from $r_p$=-0.75 to -0.83. The highest correlation of protein mass with loin area was found at 140 kg live weight. At high live weights, fat and loin area was highly associated with lipid mass for 120 and 140 kg, respectively. The highest correlation between lipid mass and BFT was at 120 kg whereas, the highest association with sidefat was at 140 kg. The correlations of carcass cuts with ash mass were high only in the group of 15 kg live weight ($r_P$=0.81 to 0.95), and therefore, are not shown.

The best predictions to estimate protein and fat mass (kg) by different carcass cuts using the multiple regression are presented in Table 3. The coefficient of determination ($R^2$) for the prediction of protein reached values from $R^2$=0.92 to 0.98 apart from the 120 kg weight group. Similarly high values were reached for the estimation of fat mass. Only at the 90 kg group, was the $R^2$ was moderate. Further carcass traits were not included in the multiple regression model because they did not meet a level of significance.

The same procedure was used to estimate the percentage of protein and fat as presented in Table 4. The best prediction of percentage of protein was the multiple regression including shoulder trimmed, loin, neck trimmed and ham at 30 kg live weight. Besides, the number and kind of predicted variables to estimate protein or fat percentage varied during the growth. In general, the coefficient of determination for percentage prediction of protein and fat of the entire body had more

variation over weight groups than for protein and fat mass. There were even weight groups, where no variable met the significance level of P<0.15.

Table1: **Correlations between carcass cuts and protein or lipid composition of the entire body for live weights from 15 to 140 kg**

| | Weight class (kg) | | | | | |
|---|---|---|---|---|---|---|
| Carcass cut | 15 | 30 | 60 | 90 | 120 | 140 |
| | Correlation with protein mass (kg) | | | | | |
| Ham | 0.96 | 0.65 | 0.78 | 0.72 | 0.43 | 0.07 |
| Ham trimmed | 0.86 | 0.65 | 0.59 | 0.52 | 0.56 | 0.66 |
| Shoulder | 0.92 | 0.41 | 0.62 | 0.39 | 0.00 | 0.71 |
| Shoulder trimmed | 0.56 | 0.01 | 0.54 | 0.27 | 0.31 | 0.68 |
| Neck | 0.82 | 0.61 | 0.31 | 0.02 | -0.32 | 0.19 |
| Neck trimmed | 0.95 | 0.85 | 0.54 | 0.43 | 0.28 | 0.42 |
| Loin | 0.74 | 0.38 | 0.70 | 0.27 | 0.11 | -0.71 |
| Loin trimmed | 0.82 | 0.50 | 0.74 | 0.33 | -0.05 | -0.20 |
| Backfat | 0.27 | 0.29 | 0.27 | 0.35 | -0.49 | -0.79 |
| Abdominal fat | 0.61 | 0.07 | -0.19 | -0.24 | -0.77 | -0.33 |
| | Correlation with lipid mass (kg) | | | | | |
| Ham | 0.88 | 0.53 | 0.09 | -0.07 | -0.18 | -0.12 |
| Ham trimmed | 0.90 | 0.68 | 0.03 | -0.22 | -0.49 | -0.36 |
| Shoulder | 0.91 | -0.09 | -0.02 | -0.36 | 0.41 | -0.33 |
| Shoulder trimmed | 0.28 | -0.08 | 0.21 | -0.41 | 0.04 | -0.30 |
| Neck | 0.73 | -0.10 | 0.15 | 0.72 | 0.17 | 0.19 |
| Neck trimmed | 0.88 | 0.09 | 0.15 | 0.09 | -0.32 | -0.31 |
| Loin | 0.78 | -0.31 | -0.18 | 0.32 | 0.01 | 0.54 |
| Loin trimmed | 0.92 | 0.64 | -0.46 | -0.16 | -0.01 | -0.26 |
| Backfat | 0.54 | 0.01 | 0.28 | 0.43 | 0.26 | 0.81 |
| Abdominal fat | 0.75 | -0.22 | 0.72 | 0.27 | 0.89 | 0.68 |

Table 2: **Correlations between carcass traits and protein and lipid composition of the entire body for live weights from 15 to 140 kg**

| | Weight class (kg) | | | | | |
|---|---|---|---|---|---|---|
| Carcass trait | 15 | 30 | 60 | 90 | 120 | 140 |
| | Correlation with protein mass (kg) | | | | | |
| Fat area | 0.68 | 0.28 | -0.61 | 0.16 | -0.75 | -0.45 |
| Loin area | 0.51 | 0.48 | 0.50 | 0.24 | 0.49 | 0.79 |
| BFT | 0.32 | 0.11 | -0.37 | -0.38 | -0.74 | -0.18 |
| Sidefat | 0.49 | -0.56 | -0.38 | 0.35 | -0.83 | -0.59 |
| | Correlation with lipid mass (kg) | | | | | |
| Fat area | 0.58 | 0.54 | 0.58 | 0.48 | 0.82 | 0.79 |
| Loin area | 0.65 | 0.52 | -0.52 | 0.02 | -0.64 | -0.84 |
| BFT | 0.36 | 0.25 | 0.40 | 0.67 | 0.80 | 0.60 |
| Sidefat | 0.27 | 0.17 | 0.69 | 0.37 | 0.76 | 0.96 |

Table 3: **Best multiple regression to predict protein and fat mass (kg)**

| Weight group (kg) | Predictor variable | $R^2$ |
|---|---|---|
| | Protein (kg) | |
| 15 | Ham, loin area, fat area | 0.98 |
| 30 | Neck trimmed, loin trimmed, shoulder trimmed | 0.97 |
| 60 | Ham, loin, neck | 0.96 |
| 90 | Ham | 0.52 |
| 120 | Sidefat (cm) | 0.69 |
| 140 | Abdominal fat, shoulder, neck trimmed | 0.92 |
| | Fat (kg) | |
| 15 | Loin trimmed, ham trimmed, shoulder trimmed | 0.97 |
| 30 | Ham trimmed, shoulder, loin trimmed, sidefat (cm), BFT, neck trimmed | 1.00 |
| 60 | Abdominal fat, BFT, fat area, shoulder trimmed, loin | 1.00 |
| 90 | Neck | 0.52 |
| 120 | Abdominal fat, neck, ham | 0.96 |
| 140 | Sidefat (cm), loin area | 0.96 |

The change of protein deposition rate during growth is presented in Table 5. High protein deposition rate was obtained between 60 and 90 kg live weight. In this weight range also lipid deposition showed its first peak (243 g/d).

After a slight reduction in lipid deposition rate in the range of 90-120 kg live weight, an exponential increase in lipid deposition was obtained. Ash deposition rate showed its highest values at 60-90 kg with 26 g/d.

The parameter estimates of protein, lipid and ash deposition fitting a Gompertz function over the entire growth period are presented in Table 6. In the present study, mature protein mass was estimated to be 24.73 kg analysing both genders together. There were no differences determined between castrates and females. In contrast to protein mass, there was a difference between genders in the estimated mature fat mass. Mature ash mass showed small differences between sexes.

Table 7 gives the estimates of muscle and fat tissue using MRT by which the volume of the tissue is measured. The estimates of mature muscle tissue were slightly higher for castrates than for females. However, the Gompertz rate of muscle tissue deposition was similar in both sexes. The estimation of the mature fat tissue indicates the high differences between sexes.

The estimates of some carcass traits using Gompertz function are presented in Table 8. All these traits showed differences between castrates and females. Loin, backfat, abdominal fat and fat area in the mature pig showed the greatest differences between sexes. In additio the traits related to fat deposition such as backfat, abdominal fat and sidefat differed substantially in their maximum deposition ($X_{max.}$). These estimations confirmed that castrates seemed to have considerably different growth curves in fat related traits than females.

Table 4: **Best multiple regression to predict percentage of entire body protein and fat**

| Weight roup (kg) | Predictor variable | $R^2$ |
|---|---|---|
| | Protein (%) | |
| 15 | Loin area | 0.51 |
| 30 | Shoulder trimmed, loin, neck trimmed, ham | 1.00 |
| 60 | Fat area | 0.51 |
| 90 | * | * |
| 120 | BFT, neck, abdominal fat, shoulder trimmed | 0.87 |
| 140 | Loin area | 0.40 |
| | Fat (%) | |
| 15 | Loin | 0.75 |
| 30 | * | * |
| 60 | Fat area, abdominal fat, backfat, BFT, sidefat, loin trimmed | 1.00 |
| 90 | Neck | 0.54 |
| 120 | Abdominal fat, loin, shoulder | 0.99 |
| 140 | Sidefat (cm), loin area, loin trimmed | 0.99 |

* no variable met the 0.15 significance level of entry into the model

Table 5. **Protein, lipid and ash deposition rate in different weight ranges measured in chemical by analysed pigs of a serial slaughter trail**

| Fraction | Weight range (kg) | | | | |
|---|---|---|---|---|---|
| | 15-30 | 30-60 | 60-90 | 90-120 | 120-140 |
| Protein (g/d) | 112 | 102 | 134 | 100 | 155 |
| Lipid (g/d) | 61 | 163 | 243 | 215 | 629 |
| Ash (g/d) | 17 | 19 | 26 | 25 | 17 |

Table 6. **Estimates of mature (∞) , maximum (max) and Gompertz rate (Gomp) for protein (P), lipid (L) and ash (A) deposition in serial by slaughtered animals**

| Item | $P_{\infty}$ | $P_{max}$ | $P_{Gomp}$ | $L_{\infty}$ | $L_{max}$ | $L_{Gomp}$ | $A_{\infty}$ | $A_{max}$ | $A_{Gomp}$ |
|---|---|---|---|---|---|---|---|---|---|
| | (kg) | (g/d) | (kg/d*kg) | (kg) | (g/d) | (kg/d*kg) | (kg) | (g/d) | (kg/d*kg) |
| Castrates | 24.73 | 126 | 0.0139 | 48.79 | 285 | 0.0159 | 5.04 | 23 | 0.0126 |
| Females | 24.98 | 125 | 0.0136 | 29.40 | 226 | 0.0209 | 4.58 | 26 | 0.0153 |
| Both | 24.73 | 126 | 0.0138 | 48.55 | 259 | 0.0145 | 5.01 | 24 | 0.0128 |

Table 7. **Estimates of mature (∞), maximum (max) and Gompertz rate (Gomp) for muscle (M) and fat (F) tissue deposition using magnetic resonance tomography**

| Item | $M_{\infty}$ | $M_{max}$ | $M_{Gomp}$ | $F_{\infty}$ | $F_{max}$ | $F_{Gomp}$ |
|---|---|---|---|---|---|---|
| | (kg) | (g/d) | (kg/d*kg) | (kg) | (g/d) | (kg/d*kg) |
| Castrates | 125.4 | 415 | 0.0090 | 62.43 | 204 | 0.0089 |
| Females | 125.6 | 416 | 0.0090 | 65.78 | 276 | 0.0114 |
| Both | 125.6 | 416 | 0.0090 | 59.50 | 243 | 0.0111 |

Table 8: **Estimates of mature (∞), maximum (max) and Gompertz rate (Gomp) for different traits (X) of the carcass in serial by slaughtered animals**

| Trait | Gender | $X_\infty$ | $X_{max}$ | $X_{Gomp}$ |
|---|---|---|---|---|
| Shoulder (kg) | Castrates | 13.06 | 49 | 0.0102 |
| | Females | 10.04 | 44 | 0.0119 |
| | Both | 10.00 | 50 | 0.0135 |
| Shoulder trimmed (kg) | Castrates | 12.99 | 33 | 0.0068 |
| | Females | 10.19 | 28 | 0.0075 |
| | Both | 12.70 | 32 | 0.0068 |
| Loin (kg) | Castrates | 21.93 | 71 | 0.0088 |
| | Females | 15.84 | 63 | 0.0108 |
| | Both | 15.96 | 66 | 0.0113 |
| Neck (kg) | Castrates | 12.90 | 32 | 0.0068 |
| | Females | 9.85 | 31 | 0.0085 |
| | Both | 9.80 | 30 | 0.0084 |
| Backfat (kg) | Castrates | 8.59 | 29 | 0.0091 |
| | Females | 6.26 | 19 | 0.0081 |
| | Both | 8.10 | 27 | 0.0090 |
| Abdominal fat (kg) | Castrates | 7.61 | 27 | 0.0096 |
| | Females | 5.21 | 14 | 0.0075 |
| | Both | 6.99 | 23 | 0.0089 |
| Sidefat (mm) | Castrates | 10.11 | 27 | 0.0073 |
| | Females | 8.86 | 19 | 0.0060 |
| | Both | 9.98 | 26 | 0.0071 |
| BFT (mm) | Castrates | 9.46 | 18 | 0.0053 |
| | Females | 8.76 | 16 | 0.0050 |
| | Both | 9.29 | 18 | 0.0053 |
| Fat area ($cm^2$) | Castrates | 37.20 | 18 | 0.0132 |
| | Females | 24.93 | 15 | 0.0161 |
| | Both | 37.29 | 17 | 0.0127 |

**Discussion and conclusion.** Based on the results shown in Table 1 and Table 2 the estimated correlations varied substantially so that an estimation of lipid and protein deposition by a single carcass cut is difficult, and thus, had no high value to predict chemical body composition over the entire test period. Combination of carcass cuts to predict protein deposition showed a higher predictability, but not in all growth periods (Table 3 and 4). The prediction also reached a high coefficient of determination except for the 90 kg class ($R^2$=0.52). However, the number and kind of predictor variable varied during the stage of growth. The percentage of entire body protein and fat was more difficult to predict by carcass cuts than the mass of protein and fat. For some weight classes a significant multiple regression equation could not even be obtained for prediction of percentage of the entire body protein and fat. Alternative regression models using other variables, for example, fat of ham or fat of shoulder or fat of neck, did not improve the predictability of chemical body composition.

Maximum protein deposition rate during growth corresponded well with estimates using enhanced breeds (Eissen, 2000). In this weight rangesthe highest heritabilities for feed intake were found. This may indicate a close association between protein deposition and feed intake (Roehe et al., 1994 and Schulze et al., 2002). Therefore, it can be used to optimise feed intake within a biological growth model. The protein deposition rate can be used for both genders, because their maximum protein deposition rates were similar. After the first peak that showed for the lipid deposition rate at 60 to 90 kg live weight a slight reduction in the range of 90 to 120 kg live weight was obtained from the literature (Eissen, 2000). Then, an exponential increase in lipid deposition at a live weight greater than 120 kg was obtained.

Also, the Gompertz rate and mature protein weight did not differ much between sexes, so the protein deposition curves can be expected to be similar for castrates and females. Differences between gender were mainly in fat deposition or traits related to fat deposition. In the present study, mature protein mass was at the lower end of the range of value that have been reported (24.5 to 38.5 kg) (Knap, 2000). This may be due to the Pietrain genotype that was involved in the F1 crosses. It may indicate that mature body mass is reduced due to selection for high lean content in Pietrain. It may also suggest that reduced feed intake capacity in Pietrain is related to the low mature protein mass.

The estimates of maximum protein deposition using Gompertz function were only slightly lower than the linear protein deposition rate at weight range between 60 and 90 kg live weight indicating the usefulness of this function. These estimates were in the range of values obtained in a literatrure review (Knap, 2000) and described by other authors (Noblet et al., 1994). For lipid deposition, the Gompertz function did not fit well, because of the extensive increase in lipid deposition at the end of the test period. The maximum lipid deposition was substantially lower than the highest lipid deposition rate during growth within 120-140 kg live weight. In contrast, maximum ash deposition corresponds well with the linear ash deposition at the weight range of 60 to 120 kg. The Gompertz rate, which is independent from the scale, of the muscle and fat tissue using the MRT was lower then the Gompertz rate for the protein and fat mass measured by chemical analysis. The difference in maximum muscle

tissue deposition and protein deposition is mainly a function of water content.

**Acknowledgement.** The authors wish to acknowledge financial support by Deutsche Forschungsgemeinschaft and PIC.

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