

Selection possibilities for uniformity in pig carcasses

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1. Introduction

Managing variation of pig weight in nursery and grow-finish facilities has major economic impacts for producers who market slaughter pigs to a slaughterhouse. Slaughterhouses have increasing discounts for 'out of range' pigs (Brumm *et al.*, 2002a). Nowadays meat processors want to have slaughter pigs in a fixed weight range, preferably not more than 10 to 15 kg difference in carcass weight. However, even at the same carcass weight, variation in carcass traits, like the weight of primals and sub-primals, is observed.

Variation starts already early in life. In the experiment of Mahan and Lepine (1991) weaning weight and associated nursery feeding programs of pigs were tested on their subsequent performance to 105 kg body weight. From the results it was concluded that variation in body weight exists already before weaning and is still present when reaching 105 kg of body weight.

Sorting pigs to create a pen of pigs with similar start weights will reduce the variation within the pen at placement. However, O'Quinn *et al.* (2002) demonstrated that sorting reduced daily gain without a reduction in variation in gain. In the study of Brumm *et al.* (2002b) various wean-to-finish treatments were tested. Treatment 1) 0.69 m²/pig and 15 pigs/pen; 2) double-stocked at 0.35 m²/pig for eight weeks (30 pigs/pen) and then divided into two pens for growth to slaughter at 0.69 m²/pig; 3) 0.35 m²/pig and 15 pigs/pen. Wean-to-finish pigs were more uniform in weight within a pen than double-stocked pigs when uniformity was expressed as the coefficient of variation of weight within a pen.

Reducing variation by selecting sires with similar indexes or by using fewer sires has been cited as a method to reduce variation in weight at market. However, Tokach (2004) pointed out that sires only account for ¼ of the genetic variance, the effect of selecting sires with similar indexes will therefore be relatively small.

Aim of current analysis is to quantify the sources of variation, especially the absence or presence of uniformity between and within lines and to explore potential of selecting sires which create greater uniformity within their litters.

2. Material and Methods

By some chance we had a dataset available from the IPG research facility Beilen where pigs were shipped on a pen basis. Shipping took place if average pen weight was around 115 kg live weight. From March 25th 2004 all pigs were shipped in the weight range of the slaughterhouse (being 82-98 kg hot carcass weight). These two phases were analysed separately. In the last phase of the analysis we added data from three commercial grow-finish operations with full information on pedigree and individual slaughter data.

Table 1. Number of pigs and litters in the datasets.

1. a) Beilen shipped by pen	1964 pigs	312 litters
b) Beilen shipped in weight range	1202 pigs	219 litters
2. Beilen + 3 Commercial farms	23491 pigs	3025 litters

Basic analysis was done on the data of individual observations with the statistical program SAS and visualisation with Excel.

For genetic analysis within litter parameters were calculated with SAS and analyzed with ASREML (Gilmour *et al.*, 2001). The following model was used for estimating heritabilities:

$$Y = \mu + \text{boarline} + \text{sowcross} + \text{mhcw} + \text{shcw} + \text{animal} + \text{error} \quad (1)$$

μ being the overall mean, mhcw the mean hot carcass weight of the pigs in the litter and shcw the within litter standard deviation in hot carcass weight. Animal and error were random variables in the model. After combining both Beilen datasets phase was added to the model to account for the two shipping approaches.

$$Y = \mu + \text{boarline} + \text{sowcross} + \text{phase} + \text{mhcw} + \text{shcw} + \text{animal} + \text{error} \quad (2)$$

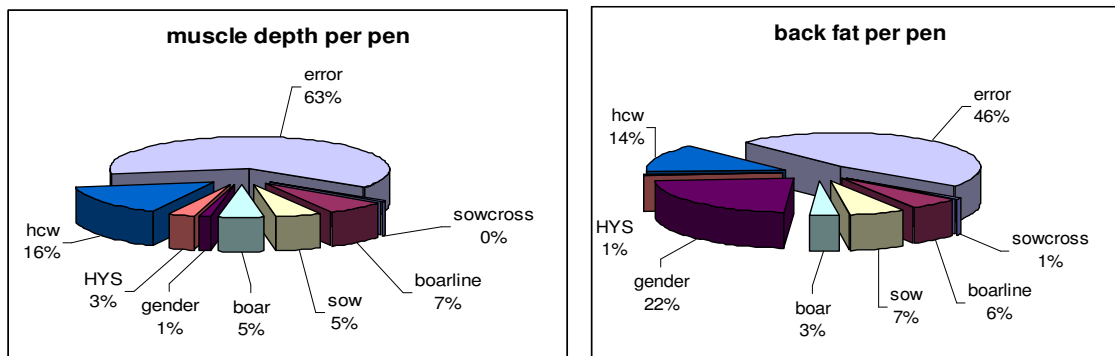
Data from three other farms with similar, but single sire line/sow cross, data were added. For analyzing this data model 3 was used. Farm was added to the model to correct for management influences. Number of pigs per litter (N) showed a significant effect and was, therefore, added to the model as well. Phase did not show a significant effect and was removed from the model. The used model was:

$$Y = \mu + \text{boarline} + \text{sowcross} + \text{farm} + N + \text{mhcw} + \text{shcw} + \text{animal} + \text{error} \quad (3)$$

3. Results and discussion

3.1 Variance components for pigs shipped on a pen basis

Results of a variation component analysis for muscle depth and back fat are shown in Figures 1 and 2 for pigs shipped on a pen basis.



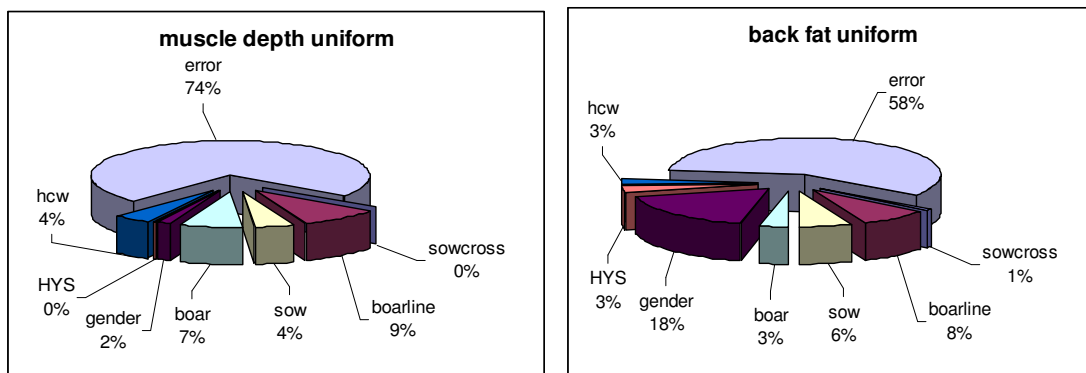
Figures 1 + 2: Sources of variation in muscle depth and back fat, pigs shipped by pen.

The error term showed to be the biggest component for variation in muscle depth (63%), indicating lack of accuracy of the measurement. Second in ranking was HCW (Hot Carcass Weight, 16 %). This was not a surprise because the pigs were not sorted on weight before going to the slaughterhouse. The highest genetic component was line of sire (7 %). Sum of the genetic components was 17 % (line of sire, line of dam, sire and dam effects). The YS (Year Season) effect was relatively small (3 %), the total variance 43.4.

For back fat a similar picture with sex as a distinct difference. Barrows clearly had more back fat than gilts, explaining 22% of the differences in back fat. This was already shown by many researchers (e.g. Tuz, 2004). For the genetic contribution the sow within sow cross component had most influence with 7 %. The total variance for back fat was 14.0

3.2 Variance components for pigs shipped on a within weight range basis

Figures 3 + 4 show the sources of variation for muscle depth and back fat for the pigs shipped within the payment grid of the slaughterhouse (uniform).



Figures 3 + 4. Sources of variation in muscle depth and back fat, pigs shipped uniform.

Starting with muscle depth, the weight component was reduced from 16% to 4%. The genetic components (boar line, sow cross, and boar within line, and sow within line) had increased from 17 % to 20 %, with boar line still being of most influence. There was no influence of HYS. The total variation was a bit smaller, 37.7.

Looking at back fat, HCW influence had decreased from 14% to 3%. Gender was still the biggest component (18%). Shipped within the grid, boar line seemed to have the highest contribution for the genetic part. This accounts for both muscle depth and back fat. The total variation in back fat was 11.2.

The differences between figures 1+3 and 2+4 showed that shipping pigs in the payment grid of the slaughterhouse can reduce the variation in muscle depth and back fat. This confirms the thoughts of the slaughterhouses.

3.3 Variance components for pigs shipped from four farms

When all data was used for estimating the components of variation (Figures 5 + 6) the influence of HCW was much higher than before, 31 % and 24 %, compared to 16 and 4, and 14 and 3. This could be due to the management of the different farms. Farm however only accounted for 3- 4% of the differences. The genetic components were reduced for both traits, with boar line still as highest influence in muscle depth. The total variance for both traits was 51.4 and 15.4, respectively.

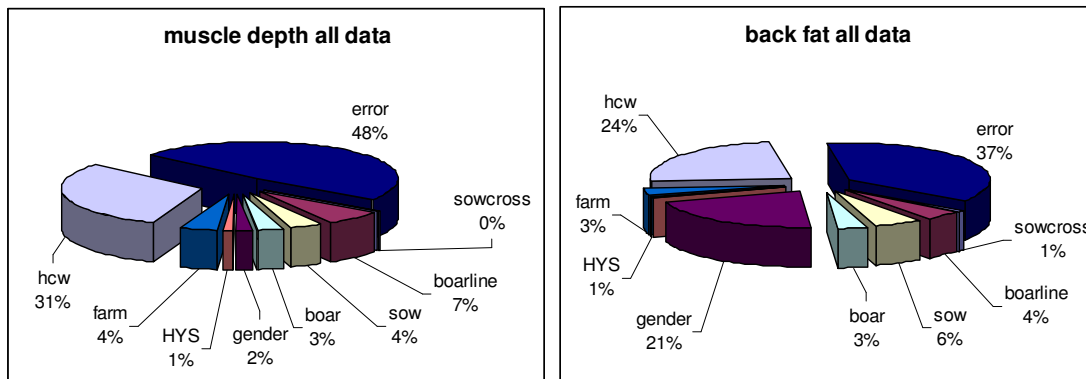


Figure 5 + 6. Sources of variation in muscle depth and back fat, all pigs.

3.4 From individual observations to litter analysis

Because boar line had the greatest genetic influence on muscle depth for all data and for back fat when looked at the uniform data, it could be possible that one boar line gave more uniformity than the other. Therefore the variation per litter was analyzed for each boar line. Figure 7 + 8 show the corrected means for the different boar lines for variation in muscle depth and back fat.

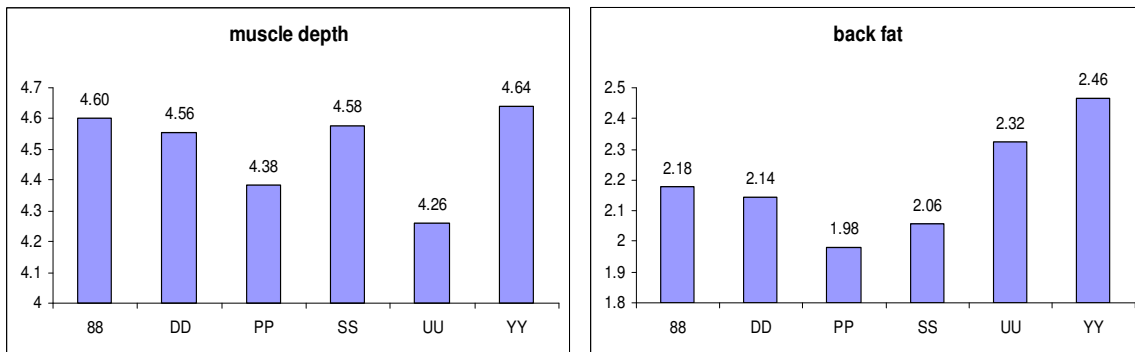


Figure 7+8: Corrected means per litter for the different boar lines for variation in back fat and muscle depth.

Statistical analyses showed that there was no significant difference for muscle depth between the boar lines. For back fat however there were differences. These differences are shown in Table 2. Figure 8 showed PP giving the least variation in back fat and YY giving the highest variation in back fat. The mean of the trait back fat was positively correlated with the variation of the trait ($R_p = 0.35$ (<0.001)). PP is known to give less back fat. With these analyses it was shown that PP not only gives less back fat but also less within litter variation in back fat.

Although the mean for back fat of the YY seemed higher than the others (Figure 8), only YY and PP were shown significantly different. The highest significance was shown between PP and UU (0.0021). To see if there were individual boars who gave more uniform litters than others the means for variation per litter for each boar were plotted (Figure 9).

Table 2: Significance tests for differences in within litter variation between the boar lines for back fat. Significant differences are gray.

	LSmean	88	DD	PP	SS	UU	YY
88	2.18		0.83	0.0385	0.15	0.17	0.19
DD	2.14	0.83		0.34	0.60	0.31	0.22
PP	1.98	0.0385	0.34		0.33	0.0021	0.0319
SS	2.06	0.15	0.60	0.33		0.0073	0.06
UU	2.32	0.17	0.31	0.0021	0.0073		0.53
YY	2.46	0.19	0.22	0.0319	0.06	0.53	

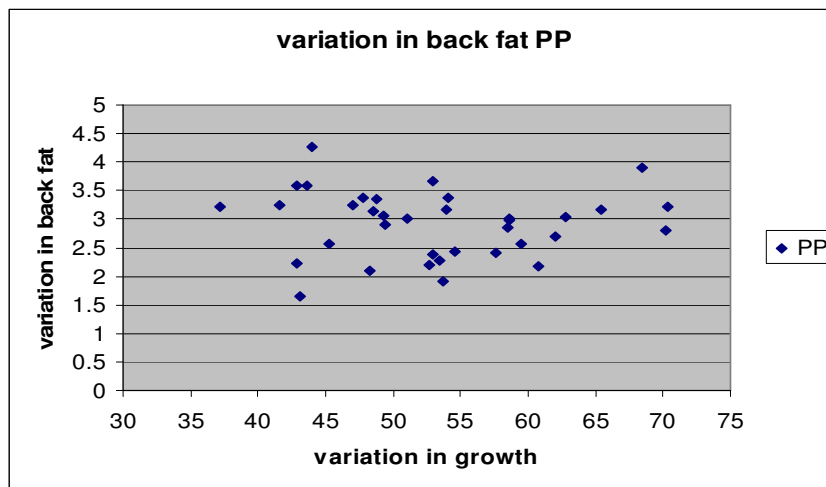


Figure 9: Means for within litter variation in back fat per boar for the P-line.

3.5 Variance components for life time daily gain

Weight is a major component for primal parts in the carcass. Therefore it is important to ship pigs within the same weight range. The age at which the pigs are at that weight range depends on the growth of the animal. If all pigs would gain the same weight every day, all pigs from the same litter could be shipped together. Unfortunately pigs differ in growth. To see what causes the variation in growth a variance component was done with SAS (Figure 10).

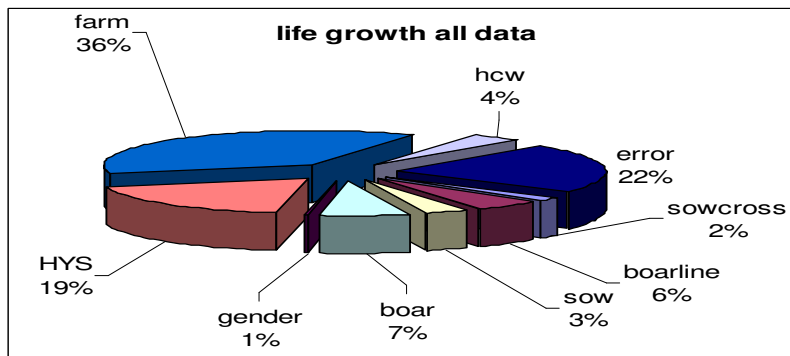


Figure 10: Sources of variation for life time daily gain.

Figure 10 shows farm as biggest source for variation in daily gain. This could be due to feed or feeding strategy (fed ad libitum or restricted). The influence of the boar and boar line were the highest for the genetic part (6 and 7 %). To see if there were differences in variation for growth between boar lines, an analysis was done to correct the means. These corrected means are shown in figure 11.

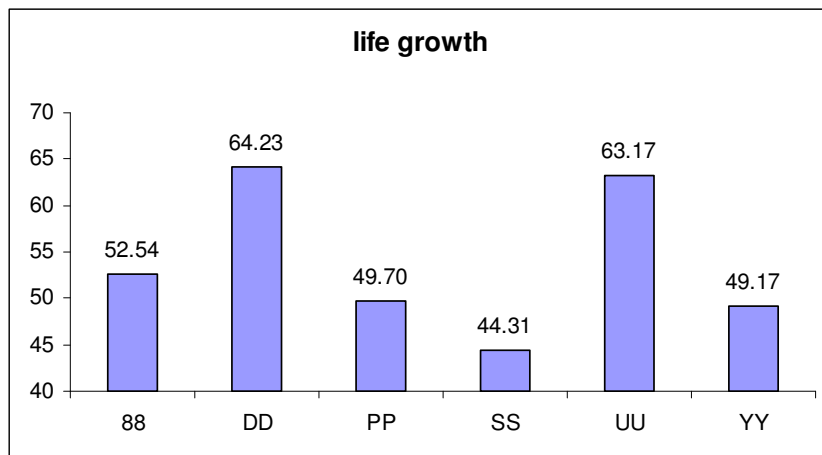


Figure 11: Corrected means per litter for variation in growth for the different boar lines.

The SS gave the lowest variation for growth while the DD gave the most variation. The analysis showed significant differences between the boar lines. Differences in Table 3.

Table 3: Differences between boar lines in within litter variation for growth. Significant differences are grey.

	LSmean	88	DD	PP	SS	UU	YY
88	52.54		0.009	0.29	0.0006	0.0005	0.60
DD	64.23	0.009		0.0029	<.0001	0.83	0.05
PP	49.70	0.29	0.0029		0.0195	<.0001	0.93
SS	44.31	0.0006	<.0001	0.0195		<.0001	0.44
UU	63.17	0.0005	0.83	<.0001	<.0001		0.0384
YY	49.17	0.60	0.05	0.93	0.44	0.0384	

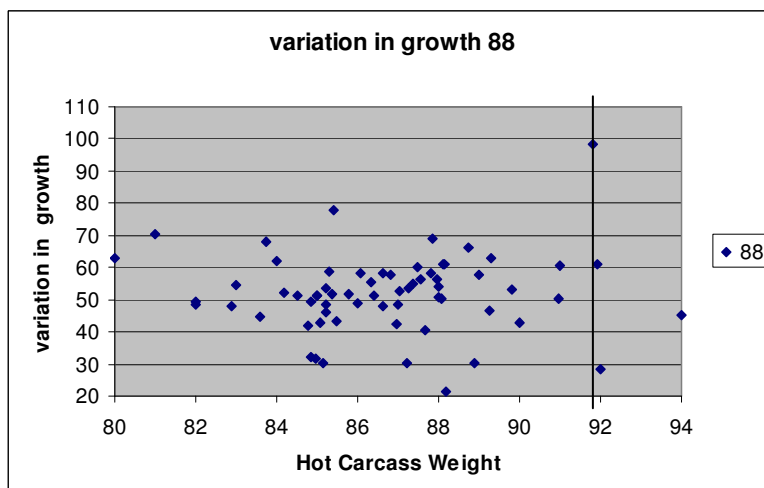


Figure 12: Mean variation for variation in growth per boar in the E-line.

Table 3 confirmed the differences shown in Figure 11. A plot for the mean variation in growth for each boar within a boar line was made to see if the individual boars differ. Figure 12 shows the results for the E-line (88).

3.6 Genetic variance components

Heritabilities were estimated using the data 'shipped per pen'. Estimates were 0.14 ± 0.08 for back fat and 0.05 ± 0.07 for muscle depth. Data 'shipped within the payment grid' yielded heritabilities of 0.14 ± 0.08 and 0.08 ± 0.18 , respectively. Using the complete Beilen data set, heritabilities for the within litter variations were 0.17 ± 0.08 for back fat and 0.04 ± 0.06 for loin depth.

Adding data of the three other farms yielded similar estimates of 0.18 ± 0.04 for back fat and 0.04 ± 0.03 for loin depth. An overview of the heritabilities is given in Table 4. The genetic correlations between this variation in back fat and trait and a number of production traits were estimated by correlating the respective breeding values (muscle depth, back fat, ham, loin, shoulder and belly). The significant results are shown in Table 5.

Table 4: Heritabilities for within litter variation in back fat and muscle depth.

<i>Data</i>	<i>Back fat</i>	<i>Muscle depth</i>
Beilen shipped per pen	0.14 (0.08)	0.05 (0.07)
Beilen shipped uniform	0.14 (0.08)	0.08 (0.18)
Beilen total	0.17 (0.08)	0.04 (0.06)
Total data	0.18 (0.04)	0.04 (0.03)

Table 5: Effect of breeding value for variation in back fat on production traits.

<i>Variable</i>	<i>Significance</i>	<i>Regr.: b</i>
Muscle depth	0.0362	-0.647
Back fat	<0.0001	1.128
Ham	0.0198	-0.222
De-boned ham	0.0313	-0.238
Belly weight	0.0210	0.238

Table 5 suggests that boars who inherit better within litter uniformity for back fat will also give better muscle depth and more ham. Variables not shown in the table (loin and shoulder) were not significant (0.56 and 0.57).

The influences of breeding value for variation in back fat on variation of the other traits were analyzed too. This was done with the same procedure as described above. Only variation in muscle depth showed significance (0.04). The direction was + 0.31 which suggests that boars who gave more uniform pigs for back fat gave more uniformity in muscle depth as well. The other traits were probably not significant because too few animals were dissected (only 755 litters left compared to 3025 litters with HGP measurements).

4. Conclusions

- Differences in back fat and loin depth exist between lines (boar line, sow cross), between animals within line (boar and sow) and within sires (significant heritability for back fat for within litter variation).
- The latter heritability was 0.18 ± 0.04 . Some boars give more uniformity in back fat in their litters than others. Possible explanations are (a) major gene allele segregation and (b) differences in behaviour.
- The correlations between breeding values for uniformity of back fat were positive with important traits like muscle depth and de-boned ham weight. Therefore the breeding value for uniformity could be implemented in the selection index.

5. References

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