Study of NBA and its relationship with other traits

Susanne Hermesch

Introduction

A cost efficient pig production is dependent on an efficient growth and a good carcase performance of the slaughtered pigs and a good reproductive performance of the sow. Genetic improvement of reproductive performance of the sow has mainly focused on number of piglets born alive. Genetic variation for this trait is low and genetic improvement of this trait has been slow in many breeding programmes.

EBV's for performance and carcass traits are obtained through multi trait animal models using best linear unbiased prediction. Animals are evaluated for these traits using all information from relatives and information from other traits. Litter size is usually analysed in a single trait analysis, assuming zero correlations to other production and carcase traits.

Genetic relationships between litter size and growth and carcase traits were summarised by Haley et al. (1988) finding wide variations from study to study and within study from herd to herd. No information was found in the literature for the genetic relationship between number born alive and meat quality traits.

Data

A data set from Bunge Meat Industries was available for the analysis of litter size. The data was recorded from 1989 until 1995 and included 3747 Large White sows and 2239 Landrace sows. A subset of these sows farrowing between July 1992 and November 1994 were mothers of the pigs participating in the project to estimate genetic parameters for production, carcass and meat quality traits.

The structure of the data set for production, carcase and meat quality as well as further information about meat quality traits has been described earlier in this workshop. After weaning, the pigs went through the normal weaner, grower and finisher shed of Bunge Meat Industries. At the age of 18 weeks pigs entered a test station where individual feed intake was measured. Pigs were single penned during the testing time. The weight of the animal at the start and at the end of this testing period was recorded giving information about growth rates before and during the test period. Feed efficiency during the test period was then calculated from this information.

Carcass information includes real time ultrasound measurements on the live animal and characteristics measured on the carcass within the abattoir. One day before slaughter real time ultrasound measurements were obtained including the fat depths at P2 and between the third and fourth last rib as well as the muscle depth between the third and fourth last rib. These measurements were then again taken with the Hennesy grading probe on the carcass within the abattoir. Lean meat percentage of the carcass was then estimated applying the following prediction equation (Ferguson et al. 1994):

$$\text{Lean\%} = 64.2704 + 0.1090 \text{ Standardized hot carcass weight} - 1.0231 \text{ Fat depth at P2 site.}$$

Analysis of fixed effects

The first step of data characterisation is the analysis of fixed effects that have an influence on the analysed traits. Fixed effects included in the models to analyse litter size were farrowing season defined in three month steps, line of the sow, farrowing unit and

whether the sow was artificially inseminated or natural mated (Table 1). The age at farrowing was included in the model as a linear covariate for litter size in the first and second parity.

Table 1: Total variation explained by the fixed effect part of the model (R^2) and fixed effects for litter size

	R^2	farrowing	line of	artificial	farrowing	farrowing
NBA_1*	0.02	✓	✓	✓		✓
NBA_2	0.02	✓	✓		✓	✓
NBA_3	0.01	✓	✓		✓	

* Abbreviations:

NBA_{123} : Litter size in the first, second or third parity

Relevant fixed effects for performance traits are summarized in Table 2 and include week, breed, parity of the sow and the weight at test entry for daily feed intake and feed efficiency. These effects explained 15 to 39 percent of the total variation.

Table 2: Total variation explained by the fixed effect part of the model (R2) and fixed effects for production traits

Trait	R^2	week	line	parity of sow	weight at test
ADG1*	0.17	✓	✓	✓	
ADG2	0.18	✓			
ADG3	0.15	✓	✓	✓	
DFDINT	0.39	✓			✓
FDEFF	0.22	✓	✓		✓

* Abbreviations:

ADG1: Average daily gain from week three to week 18
ADG2: Average daily gain within test station from week 18 to 23
ADG3: Lifetime average daily gain
DFDINT: Daily feed intake within test station
FDEFF: Feed efficiency

The model for analysing carcass traits included week, breed, and animal weight for ultrasound measurements and carcass weight for traits recorded with the Hennesy grading probe in the abattoir (Table 3). The fixed effect part of the model explained 22 to 37 percent of the total variation for carcass traits.

Table 3: Total variation explained by the fixed effect part of the model (R2) and fixed effects for carcass traits.

	R^2	week	line	live animal weight	hot carcass weight
LFD*	0.35	✓	✓	✓	
LMD	0.31	✓	✓	✓	
FD	0.30	✓	✓		✓
MD	0.37	✓			✓
LEAN%	0.22	✓	✓		✓

* Abbreviations:

LFD: Fat depth at P2 site measured with real time ultrasound on live animal

LMD: Muscle depth between third and fourth last rib measured with real time ultrasound on live animal

FD: Fat depth at P2 site measured with Hennesy grading probe on carcass

MD: Muscle depth between third and fourth last rib measured with Hennesy grading probe on carcass

LEAN%: Lean meat percentage of carcass

Analysis of variance components

Variance components were estimated using a restricted maximum likelihood procedure applying an animal model. The animal breeding value was the only random effect included in the model for litter size, daily feed intake, feed efficiency and carcass traits. Litter as a second random effect was shown through a log likelihood ratio test only to be significant for average daily gain.

Genetic correlations between traits were estimated in bivariate analysis. Environmental correlations between litter size and the other traits could not be estimated since those traits were recorded on different animals.

Genetic variation of litter size

A single trait analysis was performed for litter size separately for Australian Large White and Australian Landrace. Heritabilities for number born alive were low with values from 0.06 to 0.09 in Australian Large White sows (Table 4) and with values ranging from 0.08 to 0.11 for Australian Landrace sows (Table 5).

Table 4: Number of records (N), standard deviations (s.d.), heritabilities (h^2) with standard errors (s.e.), additive genetic variance (σ^2_a) and environmental variance (σ^2_e) for Australian Large White

	N	s.d.	h^2	(s.e.)	(σ^2_a)	(σ^2_e)
NBA_1*	3747	2.38	0.06	(0.02)	0.353	5.31
NBA_2	2722	2.45	0.09	(0.03)	0.508	5.34
NBA_3	2058	2.41	0.08	(0.03)	0.478	5.33

* Abbreviations see Table 1.

Table 5: Number of records (N), standard deviations (s.d.), heritabilities (h^2) with standard errors (s.e.), additive genetic variance (σ^2_a) and environmental variance (σ^2_e) for Australian Landrace

	N	s.d.	h^2	(s.e.)	(σ^2_a)	(σ^2_e)
NBA_1*	2239	2.52	0.11	(0.03)	0.667	5.61
NBA_2	1391	2.49	0.11	(0.05)	0.644	5.44
NBA_3	907	2.61	0.08	(0.06)	0.534	6.11

* Abbreviations see Table 1.

Genetic relationships between number born alive in different parities were estimated for Australian Large White and Australian Landrace together. Number born alive in the first parity shows genetic correlations of 0.69 to number born alive in the second parity and 0.62 to litter size in the third parity. These genetic correlations are significantly different from zero and suggest to analyse number born alive in the first parity as a different trait than litter size in following parities. The genetic correlation between litter size in the second and litter size in the third parity are one indicating to analyse these traits as repeated records.

Table 6: Genetic (first line), environmental (second line) and phenotypic correlations (third line) between litter size in parity one, two and three

	NBA_2	**NBA_3**
NBA_1*	0.69	0.62
	0.12	0.11
	0.17	0.15
NBA_2		1.00
		0.14
		0.22

* Abbreviations see Table 1.

Genetic variation of production traits

Results from single trait analysis of production traits are presented in Table 7. Growth rate in the period between 3 and 18 weeks (ADG1), life time average daily gain (ADG3) and daily feed intake are moderately heritable with values between 0.23 and 0.28. Lower heritabilities were found for growth rate within the test station and feed efficiency. The standard deviation for growth rate recorded during the test period is substantially increased in comparison to the other two growth performances which is due to an increase in environmental variation. An explanation could be the short test period of 4 to 5 weeks and differences in pigs to adapt to a single pen housing system. Feed efficiency is the ratio of feed intake to growth rate and is therefore dependent on these two measurements which could explain the low heritability found for this trait.

Litter effect was only found to be significant for different average daily gain measurements. This effect has the highest influence on growth rate within the period between 3 to 18 weeks and is of smaller importance to growth rate at the end of the growing period between 18 and 23 weeks. Life time average daily gain includes both

growth periods previously described which is reflected through an intermediate value for the litter effect of 0.10.

Table 7: Number of records (N), standard deviations (s.d.), heritabilities (h^2), litter effect (c^2), additive genetic variance (σ^2_a), variance due to litter effect (σ^2_c), and environmental variation (σ^2_e) for performance traits

Trait	N	s.d.	h^2	c^2	(σ^2_a)	(σ^2_c)	(σ^2_e)
ADG1*	3230	69.5	0.28	0.14	1160	589	2249
ADG2	3260	184.8	0.12	0.07	3539	2102	23241
ADG3	3267	68.1	0.27	0.10	1122	429	2579
DFDINT	3288	0.43	0.23		0.032		0.11
FDEFF	3224	0.57	0.09		0.02		0.24

Standard error for h^2 : 0.04 - 0.06
Standard error for c^2 : 0.03
* Abbreviations see Table 2

Genetic variation of carcass traits

Backfat measurements and lean meat percentage are highly heritable (Table 8.). The realtime ultrasound measurement of backfat shows a higher heritability than Hennesy chong measurement of fat depth. The difference in heritabilities between these two recording techniques are even more apparent for the two muscle depth measurements. Muscle depth recorded on the live animal shows a heritability of 0.21 in comparison to a heritability of 0.02 for the measurement of muscle depth recorded in the abattoir. The variation of the real time ultrasound measurements is lower than the variation of the Hennesy chong measurements and is partly an explanation for the lower heritabilities of carcass traits recorded with the Hennesy chong grading probe. Measuring carcass characteristics on the hanging carcass has to be done within the speed of the slaughter line which could be a cause of the increased variation of this measurement. Additionally the Hennesy grading probe defines fat and muscle depths using reflectance profiles of fat and protein tissues. In the case of pale meat the exact distinction between these two tissues is difficult contributing to a higher variation and a higher mean of this measurement in comparison to real time ultra sound measurements on the live animal.

Table 8: Number of records (N), standard deviations (s.d.), heritabilities (h^2), additive genetic variance (σ^2_a), and environmental variation (σ^2_e) for carcass traits

Trait	N	s.d.	h^2	(σ^2_a)	(σ^2_e)
LFD*	3223	2.59	0.60	2.72	1.79
LMD	2895	4.56	0.21	3.21	11.88
FD	2303	3.14	0.46	3.33	3.87
MD	1369	9.54	0.02	1.19	59.68
LEAN%	2302	2.94	0.46	3.49	4.05

Standard error for h^2 : 0.04 - 0.06
* Abbreviations see Table 3

Genetic relationships between NBA and performance traits

Genetic and phenotypic relationships between litter size as a trait of the sow and production traits recorded on relatives of the sow are presented in Table 9. Litter size in the first parity shows genetic correlations of -0.30 to -0.42 to the different growth rates. A high growth rate is associated with a high feed intake and therefore these genetic correlations are consistent with the negative correlation between number born alive in the first parity and daily feed intake. These genetic relationships are unfavourable, showing that high litter size in the first parity is genetically associated with a lower growth rate and a reduced feed intake.

Genetic correlations between litter size in the second and third parity and growth traits vary from 0.00 to -0.30. Litter size in the second parity is not genetically correlated to growth rate from 3 to 18 weeks. Contrary litter size in the third parity shows no genetic relationship to growth rate recorded in the test station from 18 to 23 weeks. Genetic relationships between life time average daily gain as well as feed intake and litter size in the second and third parity are moderately unfavourable

No significant genetic correlations were found between litter size and feed efficiency. Additionally, phenotypic correlations are also not significantly different from zero.

Table 9: Genetic (first line) and phenotypic (second line) correlations between litter size and production traits

	ADGl	ADG2	ADG3	DFINT	FDEFF
NBA_1*	-0.30	-0.42	-0.31	-0.19	0.09
	-0.04	-0.04	-0.04	-0.02	0.00
NBA_2	-0.01	-0.30	-0.07	-0.24	0.00
	0.00	-0.03	-0.01	-0.03	0.00
NBA_3	-0.26	0.00	-0.20	-0.05	0.08
	-0.04	0.00	-0.03	0.00	0.00

* Abbreviations see Table 1 and Table 2

Genetic relationships between NBA and carcase traits

Genetic correlations between litter size and carcass traits were estimated for backfat and muscle depth measured with real time ultrasound, fat depth of the carcass and lean meat percentage. No genetic correlations were obtained between litter size and muscle depth recorded with the Hennesy grading probe as the heritability of muscle depth was to low to give reliable estimates of genetic correlations. The magnitude of the genetic relationships between litter size and analysed carcass traits was low ranging from -0.14 to 0.24. This low magnitude and the inconsistency of genetic correlation between traits and also between parities suggests that no genetic relationships are existent between litter size and carcass traits. Phenotypic correlations between litter size and carcass traits are not significantly different from zero.

Table 10: Genetic (first line) and phenotypic (second line) correlations between litter size and carcase traits

	LFD	LMD	FD	LEAN%
NBA_1*	0.11	-0.13	-0.14	0.13
	0.02	-0.02	-0.03	0.03
NBA_2	0.15	0.24	0.12	-0.13
	0.04	0.04	0.02	-0.02
NBA_3	-0.08	-0.02	-0.08	0.08
	-0.02	0.00	-0.02	0.02

* Abbreviations see Table 1 and Table 3.

Genetic relationships between NBA and meat quality traits

Meat quality traits are lowly heritable for Large White pigs and reliable estimates of genetic correlations could not be achieved between litter size and meat quality traits. Table 11 represents genetic correlations between litter size and meat quality traits for Landrace pigs. The moderate genetic correlations between litter size in different parities and colour of the longissimus dorsi muscle are favourable in regard to the incidence of PSE meat. A high litter size is associated with a darker colour in the loin. A dark colour is also associated with a low drip loss percentage. The negative genetic correlations between litter size and drip loss percentage are therefore consistent with these results.

A high litter size in the first parity is associated with a low pH measured at 45 minutes and 24 hours after slaughter. In regard to PSE meat this is also a favourable relationship. Litter size in the second and third parity show low genetic correlations to pH measured shortly after slaughter and 24 hours post mortem. These correlations are of opposite sign and not significantly different from zero, suggesting a genetic correlation of zero for these relationships.

Table 11. Genetic correlations between litter size and meat quality traits for Australian Landrace

	CLD*[2]	DLP	pH45	pH24
NBA_1*[1]	-0.24	-0.14	-0.03	-0.34
	-0.05	-0.03	0.00	-0.05
NBA_2	-.0.50	-0.36	0.11	0.10
	-0.11	-0.07	0.02	0.02
NBA_3	-0.53	-0.41	-0.17	-0.11
	-0.11	-0.07	-0.02	-0.01

*[1] Abbreviations of litter size see Table 1

*[2] abbreviations for meat quality traits:

CLD: colour of longissimus dorsi (L-value)
DLP: drip loss percentage
pH45: pH measured 45 minutes after slaughter
pH24: pH measured 24 hours after slaughter

Discussion and conclusions

Heritabilities for litter size are slightly lower for investigated Large White sows than the Landrace population, but are within the range of literature values as summarized by Haley et al. (1988). Litter size is usually analysed with a repeatability model assuming genetic correlations of one between number born alive in different parities. The genetic correlations between litter size in the first parity and litter size in following parities are significantly different from zero and suggest to analyse number born alive in the first parity as a different trait than litter size measured in later parities. The genetic correlation between litter size in the second and third parity was one and a repeatability model is therefore the appropriate model for the analysis of these traits.

Estimates of production traits were lower than results found in the literature (de Vries et al., 1994; Hovenier et al. 1992). Heritabilities for production traits were especially low for traits recorded in the test station indicating that the short test period of 5 weeks is too short.

A genetic improvement of carcass traits can be achieved quickly as these traits are highly heritable. Heritabilities were higher for real time ultrasound measurements and show the reliability of measuring carcass traits on the live animal.

The unfavourable relationships between litter size and the production traits, growth rate and feed intake are in contrasts to results from Short et al. (1994) who found either no or a slightly favourable genetic relationship between litter size and these performance traits. The unfavourable relationship between litter size and production traits in this study could reflect the effect of a large litter of the sow on the production performance of her offspring. The influence of this effect on the production performance has to be analysed before it can be recommended to analyse litter size in a multi trait analysis.

The low magnitude of genetic correlations between litter size and carcass traits and their inconsistency between traits and parities suggest that no genetic correlations are existent between litter size and carcass traits.

Genetic correlations between litter size and meat quality traits in Landrace pigs are favourable in regard to the incidence of PSE meat for colour and drip loss percentage. pH measurements show favourable genetic correlations to litter size in the first parity. The genetic correlations between pH measurements and litter size in the second and third parity are of low magnitude and not significantly different from zero. These results indicate that a selection for higher litter size will not lead to inferior meat quality.

References

Ferguson, D.M., Chandler, R.C., Maynard, P. and Thomas, M. (1994). PRDC *Final Report Project LMA6.P* (in press)

Haley, C.S.; Avalos, E.; Smith, C. (1988) *Anim. Breed. Agstr*. **56**:317-332

De Vries, A.G., Van Der Wal, P.O., Long, T., Eikelenboom, G. and Merks, J.W.M., (1994). *Livestock Prod. Sci*. **40**: 277

Hovenier, R., Kanis, E., Van Asseldonk, TH. and Westerink, N.G., (1992) *Livest. Prod. Sci*. **32**: 309

Short, T.H., Wilson, E.R. and McLaren D.G. (1994) *Proc 5th World Conf. of Genetics Applied to Livestock Production* Vol. **17**:413.