Comparison of Genetic Parameters in PIGBLUP with UNE17P Parameters

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Introduction

Genetic improvement is based on selecting genetically superior animals. From the phenotypic performance of an animal it is not known whether an animal is genetically superior or whether good performance is caused by favourable management or environmental effects. Genetic principles are applied in genetic evaluation programs like PIGBLUP to determine genetically superior animals which is expressed in their breeding values. Unfortunately it is not possible to determine the true breeding value of an animal and therefore breeding values have to be estimated. In a single trait model Estimated Breeding Values (EBV's) are obtained for an animal based on its own performance and/or performance of relatives and knowledge of the heritability of a trait.

The efficiency of pig production is not determined by one trait but is dependent on a number of traits, and the same genes can influence more than one trait. This simultaneous effect of the same genes on different traits leads to a genetic correlation between traits. Genetic evaluation programs are based on multitrait models which require knowledge of genetic correlations.

For the main traits average daily gain, backfat and number born alive genetic parameters used in PIGBLUP were obtained from one Australian study (Klassen, 1992). Genetic parameters for other traits had to be obtained from the literature. Although this information gives a good indication it might not reflect Australian populations sufficiently. In addition, for some trait combinations no estimates were available and genetic correlations were assumed to be zero.

In this paper, genetic parameters for production traits previously used in PIGBLUP will be compared with estimates of genetic parameters obtained in a project to estimate genetic parameters for Australian pigs (UNE17P). Consequences of changes in genetic parameters will be analysed for one herd.

What is a heritability or a litter effect?

The phenotypic performance of an animal is based on environmental or nongenetic influences as well as the genotype of the animal. The magnitude of these factors differs between traits. The heritability is defined as the proportion of the phenotypic variation that is due to genetic differences. Genetic differences between animals are expressed by EBVs, and to put it in different words, the heritability is the proportion of the phenotypic variance that is caused by variance in true breeding values. By definition, heritabilities range from zero to one. A heritability of zero indicates that all differences between animals are due to environmental causes. A heritability of one indicates that all differences between animals have a genetic cause. For example, reproductive traits have generally a low heritability while backfat is highly heritable.

As mentioned earlier, the phenotypic performance of an animal is influenced by environmental effects besides genetic effects. The litter effect is the proportion of the phenotypic variation that is explained by the environment that is common to littermates in a litter. The litter effect ranges from zero to one. For example, the mothering ability of a sow influences all littermates to the same extent as well as the pen that all littermates share. Generally litter effects are of higher importance for traits that are recorded at an earlier age.

What is a phenotypic, environmental or genetic correlation?

Performance in one trait may be related to performance in another trait. Generally, this relationship is expressed through a correlation. Correlations range from minus one to one. A correlation of zero implies that no association exists between two traits while a high correlation of one or minus one shows that two traits are the same trait. Depending on a cause of a correlation we then talk about a phenotypic, environmental and genetic correlation. For example, a pig with a high feed intake is most likely to also have a high growth rate. This association based on the phenotypic observation is a phenotypic correlation. As it was mentioned earlier, phenotypic performance is influenced by environmental effects as well as genetic effects. The same environmental effects might influence different traits. Like humans, pigs don’t like to eat very much in summer when temperatures are high. This heat stress also causes a reduction in growth rate during summer. The environmental correlation is a measurement of these environmental associations. This principle of an environmental correlation can be extended to genetic correlations. The same genes that influence one trait might also influence a number of other traits which is described through the genetic correlation. It can also be thought of as the correlation between true breeding values of two traits and is of greater importance to the breeder.

Heritabilities and variance components in PIGBLUP - old and new

1. Default PIGBLUP heritabilities

Heritability estimates range from 0.25 for average daily gain measured on farm to 0.40 for backfat and carcase traits (Table 1.) The heritability for average daily gain recorded within a test station is slightly higher than growth rate recorded on farm (h^2 for TPG: 0.30). The phenotypic variation is the sum of environmental and genetic variation. Therefore by decreasing the environmental variation heritability estimates increase. Generally, it is assumed that in the test station the environment can be better controlled than on farm resulting in a lower environmental variation for test period growth in comparison to the environmental variation for average daily gain recorded on farm. The same principles apply to feed conversion ratio, the second trait obtained from central station performance testing with an assumed heritability of 0.35.

Traits describing leanness of a carcase are generally highly heritable. This is reflected in a high heritability of 0.40 for backfat measured on the live animal as well as the carcase traits carcase fat depth and lean meat percentage. Carcase muscle depth has a lower heritability of 0.30.

Table 1: Variance components, heritabilities (h^2) and litter effects (c^2) for production traits used in PIGBLUP

Trait	σ^2_a	h^2	σ^2_c	c^2	σ^2_e	σ^2_p
ADG	625	0.25	375	0.15	1500	2500
TPG	2430	0.30	810	0.10	4860	8100
BF	2.00	0.40	0.25	0.05	2.75	5.00
FCR	0.0315	0.35	0.0045	0.05	0.054	0.09
C-Fat	2.00	0.40	0.2500	0.05	2.750	5.00
C-Muscle	14.70	0.30	0.0001	0.00	34.300	49.00
% Meat	2.00	0.40	0.2500	0.05	2.750	5.00

Abbreviations:

ADG:	Average daily gain on farm
TPG:	Test period average daily gain
BF:	Backfat (P2, live animal)
FCR:	Feed conversion ratio
C-Fat:	Carcase backfat
C-Muscl.	Carcase muscle depth
% Meat:	Lean meat percentage of carcase
σ^2_a	Additive genetic variance
σ^2_e	Environmental variance
σ^2_p	Phenotypic variance
σ^2_c	Litter effect

2. New heritabilities

New variance components and heritability estimates obtained from UNE17P are presented in Table 2. Heritability and litter effects for average daily gain recorded on farm are similar to previous estimates (h^2 : 0.27; c^2 : 0.13) while variance components are higher. Most breeders also use backfat recorded on farm which has a high heritability of 0.60 while litter effects are not significant for this trait. In UNE17P only two litter mates were available per litter which might have caused this non significance of the litter effect.

In UNE17P test period gain (TPG) and feed conversion ratio (FCR) were performance recorded over a period of four weeks in the test station during the later stage of the growth curve (18 to 22 weeks). This short testing period caused a high environmental variation for average daily gain and subsequently feed conversion ratio leading to low heritability estimates for these two traits. One outcome from UNE17P is that a test period of four weeks is too short and that the obtained parameters for test period gain and feed conversion ratio (FCR) can not be used in PIGBLUP. Therefore, estimates from the literature review of Hermesch (1996) which is based on recent studies published after 1990 are used instead in Table 2. Mean literature estimates were 0.35 for the heritability for average daily gain recorded in a test station (TPG) and 0.26 for feed conversion ratio (FCR). The relatively lower heritability estimate for feed conversion ratio in comparison to growth rate is in agreement with results from UNE17P.

Results from UNE17P showed that heritability estimates are lower for carcase measurements recorded with the Hennesy Chong machine than for realtime ultrasound measurements on the live animal. The heritability estimates for carcase fat depth and lean meat percentage are 0.46 and 0.45, respectively. The prediction equations for lean meat yield as developed by Ferguson (1994) for Australian pigs are mainly based on backfat measurements which is reflected in the similar trait heritabilities. Results also showed that recording muscle depth with the Hennesy Chong machine under commercial conditions on the slaughter chain will not give a reliable measurement of muscle depth. The heritability for this trait is 0.02 and genetic improvement is therefore not possible using this measurement. In contrast, muscle depth recorded on the live animal with real time ultrasound equipment has a heritability of 0.21. It is therefore recommended to use this measurement as a measure for muscle depth.

Table 2: Variance components, heritabilities (h2) and litter effects (c2) for production traits obtained from UNE17P project

Trait	σ^2_a	h^2	σ^2_c	c^2	σ^2_e	σ^2_p
ADG	1150	0.27	532	0.13	2570	4250
TPG	5040	0.35[2]	1440	0.10	7920	14400
BF	2.70	0.60			1.80	4.50
FCR	0.0225	0.26[2]			0.0675	0.090
C-Fat	3.33	0.46			3.90	7.20
Muscle[1]	3.20	0.21			11.90	15.10
% Meat	3.50	0.45			4.05	7.55

[1] Muscle: Muscle depth recorded with real time ultrasound

[2] Heritabilities are obtained from literature review of Hermesch (1996)

Genetic and residual correlations in PIGBLUP

Genetic correlations and environmental correlations (also called residual correlations) between traits are presented in Table 3 as currently used in PIGBLUP and in Table 4 as obtained from UNE17P. Currently a high genetic correlation of 0.70 is used for the genetic relationship between average daily gain on farm (ADG) and average daily gain recorded in the test station (TPG). This assumes that growth rate on farm and on test are similar traits and that genotype by environment interactions are of minor importance. Results from UNE17P contradict this assumption with an estimate of the genetic correlation between growth rate before test and within the test station of 0.32. Two factors contribute to this low genetic relationship in UNE17P. Firstly, both growth traits are recorded over different age and therefore different weight range of the animal. Secondly, pigs were group penned from three to 18 weeks and single penned during the test period. These two effects are confounded and can not be distinguished. However, von Felde (1996) presented a genetic correlation of 0.45 between growth rate recorded in single pens and average daily gain recorded in groups thus supporting a low genetic correlation between test period gain and average daily gain measured on farm with group penning.

The default genetic correlation in PIGBLUP between backfat and growth rate is slightly positive and therefore unfavourable (r_g with ADG: 0.10, r_g with TPG: 0.11; Table 3). This is expressed through genetic correlations of 0.11 and 0.10 for growth rate recorded on farm and average daily gain recorded during the test period with backfat. In contrast, a negative and therefore favourable relationship was found between backfat and farm average daily gain in UNE17P. A number of factors contribute to this favourable relationship. Firstly, only boars were included in the analysis who have a high protein deposition rate in regard to feed intake capacity (Campbell and Taverner, 1988). Secondly, growth rate was recorded in the earlier growth phase which is the predominantly protein accretion phase. Thirdly, pigs were group penned until they entered the test station and their reduced feed intake in comparison to single penned pigs as found in a new project (UNE21P) might be an indication that the housing system restricts their feed intake. McPhee et al. (1988) showed that restricted feeding leads to a favourable genetic correlation between average daily gain and backfat. Therefore these three factors contribute to the favourable genetic correlation between average daily gain and backfat as estimated in UNE17P. PIGBLUP users however will analyse boars and gilts simultaneously and pigs will be grown to higher weights beyond 70 kg liveweight. It is therefore recommended to use a more conservative genetic correlation of zero between backfat and growth rate recorded on farm given that other studies find a positive genetic correlation between these two traits under ad libitum feeding.

Table 3: Genetic correlations (above diagonal) and residual correlations (below diagonal) currently used in PIGBLUP

	ADG	**TPG**	**BF**	**FCR**	**C-Fat**	**C-Musc**	**% Meat**
ADG		0.70	0.11	-0.20	0.11	0.00	0.00
TPG	0.35		0.10	-0.20	0.10	0.00	0.00
BF	-0.06	-0.06		0.10	0.80	-0.05	-0.60
FCR	-0.40	-0.39	0.00		0.00	0.00	0.00
C-Fat	-0.06	-0.06	0.69	0.00		-0.05	-0.60
C-Musc	0.00	0.00	0.00	0.00	0.00		0.25
% Meat	0.00	0.00	-0.47	0.00	-0.91	0.10	

Feed conversion ratio is defined as feed intake over growth rate. This implies that a high growth rate is associated with a low feed conversion ratio. This relationship is stronger between feed conversion ratio and average daily gain both recorded in the test station (r_g: -0.48, Table 4) than between feed conversion ratio and average daily gain measured on farm (r_g: -0.10). The default genetic correlations, currently used in PIGBLUP, do not make a distinction between the two growth rate traits (r_g with FCR: -0.20, Table 3).

Currently, a number of genetic correlations between carcase traits and other traits are set to zero in PIGBLUP (Table 3). Besides filling these holes changes include higher genetic correlations between both backfat measurements and lean meat percentage (Table 4). These high genetic correlations also imply that genetic correlations between these three traits and other traits are similar. In summary, leaner pigs have a lower test period gain and a lower (better) feed conversion ratio while no genetic association is assumed between leanness and average daily gain recorded on farm.

Table 4: Genetic correlations (above diagonal) and residual correlations (below diagonal) obtained from UNE17P

	ADG	TPG	BF	FCR	C-Fat	Muscle	% Meat
ADG		0.32	0.00	-0.10	0.00	0.10	0.00
TPG	0.02		0.31	-0.48	0.33	-0.13	-0.33
BF	0.06	0.00		0.19	0.90	-0.16	-0.90
FCR	0.00	-0.70	0.17		0.20	0.07	-0.15
C-Fat	0.05	0.03	0.36	0.06		-0.10	-0.95
Muscle	0.05	-0.03	-0.01	-0.02	-0.02		0.10
% Meat	-0.05	-0.03	-0.36	-0.12	-0.48	0.02	

Heritabilities and genetic correlations as presented in Table 2 and Table 4 are recommended to be used in PIGBLUP as new genetic parameters. One exception might be the high heritability for backfat and its zero genetic correlation with average daily gain. However, in order to analyse changes in genetic parameters these presented parameters will be used to analyse implications of different genetic parameters.

How do these changes affect EBV's

1. Data set from Aztec Farms

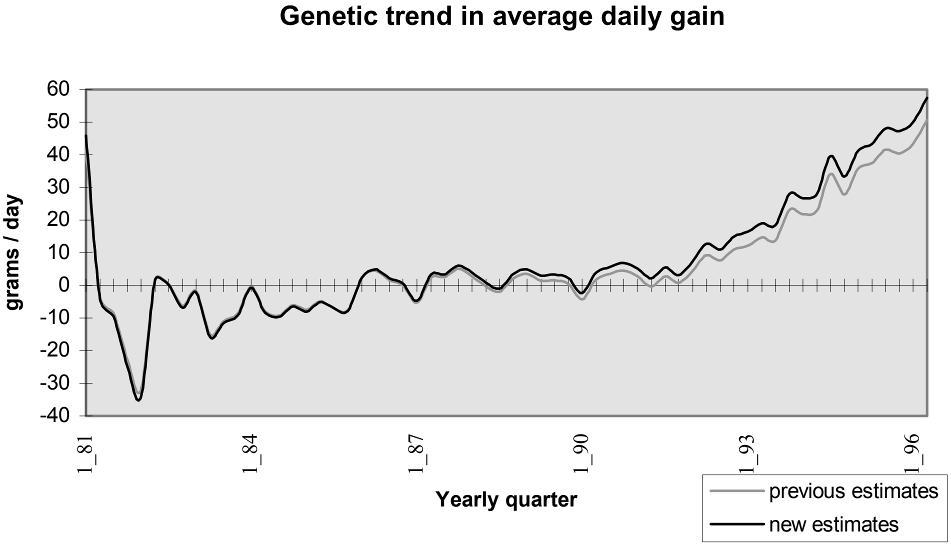
To quantify effects of these parameter changes, the PIGBLUP data file of Aztec Farms was used. This data set includes performance records from 1981 to 1996 comprising approximately 178,000 animals. All animals have average daily gain recorded while only 55,000 animals have information on backfat available. Since 1992 backfat was recorded on all animals. The size of this data set should guarantee that changes in EBV's are due to changes in genetic parameters and other factors that influence EBV's but can not be quantified are minimised.

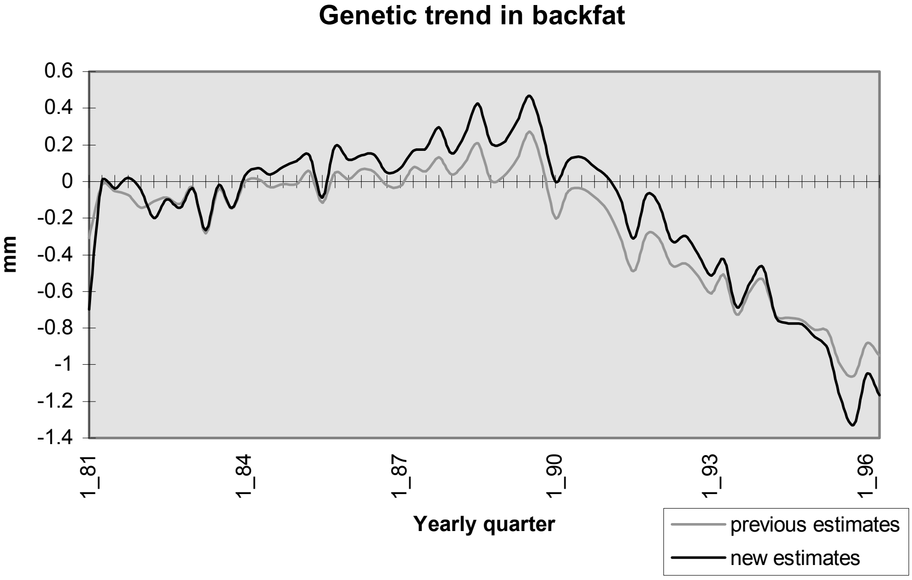
2. Genetic trend

The genetic trend shows how mean EBV's changed over time. Changes in genetic parameters will influence EBV's and might therefore lead to a different genetic trend. Genetic trends applying previous estimates and new estimates are shown in Figure 1 for average daily gain and in Figure 2 for backfat. Generally the genetic trend for average daily gain is similar from 1981 to 1991 for both sets of estimates, and slightly higher from 1991 to 1996 using new estimates. This higher progress for average daily gain is due to changing the genetic correlation between average daily gain and backfat from 0.10 to 0.00. Previously, the slightly positive and therefore unfavourable genetic correlation inhibited genetic progress in average daily gain with correlated response in backfat.

Changes are slightly higher in genetic trends for backfat which is due to changes in heritability estimate from 0.40 to 0.60 as well as a change in genetic correlation with average daily gain. The shift to higher EBV's for backfat is caused by a zero genetic correlation between backfat and average daily gain. Only a proportion of animals have backfat recorded and additional information from average daily gain is not used. This information is currently used when a genetic correlation of 0.1 is applied in PIGBLUP with the consequence of earlier information and a lower EBV for backfat.

Besides these differences in genetic trend for the two traits it can be seen that genetic trends using old and new parameters follow the same patterns. This indicates that these changes do not cause major reranking of animals. This is confirmed by rank correlations between EBV's for average daily gain and backfat of 0.99 and 0.98, respectively. Some individual animals might rerank due to less information available but, more importantly, the overall ranking in average daily gain and backfat is not significantly affected by these changes.





Although this might convince a scientist who is more interested in the overall changes, breeders are more interested in individual animals. Changes for individual pigs are therefore summarised below.

3. Changes in individual EBV's

Changes in EBV's have to be seen in context with the mean and variation between EBV's. This information is presented in Table 5. The mean EBV for average daily gain increased from 7.26 to 9.44 while the variation of EBV's remained the same. The increase in mean EBV is due to a shift of genetic correlation from 0.10 to 0.00 between average daily gain and backfat. The heritability did not change for average daily gain and it is therefore expected that variation in EBV's for average daily gain does not change. In contrast, variation in EBV's for backfat is increased. Given the higher heritability this is expected.

Table 5: Means, standard deviations (s.d.), minimum and maximum for EBV's for average daily gain (ADG) and backfat (BF) using old and new parameters

EBV for	Mean	s.d.	Minimum	Maximum
ADG - old parameters	7.26	25.52	-88.49	115.6
ADG - new parameters	9.44	25.29	-88.32	114.4
BF - old parameters	-0.27	0.93	-3.50	3.63
BF - new parameters	-0.20	1.15	-4.17	4.91

Breeders might be more interested in changes in EBV's for individuals. The percentage of animals with differences in EBV's are presented for average daily gain and backfat in Table 6.

Table 6: Number of animals with an absolute difference in EBV's for average daily gain from 0 to > 10 grams and for backfat from 0 to > 1mm

Change in ADG EBV	Percentage of animals	Change in BF EBV	Percentage of animals
0 gram	12.4	0 mm	13.7
1 gram	22.0	0.1 mm	26.2
2 grams	18.9	0.2 mm	20.1
3 grams	12.9	0.3 mm	14.6
4 grams	10.1	0.4 mm	11.0
5 grams	8.8	0.5 mm	6.4
6 grams	6.8	0.6 mm	4.3
7 grams	4.6	0.7 mm	1.8
8 grams	2.3	0.8 mm	1.1
9 grams	1.0	0.9 mm	0.5
> 10 grams	0.2	> 1 mm	0.3

For 12.4% and 13.7% of all animals EBV's did not change at all for average daily gain and backfat. For further 40.9% of all animals average daily gain changed only one or two grams. Changes in backfat were only 0.1 to 0.2 mm for 46.3% of all animals. The large changes in EBV's are observed for animals with extreme EBV's for average daily gain and backfat.

Overall, the magnitude of these changes is minimal and shows that changes in genetic parameters for backfat and average daily gain influence EBV's only slightly.

Interested in EBV's for meat quality traits?

Even without recording meat quality traits, results from UNE17P can be used in PIGBLUP to obtain first information about meat quality traits. Most PIGBLUP users do not record carcase traits and by replacing genetic parameters of carcase traits with genetic parameters for meat quality traits, EBV's and genetic trends can be obtained for meat quality traits based on correlated response from other recorded traits. It is only possible to substitute parameters for carcase traits since these traits are not included in the $Index. The required genetic parameters, including heritability estimates and variance components as well as genetic correlations, are presented in Table 7 and Table 8 for colour, drip loss percentage and intramuscular fat content. When measurements of meat quality traits are not available, environmental effects can not be estimated for these traits so it is not possible to obtain an environmental trend. These genetic parameters were discussed in detail during the previous workshop.

Table 7. Variance components and heritabilities for selected meat quality traits

Trait	**h**2 *	σ2a	σ2e	σ2p
colour of *m. longissimus dorsi*	0.29	5.87	14.39	20.25
drip loss percentage	0.23	0.71	2.36	3.07
intramuscular fat content	0.35	0.120	0.219	0.339

* for abbreviations see Table 1

Table 8. Genetic correlations between meat quality traits and production traits

	ADG*	**TPG**	**BF**	**FCR**	**DLP**	**IMF**
colour of *m. longissimus dorsi* (CLD)	-0.21	0.23	-0.08	-0.59	0.80	0.26
drip loss percentage (DLP)	0.02	0.10	-0.16	-0.58		-0.06
intramuscular fat content (IMF)	0.01	-0.21	0.26	0.21		

* for abbreviations see Table 1

Currently, PIGBLUP does not allow you to change names and units of measurement for different traits. However, by using these genetic parameters instead of those for carcase traits it is possible to obtain a genetic trend for meat quality traits, although the labelling of the graph does not reflect these changes. In the future, PIGBLUP will become more flexible and accommodate for these type of changes. However, breeders who don't want to wait any longer can get a first indication of meat quality traits by implementing these genetic parameters. **Finally one note of caution, implementing meat quality traits into PIGBLUP this way is only possible when no data on meat quality traits is available.** Should measurements of meat quality traits become available, appropriate models for these traits would have to be included in PIGBLUP.

4. Summary

The real benefit of results from UNE17P is the knowledge of genetic parameters for traits that have not been analysed frequently before. It was shown how the knowledge of genetic parameters for meat quality traits could already be used by breeders in PIGBLUP.

Heritabilities and genetic correlations as presented in Table 2 and Table 4 are recommended to be used in PIGBLUP as new genetic parameters. One exception might be the high heritability for backfat and its zero genetic correlation with average daily gain.

Changes in genetic parameters influence EBV's and implications of these changes were shown for one herd. Although there was a shift in genetic trend for average daily gain and backfat, the overall ranking of animals did not change significantly. This was demonstrated through rank correlations of 0.99 between EBV's for average daily gain using old and new parameters and 0.98 for EBV's for backfat implementing the two sets of genetic parameters. Changes in genetic parameters are therefore of minor importance for these traits which have been researched many times and are used most frequently.

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