# LEVELS OF GENETIC VARIATION FOR GROWTH, CARCASS AND MEAT QUALITY TRAITS OF PUREBRED PIGS

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## Summary

Levels of genetic variation for key growth and carcass, and meat quality traits were estimated for 3200 pigs, representing 4 pure breeds (Duroc, Hampshire, Yorkshire, Landrace), coming from 118 different breeder sources in Ontario. Pigs were reared in a single test station, were slaughtered at about 105 kg, and went for detailed carcass dissection. Mixed model analyses had herd origin, sire, litter and error as random effects, and sex, breed, PSS genotype, fill number and interaction terms as fixed effects. For all traits except meat quality attributes, differences among sources of breeding stock (herds) within breed were as large or larger than differences among breeds. While breed differences in meat quality traits (drip loss, marbling colour, structure) were relatively large, differences among herds were fairly small. For all traits, the variation among breeding values of animals within a herd and breed was considerably larger than between herds and breeds. Thus, for most traits, it is more important to choose the best source of breeding stock than the best breed. In the longer term, within line selection will produce the largest gains.

Keywords: genetic variation, breeds, growth, carcass, meat quality, pigs

#### Introduction

Genetic improvement of pigs over the past 30 years or so has focused primarily on improving growth rate and carcass leanness, and the success of such breeding programs is well accepted. In many cases breeding stock now have back fat levels that are at, or are approaching, a commercial optimum.

Rad je priopćen na "6<sup>th</sup> World Congress Genetics Applied to Livestock production", Armidale, 1998.

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Consumers in many markets are increasingly demanding higher quality products, and a plausible argument can be made that the quality of pork will have to increase if the pork industry is to maintain or increase its share of the meat market. The result is that many breeders are questioning what should be their breeding goals for the future, while many producers are seeking breeding stock that can bring them better profits in markets that are, or will in the future, pay premiums for carcass and meat quality.

Performance recording for pigs in Canada began in the 1920s, and since the 1960s there have been performance summaries and indexes for growth and ultrasonic measures of back fat for both station tested and home tested animals. National genetic evaluations based on an anima model BLUP were implemented in 1985, which is believed to be the first large scale use of animal model EBV in any species. There are many breeders in Canada ranging in size from large groups essentially running closed nucleus herds through to smaller breeders who rely on movement of genetic material between herds to maintain genetic progress. The result is that there are a large number of sources of breeding stock available to producers.

The Ontario Pork Carcass Appraisal Project was set up in 1992 to detail the genetic diversity for growth, carcass and meat quality traits of pigs in Ontario. We here present results on the genetic variation observed between breeds versus that between sources of breeding stock within breeds versus that within breeding stocks.

#### Methods

Some 3200 pigs from 4 breeds (Duroc, Hampshire, Yorkshire, Landrace), coming from 118 different sources in Ontario, were reared in a test station from 25 to 105 kg before going to slaughter followed by detailed carcass dissection. A variety of growth, carcass and meat quality traits were recorded.

Data was analysed using a mixed model with herd of origin, sire, litter and residual error as random effects, and breed, sex (gilt, barrow, boar), PSS genotype, and their interactions, and fill number, as fixed effects. There were relatively few relationships among sires or dams and these were ignored in the analysis. Since most dams had only one litter, the dam effects were subsumed into the litter effects. Dressing %, estimated carcass yield and carcass index (a payment grid) included slaughter weight as a covariate, while all other carcass traits included carcass weight as a covariate.

### Results

Comparison among the observed levels of genetic variation are given in Table 1. The breed range is the difference in least squares means between the highest and lowest performing breed for each trait. The difference between the top versus bottom 10% of herds is estimated as  $3.51^*$ ,  $\sigma_{\text{herds}}$ , where  $\sigma_{\text{herds}}$  is the estimated standard deviation of herd effects. The difference between the top and bottom 10% of BV is estimated as  $3.51^*$   $\sigma_{\text{a}}$ , where  $\sigma_{\text{a}}$  is the additive genetic s.d. estimated as 4 times the between sire variance. This is provided as an indication of the genetic variation available for improvement within a genetic stock on the same scale as choosing between the top versus the bottom 10% of herds. Also given in Table 1 is the estimated heritability obtained from the between sire variance in relation to the within stock variance, obtained as the sum of sire, litter and error variance.

There were substantial differences among breeds growth rate, but only modest differences for most aspects of carcass quality. Comparison with estimates of genetic trend from National genetic evaluations (B Sullivan, pers comm), indicates that breed differences for growth rate have been increasing over time, while differences in backfat, and presumably therefore in carcass lean yield, have been decreasing over time. There were substantial differences among breeds for Marbling score (Durocs being higher than other breeds) and drip loss (Hampshires being higher than other breeds). Despite being below average for physical measures of meat quality, Hampshires in this same trial scored well above other breeds for taste panel assessments of meat quality (Jeremiah et al., 1996).

The range in performance between the top and bottom 10% of breeding stocks (herds) within breeds was higher than that between breeds for growth traits, and much greater for measures of carcass leanness. The range between herds was, however, much smaller than the breed range when it came to physical measures of meat quality. There were relatively small differences between both breeds and herds when it came to carcass distribution traits (proportion of carcass or carcass lean in shoulder, loin, ham or belly). It seems that in the Ontario population, breed differences are not as important as difference between stocks within breeds when it comes to traits that are economically important today (growth, feed efficiency, carcass lean). If meat quality traits becomes economically important from a producer perspective, then choosing the right breed is more important than choosing the right stock within breed.

Table 1. - VARIATION BETWEEN BREEDS, HERDS WITHIN BREED, AND BV OF ANIMALS WITHIN HERDS

Trait	Breed range	Top vs bottom 10% of herds	Top vs bottom 10% of BV	h <sup>2</sup> sire
Days to 100 kg	10.6***	14.0***	24.32**	.38
ADG (kg/d)	.088***	.087***	.227***	.43
Backfat at 100 kg (mm)	1.01**	3.40***	5.63***	.53
Feed conversion (kg/kg)	0.08	0.24**	0.48**	.40
Dressing %	1.0***	1.2 <sup>ns</sup>	2.32 <sup>ns</sup>	.12
Estimated yield %	0.70 <sup>ns</sup>	2.60**	4.81*	.69
Carcass index	1.8**	3.3**	7.09*	.21
Carcass length (cm)	3.5***	2.2***	4.56***	.45
Carcass moisture loss (kg)	0.11 <sup>ns</sup>	0.05 <sup>ns</sup>	0.0	0.0
Max fat depth shoulder (mm)	4.8***	4.1***	10.20**	.29
Min back fat depth (mm)	0.8 <sup>ns</sup>	4.2***	6.37*	.21
Min loin fat depth (mm)	2.1 <sup>ns</sup>	5.7***	8.87**	.35
Shoulder as % of side	1.0***	0.9*	2.13*	.22
Loin as % of side	1.2***	1.0**	2.15*	.20
Ham as % of side	1.4***	0.9**	1.73*	.21
Belly as % of side	1.0***	1.2***	1.77*	.19
oin eye area (cm²)	4.5***	6.9***	10.7 <sup>ns</sup>	.37
ean content of shoulder (%)	1.2**	3.3***	3.9 <sup>ns</sup>	.19
ean content of loin (%)	1.8***	5.6***	10.5***	.55
ean content of ham (%)	2.6***	3.8***	8.5***	.72
ean content of 3 primals (%)	1.8***	4.1***	7.61***	.62
Chemical fat in belly (% of DM)	7.7**	8.4**	16.51 <sup>ns</sup>	.37
Chemical N in belly (% of DM)	0.8**	1.2**	1.99 <sup>ns</sup>	.31
hld lean (% of 3 primals)	0.2 <sup>ns</sup>	1.1*	3.25***	.37
oin lean (% of 3 primals)	1.6***	1.6***	1.94 <sup>ns</sup>	.13
am lean (% of 3 primals)	1.6***	1.3***	2.14 <sup>ns</sup>	.18
rip loss, loin (%)	4.0***	2.1*	4.38 <sup>ns</sup>	.12
arbling score, loin	1.21***	0.54***	0.88 <sup>ns</sup>	.15
olour score, loin	0.44***	0.24 <sup>ns</sup>	0.68 <sup>ns</sup>	.11
tructure score, loin	0.55***	0.13 <sup>ns</sup>	0.60 <sup>ns</sup>	.08

The range between the top and bottom 10% of animals within a stock based on breeding value is considerably larger than either the breed or herd range for all traits except the meat quality traits. The heritabilities estimated from sire variances here are generally very close to those estimated using a full animal model from the same data (Vandervoort and Gibson, 1996), and by others from independent data sets (eg Hovenier, 1993; Johansson et al., 1987). The exceptions were the heritabilities for the meat quality traits, drip loss, colour and structure, which were about half those we estimated from a full animal model and those obtained by Hovenier (1993). In our data, the litter component accounted for much more variance than the sire component, suggesting that common family effects are important for these traits, and in our data structure these cannot adequately be separated from additive genetic effects even under an animal model. Thus our sire variance estimates of additive genetic variance are probably less biased than those from a full animal model.

The range in BV among animals is slightly misleading, since it cannot be accessed directly. For a trait of average heritability, with a reasonably efficient selection program, it would take 4 to 10 generations to produce a change in the population average performance equal to the difference in breeding value between top and bottom 10% of animals. Nevertheless, for all traits the results clearly indicate that the greatest changes can be made in the long term by within line selection. In the short term, choice of optimum breed and source of breeding stock would have the most impact on profitability.

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## RAZINE GENETSKE VARIJACIJE ZA OSOBINE RASTA, POLOVICA I KAKVOĆE MESA U ČISTOKRVNIH SVINJA

#### Sažetak

Razne genetske varijacije za ključni rast i polovice, te osobine kakvoće mesa procjenjivane su za 3200 svinja, što su predstavljale 4 čiste pasmine (Duroc, Hampshire, Yorkshire, Landrace) iz 118 raznih uzgoja u Ontariju. Svinje su uzgajane na jednoj testnoj stanici, zaklane s oko 105 kg te išle na detaljno seciranje polovica. Analize miješanog modela uključile su podrijetlo stada, rasplodnjaka, leglo i pogrešku kao slučajne učinke, a spol, pasminu, genotip PSS, broj mjesta i uvjete interakcije kao stalne učinke. Za sve osobine, osim atributa kakvoće mesa, razlike među izvorima uzgojne loze (stada) unutar pasmine bile su velike ili veće od razlika među pasminama. Dok su pasminske razlike u osobinama kakvoće mesa (gubitak tekućine, mramoriranje, boja, struktura) bile razmjerno velike, razlike među stadima bile su prilično male. Za sve osobine odstupanja/variranja među uzgojnim vrijednostima životinja unutar stada i pasmine bilo je znatno veće nego između stada i pasmina. Prema tome, za većinu osobina važnije je izabrati najbolji izvor uzgojne loze nego najbolju pasminu. Dugoročno, selekcija unutar linije proizvest će najveće dobitke.

Ključne riječi: genetska varijacija, pasmine, rast, polovice, kakvoća mesa, svinje

Primljeno: 15. 2. 1999.