

Selection for Lean Growth Rate in a Synthetic Line of Yorkshire-Meishan Pigs

1. Selection Pressure Applied and Direct Response

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Summary and Implications

Selection for lean growth rate (LGR) was conducted for four generations in a synthetic line of Yorkshire-Meishan pigs. In the select line, seven boars and 20 gilts with the highest LGR were selected from each generation to produce the subsequent generation. A contemporaneous control line was maintained by randomly selecting five boars and 15 gilts to produce the next generation. Inbreeding coefficients averaged .198 and .207 for the select and control line pigs and .173 and .162 for the select and control line dams, respectively, in the fourth generation. LGR was estimated from ultrasound measures of 10th-rib backfat thickness and longissimus muscle area from 1,057 pigs. These pigs were sired by 58 boars and out of 133 sows. The generation interval was 13 months and the average selection differential per generation was 1.1 phenotypic standard deviation units for LGR. Heritability and response were estimated from the deviation of select line from the control line and multiple trait derivative free restricted maximum likelihood (MTDFREML) on the same material. Realized heritability was $.29 \pm .12$ for LGR in the control line. Corresponding estimates from MTDFREML were .32 and .37. The estimate of direct genetic change per generation using the deviation from the control line was 9.4 g/day for LGR. Corresponding estimates from MTDFREML were similar but were more precisely estimated.

Introduction

Lean growth rate (LGR) and litter traits are economically important traits of swine production, and thus, both should be emphasized in a swine selection program. Selection for LGR in swine has been practiced for several decades, and has been effective (4,5,11,14). However, several studies have demonstrated it is difficult to improve litter traits through selection (3,12). Moreover, other studies have demonstrated that selection for LGR had an effect on litter traits. An important question at the

moment for the pork industry is how to improve both groups of traits simultaneously.

Several studies have been conducted to document the superior reproduction of native Chinese pig breeds relative to American and European breeds (6,16). An alternative way to increase litter traits in swine is to incorporate them as a component of the maternal line in a crossbreeding program. Sellier and Legauet (13) proposed that various crossbreeding schemes could be implemented to take advantage of the high prolificacy of Chinese breeds. Several studies have demonstrated the usefulness of crossbred females produced from these Chinese breeds relative to American and European breeds. Unfortunately, the disadvantages in growth rate and composition traits in Chinese pure breeds have hampered realization of a commercial boost to litter productivity. Thus, this problem could be overcome by creating a synthetic line which contains both some native Chinese breeds such as Meishan, which has been reported to be the most prolific (3,6,10), and some American and European breeds and then selecting for LGR (1). Similar synthetic lines have been started in Europe (15).

A selection experiment was started in 1993 at the Iowa State University Bilslund Memorial Research Farm near Madrid, IA, to study the efficiency of selecting for LGR and the correlated responses in litter traits in a synthetic line of Yorkshire-Meishan pigs. Select and control lines were established using crosses of the Yorkshire and Meishan breeds. This paper evaluates the selection pressure applied and responses achieved for LGR over four generations.

Materials & Methods

Source of data. The experiment was conducted at the Iowa State University Bilslund Memorial Research Farm from 1993 to 1998. Foundation stock consisted of nine Meishan sows that were descendants of individuals imported from the People's Republic of China in 1989 and were considered to be representative of the Meishan breed. Semen from six American Yorkshire boars from two commercial AI companies was used to randomly inseminate Meishan sows at the Bilslund Farm to produce the base population (generation 0) of pigs in 1994. Selection criteria for the Yorkshire boars emphasized high expected progeny difference for 10th-rib backfat thickness and number of piglets born alive per litter. From the base generation and in each subsequent generation, five boars were randomly selected after ultrasound scanning to sire the next generation of the control line. An additional two boars, also randomly selected, were kept as alternates and used when any of the originally designated boars were unable to

service sows successfully. In each generation, 15 gilts were randomly selected to produce the next generation of control line pigs. In the select line, seven boars, along with two or three alternates, and 20 gilts with the highest LGR, were selected each generation without regard to pedigree to produce the next generation. One of the seven designated control line boars in the base population had high LGR and was also used to sire select line pigs for generation one. In each of the succeeding generations, all boar and gilt replacements came from their respective lines, and no matings were made across lines.

Ultrasound scanning was used to estimate LGR on all boars and gilts in the select and control lines in each generation. Therefore, all boars and gilts were available for selection in both lines. Matings were made within each line to minimize inbreeding. The generation interval in both the select and control lines was designated to be 13 months because females farrowed only one litter and boars were retained for use in only one five-wk breeding period. Litters were sired by 58 boars and out of 133 sows. During the course of the experiment, ultrasound loin muscle area and 10th-rib backfat thickness were collected on 1,057 pigs.

All sows were housed during gestation in open-fronted buildings with concrete-floored pens. As the expected date of farrowing approached, individual sows were moved to farrowing pens in an environmentally controlled building. Approximately one week after farrowing, sows and litters were moved from the farrowing house to an open-fronted, concrete-floored nursery. Pigs were weaned at approximately six weeks of age and moved to growing pens to start the test. Commercially prepared corn-soybean meal diets containing 18, 16, and 14% crude protein were fed to pigs when they reached 30, 70, and 105 kg, respectively. Pigs were weighed off test on an individual basis at weekly intervals upon reaching a weight of 105 kg. Pigs were allowed ad libitum access to feed and water. Ultrasound scanning for 10th-rib backfat thickness and loin muscle area was conducted by a National Swine Improvement Federation certified ultrasound technician. Selection was based on LGR adjusted to 105 kg.

Statistical analyses: Weighted cumulative selection differentials (WCSD) and inbreeding. WCSD were calculated by deviating the record of each selected individual from its generation-line-sex subclass mean and adding it to the average cumulative selection mean of the individual's parents. Individual cumulative selection differentials were weighted by the number of progeny alive at the time of ultrasound scanning. Lean growth rate was analyzed with a statistical model that included the effects of generation-line (GL), sire/GL, dam/sire/GL, sex, and GL x sex interaction. Sire and dam effects were considered random effects. Inbreeding coefficients of dams and litters were calculated directly from pedigree information for the base population in 1994.

Direct response to selection. Responses to selection were evaluated by two methods: 1) deviation from control line (method 1), and 2) estimation of (co)variance components and prediction estimation trend with multiple trait derivative free restricted maximum likelihood (MDFREML) (method 2) (2). In method 1, direct cumulative genetic response for LGR was calculated as the deviation of the mean phenotypic performance of the select line from the mean performance of the control line. To provide a measure of average response over generations, WCSD were regressed on generation of selection. To take into account the covariances between cumulative responses, realized heritability for LGR was estimated by the weighted regression of cumulative response on cumulative selection differential. The weighted regression of cumulative response on cumulative selection differential was based on the vectors of cumulative response, selection differentials, and the variance-covariance matrix of cumulative responses (7,8).

Method 2 used the estimation of (co)variance components and genetic trend by MTFREML. Additive genetic and common environmental variances were estimated with an animal model in a single-trait analysis. Analysis was carried out for LGR in the select line only (LGRL) and in the select line plus the control line (LGRL + CTL). Pedigree information on all animals, including the base generation, was included in the analysis. Fixed effects of sex, batch, and month within a particular year at the start of the performance test were included in the model. Estimates of genetic change per generation were obtained by regressing the mean breeding value of each generation on generation.

Results and Discussion

WCSD and inbreeding. The number of animals tested and the number of litters per generation were similar in the selection and control lines (Table 1). On average, in the select and control lines, there were, respectively, 7.3 and 5.8 sires with 17.3 and 12.8 dams per generation. The mean WCSD by generation and line are illustrated in Figure 1. Total WCSD over the four generations of selection was 141 g/day in the select line and 16.2 g/day in the control line, a difference of 124.8 g/day. This corresponds to a standardized WCSD of 4.1 phenotypic standard deviation units. The regression of WCSD on generation showed that the average increase in WCSD was 33.9 g/day per generation, 1.1 phenotypic standard deviation units. Average inbreeding coefficients are presented by line and generation in Table 2. Select and control line inbreeding coefficients usually differed by less than .02 in each of the generations for both the litters and dams. Therefore, the data were not adjusted to correct for these differences. The goal for all matings was to minimize the inbreeding coefficients in each of the generations. In the fourth generation, the cumulative inbreeding coefficients averaged .198 and .207 for the select and control line litters, and .173 and .162 for the select and control line dams, respectively.

Realized heritability. The estimate of realized heritability from method 1 was $.29 \pm .12$. The heritabilities and variance components from MTFREML in the select line only (LGRL)

and in the select line plus the control line (LGRL + CTL) are presented in Table 3. The estimate of heritability for LGR in the select line only was lower than that from the select line plus the control line; however, both were higher compared with the estimate from method 1. Generally, the heritability estimates from MTDFREML with increased population size were more precise.

Responses achieved. Direct cumulative responses for LGR from method 1 and method 2 are presented in Figure 2. Direct genetic change was 9.4 g/day per generation for LGR from method 1. Corresponding estimates from MTDFREML were generally similar to those from method 1 (Table 4), but were more precise than the estimate from method 1.

Inbreeding coefficients in the fourth generation in this study were higher when compared with other studies. Leymaster et al. (11) reported inbreeding coefficients were .172 and .152 for litters and dams, respectively, after index selection in the fourth generation. Stern et al. (14) observed the inbreeding coefficient was .03 after selecting for LGR over four generations. This low inbreeding level can be explained by individual selection on phenotypic values and within family selection for the males. Cameron (4) reported that inbreeding coefficients in high and low selection lines after index selection for LGR in the fourth generation in a Large White herd were .060 and .051, respectively. Cameron and Curren (5) also reported that inbreeding coefficients in high and low selection lines in the fourth generation after index selection for LGR in a Landrace herd were .032 and .029, respectively. The relatively high inbreeding coefficients in this experiment may be due to the small sample size. However, high inbreeding coefficients could be tolerated in a short

experiment such as this to increase rate of lean growth. Although high inbreeding levels were found after selection, the difference in the inbreeding coefficients between the two lines was small, which was similar to reports in other experiments (9).

The realized rate of genetic change indicated that selection for LGR had been effective. The average annual rate of genetic change for LGR was 9.9 g/day which was higher than the annual rate of 8.28 g/day and 7.67g/day in the high- and low-protein lines in Swedish Yorkshire pigs reported by Stern et al. (14). This result was also higher than reported by Cameron (4), and Cameron and Curren (5) with index selection. The higher rate of change observed for LGR in this study may be due to effective selection, the rapid rate of generation turnover, and the medium-to-high heritability estimate.

The estimate of heritability based on method 1 was lower than with method 2 in this study, which agrees with the work of Cameron (4). The standard errors of heritability estimates from MTDFREML were not available. Generally, mixed model methodology uses more information than only the selection differentials and responses each generation and the standard error should be lower than that from method 1.

This experiment has demonstrated that selection for lean growth rate over four generations was effective in a synthetic line of Yorkshire-Meishan pigs. The estimates of heritability indicate that the trait is associated with a moderate to high degree of additive genetic variation, which has been confirmed by the positive rates of response estimated. These results also indicate that it is feasible to improve lean growth rate in a synthetic line. In a subsequent paper, the correlated responses of litter traits will be examined.

Table 1. Distribution of parents and offspring by line and generation.

Generation	Select line				Control line			
	Sires	Dams	Offspring		Sires	Dams	Offspring	
			Boars	Gilts			Boars	Gilts
0	-	-	-	-	6	9	40	50
1	7	16	48	75	5	14	50	62
2	7	17	51	74	6	13	49	58
3	7	18	60	70	6	14	48	60
4	8	18	75	81	6	14	50	56
Totals	29	69	234	300	29	64	237	286

Table 2. Average inbreeding coefficients by line and generation.

Generation	Select line		Control line	
	Litter	Dam	Litter	Dam
0	-	-	.015	.012
1	.061	.057	.067	.047
2	.083	.072	.091	.078
3	.143	.136	.153	.121
4	.198	.173	.207	.162

Table 3. Variance components and heritability estimates for LGR from MTDFREML.

Population	Additive genetic	Common environment	Residual	Phenotypic	Heritability
LGRL	349	85	592	1092	.32
LGRL + CTL	347	79	511	937	.37

Table 4. Direct response (per generation) for LGR.

Trait	Method 1	MTDFREML	
		LGRL	LGRL + CTL
LGR, g/day	9.4	10.5	9.8

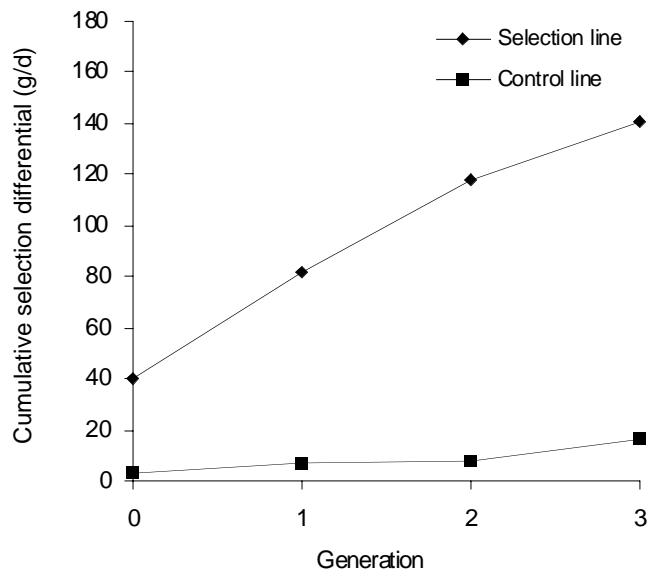


Figure 1. Cumulative selection differential for LGR in the select line and the control line.

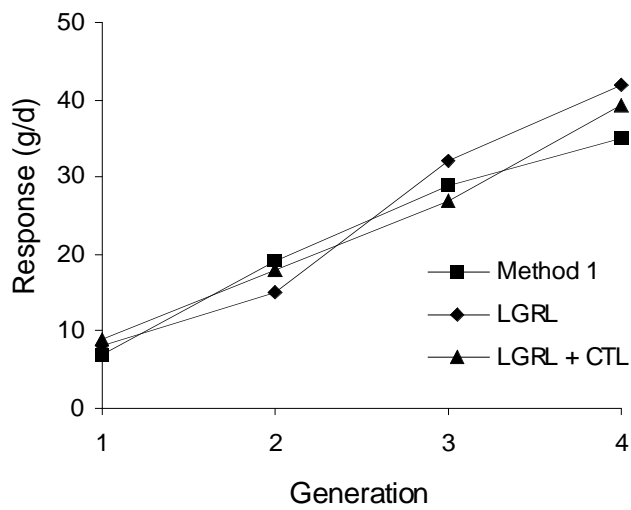


Figure 2. Cumulative response for LGR in the selection line only and in the select line plus the control line using MTDFREML compared with Method 1.

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