

# EFFECTS OF SELECTION OF LITTER SIZE AT BIRTH AND LITTER WEIGHT AT WEANING BASED ON A MULTIPLE-TRAIT ANIMAL MODEL IN GOLDEN HAMSTERS

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## SUMMARY

An experiment was conducted on hamsters to examine response to selection using information on a correlated trait in combination with reproductive traits based on BLUP under a multiple-trait animal model. The base population was established with progenies of 4-way cross sires and dams using 4 inbred lines. The population was subdivided into a selection line for litter size at birth, litter weight at weaning and 8-week body weight (line W), a selection line for litter size and litter weight (line R) and a control line (line C). Lines W and R were selected from a high aggregate genotype based on a multiple-trait animal model. Line C was maintained as a randomly breeding control. Line W showed much larger response to selection than line R for each trait. Mean litter sizes at generation 15 were 12.5, 12.1 and 10.3 for the lines W, R and C, respectively. Deviations in W and R from C, 2.2 and 1.8 pups, respectively were statistically significant ( $P < 0.01$ ). Mean litter weights at generation 15 were 275 g, 240 g and 204 g for lines W, R and C, respectively. Deviations of the selected lines from the control line were significant ( $P < 0.01$ ). For selected populations, inbreeding was higher in line R than line W. The use of 8-week body weight along with litter size and litter weight as a selection criterion brought larger response in the two traits.

## INTRODUCTION

Improvement in reproductive traits has major influence on the efficiency of animal production. However, only the results of selection experiments to improve litter size at birth in pigs are available (Lamberson *et al.*, 1991), because of low heritability and low selection intensity due to the sex-limited nature of the traits.

Avalos and Smith (1987) examined the efficiency of selection indices using family information, and the results were useful for increasing litter size in pigs. For comparison of animals with different amounts of information, such as a sow with a sister versus a sow with three sisters, Best Linear Unbiased Prediction (BLUP) may be applied to the data. BLUP gives the greatest benefit in selection for traits of low heritability or which are measurable in only one sex. De Vries and Sorensen (1990) estimated that using all family information increases genetic response by as much as 40 % for reproductive traits compared with only 10 % for growth traits. However, BLUP uses information on all known relatives, and thus the potential exists for an increase in the rate of inbreeding, as has already been shown by several researchers (Belonsky and Kennedy, 1988; Toro *et al.*, 1988; de Vries *et al.*, 1989). Their studies indicated that selection using BLUP increases inbreeding levels over selection on phenotype or index selection, especially when selection is on a trait of low heritability, such as litter size (Long *et al.*, 1991).

For traits such as low heritability and measurable only in one sex, selection of a genetically correlated trait in combination with desired traits can be advantageous (Haley *et al.*, 1988). With selection of growth and carcass traits in combination with litter size, the rates of inbreeding may be similar to those in conventional pig selection units (Avalos and Smith, 1987). This study was conducted to examine response to selection and the rate of inbreeding using information on a correlated trait in combination with reproductive traits based on BLUP under a multiple-trait animal model in golden hamsters.

## MATERIAL AND METHODS

The base population was established with progenies of 4-way cross sires and dams using 4 inbred lines of hamsters. Population parameters were estimated using data of the 4-way cross and base population as shown in Table 1. Base population was divided into three lines, a selection line for litter size at birth, litter weight at weaning and body weight at 8 weeks of age (line W), a selection line for litter size and litter weight (line R) and a control line (line C). Breeding population size of lines W and R was about 35 sires and 70 dams, respectively and of line C, about 35 sires and 35 dams, respectively for each generation. One male and two females were mated randomly avoiding sib and cousins for 12 days.

Table 1. Estimates of population parameters

		(1)	(2)	(3)
Litter size at birth	(1)	0.07	0.15	0.26
Litter weight at weaning (g)	(2)	0.36	0.34	0.04
8-week body weight (g)	(3)	0.39	-0.26	0.42

Heritability on diagonal; genetic correlation on below diagonal; phenotypic correlation on above diagonal.

Litter size as the number of pups born alive was counted within 12 hours after birth. It was then standardized to eight, four males and four females, as much as possible within each litter without fosterage on the day after birth. All young were weaned and males and females were separated at 3 weeks of age. They were reared in groups of 6 or 7 in cages up to about 9 weeks of age. For progeny, individual body weight was taken at 3, 5 and 8 weeks of age. Five-week weight was not considered in this paper.

The animals in lines W and R were selected based on a high aggregate genotype using the mixed model:

$$y = Xb + Zu + e$$

where  $y$  is a vector of observations;  $b$  is a vector of fixed generation effects;  $u$  is a vector of random additive genetic effects of  $q$  traits;  $e$  is a vector of random residual effects;  $X$  is an incidence matrix relating elements of  $b$  to each  $y$ ; and  $Z$  is a incidence matrix relating elements of  $u$  to elements of  $y$ .  $E(y) = Xb$  is assumed, and the expectations of the random effects are assumed to be zero. The variance-covariance matrix of the random effects is as follows:

$$\text{var} \begin{bmatrix} u \\ e \end{bmatrix} = \begin{bmatrix} A \otimes G_0 & 0 \\ 0 & I \otimes R_0 \end{bmatrix}$$

where  $A$ ,  $G_0$ ,  $I$  and  $R_0$  represent the additive genetic relationship matrix, additive genetic variance-covariance matrix, identity matrix and residual variance-covariance matrix, respectively and  $\otimes$  denotes the right direct product operator. The animals in line C were maintained as randomly breeding controls. Economic weights of litter size, litter weight and 8-week body weight were determined to be 1.69, 0.0260 and 0.199, respectively, based on the inverses of the estimated genetic standard deviations of these traits. The maximum numbers of individuals from one litter were 2 males and 4 females in the selected lines and 2 males and 2 females in the control line. This selection was made for fifteen generations.

Hamsters had free access to pellet feed and water at a temperature maintained at  $21.0 \pm 1.0$  °C and humidity of 50 %. The period of light was 14 hours from 6:00 to 20:00 throughout the study.

## RESULTS AND DISCUSSION

Responses to selection for litter size at birth and litter weight at weaning are given in Figures 1 and 2, respectively as deviations of selected lines from means of the control. Deviations in generation means obtained for each selected line from the control line for litter size increased and line W reached a plateau after about 10 generations. Line R also plateaued around generations 13–15. Mean litter sizes pooled over generations from 11 to 15 for each line were 12.7, 12.1 and 10.6 for lines W, R and C, respectively. Deviations in lines W and R from line C, 2.1 and 1.5 pups, respectively were statistically significant at  $P < 0.01$ . Mean litter weights for the last five generations were 274 g, 236 g and 193 g for lines W, R and C, respectively. Differences between selected lines and control line were highly significant ( $P < 0.01$ ).

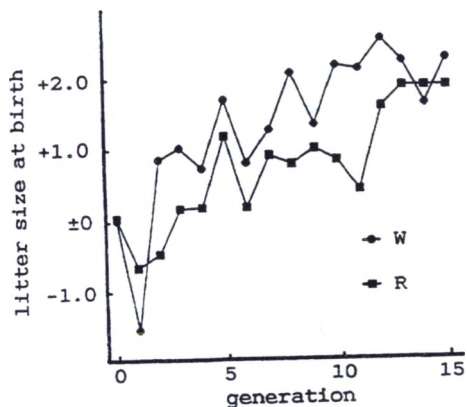


Fig. 1 Response to selection for litter size at birth as deviation from control line.

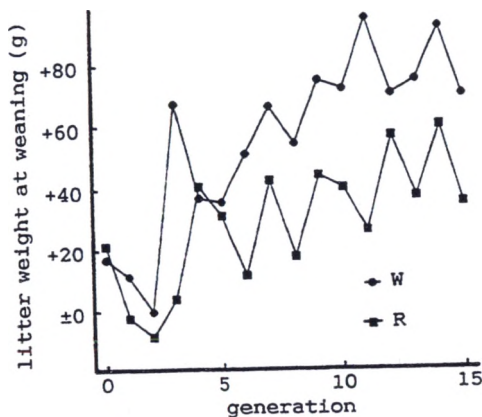


Fig. 2 Response to selection for litter weight at weaning as deviation from control line.

Response to selection for increased body weight at 8 weeks of age is indicated in Figure 3 as deviations in selected lines from means of the control. Mean 8-week body weights at generation 16 were 130.0 g, 95.1 g and 98.6 g for lines W, R and C, respectively. Deviation in generation means obtained for line W from line C increased almost linearly. The difference between line W and C attained the largest value of 31.4 g at generation 16 and it was highly significant at  $P < 0.01$ . However, deviation in generation means in line R from line C hardly increased.

Average inbreeding coefficients of progeny at generations 5, 10 and 15 for each line are given in Table 2. Inbreeding was the lowest in the control. For selected populations, inbreeding was higher in line R than line W. At generation 16, average inbreeding was 0.13 and 0.19 for lines W and R, respectively.

A multiple trait model should provide more accurate evaluation than a single trait model (Schaeffer, 1984). The use of 8-week body weight along with litter size and litter weight as a selection criterion indicated greater response in these two traits in line W. This may have been due to positively correlated response caused by selection for 8-week body weight. Differences between lines in average inbreeding coefficients were large at generation 16. Since the full-sib selection based only on the litter records in line R can accelerate the rate of inbreeding more than the selection based on the litter records and the individual body weight in the line W, and then the line differences in the average inbreeding coefficients should increase in subsequent generations. High levels of inbreeding may lead to inbreeding depression if non-additive genetic effects are significant. Consequently, inbreeding depression in reproductive traits should be less in line W than line R. It follows from the present results that the selection of a correlated trait in combination with desired traits may lead to the highly correlated response to selection and lower inbreeding level.

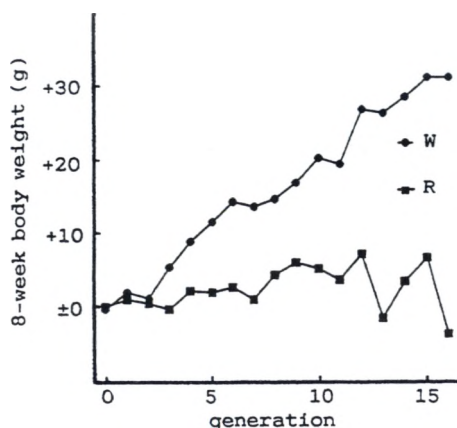


Fig. 3 Response to selection for body weight at 8 weeks of age as deviation from control line.

Table 2. Average inbreeding coefficients of progeny at generation 5, 10 and 15

Generation	Line		
	W	R	C
5	.030±.021 <sup>a</sup> )	.030±.012	.011±.007
10	.068±.010	.107±.009	.043±.014
15	.121±.009	.177±.010	.076±.009

<sup>a</sup>Standard error.

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