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Genetic correlations for daily gain between ram and ewe lambs fed in feedlot conditions and ram lambs fed in Pinpointer units¹

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ABSTRACT: When performance is recorded in automated facilities that measure feed intake of individual lambs that are penned in a group, such as Pinpointer units, a legitimate question is the degree to which daily gain is genetically correlated with daily gain achieved under feedlot conditions. Lambs were from a composite population ($\frac{1}{2}$ Columbia, $\frac{1}{4}$ Suffolk, and $\frac{1}{4}$ Hampshire germplasm) and of the F₂ or more advanced generations. Data were daily gains of 1,101 rams (PR) fed in Pinpointer units (11 to 17 wk of age) and 2,021 rams (FR) and 3,513 ewes (FE) fed under feedlot conditions (9- or 10-wk period starting at 9 wk of age). The FR and FE lambs were born from 1983 through 1995, whereas the PR lambs were born from 1986 through 1995. Measurements of daily gain in PR, FR, and FE lambs were considered to represent three correlated traits. Unadjusted means were .411, .406, and .326 kg/d for PR, FR, and FE, respectively. Random effects in the model were animal direct genetic, maternal genetic,

and maternal permanent environmental. Fixed effects were associated with age of dam (1 to 6 yr), type of rearing (1 to 4), and contemporary group (test date). Variances due to maternal genetic effects with single-trait analyses were near zero, so those effects were eliminated from the three-trait analysis although a random uncorrelated effect due to dam was included in the model. Estimates of heritability were .22, .14, and .23 for PR, FR, and FE, respectively, with fractions of variance due to dam effects ranging from .02 to .05. Estimates of genetic correlations were .86 for PR with FR, .83 for PR with FE, and 1.00 for FR with FE. Estimated phenotypic variances were similar for PR and FR, but one-third less for FE. The similarity of heritability estimates and estimates of genetic correlations all exceeding .83 suggest that daily gain of rams fed in Pinpointer units will reflect genetic expression for daily gain in both ram and ewe lambs fed under feedlot conditions.

Key Words: Genetics, Growth, Sheep

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Introduction

Measurement of individual feed intake is often costly. Automated facilities for measuring feed intake of individual lambs that are penned in a group may cause a change in natural feeding behavior for some classes of livestock (Jenkins and Leymaster, 1987). An important question then is whether daily gain achieved in automated facilities is correlated with daily gain under common feedlot conditions. The genetic question asks what

is the magnitude of the correlation between daily gain of a genotype in one environment (e.g., automated facilities) and daily gain of the genotype in another environment (e.g., feedlot conditions). This idea was formulated in a general sense by Falconer (1952), and the genetic correlation has been used as a way to measure genotype \times environment interaction. The objective of this research was to estimate genetic correlations where expressions of daily gain for a genotype were in ram lambs in automated facilities, ram lambs in feedlot conditions, and ewe lambs in feedlot conditions. Obviously, the genotype of an individual lamb can be expressed in only one of those "environments." Related lambs, however, can be considered to be partial genetic replicates of each other. For example, the most common relationship that forms partial genetic replications in the three environments is that of lambs with the same sire (paternal half-sibs), although other relatives will also be partial genetic replications of each other.

¹Mention of a trade name, proprietary product, or specific equipment does not constitute a guarantee or warranty by the USDA and does not imply approval to the exclusion of other products that may be suitable.

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Materials and Methods

Data were collected on a terminal sire composite population that was formed by mating Columbia rams to Hampshire-Suffolk crossbred ewes. Leymaster (1991) described the derivation of the population and the management of the flock. Briefly, 27 Columbia, 31 F₁, and 27 F₂ rams produced progeny from 1980 through 1987; subsequent generations were not discerned. A relatively large effective population size was maintained thereafter by use of at least 24 rams per year and avoidance of matings among paternal half-sibs. For these analyses, the base generation was made up of Columbia sires and Suffolk-Hampshire crossbred dams. The trait analyzed was postweaning average daily gain of lambs born from 1983 through 1995. These lambs were from the F₂ and advanced generations.

Ram lambs were not castrated and all lambs were offered a pelleted, total-mixed creep diet (2.90 Mcal ME per kg DM with 17.5% CP) by about 14 d of age. Lambs were weaned by groups at about 7 wk of age and, following a 2-wk adaptation period, the first postweaning weight was recorded at about 9 wk of age. Each year, from 1986 through 1995, a sample of ram lambs was randomly chosen within sire groups and moved into Pinpointer units at about 10 wk of age. Pinpointer units were located within an enclosed building. Each unit consisted of an elevated pen with a woven-wire floor, an entrance chute, a scale-feeder unit, and a microcomputer. The entrance chute limited access to the scale-feeder unit to one lamb at a time. Each lamb was electronically identified in the entrance chute, allowing measurement of feed intake of each lamb while penned in a group. Ram lambs forming a contemporary group (common on-test date) were assigned to three to five pens so that distributions of 9-wk weights were similar among pens. Progeny of a sire were often placed into each pen. From 1986 through 1989, 11 rams were grouped per pen, whereas pens contained 9 rams each from 1990 through 1995. These numbers of rams per pen allowed full expression of daily feed intake per ram in previous research reported by Jenkins and Leymaster (1987). Pinpointer rams remained on the creep diet to ensure that protein availability would not limit muscle development of these rams. Following a 1-wk adaptation period in the automated facilities, weights of Pinpointer rams were recorded from 11 to 17 wk of age and daily gains were calculated for the 42-d interval. The mean weights on test at 11 and off test at 17 wk of age were about 32 and 50 kg.

The remaining ram and ewe lambs were managed under feedlot conditions with access to a pole-shed facility. Rams and ewes were penned separately with about 100 to 120 lambs per pen. Feedlot lambs were switched to a total-mixed growing diet (2.96 Mcal ME per kg DM with 14.5% CP) at approximately 10 wk of age. Daily gains of feedlot lambs born in 1983 through 1989 were calculated over the 63-d interval from 9 to 18 wk of age, whereas daily gains of feedlot lambs born in 1990

Table 1. Number of lambs, sires, and dams and unadjusted means and standard deviations (SD) for daily gain (kg/d) by environment (feeding method and sex)

Environment	Number			Mean	SD
	Lambs	Sires	Dams		
Feedlot ram	2,021	269	1,348	.406	.073
Pinpointer ram	1,101	122	825	.411	.080
Feedlot ewe	3,513	271	1,898	.326	.062

through 1995 were based on the 70-d interval from 9 to 19 wk of age. Mean weights on test at 9 and off at 19 wk of age were about 26 and 55 kg for rams and 24 and 47 kg for ewes.

The numbers of lambs in the three environments (Pinpointer rams, feedlot rams, and feedlot ewes) are listed in Table 1, which also summarizes the unadjusted means and phenotypic standard deviations.

Statistical analyses were based on the concept of Falconer (1952). Data were divided according to the three environments defined by feeding method and sex (Pinpointer rams, feedlot rams, and feedlot ewes). Analyses were conducted for each environment separately and also together as three separate, but correlated traits. For the three-trait analysis, numerator relationships among lambs across environments created the partial genetic replications needed to estimate the genetic covariances (correlations) among expressions of daily gain in the three environments.

The initial statistical model included fixed effects of age of dam (1 to 6 yr), type of rearing (1 to 4 litter mates), and contemporary feeding group (common on-test date, $n = 53$). Random effects were animal direct genetic, maternal genetic, maternal permanent environmental, and residual. For each environment, the estimate of maternal heritability was .01 or less with little improvement in the likelihood compared with a model ignoring maternal genetic effects. Consequently, the model for the three-trait analysis (and the single-trait analyses reported herein) included animal genetic effect and a general maternal effect that did not account for relationships that would encompass both maternal genetic and maternal permanent environmental effects.

For the three-trait analysis, covariances were estimated among direct genetic expressions in the three environments and among maternal expressions in the three environments. As an animal could be in only one environment, the residual covariances were zero.

Estimates of variance and covariance components were obtained by REML with a derivative-free algorithm (Smith and Graser, 1986; Graser et al., 1987) with the MTDFREML package (Boldman et al., 1995). To help ensure global convergence, the algorithm was restarted with estimates at apparent convergence until the log likelihood did not change at the second decimal.

Table 2. Estimates (standard errors) of heritability (h^2), fraction of variance due to maternal effects (d^2), and phenotypic standard deviation (σ) from separate analyses of daily gain (kg/d) for the three environments (feeding method and sex)

Environment	Parameter estimates		
	h^2	d^2	σ
Feedlot ram	.13 (.05)	.04 (.04)	.056
Pinpointer ram	.19 (.06)	.04 (.06)	.054
Feedlot ewe	.23 (.04)	.02 (.02)	.043

Standard errors for single-trait estimates of genetic parameters were calculated using the inverse of the information matrix as described by Dodenhoff et al. (1998).

Results and Discussion

Table 2 lists estimates of heritability and fractions of variance due to maternal effects together with standard errors for data from the three environments analyzed separately. Although the standard errors are large relative to the difference between estimates, the heritability estimate for feedlot rams was less than for Pinpointer rams and for feedlot ewes. The reason may be that the lower content of CP in the diet of feedlot rams may have limited genetic expression of daily gain in these rams. The fractions of variance due to maternal effects were relatively small (.02 to .04). The phenotypic standard deviations were similar for the two ram groups, which were considerably larger than for the feedlot ewes.

The estimates of parameters for the genotype \times environment analysis with expressions for each environment as separate traits are given in Table 3. The estimates of heritability were similar to estimates from single-trait analyses and within the moderate range (.2 to .4) typically reported for postweaning daily gain (e.g., Olson et al., 1976), although the estimate of .14 for feedlot rams is rather low. The estimate of genetic correlation between expression in feedlot rams and ewes approached unity. The estimates of the genetic correlations between expression of Pinpointer rams with feed-

lot rams and ewes were similar and large (.86 and .83, respectively). Robertson (1959) presented a useful guide for the importance of the difference in such correlations from unity. A genetic correlation greater than .80 would suggest that the expression of the trait in two environments could be considered to be a single trait (i.e., a multiple-trait analysis would not be needed). The likelihood for the three-trait model was significantly different from that for a three-trait model with covariances assumed to be zero ($-2 \log$ likelihoods were $-20,591.96$ and $-20,525.15$, respectively). The $-2 \log$ likelihood for a three-trait model, assuming the genetic correlations between pairs of environments were .995, was similar to that using estimates from the data ($-20,588.49$ vs $-20,591.96$, respectively). This similarity of likelihoods is further justification that average daily gain measured in these three different ways can be considered to be one trait rather than three separate traits.

These results indicate that lambs and automated facilities can be managed to provide growth data that genetically reveals expression of growth under feedlot conditions. Several procedural factors may be relevant. Pinpointer rams were randomly chosen from within a single flock in which management of ewes and lambs was standardized to the extent possible. Prior to collection of postweaning weight data that determined daily gain, all lambs were allowed time to respond to varying preweaning environmental effects and Pinpointer rams to adapt to automated facilities. Lambs were of similar age within a contemporary group with a mean range of 13 d. Under these conditions, Pinpointer facilities can be used as an effective evaluation tool. The high genetic correlation of daily gain in automated facilities with daily gain in feedlot conditions justifies the current use of automated facilities for evaluation purposes by some producers of beef seedstock. The authors are not aware that producers of sheep seedstock have invested in automated facilities to record feed intake.

Waldron et al. (1990) reported that daily gain of Suffolk rams in central test stations was not significantly associated with daily gain of their progeny measured under experimental conditions. Daily gains of rams were measured over a 63-d period starting at about 60

Table 3. Estimates of genetic and phenotypic parameters for daily gain (kg/d) in the three environments (feeding method and sex)

Environment	Genetic ^a			Maternal ^b			Other ^c	
	FR ^d	PR	FE	FR	PR	FE	e^2	σ
Feedlot ram	.14	.86	1.00	.05	.91	.53	.81	.061
Pinpointer ram		.22	.83		.04	.13	.74	.062
Feedlot ewe			.23			.02	.75	.050

^aDiagonals are h^2 = heritability and off-diagonals are r_g = genetic correlations.

^bDiagonals are d^2 = fraction of variance associated with total maternal effects of dam and off-diagonals are r_d = correlations between total maternal effects of dam.

^c e^2 = fraction of variance due to residual effects, σ = phenotypic standard deviation.

^dFR, feedlot ram; PR, Pinpointer ram; FE, feedlot ewe.

d of age and daily gains of progeny were evaluated for 60 d, also beginning at 60 d of age; these conditions were similar to those reported herein. It seems likely that pretest environmental effects, both among and within flocks, may have affected performance of the rams at the central test stations.

The estimates of proportions of variance due to maternal effects with the three-trait analysis were similar (.02 to .05) to estimates from the single-trait analyses. The estimate of correlation between dam effects was largest for Pinpointer rams with feedlot rams (.91) and was smallest between Pinpointer rams and feedlot ewes (.13). The small amount of variance due to maternal effects for feedlot ewes makes such estimates of correlations have little importance.

As with the single-trait analyses, the estimate of phenotypic standard deviation for feedlot ewes is less than for Pinpointer and feedlot rams (.050 vs .062 and .061 kg/d, respectively), which had essentially equal phenotypic variance.

Implications

The large correlations between genotypic expression of daily gain in Pinpointer facilities and feedlot conditions indicate that the change from normal feeding behavior does not affect ranking of genotypes for daily gain. These results for growth suggest that such automated feeding facilities might be used to reflect differences in feed intake under normal feedlot conditions. The reduced heritability and increased variation for feedlot rams compared with feedlot ewes implies that rams may need a diet with more CP than ewes to express genetic differences for postweaning daily gain. A genetic evaluation system for rams and ewes might

be improved by standardizing phenotypic variance, by considering expression to be two separate traits for rams and ewes with different heritabilities and phenotypic variances, or by use of a heterogeneous variance model.

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