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L. K. Hutchens
Oklahoma State University, Stillwater

R. L. Hintz
Oklahoma State University, Stillwater

R. K. Johnson
University of Nebraska-Lincoln, rjohnson5@unl.edu

GENETIC AND PHENOTYPIC RELATIONSHIPS BETWEEN PUBERTAL AND GROWTH CHARACTERISTICS OF GILTS[1]

L. K. Hutchens[2], R. L. Hintz[2] and R. K. Johnson[3]

Oklahoma State University, Stillwater 74078

Summary

Data on 737 crossbred and purebred gilts were used to obtain heritability estimates for age at puberty (AGEPUB) and weight at puberty (WTPUB) and their genetic and phenotypic correlations with birth weight (BW), weaning weight (WW), postweaning daily gain (ADG), adjusted age at 90.7 kg (AGE) and adjusted backfat at 90.7 kg (BF). The heritability estimates for AGEPUB were low to moderate (.19 and .40, based upon paternal and maternal half-sib estimates, respectively.) The genetic (r_g) and phenotypic (r_p) correlations between AGEPUB and BW ($r_g = -.07$; $r_p = -.09$), WW ($r_g = -.25$; $r_p = -.19$), ADG ($r_g = -.38$; $r_p = -.34$) and AGE ($r_g = .56$; $r_p = .38$) were favorable. The genetic and phenotypic correlations between AGEPUB and BF were .27 and .01, respectively.

(Key Words: Puberty, Swine, Heritabilities, Genetic Correlations, Growth.)

Introduction

The cost of developing replacement gilts will be reduced by decreasing age at puberty because gilts can be brought into production at an earlier age. Current selection practices emphasize increased growth rate and decreased backfat thickness, and thus, the magnitude and direction of the correlated response of age of puberty are of interest. The purpose of this study was to estimate the heritability of age at puberty and the genetic and phenotypic correlations of age at puberty with growth characteristics.

Materials and Methods

Data were collected on 819 purebred and crossbred gilts (33 sire and 131 dam groups) produced in a four-breed diallel mating system involving Duroc, Yorkshire, Spot and Landrace breeds. Each sire was mated at random to at least one dam of each breed. At least one sire of each breed was replaced each season. Gilts were born during the fall months of 1976 and 1977 and the spring months of 1977 and 1978. Farrowing took place in a central confinement building. One to 2 weeks later, gilts were moved either to pasture lots with three or four litters per lot or to an open-front confinement building with one litter per pen. Creep fed was made available to gilts at 3 week of age and litters were weaned at 6 weeks. At approximately 8 weeks of age, gilts were randomly assigned within litter to be fed either in an open-front confinement building (10 gilts per pen) adjacent to at least one pen of littermate boars or in pasture lots (approximately 50 per lot) along with littermate barrows for a gain test (two to 12 gilts per breed group-management regimen-season-year subclass).

All gilts were fed a 14% protein corn- or milo-based diet during the gain test. Gilts were removed from test on a weekly basis at approximately 90.7 kilograms. They were then probed for backfat, placed together in pasture lots and fed daily 1.8 to 2.2 kg of a 15% protein diet.

Puberty was defined as the first detected estrus, indicated by a standing response to a teaser boar. Average age when estrus detection began ranged from 163.5 to 172.9 days for the various breed groups. The distribution of age at puberty approximated a normal distribution, because 66.4, 95.1 and 99.6% of the records were within 1, 2 and 3 standard deviations of the overall mean, respectively. After the gilts were placed in pasture lots (approximately 30 per lot), tests for estrus were started on a daily

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basis by exposure to teaser boars for 15 to 30 minutes. Tests for estrus were continued each season until the youngest gilt was at least 219 days of age. Eighty-two gilts were not detected in estrus, and they were not used in the analysis. These gilts either were slow to express estrus, were not observed in estrus or might never have cycled. Data used in the analysis consisted of information on gilts from 32 sire and 128 dam groups.

Birth weights were taken within 12 hr of farrowing, and weaning weights were adjusted to a 42-day basis. The age at which gilts came off gain test was adjusted to a 90.7-kg basis. Average daily gain was measured as the actual rate of gain during the gain test. The average of the backfat measurements taken at the shoulder, loin and rump (approximately 4 cm from the midline) was adjusted to a 90.7-kg basis. The actual age and weight were recorded when gilts reached first detected estrus.

The experiment was conducted primarily for the purpose of breed evaluation. The sires sampled for each breed were selected on the basis of the National Swine Improvement Federation Test Station index of growth and backfat (Hubbard, 1976). Replacement gilts were selected from within herd on the basis of a similar index.

The following linear model was assumed:

$$Y = X\beta + Z_1 s + Z_2 d + e,$$

where

Y is a vector of observations;

X is a known design matrix;

β is a vector of breed-of-sire effects, breed-of-dam effects, season effects, year effects, management during gain test effects, breed-of-sire × breed-of-dam effects, breed-of-sire × management effects, breed-of-dam × year effects, breed-of-dam × management effects, year × season effects, management × season effects, breed-of-sire × breed-of-dam × management effects and breed-of-sire × breed of dam × year effects and a common constant u;

Z_1 is a known design matrix;

s is a vector of one-half the additive genetic effects of the sires having multivariate distribution with mean zero and a nonsingular variance-covariance matrix G_1;

Z_2 is a known design matrix;

d is a vector of one-half the additive genetic effects and any maternal effects of the dam

having a multivariate distribution with mean zero and a nonsingular variance-covariance matrix G_2; e is a vector of residual effects including environmental and other genetic effects having a multivariate distribution with mean zero, and variance-covariance matrix R, s, d and e are mutually uncorrelated.

The decision as to which interactions would be included in the model for each trait was based on the results of preliminary analyses. Inclusion of all possible interactions would have created a sparce matrix. Litter size was not included as a covariate in the model, because adjustment of the data for litter size weaned did not appreciably alter the heritability and correlation estimates (maximum change of .02). It was assumed that $R = I^2 \sigma_e$, where I is an identity matrix with order equal to the number or records, which implies that the elements of e are uncorrelated and that all records have common variance, σ^2_e. The variance-covariance matrix G_1 was assumed to be $I\sigma^2_s$, where I is an identity matrix with order equal to the number of sires and σ^2_s is equal to one-fourth the additive genetic variance. The variance-covariance matrix G_2 was assumed to be $I\sigma^2_d$, where I is an identity matrix with order equal to the number of dams and σ^2_d is equal to one-fourth the additive genetic variance plus any maternal variation. Theoretically, covariances among half-sibs are not the same for purebreds and crossbreds. Also, genetic parameters may not be the same for gilts raised on pasture and gilts raised in confinement. In this study, numbers were not large enough for either hypothesis to be tested.

Henderson's (1953) Method 3, often called the "fitting constants method," was used to obtain unbiased estimates of the variance and covariance components. Heritability (h^2) estimates were obtained by the following equations:

$$\hat{h}^2 = 4\hat{\sigma}^2_s / (\hat{\sigma}^2_s + \hat{\sigma}^2_d + \hat{\sigma}^2_e) \text{ (paternal)};$$
$$\hat{h}^2 = 4\hat{\sigma}^2_d / (\hat{\sigma}^2_s + \hat{\sigma}^2_d + \hat{\sigma}^2_e) \text{ (maternal)}.$$

Approximate standard errors of the heritability estimates were obtained with an approximate formula (Swiger et al., 1964). Genetic correlations were calculated from sire variance and covariance components as follows:

$$\hat{r}_g = \hat{\sigma}_{s_x s_y} / \sqrt{\hat{\sigma}^2_{s_x} \hat{\sigma}^2_{s_y}},$$

where $\hat{\sigma}_{s_x s_y}$ represents the estimated covariance of trait x and y for sires, and $\sigma^2_{s_x}$ and $\sigma^2_{s_y}$ represent the estimated sire components of variance for traits x and y, respectively. Standard errors of the genetic correlations were not calculated, because the estimated standard errors for genetic correlations between age at puberty and the growth traits (correlations of major interest in this study) would have been biased upward on the basis of the magnitude of the heritabilities and number of animals involved (Van Vleck and Henderson, 1961). Phenotypic correlations were calculated from the sum of the variance and covariance components. Computer programs developed by R. L. Hintz (*unpublished*) were used for the analysis.

Results and Discussion

Heritabilities. The paternal half-sib heritability estimate for age at puberty was .19 (table 1). While this is not a high heritability, it does suggest that improvement can be made through selection. The estimate is lower than the weighted average (by number of offspring) of .34 for swine calculated by various methods (Reutzel and Sumption, 1968; Legault, 1973; Cunningham *et al.*, 1974; Young *et al.*, 1978).

The maternal half-sib heritability estimate for age at puberty was considerably larger than the paternal half-sib estimate (.40 *vs* .19). The dam component of variance included all of the maternal additive genetic variance, the covariance between direct and maternal additive effects and both the maternal dominance and maternal environmental variances. These were not included in the sire component of variance and four times their contributions would lead to differences between paternal and maternal

estimates of heritability. A suggestion of possible maternal effects upon age at puberty would agree with other reports. The paternal half-sib estimate and the offspring-on-dam regression estimate were −.20 and .49, respectively (Reutzel and Sumption, 1968). Variance components for dams were larger than variance components for sires for age at breeding (Reddy *et al.*, 1958) and age at puberty (Legault, 1973). Furthermore, in studies by Dyck (1971) and Burger (1952), 49.0 and 53.5%, of full sisters, respectively, reached puberty within a period of 5 days.

The paternal half-sib estimate for weight at puberty was .35 (table 1). This estimate agrees with a weighted average of .31 (Reutzel and Sumption, 1968; Legault, 1973; Young *et al.*, 1978).

In general, heritability estimates for the growth traits were higher than those previously reported (Hutchens, 1980). Reasons for the higher estimates may be the differences in statistical models used, the differences in methods used (e.g., paternal half-sib *versus* regression of offspring on parent) and sampling error. However, we have no specific explanation as to why the heritability estimates for both weight and weaning weight were greater than 1.

Correlations. The genetic correlations of age at puberty with birth weight (−.07), weaning weight (−.25), postweaning daily gain (−.38) and age at 90.7 kg (.56) increased in magnitude as the age at which growth was measured increased (table 2). The direction of the genetic correlations indicates that continued selection for growth rate would tend to decrease the age at puberty. Similar favorable genetic relationships of birth weight (−.14), weaning weight (−.04) and postweaning daily gain (−.33) with

TABLE 1. HERITABILITY ESTIMATES AND MEANS FOR PUBERTAL AND GROWTH CHARACTERISTICS AND THEIR STANDARD ERRORS

Trait[a]	Paternal half sib	Maternal half sib	Mean
AGEPUB, days	.19 ± .09	.40 ± .13	190.9 ± .80
WTPUB, kg	.35 ± .12	.26 ± .12	94.2 ± .37
BW, kg	1.53 ± .26	.32 ± .12	1.5 ± .01
WW, kg	1.20 ± .24	.80 ± .15	11.8 ± .10
ADG, kg	.69 ± .18	.54 ± .14	.69 ± .003
AGE, days	.60 ± .17	.79 ± .15	170.0 ± .38
BF, cm	.51 ± .15	.55 ± .14	2.52 ± .10

[a]AGEPUB = age at puberty, WTPUB = weight at puberty, BW = birth weight, WW = weaning weight, ADG = postweaning daily gain, AGE = age at 90.7 kg and BF = adjusted backfat at 90.7 kilograms.

TABLE 2. GENETIC AND PHENOTYPIC COMPONENTS OF VARIANCE AND COVARIANCE AND CORRELATIONS[a]

Trait[b]	Component	AGEPUB, days	WTPUB, kg	BW, kg	WW, kg	ADG, kg	AGE, days	BF, cm
AGEPUB	Genetic	89.2	1.57	-.244	-6.98	-.251	68.6	.632
	Phenotypic	473.4	117.3	-.568	-11.48	-.623	137.9	.079
WTPUB	Genetic	-.03	34.8	.993	12.13	.330	-53.7	.408
	Phenotypic	.54	98.3	.702	7.97	.286	-62.1	.105
BW	Genetic	-.07	.46	.136	.599	.013	-2.94	.002
	Phenotypic	-.09	.24	.089	.414	.007	-2.09	-.003
WW	Genetic	-.25	.69	.54	8.93	.102	-33.9	-.009
	Phenotypic	-.19	.29	.51	7.47	.071	-121.0	-.041
ADG	Genetic	-.38	.81	.50	.49	.005	-.656	.003
	Phenotypic	-.34	.34	.29	.31	.007	-1.156	.002
AGE	Genetic	.56	-.70	-.61	-.88	-.73	168	-.009
	Phenotypic	.38	-.38	-.42	-.58	-.83	278	.061
BF	Genetic	.27	.28	.19	-.01	.16	.00	.060
	Phenotypic	.01	.01	-.03	-.04	.05	.01	.119

[a]Variances are presented on the diagonal; covariances are above the diagonal; correlations are below the diagonal.

[b]AGEPUB = age at puberty, WTPUB = weight at puberty, BW = birth weight, WW = weaning weight, ADG = postweaning daily gain, AGE = age at 90.7 kg and BF = adjusted backfat at 90.7 kilograms.

age at puberty have been reported (Young *et al.*, 1978). However, an unfavorable genetic covariance between postweaning daily gain and age at puberty was reported by Reutzel and Sumption (1968). Other researchers estimating between-line correlations found that lines having the highest average 154-day weight tended to be the slowest to reach puberty, which may suggest a nonfavorable genetic relationship (Phillips and Zeller, 1943; Warnick *et al.*, 1951). However, unless lines have been selected under similar environments and for similar objectives, between-line correlations may not reflect within-line genetic correlations.

The phenotypic correlations of age at puberty with birth weight (−.09), weaning weight (−.19), postweaning daily gain (−.34) and age at 90.7 kg (.38) also generally increased with the age at which growth was measured. The estimates between age at puberty and birth weight and weaning weight agree with the weighted averages from the literature, −.01 and −.12, respectively (Hutchens, 1980). The phenotypic correlation between postweaning daily gain and age at puberty (−.34) was higher than the weighted average of −.17 (Hutchens, 1980). A possible explanation for the higher phenotypic correlation is that faster-growing gilts were exposed to boars at a younger age and, hence, could be detected in estrus earlier; however, this estimate is similar in magnitude to many of the phenotypic correlations reported between 154-day weight and age at puberty (Warnick *et al.*, 1951; Robertson *et al.*, 1951a,b; Self *et al.*, 1955; Foote *et al.*, 1956). Estimates from this investigation indicate that gilts with a faster growth rate would tend to reach puberty at a younger age.

The genetic correlation between age at puberty and backfat was low and positive (.27). This estimate is higher than the genetic correlation estimate of .00 reported by Young *et al.* (1978). If any genetic relationship exists between age at puberty and backfat, it appears to be low and positive. The phenotypic correlation between age at puberty and backfat was .01, which is similar to the weighted average of .07 reported by Hutchens (1980). There appears to be little, if any phenotypic association between age at puberty and backfat.

The genetic correlations of growth traits with weight at puberty were consistently higher than those of growth traits with age at puberty, suggesting that weight at puberty is more closely related to growth than is age at puberty.

The genetic correlation estimates of weight at puberty with weaning weight and postweaning daily gain, .69 and .81, respectively, fall between those reported by Young *et al.* (1978), .01 and .19, respectively, and Reutzel and Sumption (1968), .70 and 1.01, respectively. The greatest correlation was with growth measured later in life.

Estimates of the phenotypic correlations of weight at puberty with birth weight, weaning weight, postweaning daily gain and age at 90.7 kg were low to moderate (.24, .29, .34 and −.38, respectively). These values agree quite well with weighted averages of .27, .28 and .39 for the correlation of weight at puberty, birth weight, weaning weight and postweaning daily gain, respectively (Reutzel and Sumption, 1968; Young *et al.*, 1978). Thus, gilts with a faster growth rate would tend to be heavier at puberty.

The phenotypic correlation between weight at puberty and backfat was .01, indicating no phenotypic association between the two traits. The weighted average of two estimates reported in the literature is −.12 (Reutzel and Sumption, 1968; Young *et al.*, 1978).

The genetic correlation between age at puberty and weight at puberty was −.03. This value disagrees with that of .90 reported by Young *et al.* (1978). The phenotypic correlation between age at puberty and weight at puberty was .54, which agrees with the weighted average of .65 reported by Hutchens (1980). This suggests that gilts reaching puberty at later ages would also be expected to be heavier at puberty.

Conclusions

The heritability estimates indicate that age at puberty is low to moderately heritable and that age at puberty may be reduced through selection. However, the estimated genetic correlations with growth in this study indicate that continual selection for growth rate would result in a correlated decrease in age at puberty. These data also suggest a low, favorable genetic association between age at puberty and backfat.

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