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ADDITIVE AND DOMINANCE GENETIC EFFECTS ON POST-WEANING GROWTH IN NEW ZEALAND WHITE RABBITS

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ABSTRACT

Animal model analyses were performed using REMLF90 software to estimate variance components for body weights (BW) in New Zealand White rabbits. From 1985 through 1995, BW was first measured within one week after weaning (28 d) and then, in most cases, weekly for a maximum of five weeks until minimum market weight of 1.6 kg was observed. Data were recorded on 5,964 weanling animals from 43 sires, 273 dams (including 101 base animals), 1,218 litters, and 855 full-sib families. Four univariate genetic models were compared in estimating additive and dominance effects. The full model included fixed effects of contemporary groups (year-season of weaning) and linear covariates of age and inbreeding of animal and litter size at weaning, and random animal (additive genetic), full-sib (fraternal and non-fraternal members), permanent maternal, common litter, and residual effects. Remaining models either included or excluded maternal or full-sib sources or both. In the model which included the maternal source, additive (heritability) and dominance effects on BW's ranged from 0.01 to 0.07 and 0.02 to 0.07, respectively, compared to 0.08 to 0.26 and 0.10 to 0.30 for the model which excluded the maternal source. Further research is warranted to confirm these premiere results.

INTRODUCTION

In recent years, mixed-model techniques originally developed by HENDERSON (1975, 1976), the so-called animal model, have been widely adopted by rabbit breeders and scientists in performing genetic evaluations (*e.g.,* breeding value and heritability estimation) of animals and populations for economic traits. HENDERSON (1977) also developed mixed models using REML algorithms to estimate an animal's additive and dominance genetic merit. According to WEI & VAN DER WERF (1993), the preferred method for obtaining unbiased estimates of variance components and breeding value is REML using a mixed linear model which utilizes matrices for additive and dominance genetic relationships among animals. Potential applications of using total genetic merit (sum of an animal's estimated additive and dominance values) as production criterion are planning of specific matings and prediction of straightbred or crossbred performance, based on among- and within-breed (line) additive and dominance genetic variation and pedigree relationships. Recent papers have promoted additive genetic and dominance models for beef cattle (RODRIGUEZ-ALMEIDA *et al.,* 1995; GENGLER *et al.,* 1998), poultry (WEI & VAN DER WERF, 1993), and swine (CULBERTSON *et al.,* 1998).

On the occasion of the 5th World Rabbit Congress, LUKEFAHR (1992) proposed various animal models applicable to commercial meat and wool production systems. However, these models were appropriate only for obtaining estimates of additive genetic (breeding) values. Previously, it has not been possible to estimate dominance genetic values from available software packages that use animal model methods. To date, no reports have been published involving estimates of additive and dominance variances from animal model analyses for economic traits in rabbits. Hence, our objective was to simultaneously estimate additive and non-additive (dominance) genetic effects for body weight (**BW**) traits measured in growing rabbits.

MATERIALS AND METHODS

Stock housing, diet, and management aspects of the breeding experiment were previously described by MCNITT & LUKEFAHR (1993, 1996). Data used in these studies consisted of growth measurements involving 3,939 New Zealand White rabbits, which were collected from 1985 to 1992 at the Small Farm Family Resource Development Center at Southern University and A&M College, Baton Rouge, LA. For the present investigation, data were extended to 1995 to accumulate records from 2,025 additional animals.From a total of 6,065 animals, BW's were recorded from 5,964 weanling animals from 43 sires, 273 dams (including 101 base animals), 1,218 litters, and 855 full-sib families. Repeated matings were commonly practiced to minimize possible individual sire x dam interaction effects on fryer performance, and, in retrospect, to estimate dominance variance as found in full-sib families. The BW's were first measured within one week after weaning (28 d; BW1). Generally, BW was measured weekly for a maximum of five consecutive weeks or until minimum market weight of 1.6 kg was observed (*i.e.,* BW1 through BW5).

Four univariate genetic models (**I-IV**) were compared in estimating additive and dominance effects on BW's. Genetic models using matrix notation were as follows:

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{b}\,\Delta + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_2\mathbf{m} + \mathbf{Z}_3\mathbf{l} + \mathbf{e} \qquad [\mathbf{I}]$$

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{b}\,\Delta + \mathbf{Z}_1\mathbf{a} + \mathbf{Z}_3\mathbf{l} + \mathbf{e} \qquad [\mathbf{II}]$$

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{b}\,\Delta + \mathbf{Z}_1\mathbf{a} + \mathbf{W}\mathbf{f} + \mathbf{Z}_3\mathbf{l} + \mathbf{e} \qquad [\mathbf{III}]$$

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_1\mathbf{b}\,\Delta + \mathbf{Z}_1\mathbf{a} + \mathbf{W}\mathbf{f} + \mathbf{Z}_2\mathbf{m} + \mathbf{Z}_3\mathbf{l} + \mathbf{e} \qquad [\mathbf{IV}]$$

where **y** is the vector of body weight records (g), $\boldsymbol{\beta}$ is the vector of contemporary groups (year-season of weaning; classes = 43) and the linear regressions of **y** on age and on litter size at weaning, Δ is the linear regression of **y** on inbreeding coefficient, **b** is the vector of inbreeding coefficients, and **a**, **f**, **m**, **l**, and **e** are vectors of random additive animal, parental dominance, permanent maternal, common litter, and residual effects, respectively, and **X**, $\mathbf{Z_1}$ through $\mathbf{Z_3}$, and **W** are incidence matrices associated with corresponding fixed and random effects. Variances of random effects **a**, **f**, **m**, **l**, and **e** were

$$\mathrm{var}\begin{bmatrix}\mathbf{a}\\ \mathbf{d}\\ \mathbf{m}\\ \mathbf{l}\\ \mathbf{e}\end{bmatrix} = \begin{bmatrix}\mathbf{A}\sigma^2_{\mathbf{a}} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{F}\sigma^2_{\mathbf{f}} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{\mathbf{m}} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{\mathbf{l}} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{I}\sigma^2_{\mathbf{e}}\end{bmatrix}$$

where σ_a^2 is the additive genetic variance, σ_f^2 is the parental dominance variance (¼ of total dominance variance, σ_d^2), σ_m^2 is the general maternal variance (combined genetic and permanent environmental effects), σ_l^2 is the common litter variance, and σ_e^2 is the residual variance. The residual variance was calculated after subtraction of three times the estimate of σ_f^2. Because of relatively small numbers of dams in proportion to fryers, and the complexity of models including dominance effects, an estimate of the maternal genetic effect was not partitioned from the general maternal source (σ_m^2). In preliminary analyses, univariate and bivariate (BW1 and a second BW) animal models yielded similar estimates of variance. Therefore, only results from univariate models are presented. Variance components were estimated using REMLF90 software (MISZTAL, 1999) which integrate dominance models (MISZTAL, 1997). However, REMLF90 does not directly provide standard errors for the variance estimates. Convergence (criterion of 1 x 10^{-9}) was achieved at a global maximum of the likelihood function.

RESULTS AND DISCUSSION

Simple means (standard deviations) for BW1 through BW5 were 657 (162), 946 (197), 1,228 (222), 1,468 (212), and 1,649 (202) g, respectively. In addition, rabbits weighing more than 1.6 kg represented 0.0, 0.1, 5.2, 27.4, and 59.1% of the records for BW1 through BW5, respectively. Also, mean ages (standard deviations) for BW1 through BW5 were 32.3 (2.5), 39.4 (2.7), 46.6 (2.9), 53.5 (2.9), and 60.2 (2.8) d, respectively. Mean (standard deviation) litter size weaned was 6.6 kits (2.0) with a range of 1 to 12 kits.

The largest full-sib family size consisted of 71 members from 10 different litters. Breeding bucks and does tended to remain in the experimental herd for several years (*e.g.,* one doe produced 28 litters), which should enhance statistical partitioning of maternal influences from the litter variance. However, this aspect also explains the proportionately small numbers of bucks and does used over the 11–year experimental period. Consequently, this aspect related to 2,576 animals (42.5% of the population) that were inbred (mean 9.4%; range 0.4 to 28.5%), although 566 animals (22.0%) actually had inbreeding coefficients greater than 12.5%. Of relevance, while some selection was applied for increased BW and loin width, genetic trends from 1984 to 1993 for weaning weight and average daily gain indicated insignificant genetic progress (MCNITT & LUKEFAHR, 1996). QUAAS & POLLAK (1980) recommended the inclusion of inbreeding coefficients of animals as a model covariate source for populations in which confounding might occur between the effects of selection and inbreeding; however, such confounding should have been minimal in our population because of minor genetic trends.

In Table 1, variance component estimates for BW's from the conventional model **I** tend to agree with previous reports (ESTANY *et al.,* 1992; FERRAZ *et al.,* 1992; LUKEFAHR *et al.,* 1993, 1996; MCNITT & LUKEFAHR, 1996). Despite our low heritability estimates, the cited studies, which used animal models, also reported heritabilities ranging from only 0.0 to 0.19. In addition, variance estimates due to common litter effects were generally lower than those reported in the literature, probably because the weaning method involved the random transfer to growing cages of only four rabbits from the same or different litters. Although higher heritabilities were obtained from model **II**, it was apparent that a statistical confounding problem occurred in the analyses, largely involving additive genetic and maternal sources. Generally, residual variances decreased while additive genetic variances increased for BW's between the two models. A more ideal population would have involved larger numbers of sires and dams that would have also contributed more genetic relationships.

Table 1 : Additive genetic (a), dominance genetic (d), maternal (m), common litter (l), and residual (e) variances as proportions of total phenotypic variance (σ_p^2) by genetic model for weekly body weight (BW)[a]

Genetic model	a^2	d^2	m^2	l^2	e^2	σ_p^2
I (conventional additive genetic model with maternal source)						
BW1	0.03	__	0.11	0.46	0.39	14,653
BW2	0.02	__	0.12	0.44	0.42	23,496
BW3	0.02	__	0.11	0.37	0.50	31,077
BW4	0.02	__	0.10	0.34	0.54	31,008
BW5	0.11	__	0.08	0.26	0.55	30,660
II (conventional additive genetic model without maternal source)						
BW1	0.10	__	__	0.54	0.35	14,746
BW2	0.16	__	__	0.50	0.34	24,110
BW3	0.21	__	__	0.41	0.39	32,447
BW4	0.25	__	__	0.36	0.39	32,962
BW5	0.33	__	__	0.27	0.41	32,747
III (additive and dominance genetic model without maternal source)						
BW1	0.08	0.27	__	0.48	0.16	14,617
BW2	0.10	0.30	__	0.44	0.15	23,633
BW3	0.16	0.23	__	0.37	0.25	31,818
BW4	0.23	0.10	__	0.34	0.34	32,683
BW5	0.26	0.17	__	0.24	0.32	31,918
IV (full additive and dominance genetic model with maternal source)						
BW1	0.03	0.04	0.11	0.46	0.37	14,690
BW2	0.02	0.02	0.12	0.43	0.40	23,587
BW3	0.01	0.02	0.11	0.37	0.49	31,153
BW4	0.02	0.02	0.10	0.34	0.52	31,202
BW5	0.07	0.07	0.08	0.26	0.53	30,196

[a] In addition to the above specified random effects, all genetic models included fixed effects of year-season of weaning and linear covariates of inbreeding of animal, litter size at weaning, and age at weekly weighing. See text for description of body weight traits.

Models **III** and **IV** included dominance genetic effects (Table 1). In this breeding experiment, the relatively large size of full-sib families (fraternal and non-fraternal members) versus contemporary litters was critical in partitioning dominance genetic effects from litter and residual (within-litter) model sources, as well as in reducing bias or confounding problems between other random sources and time (*e.g.,* contemporary groups). Comparison of models **I** and **IV** show very similar variance fractions for all shared sources. Upon closer examination, however, the residual fractions for model **IV** are slightly lower which can be explained by the larger ¾ proportion of dominance variance which was partitioned. For BW5, there is an indication that some confounding existed between additive and dominance effects. In genetic models which exclude dominance effects, additive genetic parameters may be upwardly biased (WEI & VAN DER WERF, 1993). In model **III**, which excluded maternal effects, higher additive (0.08 to 0.26) and dominance (0.10 to 0.30) variance fractions were observed, although the common litter source remained relatively stable. While it is not possible to determine which genetic model yielded the most accurate or unbiased results, it is evident that variances were sensitive to the models employed. However, in support of model **IV** results, inbreeding coefficients were very small across all models. For example, in model **I**, inbreeding coefficients for BW's ranged from only –5.8 to –3.6 g/10% increase in inbreeding. However, FERRAZ *et al.* (1992) reported greater inbreeding depression for growth traits. In addition, on the premise that heterosis levels are higher in crossbred versus straightbred animals, and that dominance is a major cause of heterosis as well as inbreeding depression, rabbit crossbreeding experiments (BRUN & OUHAYOUN, 1989; AFIFI & KHALIL, 1992; MEDELLIN & LUKEFAHR, 1999) generally suggest low heterosis (≤|10|%) levels for BW's. In conclusion, our results suggest the existence of dominance effects for growth traits which may be at least as important as additive genetic effects. If true, mating strategies might need to be modified to evaluate animals on the basis of total genetic merit. However, further research is warranted to confirm these premiere results.

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