

GENETIC AND ENVIRONMENTAL PARAMETER ESTIMATION FOLLOWING MASS SELECTION FOR 70-DAY BODY WEIGHT IN RABBITS USING AN ANIMAL MODEL

S.D. Lukefahr^{1,2}, H.B. Odi¹ and J.K.A. Atakora³

¹International Small Livestock Research Center, Alabama A&M University, Huntsville, AL 35762, USA.

³National Rabbit Project, Ministry of Agriculture, Accra, Ghana.

SUMMARY

Phenotypic mass selection for increased 70-d body weight (BW) was carried out for five generations in a synthetic sire line of rabbits (n=1,453). Additional growth and carcass traits recorded were: 28-d weaning weight; 28 to 70 d average daily gain; carcass yield, and proportion and lean-to-bone ratio of the loin primal cut. A full animal model (univariate and bivariate) utilizing a derivative-free restricted maximum likelihood algorithm was used to estimate genetic parameters and trends. Heritabilities for direct genetic effects ranged from .02 to .14 for growth traits, and from .42 to .50 for carcass traits. Divergence between select and control line rabbits for BW was 111 g (5.4%) after five generations of mass selection. Genetic and environmental (common dam and (or) litter and residual) correlations were all positive and moderate to high in magnitude (range of .38 to .96) between BW and growth and carcass traits.

INTRODUCTION

Application of animal model methodologies (Henderson, 1977) that account for additive genetic relationships and selection bias, in particular, is a recent computational tool used in rabbit breeding/selection experiments and genetic evaluation procedures (Baselga and Camacho, 1993; Blasco et al., 1993; Estany et al., 1989; 1992; Ferraz et al., 1992; Lukefahr et al., 1992, 1993). Moreover, estimates of BLUP for breeding value and REML genetic (co)variance components for economic traits are valuable in genetic evaluation of seedstock, in determination of genetic trend, and ultimately in designing rabbit breeding programs.

This paper employed animal model procedures to analyze rabbit data involving five generations of phenotypic mass selection for 70-d body weight. Specifically, the research objectives were to estimate genetic and environmental parameters, and determine direct genetic trends for growth and carcass economic traits.

MATERIALS AND METHODS

Population Background. The base population of the synthetic sire line consisted of the breed composition of $\frac{1}{2}:\frac{1}{4}:\frac{1}{4}$ for Flemish Giant, Californian and Champagne D'Argent, respectively. Details on the rationale and development of the sire line, and also diet, housing and management systems, were previously reported by Ozimba and Lukefahr (1991). In 1989, the synthetic base population was randomly subdivided on a within-litter basis into control (C) and select (S) lines.

²Present address: Department of Animal & Wildlife Sciences, Texas A&M University-Kingsville, TX 78363, USA.

Random matings were made in the C line, except that sibling matings were avoided. In the S line, 10 bucks and a minimum of 40 does having the heavier phenotypic body weights (BW) at 70-d of age were selected (regardless of pedigree) for breeding in the next generation. Litters in both lines were primarily from primiparous does. Weighted cumulative selection differentials (WCSD) were calculated by generation-line-sex group. By generation five, the WCSD line difference between S and C lines was 1,016 g. Progeny numbers by line and generation are shown in Table 1.

Table 1. Number of sires and dams contributing offspring by line and generation

Generation	Select line			Control line		
	Sires	Dams	Offspring	Sires	Dams	Offspring
1	10	46	232 (30)*	10	19	88 (28)
2	10	30	142 (31)	9	22	107 (22)
3	10	29	132 (32)	9	25	114 (22)
4	10	35	176 (33)	9	27	126 (26)
5	10	23	121 (25)	9	19	130 (27)
Total	50	163	803 (151)	46	112	565 (125)

*Number in parentheses is the number of fryers evaluated for carcass trait merit.

Traits and Data Collection. Litters (n=289) were weaned by removing the dam from the cage at 28 d, whereby the litter remained as an intact unit during the postweaning 28 to 70 d growth period. Growth traits included 28-d weaning (WW) and 70-d body weights (approx. market age) BW, and calculated 28 to 70-d average daily gain (ADG). One rabbit was randomly chosen from each litter for carcass evaluation following a 24-hr fast of feed (Table 1). Carcass traits measured were carcass yield (hot carcass/ preslaughter weight) (CY), loin primal cut proportion of hot carcass weight (LP), and lean-to-bone ratio (LBR) of loin primal cut. "Base population" means and standard deviations were 501 ± 115 and $2,067 \pm 307$ g for 28-d WW and BW, 37.3 ± 5.7 for ADG, $.50 \pm .03$ for CY, and $.21 \pm .02$ and 8.50 ± 1.5 for LP and LBR, respectively.

Mixed-Model Procedures. A complete animal model was used to estimate genetic and environmental parameters, and genetic trends, employing the DFREML software package developed by Meyer (1988). Individual rabbit performance records (n=1,368) and complete pedigree information tracing to the synthetic base population (85 "base animals") were involved. A univariate, mixed model for 70-d body weight (BW) was used: $y = X\beta + Z_1d + Z_2m + Z_3c + \epsilon$, where y is the observational vector of BW records, β is a vector of the unknown fixed effect due to generation, X, Z₁, Z₂ and Z₃ are known incidence matrices relating records to appropriate fixed and random effect classes, d, m and c are vectors of unknown random direct and maternal additive genetic and common environment effects (associated with dam and[or] litter), and ϵ is the random residual vector of environmental effects. All random effects were assumed to uncorrelated.

Bivariate analyses involving the same model effects above (except the c effect was not fitted and residual environmental correlations were set to zero for carcass traits) were carried out that

considered **BW** together with each growth and carcass trait. For **BW** with each growth trait, sets of correlations were estimated between BLUP for direct genetic (breeding value), and common and residual environmental deviations. In preliminary analyses pertaining to univariate and bivariate models, the maternal genetic effect was non-zero for only **WW**, and therefore was eliminated as a random source for all other traits. For each animal and trait, direct breeding value were estimated, and then averaged according to generation-line to determine genetic trends for growth and carcass traits.

RESULTS

Genetic and Environmental Parameters. Direct heritability estimates (h^2_d) for **WW**, **BW** and **ADG** were .02, .12 and .14, respectively (Table 2). Maternal heritability (h^2_m) for **WW** was estimated at .05, being larger in magnitude than direct heritability. Carcass traits were more highly heritable, as expected, estimates being .50, .50 and .42 for **CY**, **LP** and **LBR**, respectively. For growth traits, common environmental variance was larger than residual environmental variance, except for **ADG**.

Table 2. Direct and maternal heritabilities and variance component estimates for commercial traits*

Parameter	WW, g	BW, g	ADG, g/d	CY	LP	LBR
h^2_d	.02	.12	.14	.50	.50	.42
h^2_m	.05	-	-	-	-	-
σ^2_d	351	9,281	3.686	.00032	.00014	.67316
σ^2_m	721	-	-	-	-	-
σ^2_c	9,529	40,809	11.08	-	-	-
σ^2_ϵ	3,472	29,526	11.65	.00032	.00014	.92427

***d** = direct genetic; **m** = maternal genetic; **c** = common environmental, and ϵ = residual environmental effects.

Genetic correlations for direct breeding value between the selected trait, **BW**, together with **WW**, **ADG**, **CY**, **LP** and **LBR** were .84, .96, .38, .49 and .78, respectively. For growth traits, the environmental correlation, due to common dam and(or) litter effects, between **BW** and **WW** was .80, and between **BW** with **ADG** was .89. In contrast, residual environmental correlations between **BW** and **WW**, and between **BW** and **ADG**, were .62 and .95, respectively.

Genetic Trends. Genetic trend calculations for direct breeding value for **BW** revealed a cumulative 111.35 g (5.4%) difference between **S** and **C** line rabbits, following five generations of phenotypic mass selection (approx. 22 g per generation). Direct and maternal genetic trends for breeding value for **WW** showed cumulative line differences of 18.0 and 5.0 g between **S** and **C** lines. A 4.2 g increase in direct breeding value for **WW** per generation of phenotypic selection for **BW** was observed ($P < .01$) in the **S** line, other computed regression coefficients for **WW** being non-significant. Correlated response for direct breeding value for **ADG** indicated 2.22 g/d progress

($P < .01$) in S compared to C line rabbits. For carcass traits, direct breeding value trends for CY, PL and LBR portrayed some improvement in both lines; a plausible explanation is possibly genetic drift in C line and the high genetic correlation in S line as associated positively with mass selection for BW. In mice, Eisen and Prasetyo (1988) reported a high genetic correlation ($r_g = .74$) between 12 wk body weight and lean weight index score.

DISCUSSION

For growth traits, direct and maternal additive genetic variances were low as opposed to common and residual environmental variances. Our heritability estimates for growth traits are comparable to those of Estany et al. (1992) and Ferraz et al. (1992), both studies of which used an animal model procedure, reporting direct heritability values of .15 and .01 for WW (28 d), and .17 and .08 for BW (77 d), respectively. Common environmental variance due to dam and(or) litter effects was consistently larger than residual environmental variance, except for ADG. In rabbits, the relatively large common environmental effects associated with the dam and(or) litter pertain to unique biological and management systems, and also the young age at which rabbits are marketed; this is in contrast to beef cattle, sheep and swine which are marketed at later ages. Thus, common environmental factors have indirect bearing on predicted rates of genetic progress.

After five generations of phenotypic mass selection, genetic improvement, via direct breeding value, for BW was a cumulative 111.35 g (5.4%) difference between S and C line rabbits. Recent reports confirm the slow rate of genetic response at 1 to 2% per generation for postweaning growth traits in rabbits (Rochambeau et al., 1989; Estany et al., 1992). Conversely, since BW was estimated to be highly genetically correlated with LBR ($r_g = .78$), selection for BW would be expected to favor rabbits with high lean yield merit.

Further research is warranted comparing BLUP selection for breeding value and employing an animal model procedure (while accounting for common environmental effects of the dam and(or) litter, as well as full pedigree additive genetic relationships), as opposed to phenotypic mass selection for improving economic trait performance in rabbits.

REFERENCES

- Baselga, M. and Camacho, J. (1993) *J. Anim. Breed. Genet.* 110 : 253-236.
- Blasco, A., Santacreu, M.A., Thompson, R. and Haley, C.S. (1993) *Livest. Prod. Sci.* 34 : 163-174.
- Eisen, E.J. and Prasetyo, H. (1988) *J. Anim. Sci.* 66 : 1153-1165.
- Estany, J., Baselga, M., Blasco, A. and Camacho, J. (1989) *Livest. Prod. Sci.* 21 : 67-75.
- Estany, J., Camacho, J., Baselga, M. and Blasco, A. (1992) *Genet. Sel. Evol.* 24 : 527-537.
- Ferraz, J.B.S., Johnson, R.K. and Van Vleck, L.D. (1992) *Proc. 5th World Rabbit Congr. (J. Appl. Rabbit Res.)* 15 : 131-142.
- Henderson, C.R. (1977) *J. Dairy Sci.* 60 : 783-787.
- Lukefahr, S.D., Opoku, E.M. and Atakora, J.K.A. (1992) *J. Hered.* 83 : 105-108.
- Lukefahr, S.D., Roberts, J.D. and Van Vleck, L.D. (1993) *Prof. Anim. Sci.* 9 : 89-97.
- Meyer, K. (1988) *J. Dairy Sci.* 71(Suppl.2) : 33-34.
- Ozimba, C.E. and Lukefahr, S.D. (1991) *J. Anim. Sci.* 69 : 3494-3500.
- Rochambeau, H. de, Fuente, L.F., Rouvier, R. and Ouhayoun, J. (1989) *Genet. Sel. Evol.* 21 : 527-546.