Proceedings 5th World Rabbit Congress, 25-30 July 1992, Corvallis – USA, 131-142.

ESTIMATION OF GENETIC TRENDS AND GENETIC PARAMETERS FOR REPRODUCTIVE AND GROWTH TRAITS OF RABBITS RAISED IN SUBTROPICS WITH ANIMAL MODELS.

Ferraz, J.B.S.[1]**; Johnson, R.K.**[2] **and Van Vleck, L.D.**[3]

(1) -Departamento de Producao Animal da Faculdade de Medicina Veterinaria e Zootecnia, Universidade de Sao Paulo, Depto. de Producao Animal, Cx.Postal 23, 13630 Pirassununga, SP, Brasil
(2) -University of Nebraska, Department of Animal Sciences, Lincoln, Nebraska 68583-0908, USA
(3) - Roman Hruska Meat Animal Research Center, ARS-USDA, A218 Animal Sciences, Lincoln, Nebraska, 68583-0908, USA

ABSTRACT

Records of 1,331 parturitions of 130 Californian (CAL) and 146 New Zealand White (NZW) does, individual weekly weights from weaning to 11 weeks of 2,882 rabbits (1,512 CAL and 1,370 NZW) and traits observed at slaughter of 1,731 fryers (908 CAL and 823 NZW) were analyzed by mixed model procedures with an animal model to estimate genetic and environmental parameters (REML estimates of variance components) and genetic trend by year, considered the average estimated breeding value of rabbits born in each year. Estimates of total heritability (h_t^2) were low for litter size at birth (LSB), 21 days (LS21) and weaning (LSW). Estimates of h_t^2 for preweaning mortality and gestation length were very low, were low for litter weights at birth and 21 days. The estimate was moderate for litter weight at weaning. The contribution of the permanent environmental effect of the doe was moderate for litter traits. Estimates of h_t^2 for growth traits were moderate with largest estimates for individual weights at 10 or 11 weeks. Litter effects explained from 30 to 50% of variation in growth traits and were progressively less important with increase in age. The largest estimate of h_t^2 for slaughter traits was for weight at slaughter. Future multivariate mixed model analyses are needed to decide the best traits to be used as selection criteria.

INTRODUCTION

In development and evaluation of breeding programs, both genetic parameters and genetic trends need to be evaluated accurately. Compared to other livestock species, very few estimates have been reported on rabbits for either genetic parameters or genetic trends. The importance and use of genetic parameters to improve the productivity in rabbits was discussed by Lukefahr (1988). Khalil et al. (1986) reviewed estimates of phenotypic and genetic parameters of reproductive and growth traits associated with rabbit meat production.

In general those traits had low or moderate heritabilities. Neither study used mixed model procedures under an animal model.

Mixed model methods under an animal model, that give best linear unbiased predictors (BLUP) of genetic values, are also accepted as the best methods to estimate genetic parameters (Henderson, 1988).

Lukefahr et al. (1992) used Restricted Maximum Likelihood (REML) to estimate genetic parameters for carcass traits in rabbits and reported heritabilities of 0.10 for preslaughter weight, 0.08 for hot carcass weight, and 0.01 for pelt and viscera percentage. Ferraz et al. (1991a,b), using least squares and mixed model (sire model) procedures reported genetic parameters for reproductive, growth and carcass traits of rabbits raised in Brasil.

The estimation of genetic trends in populations undergoing selection has been discussed by several authors (Dickerson, 1961; Van Vleck and Henderson, 1961; Smith, 1962) and recently, mixed model methodology has been applied to evaluate those trends (e.g., Sorensen and Kennedy, 1986). Estany et al. (1989) applied mixed model methodology to estimate genetic response to selection for litter size of rabbits.

The objective of this study was to apply mixed model methods, under an animal model, to estimate genetic trends and genetic parameters for an experimental herd of Californian and New Zealand White rabbits raised in a subtropical area of Brasil.

MATERIAL AND METHODS

The two data sets used in this study came from the Rabbit Research Sector of the University of Sao Paulo, campus of Pirassununga, Brasil, located approximately at 22° S and 47° W and 750 m above sea level, where average temperatures range from 15°C in winter up to 30°C in summer. The animals were confined in metal cages in a closed building with lateral openings, where the internal temperatures varied from 18°C to 35°C.

The first data set, used to study the reproduction data, had 1,331 litters (616 from 130 Californian does and 715 from 146 New Zealand White does) born from 1982 to 1990. The second set, used to estimate parameters of growth and carcass traits had 2,882 records for growth traits (1,512 Californian and 1,370 New Zealand White rabbits) and 1,731 records for traits measured at slaughter (908 Californian and 823 New Zealand White animals), for animals born from September of 1988 to December of 1990.

Females were mated, after 130 days of age, at the buck's cage and logged individually. Sire-daughter, full and half sib matings were avoided to reduce inbreeding. Wood nests were provided 27 days after mating. The number and weights of rabbits of each litter were recorded, at parturition, at 21 days of age and at weaning. At 21 days the nests were removed. Weaning age varied from 25 to 42 days of age. Reproductive traits measured and analyzed were litter sizes at birth, total (LSB) and alive (LSBA); at 21 days of age (LS21) and weaning (LSW), stillbirth (STILL), mortality from birth to 21 days of age (MORTB21) and from birth to weaning (MORTBW), gestation length (GESTL) and litter weights at birth (LWTB), 21 days (LWT21) and weaning (LWTW).

At weaning the rabbits were identified by tattooing and their sex and weights recorded. After weaning, the animals were raised with their littermates in metal cages (85 x 95 x 45 cm) having automatic waterers and feeders. A commercial pelleted feed (minimum of 18%

crude protein and 17% fiber), supplemented with 20% of dry matter with green elephant grass or rami was used.

Animals were weighed weekly from weaning to slaughter. The measurements were called individual weights at weaning, 5, 6, 7, 8, 9, 10 and 11 weeks (IWW, IW5, IW6, IW7, IW8, IW9, IW10 and IW11). Slaughter occurred at 87 days as an average. At that time individual weight at slaughter (IWSL), carcass weight (CWT ,warm washed carcass, without head, skin and viscera), viscera weight (VISWT, all the internal organs, including the gastro-intestinal content), head weight (HEADWT, head with ears and head skin, eyes and brain, plus the paws and tail, used in crafts) and skin weight (SKINWT) were measured. Dressing percentage (DRESS%) was defined as the ratio CWT/IWSL.

No selection pressure was applied in the herd from 1982 until 1988, when the criterion for mass selection became IW10. After August of 1988, IW10 was used as the only selection criterion for males and females. The rabbits were weaned in groups of 50 as an average every two weeks, with the group being considered a contemporary group. TABLE 1 presents the number of males and females selected and the average selection differentials applied in actual weight and units of standard deviation, calculated as differences from averages of contemporary groups. Migration occurred in 1984, 1986 and 1987. In CAL, 15.2% of males and 5.4% of females came from other herds, while in NZW those proportions were, respectively 11.3 and 4.1%.

The coefficients of inbreeding for each animal (F), were calculated using an adaptation of DFNRM, part of K. Meyer's DFREML program (Meyer, 1988a,b) using all the pedigree information available, since the herd was founded. Inbreeding coefficients were included, as a covariate, in the animal model as suggested by Kennedy et al. (1988).

The animal models followed the basic linear model:

$y = X\beta + Zu + e$, where:

X = incidence matrix for fixed effects;

β = vector of fixed effects, including covariates. The fixed effects considered, for each trait, are specified in TABLE 2.

Z = incidence matrix for random effects;

u = vector of random effects (animal, litter as a common permanent environment effect and maternal, depending on the model; ;

e = vector of environmental effects, $N(0,\sigma^2_e)$.

Among the four animal models proposed, model 1 included only the animal effect, model 2 included the animal and permanent or common environmental effect of doe (for reproductive traits) or litter (for growth and slaughter traits), model 3 included the additive genetic value of the animal, the maternal genetic value, uncorrelated with the direct genetic value and permanent or common environmental effect (the same used in model 2) and model 4, the same as in model 3, but with correlated animal and maternal genetic effects. Estimates from model 4, the most complete model, were chosen to be reported for both variance components and the breeding values, as that model had the largest logarithm of the likelihood function for the majority of traits.

The mixed model equations under the proposed animal models were used to obtain Restricted Maximum Likelihood (REML) estimates of variance components with the DFREML programs of Meyer (1988a,b, 1989), modified by Boldman & Van Vleck (1991) to use SPARSPAK (George et al., 1980), a sparse matrix solver package.

The genetic parameters estimated were heritability for direct animal genetic value (h^2),

heritability for maternal genetic effects (m^2), correlation between direct and maternal genetic effects (r) and total heritability (Dickerson, 1947, 1970) ($h^2_t = h^2 + .5m^2 + 1.5\ cov(a,m)/\sigma^2_p$), where cov(a,m) is estimate of covariance between direct and maternal genetic effects and σ^2_p is the estimate of phenotypic variance.
The environmental parameter estimated, in addition to σ^2_e was the relative variance of permanent environmental effects for reproductive traits (associated with the dam) or of permanent common environmental effects (associated with the litter) for growth and slaughter traits (c^2)
The software used to set up the mixed model equations, DFREML (Meyer, 1988 a,b) considers all the pedigree information available, since the foundation of the herd, to set up the inverse of the numerator relationship matrix (A^{-1}) . The direct and maternal breeding values for the traits are estimated for all animals, including those without records and base animals, which are evaluated by their relationships with animals with records. Average breeding values per year of birth were plotted to estimate genetic trend. The averages for 1980 and 1981 are for base animals.

RESULTS AND DISCUSSION

TABLE 3 shows the estimates of genetic and environmental parameters. As the actual results to be expected from individual selection for a given trait are affected not only by the fraction of the variance due to an animal's own genes, but also by that due to heritable differences in the dam's direct environmental influence and the interaction between those two inheritances (Dickerson, 1947), h^2_t is the best estimate of heritability as a measure of possible selection response. For reproductive traits, the trait with the larger heritability for direct effects is STILL, but when h^2 and m^2 are pooled in h^2_t, LS21 and LSW have the largest values. So, in terms of litter sizes, the largest genetic progress is expected in LS21 or LSW. As weaning age can vary, LS21 seems to be the most consistent trait that could be used as selection criterion among preweaning litter sizes in this population, not only because of the moderate heritability, but because the correlation between animal effects is high and positive so that with selection for direct effects the maternal effects should change in the same direction. All the other preweaning litter sizes have negative correlations between the animal effects. The estimates for heritabilities for these traits are smaller than the majority of estimates reported (Khalil et al., 1986; Ferraz et al.,1991).
The direct, maternal and total heritabilities estimated for MORTB21 and MORTBW are very low and the correlation (r) is -1.000 for both, indicating that not only almost no genetic progress is expected in this trait but also an antagonism between direct and maternal inheritance. The same can be applied to GESTL.
The preweaning litter weight traits had low heritability, except for LWTW that had an estimate close to 0.2 with a negative estimate for r. As the weights at 21 days and weaning differ by only about 1 week, the difference observed in estimates seems to be too large. The estimate of h^2_t for LS21 is less than that estimated for LWTB, but the value for r is much larger and positive. Although little genetic progress is expected, the most genetic progress would be expected for this trait, among preweaning litter weights.
The estimates for c^2, the proportion of variation due to the permanent environment of the

dam, for the preweaning litter traits are small, generally less than 0.10, except for LS21, where the value is 0.175, indicating also that this maternal effect is not of much importance and is not the main cause of variation.

Estimates of heritabilities for growth traits are from low to moderate so that reasonable genetic progress can be obtained when IW10 or IW11 are adopted as selection criteria. Both traits had estimated values of r very large and positive, so that both traits could be selected for. However, slightly more progress is expected for IW11 than for IW10, due to larger values for h^2 and m^2. If slaughter occurs before the 11th week, IW10 can be a good criteria too. Earlier individual weights do not seem to be good traits for selection due to small estimates of h^2 and h, in agreement with those reported by Khalil et al. (1986) and Ferraz et al. (1991).

The values of c^2 estimated for growth traits, the common permanent environmental effects of littermates, are high, varying from .31 to .50 but decrease as age increases, implying that the litter influence is progressively smaller as the time between the target age and weaning is longer. Small estimates of c^2 for IW10 or IW11 reinforce those traits as selection criteria.

The estimated values of h^2, m^2 and h_t^2 for slaughter traits varied from low to moderate. Selection would not be effective if the selection criterion is VISWT or DRESS%, but approximately equal relative genetic progress could be obtained if selection is based on IWSL or CWT. As carcass weight is not easy to obtain under slaughterhouse conditions and as both r and c^2 values are similar for IWSL and CWT, IWSL seems to be the best trait to select for among slaughter traits. In places where the rabbit skin is important for fur and can make a substantial contribution to the total value, selection for SKINWT can be moderately effective. The values observed for h_t^2 for slaughter traits are similar to those obtained by Lukefahr et al. (1992).

The values of c^2, representing the relative contribution of litter effects to the total phenotypic variance in slaughter traits, are similar to those observed for IW10 and IW11, except for HEADWT and DRESS%. Litter effects explain about 30% of the total variance and have to be considered in a breeding program as an important source of variation.

Further studies using multivariate mixed models under an animal model to estimate the genetic covariances can modify this scenario. The selection criteria should be chosen based not only on values of h^2, m^2, h_t^2, r and c^2, but also on the genetic correlations with other important traits and especially on the relative economic values of the traits.

The genetic trends for direct animal effects, as means of estimated breeding values by year of birth of rabbit for LSB, LSBA, LS21 and LSW are shown in FIGURE 1, for LWTB, LWT21 and LWTW in FIGURE 2 and for IW10, IW11 and IWSL in FIGURE 3. Only those trends are shown because those traits are the most important. The genetic trends for maternal effects could be obtained by this method.

The trends for litter sizes (FIGURE 1) were similar and positive for LSB, LSBA, LS21 and LSW. Litter sizes increased from .15 to .30 rabbits from the foundation of the herd to 1990. That trend could be improved if litter size is the selection criterion. The genetic gain observed showed that genetic progress is possible in any of the measured litter sizes, despite the low heritabilities.

The trends observed for litter weights (FIGURE 2) are positive, but the plot indicates that a plateau may soon be reached.

The genetic gain observed in IW10, the selection criteria from 1988 to 1990, was positive and about 10 g (about .5% of the average). The same was true for IW11, but although the same trend was shown for IWSL, the trend from 1988 to 1991 in this trait was slightly down. The average estimates of breeding values were not regressed on year because the variation in changes from year to year is important not only to evaluate migration that has occurred, but also to monitor effects such as changes in management or disease outbreaks. The methodology used was useful for not only estimating genetic parameters, but in evaluating the breeding program.

CONCLUSIONS

1)The genetic parameters estimated for litter sizes show those traits had low heritability with the largest responses to selection expected in LS21, followed by LSW.
2)MORTB21, MORTBW and GESTL had very low heritabilities and negative estimates of correlation between direct and maternal genetic effects.
3)Heritabilities were small for LWTB and LWT21 and moderate for LWTW, but LWTW had a large negative correlation between direct and maternal genetic effects.
4)The values of c^2 were small for almost all reproductive traits, meaning that the effect of dam is not a main cause of variation, accounting for less than 10% of the phenotypic variation.
5)The genetic parameters estimated indicate largest expected responses to selection for IW10 or IW11, among the growth traits of rabbits.
6)Litter effects can explain from 30 to 50% of the phenotypic variation for growth traits. Those effects are progressively less important as age at measurement increases.
7)Multivariate mixed model estimation of covariances in the future, under an animal model are needed to account for correlated responses and to define the best selection criteria.

ACKOWLEDGEMENTS

-To K. Meyer and K.G. Boldman for the programs;
-To Prefeitura do Campus da USP em Pirassununga, Brasil, where the data came from;
-To University of Nebraska, where the data were analyzed.

REFERENCES

BOLDMAN, K.G. and VAN VLECK, L.D. 1991. Derivative-free Restricted Maximum Likelihood estimation in animal models with a sparse matrix solver. J. Dairy Sci., 74 :(12):4337- 4344.

DICKERSON, G.E. 1947. Composition of hog carcasses as influenced by heritable differences in rate and economy of gain. Ag. Exp. Sta. Iowa State College of Agriculture and Mech. Arts. Res. Bull.354:491-524.

DICKERSON. G.E. 1961. Effectiveness of selection for animal improvement.

In:Germ Plasm Resources, Am. Ass. for the Advanced of Science, Washington.

DICKERSON. G.E. 1970. Research in quantitative animal genetics. In: Techniques and procedures in animal science research, Am.Soc. Anim. Sci., Albany, New York.

ESTANY, J.; BASELGA, M.; BLASCO, A. & CAMACHO, J. 1989. Mixed model methodology for the estimation of genetic response to selection in litter size of rabbits. Livest. Prod. Sci.21 (1):67-75.

FERRAZ, J.B.S.; JOHNSON, R.K. & ELER, J.P. 1991a. Genetic parameters for growth traits of rabbits raised in Brasil. Accepted to publication in J. Appl. Rabbit Res.,paper # 133.

FERRAZ, J.B.S.; JOHNSON, R.K. & ELER, J.P. 1991b. Genetic parameters of reproductive traits of rabbits in Brasil. Accepted to publication in J. Appl. Rabbit Res.,paper # 135.

GEORGE, A.; LIU, J. and Ng., E. 1980. User guide for SPARSPAK : Waterloo sparse linear equations package. CS-78-30, Depto. Computer Science, Univ. of Waterloo, Ontario, Canada.

HENDERSON, C.R. 1988. Theoretical basis and computational methods for a number of different animal models. J.Dairy Sci., 71 (supplement 2):1-16.

KHALIL, M.H.; OWEN, J.B. & AFIFI, E.A. 1986. A review of phenotypic and genetic parameters associated with meat production traits in rabbits. Animal Breeding Abstracts,54(9):725-749.

KENNEDY, B.W., SCHAEFFER, L.R. and SORENSEN, D.A. 1988. Genetic properties of animal models. J.Dairy Sci., 71 (supplement 2):17-26.

LUKEFAHR, S.D. 1988. Progressive genetic applications for improved commercial production efficiency in the rabbit industry.J.Appl. Rabbit Research, 11(3):161-175.

LUKEFAHR, S.D.; VAN VLECK, L.D. & ROBERTS, J.D. 1992. Estimates of components of variance and covariance for carcass traits in rabbits using an animal model. J.Appl. Rabbit Research (in print) , ARD Journal #9728.

MEYER, K. 1988a. DFREML - a set of programs to estimate variance components under an individual animal model. J.Dairy Sci. 71(Suppl.2):33.

MEYER, K. DFREML. 1988b. Programs to estimate variance components for individual animal models by restricted maximum likelihood. User Notes. Edinburgh Univ., Scotland.

MEYER, K. 1989. Estimation of variance components for individual Animal Models. I. Univariate analyses. Genet. Sel. Evol.,21:317-340.

SMITH, C. 1962. Estimation of genetic change in farm livestock using field records. Anim. Prod., 4:239-251.

SORENSEN, D.A. & KENNEDY, B.W. 1986. Analysis of selection experiments using mixed model methodology. J. Anim. Sci., 63:245-258.

VAN VLECK, L.D. & HENDERSON, C.R. 1961. Measurement of genetic trend. J. Dairy Sci., 44:1705-1710.

TABLE 1. Selection differentials for individual weight at 10 weeks (IW10), in grams, of Californian (CAL) and New Zealand White (NZW) rabbits selected from 1988 to 1990.

	CAL			NZW			TOTAL		
SEX	N	IW10	SD	N	IW10	SD	N	IW10	SD
males	16	439.0	1.41	19	429.1	1.34	35	433.6	1.34
females	39	242.1	0.88	49	234.3	0.92	88	237.7	0.91

TABLE 2. Effects considered as fixed for reproductive and growth traits of rabbits raised in a subtropical area of Brasil.

TRAIT	SEX	BREED	YS	PAR	Fdoe	Flit	Frab	LSW	AGEw	AGEs
Reproductive Traits										
LSB, LSBA, STILL, LS21, MORTB21, GESTL, LWTB and LW21		X	X	X	X	X				
LSW, MORTBW and LWTW		X	X	X	X	X			X	
Growth traits										
IWW, IW5, IW6, IW7, IW8, IW9, IW10 and IW11	X	X	X	X			X	X		
Slaughter traits										
all *	X	X	X	X			X	X		X

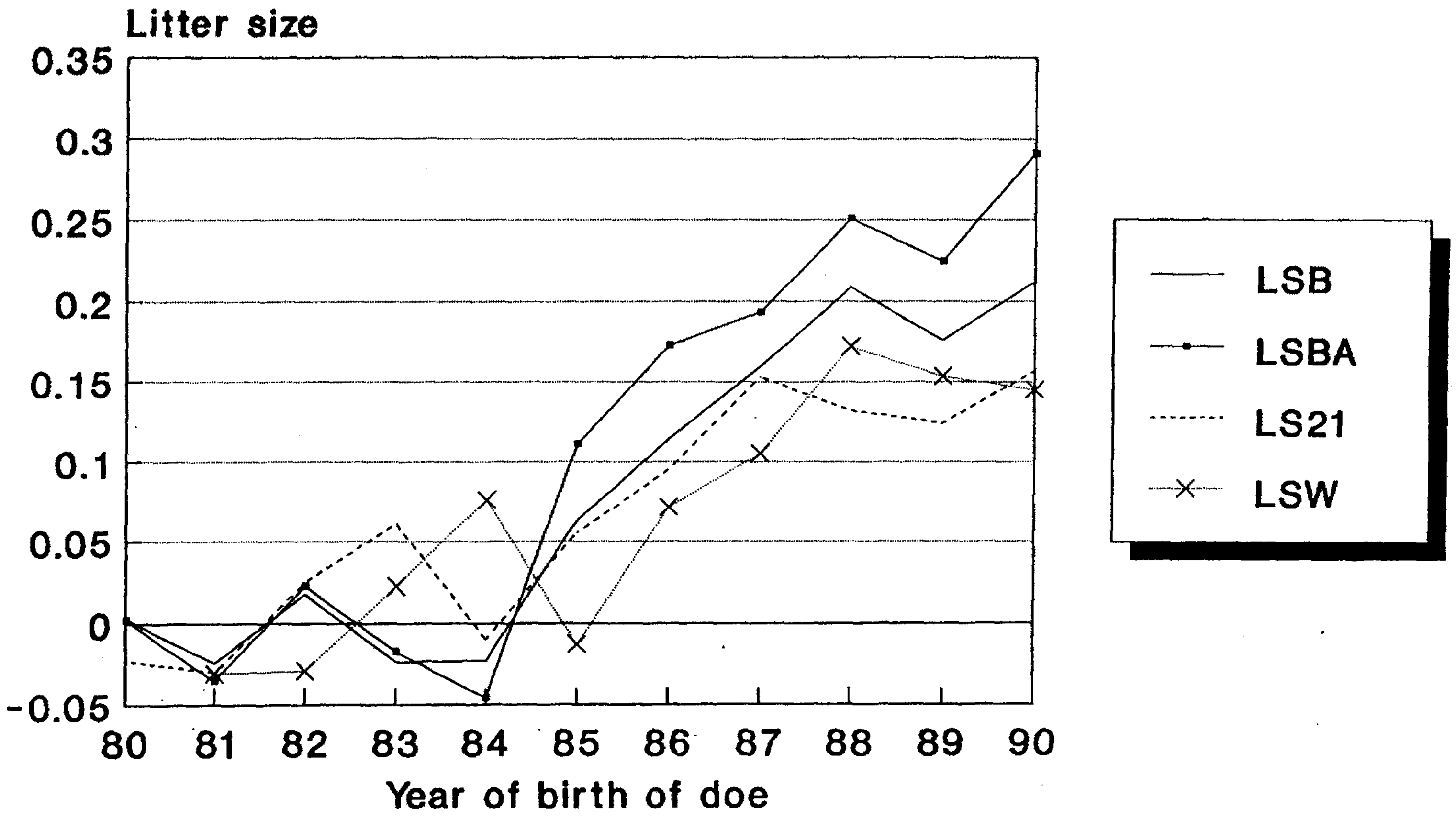
YS= year x season; PAR= parity of doe; Fdoe= inbreeding of doe (linear and quadratic effects); Flit= inbreeding of litter (linear and quadratic effects); Frab= inbreeding of rabbit (linear and quadratic effects); LSW= litter size at weaning (linear and quadratic effects); AGEw= age at weaning (linear effects); AGEs= age at slaughter (linear effects).
LS = litter size; LWT= litter weight; B=birth; BA= birth alive; 21= 21 days of age; W= weaning; STILL = number of stillbirths; MORTB21= mortality from birth to 21 days of age; MORTBW= mortality from birth to weaning; GESTL= gestation length; IW= individual weight; 5,6,.....11= age in weeks;
(*)- IWSL= individual weight at slaughter; CWT= carcass weight; VISWT= viscera weight; HEADWT= head weight; SKINWT= skin weight; DRESS%= dressing percentage.

TABLE 3. Estimates of genetic and environmental parameters under an animal mo
reproductive and growth traits of rabbits raised in a subtropical area of Brasil.

TRAIT	h^2	m^2	h_t^2	r	c^2
Reproductive Traits					
LSB	.054	.020	.045	-.384	.049
LSBA	.063	.035	.060	-.297	.036
STILL	.176	.112	.043	-.898	.007
LS21	.056	.007	.089	1.000	.088
LSW	.139	.008	.101	-.820	.070
MORTB21	.023	.017	.002	-1.000	.090
MORTBW	.002	.010	.001	-1.000	.099
GESTL	.056	.033	.016	-.871	.063
LWTB	.043	.004	.051	.295	.089
LWT21	.001	.048	.035	.999	.175
LWTW	.199	.000	.197	-.975	.015
Growth traits					
IWW	.007	.091	.089	.980	.496
IW5	.003	.055	.051	1.000	.480
IW6	.007	.050	.060	1.000	.416
IW7	.013	.087	.105	1.000	.380
IW8	.043	.168	.026	-.790	.374
IW9	.024	.067	.117	1.000	.365
IW10	.049	.0456	.143	1.000	.307
IW11	.082	.033	.177	.999	.314
Slaughter traits					
IWSL	.042	.039	.121	.999	.343
CWT	.021	.072	.114	.997	.310
VISWT	.007	.037	.026	.040	.316
HEADWT	.159	.008	.166	.064	.229
SKINWT	.081	.011	.130	.993	.383
DRESS%	.002	.076	.026	-.779	.175

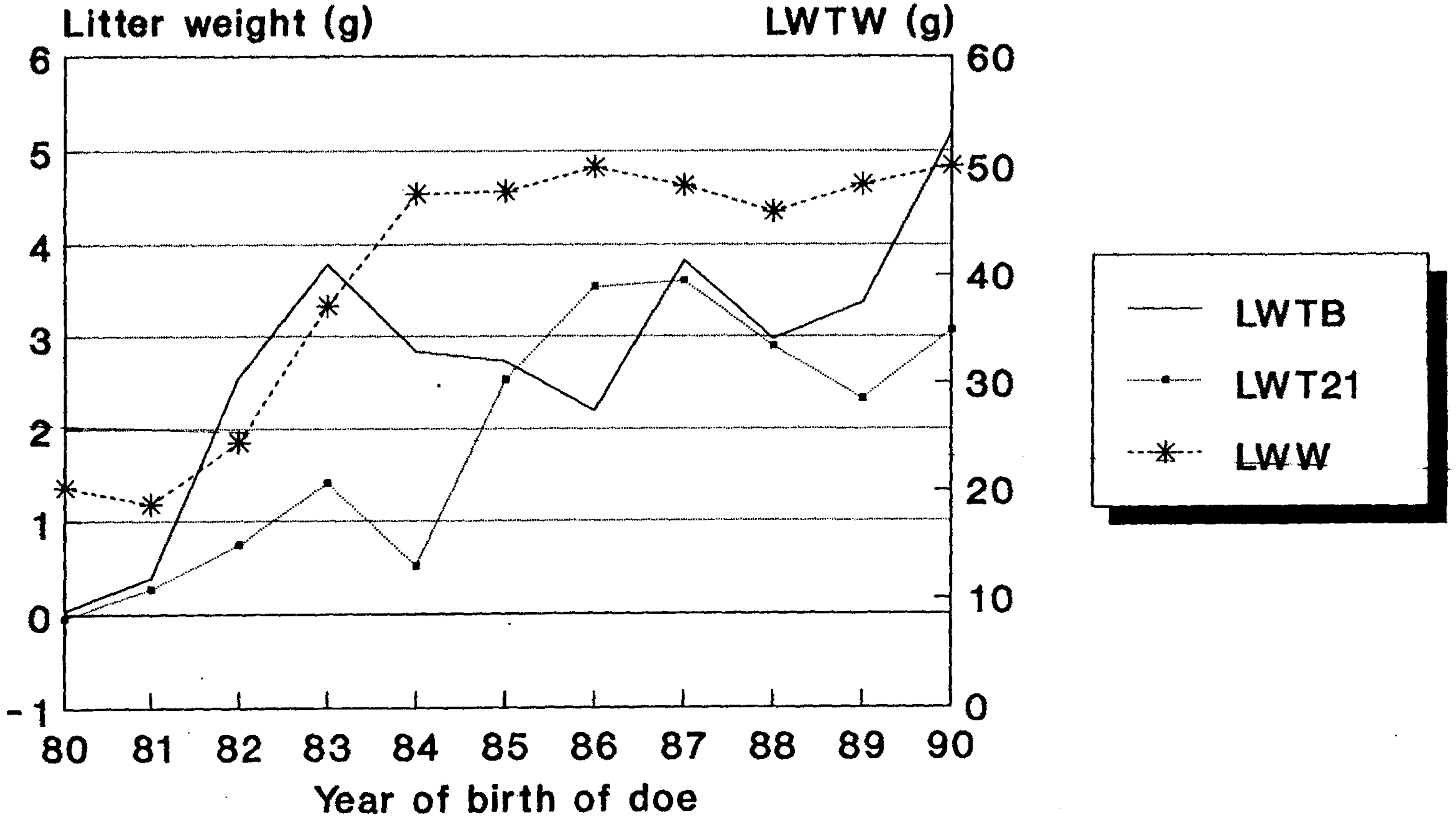
h^2= heritability for direct genetic effects; m^2= heritability for maternal genetic ef
h_t^2= total heritability; r= correlation between animal effects; c^2= perm
environmental effects for reproductive traits (doe x parity) or common perm
environmental effect for growth and slaughter traits (litter effects). LS = litter
LWT= litter weight; B=birth; BA= birth alive; 21= 21 days of age; W= weaning; S
= number of stillbirths; MORTB21= mortality from birth to 21 days of age; MORT
mortality from birth to weaning; GESTL= gestation length; IW= individual weight
..11= age in weeks; SL= at slaughter; CWT= carcass weight; VISWT= viscera w
HEADWT= head weight; SKINWT= skin weight; DRESS%= dressing percentag

FIGURE 1. Genetic trend of LSB, LSBA, LS21 and LSW of Californian and New Zealand White rabbits in subtropics*



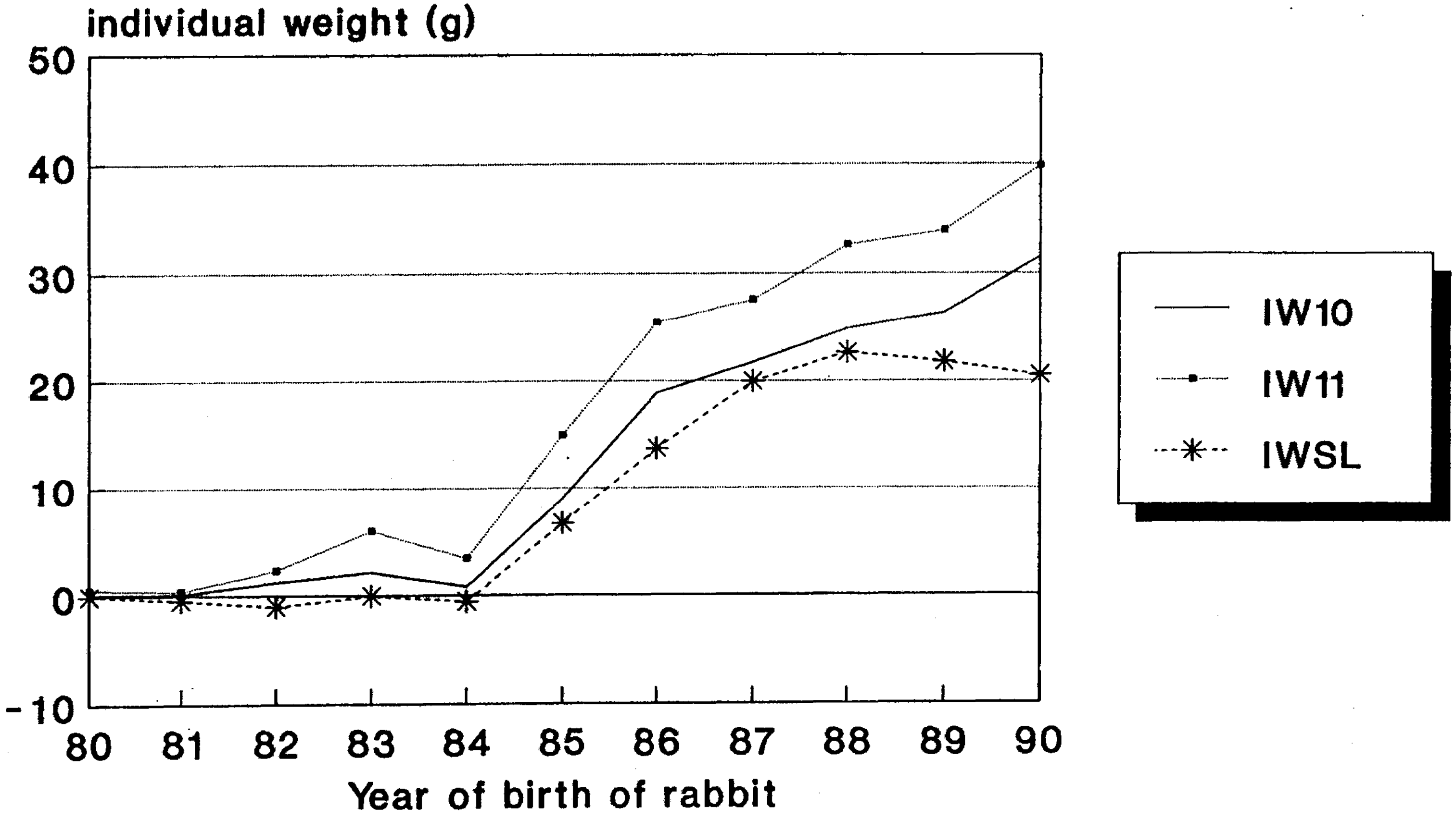
(*)- LS=Litter size; B= birth; BA= birth alive; 21= 21 days of age, W = weaning
Estimated by animal model

FIGURE 2. Genetic trends of LWTB, LWT21 and LWTW of Californian and New Zealand White rabbits raised in subtropics*



(*)-LW=Litter weighT, B= birth; BA=birth alive; 21= 21 days of age, W = weaning
Estimated by animal model

FIGURE 3. Genetic trends of IW10, IW11 and IWSL of Californian and New Zealand White rabbits raised in subtropics*



(*)-IW=rabbit weight, 10, 11 = age in weeks, SL = at slaughter
Estimated by animal model