GENETIC ANALYSIS AND SIRE EVALUATION FOR POSTWEANING GROWTH TRAITS IN THREE LINES OF RABBITS RAISED UNDER INTENSIVE PRODUCTION SYSTEM

By

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ABSTRACT: Data on 15435 of weaned rabbits for three lines (N, Z and G) from 359 sires born between 1987 and 1995 were analyzed to estimate sire transmitting abilities and to evaluate the effect of various genetic and some environmental factors on body weight (at 8, 12 and 16 weeks of age) and daily gain (during the intervals of 8-12, 12-16 and 8-16 weeks). Two methods of Henderson method 3 (MM3) and restricted maximum likelihood (REML) procedure taking into account the relationships among sires, A⁻¹ were compared in estimating variance components and heritability estimates.

Line N was intermediate in growth traits between the lowest line Z and the highest line G. Year and season of birth were the most important non-genetic factors affecting body weight and gain. Parity effect constituted a significant source of variation in most growth traits at different ages. Body weight and daily gain of the rabbits nursed in small-sized litters were the highest until a certain litter size (≤ 4 or 5 for N; ≤ 7 for Z and ≤ 6 for G) and decreased thereafter. Males were significantly heavier and grew more than females in all lines.

REML method caused in general an increase in sire variance and a decrease in error variance. MM3 method gave underestimated heritability because it ignored relationships among sires. Analysis using mixed models, which account

for relationships among sires should therefore give more accurate genetic parameters than MM3 analysis. Heritability estimates were high for most growth traits studied within lines, i.e. selection to improve these traits would be successful. For most postweaning growth traits in the three lines, heritability estimates in line G were the largest, while estimates in line Z were the lowest. In situations where considerable relationship among parents exists in rabbits data, methods of analysis that account for these relationships should be used to obtain unbiased estimates of heritability.

Genetic and phenotypic correlations among body weights at all ages were positive and high. The feasibility of including daily gain from 8 to 12 weeks of age in selection objectives is of considerable importance to improve postweaning growth performance in rabbits.

Sire evaluation using BLUP considering relationships among sires (A⁻¹) was better than BLUP without A⁻¹ because it allowed a fair comparison between bucks.

INTRODUCTION

The genetic potential for improvement of rabbits is dependent largely on heritability of the trait measured and its relationship with other traits of economic importance. Prior to developing any breeding plan, new methodologies are necessary to obtain accurate estimates of genetic parameters. Procedures for estimating genetic parameters of several traits of rabbits have typically involved using Henderson's method 3 mixed model estimators (Khalil et al., 1986). Recently, genetic evaluation of rabbits was most often performed using an animal model, where all relationships among all animals are considered (Lukefahr et al., 1994 and 1996; and McNitt and Lukefahr, 1996), or using reduced animal model, which accounts for relationships among sires and dams (Besbes et al., 1992). Best linear unbiased predictor (BLUP), under methodology of mixed models, is becoming the preferred method of estimation for animal breeders (Henderson, 1988). Restricted maximum likelihood (REML) for estimating variance or covariance components is also becoming the most commonly algorithm used in such estimations.

In rabbits breeding, selection of sires for postweaning growth traits is an important aspect for genetic improvement. Therefore, sire evaluation programs should be used Procedure of best linear unbiased predictor (BLUP) was developed by Henderson (1972), and it was used throughout the world for sire evaluations.

The objectives of this study were (1) to analyze the effect of year of birth, season ,parity, litter size and sex on postweaning growth in three lines of rabbits, (2) to compare the variance component estimates of Henderson's method and restricted maximum likelihood (REML) considering relationship among sires for growth traits, and to evaluate the sire transmitting ability for these traits using two methods of sire evaluation.

MATERIALS AND METHODS

Breeding plan and management:

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Data from three lines of rabbits (N, Z and G) were collected from 15435 weaned rabbits, sired by 359 bucks, born in the nucleus breeding farm ZIKA (Schweizerhof, Untergröningen, Germany) between 1987 and 1995. Line N was originated from New Zealand White breed. Line Z was produced by mating various local German strains, while line G was developed from Giant breed. All these lines were selected for productive and reproductive ability. An account of these lines was reported by El-Raffa (1994).

During the whole period of the investigation, the rabbits were housed in windowed environmentally controlled rabbitry. At weaning (litters were weaned at the mean age of 28 days), the young rabbits were removed from the does' cages, ear tagged and raised in collective cages in groups of 8 members to eight weeks of age and 4 ones afterthat, therefore, the group size effect on growth traits was reduced. Breeding animals and young were fed ad libitum pelleted rabbit rations, in which minimum rate of crude protein was 16 % and maximum rate of crude fibers was 14 %. Water was available continuously. A minimum temperature of 14°C was maintained during the winter (optimum 18°C). The relative humidity was 60 % \pm 10 %. Brood spectrum fluorescent bulbs were used to provide 14 hours light per day, 4 watt/m². Manure was collected in deep pits and removed twice a week in winter and three times a week in summer.

Data and statistical analyses:

Individual rabbits were weighed at 8, 12 and 16 weeks of age. Daily gain was also computed for each rabbit at intervals of 8-12, 12-16 and 8-16 weeks of age. Data of the growth traits (individual body weights and daily gains) for N, Z and G lines of rabbits were analyzed separately using Henderson's method 3 mixed model estimators (MM3), (Henderson, 1984) as described by Harvey's LSMLMW (1990) program.

The data set of Z and G lines was analyzed using the following sire model:

$$Y_{ijklmno} = \mu + s_i + KY_j + KS_k + P_l + LS_m + SX_n + e_{ijklmno}$$

where $Y_{ijklmno}$ = the observation on the ijklmnoth rabbit; U = overall mean; s_i = random effect of i^{th} sire; KY_j and KS_k = fixed effect of j^{th} year and k^{th} season of birth, respectively; P_1 = fixed effect of l^{th} parity; LS_m = fixed effect of m^{th} litter size at birth; SX_n = fixed effect of n^{th} sex and $e_{ijklmno}$ = random error.

Due to partial confounding between sires and year of birth in line N (i.e. most of sires were used only for one year, sires were treated as nested effect within year), data were analyzed using the following nested sire model:

$$Y_{ijklmno} = \mu + KY_i + s_{ij} + KS_k + P_l + LS_m + SX_n + e_{ijklmno}$$

where KY_i = fixed effect of i^{th} year of birth and s_{ij} = random effect of j^{th} sire nested to i^{th} year of birth. The other effects were similar to those presented in the previous model.

Due to missing numbers in some subclasses, the interactions between the fixed effects were not fitted in the models of analysis. For growth traits including 16 weeks of age, data were recorded only on males, so sex effect was excluded from the models.

Estimates of variance components for the growth traits were computed with Harvey's (1990) LSMLMW program. Henderson's method 3 (MM3) and Restricted Maximum Likelihood (REML) taking the relationship among sires into consideration (A⁻¹) were used for estimating variance components of random effects. Estimates of covariance components were only computed using MM3 method. Heritability and correlation estimates were obtained from sire component of variance and covariance. Standard errors for the heritability and

correlation estimated by Henderson method were calculated by the methods of Tallis (1959) and Swiger et al. (1964) as described by Harvey (1990), while those estimated for heritability using REML was calculated approximately by the formula given by Becker (1984).

Sire transmitting abilities (STA):

Two methods described below were used for estimating sire transmitting abilities for postweaning growth traits:

1-Best linear unbiased predictor (BLUP) using restricted maximum likelihood (REML) procedure with sires relationship coefficient matrix (A⁻¹). In this method, REML was used for estimating variance components to be used in estimation of BLUP. In this case, the mixed-model equations of Henderson were used to obtain best linear unbiased predictor (BLUP) of the random effects, best linear unbiased estimators (BLUE) of the fixed effects and minimum normal quadratic unbiased estimators (MINQUE) of the variance components. In this situation, the random effects may be correlated and Henderson's mixed model in matrix notation was:

$$y = X\beta + Zs + e$$

where y = vector of observations; X and Z = known incidence matrices for fixed and random effects, respectively; $\beta = unknown$ column vector of fixed effects; s = unknown column vector of random effects of sires, and e = a column vector of random error. The mixed model equations used were:

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + k A^{-1} \end{bmatrix} \begin{vmatrix} \hat{\beta} \\ \hat{s} \end{vmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

where $k = \sigma_e^2/\sigma_s^2$ estimated by REML procedure and A^{-1} = the inverse of the numerator relationship sire matrix. The minimum variance normal quadratic unbiased estimates (MINQUE) of sires (σ_s^2) and error (σ_e^2) variance components as described by Henderson (1984) were calculated using LSMLMW program of Harvey (Harvey, 1990). Searle (1989) found that iterative MINQUE estimators were equal to REML estimators and therefore, σ_s^2 and σ_e^2 were obtained as REML estimators.

2-Best linear unbiased predictor (BLUP) procedure without sires relationship coefficient matrix (A⁻¹). In this method, one set of crossclassified non-interacting random effects (sire) was absorbed (Harvey, 1990). Accordingly, BLUP estimates for random sire effects absorbed by maximum likelihood were obtained. BLUP procedures were used to evaluate directly the sires from records of their progeny according to the previous models used in the present study with regard to the sire as a random effect. This procedure account for heritability, number of progeny, genetic trend and differences in levels of herdmate sires (Freeman, 1988). The solution of mixed model equations in simplified form was:

where I = Identity matrix, and $k = \sigma^2 e/\sigma^2$ s and solution to s, was called BLUP predictor of s.

RESULTS AND DISCUSSION

Means and variation

For each separate line, means, standard deviations and percentages of variation (V%) of growth traits (postweaning body weights and weight daily gains) are presented in Table 1. Mean body weight of line N ranged from 1613 g at 8 weeks of age to 3715 g at 16 weeks of age which was intermediate between the lightest line Z and the heaviest line G. The same trend was observed for daily gain. Percentages of V for daily gain in all lines were high, which mean that improvement of weight gain in rabbits through phenotypic selection is quite possible. For most growth traits, V% for body weights decreased in value as the rabbit advanced in age. Reviewed estimates of V% (Khalil et al., 1987; Afifi and Emara, 1990; Khalil et al., 1993 and Afifi et al., 1994) showed a general trend indicating that variations of postweaning weights in growth of a certain breed of rabbits decreased with advancing of age.

Non-genetic effects

Year and season of birth. Across all lines, year and season of birth effects were significant for most growth traits studied (i.e. body weight and daily gain). Year and season of birth were the most important non-genetic factors affecting postweaning body weights and gains. An evidence for such considerable year and season effect was given by Khalil et al (1987), Ferraz et al. (1991), Baselga et al. (1992), Afifi et al. (1994), Ayyat et al. (1995) and De Paula et al. (1996). Postweaning growth performance of rabbits born during autumn were generally higher than those born during the other seasons (Tables 2, 3, 4). This may be can be explained by mild temperatures when animals are growing.

Parity. Parity effect constituted a significant source of variation in most growth traits at different ages. Lines had different behaviour in growth traits from parity to parity and no consistent pattern was observed (Tables 2, 3 and 4). These changes with parity are mostly a reflection of the efficiency of the dam as a mother (especially those associated with the sustained ability of the lactating dam to suckle her young until weaning). Khalil et al. (1993) reported that postweaning body weight increased with advance of parity until certain parity and decreased thereafter. On the other hand, mothering ability increases with advance of parity until a certain age, then remains constant for a period and decreases thereafter due to aging (Emara, 1982).

Litter size. For all lines studied, figures of F-ratios obtained in ANOVA reveal that litter size at birth contributed significantly to the variance of body weights at 8 and 12 weeks of age and 8-12 weeks daily gain (Tables 2, 3 and 4). Therefore, litter size at birth was one of the most non-genetic maternal factors influencing postweaning growth performance of these lines. Szendro et al. (1996) reported a negative relationship between litter size and body weight in every age category (3, 6, 10 and 12 weeks). Opposite to data of both sexes, litter size at birth had a little effect on 16-week body weight in males. In addition, it had no effect on 12-16 weeks daily gain. Body weight and daily gain of the rabbits nursed in small-sized litters were the highest until a certain litter size (\leq 4 or 5 for N; \leq 7 for Z and \leq 6 for G) and decreased thereafter. Khalil et al. (1987) attributed the decrease of body weight with the increase of litter size at birth to the fact that each dam has a limited capacity for providing her young

with nourishment during pre- and post-natal growth until weaning and accordingly the share of each young decreases and results in light weights. The continuation of the same trend of carry over effect of litter size as a maternal factor on body weight, at a decreasing rate, up to 12 weeks of ages may be due to the fact that the maternal effects do not disappear rapidly after weaning and to the high positive association that exists between body weights at weaning and successive ages, i.e. part-whole relationship.

Sex. Males were significantly heavier and grew more than females in all lines (Tables 2, 3 and 4). These results are in contrast with those reported by many investigators (Mgheni and Christensen, 1985; Afifi and Emara, 1991; Ferraz et al., 1991; Lukefahr et al., 1992; McNitt and Lukefahr, 1993). They noted that, no sex effect was detected on body weight or weight gain during the postweaning period. In this respect, El-Raffa (1994) suggested that the significant differences obtained between sexes in these lines could chiefly be attributed to a bias due to the effect of selection, as only small numbers of tested males were chosen when compared with the number of tested females. Thus, the chance to select and improve body weight is better in males than in females. He also concluded that, although these differences were statistically significant, the biological importance is questionable.

Variance components and heritability estimates

Table 5 presents variance components and heritabilities estimated from Henderson method 3 (MM3) and restricted maximum likelihood (REML) procedure with sires relationship coefficient matrix (A-1) for postweaning body weights and daily gains at different ages by line. For most growth traits studied, heritability estimates observed in line G were the largest. In addition, heritability estimates of line N were higher than those in line Z. One explanation may be that line G has had only a short history of selection. The estimates of heritability for growth traits within lines show some marked effects of age (Table 5). Heritability estimates of body weight for N and G lines increased with age. In contrast, for line Z, these estimates decreased by advancing of rabbit age. Except for line G, heritability estimates of daily gain at earlier stage (8-12 weeks) were high, while they were low at later one (12-16 weeks). In this respect, the average of the reviewed estimates for heritability for body weight at different ages were generally higher at younger ages (8 weeks) than at older ages (Mostageer et al., 1970; Niedzwiadek, 1978 and Khalil et al., 1987).

The more precise ratio of variances (σ^2/σ^2) for the growth traits in the three lines indicated that two third of these ratio estimates of the REML method considering relationships among sires were lower than those for the MM3 method (Table 5). It may be concluded that REML considering A caused an increase in sire variance and a decrease in error variance Twelve heritability estimates from sixteen calculated for growth traits across all lines were found to be of higher values when REML considering the relationships of sires was applied than when using MM3. These results mean that MM3 method gave underestimates of heritability because it ignores relationships among sires Similar conclusion was reported by Van der Werf and de Boer (1990) It seems clear that genetic parameters estimates obtained under animal model where all relationships among all animals are considered would be most accurate (Henderson, 1984). Analysis under mixed models, which account for relationships among sires should therefore give more accurate genetic parameters than MM3 analysis.

The higher heritability estimates of the growth traits obtained in the present study than those reported in the literature could be explained by a large amount of genetic variability in the populations, the high standard of hygiene and the uniformity of the environment (El-Raffa, 1994).

In conclusion, heritability estimates were high for most growth traits studied within lines. This suggests that selection to improve these traits would be successful. In situations where a considerable relationship among parents exists such as in poultry data, method of analysis that account for these relationships should be used to obtain unbiased estimates of heritability

Correlations

All phenotypic correlations among body weights at 8, 12 and 16 weeks of age for N, Z and G rabbits were positive and highly significant (Table 6). Genetic correlations between body weight traits were, in general, high and positive. Both estimates of phenotypic and genetic correlation averaged 52. Most estimates of the genetic correlation among daily gain traits were high and positive (Table 6). In addition, the phenotypic correlations between 8-16 weeks daily gain and each of daily gain at 8-12 and 12-16 weeks of age were positive and highly significant. The reverse trend was observed for the phenotypic correlations between daily gain at 8-12 and 12-16 weeks of age Estimates of

phenotypic and genetic correlations obtained in the present study fall within the range of literature (e.g. Mostageer et al., 1970; Khalil et al., 1987; El-Maghawry, 1990 and Khalil et al., 1993). In practice, high and positive estimates of phenotypic correlation in the present and reviewed studies among body weight or daily gain traits at different ages give a considerable advantage for rabbit breeders in management and culling decisions. Moreover, the high genetic correlations obtained here and those reviewed in the literature (Khalil et al., 1993), gives an encouragement for rabbit breeders to improve body weight and gain of their breeds at later ages (i.e. at marketing age) through early selection at younger ages.

Regarding the correlations among body weights and daily gains at different ages (Table 6), it was clear that genetic correlations between body weight at 8 weeks of age and 8-12 weeks daily gain were lower than the corresponding correlations between body weight at 12 weeks of age and daily gain in the same period. In this respect, Randi and Scossiroli (1980) and Szendro et al. (1988) concluded that body weight at younger age gives no reliable information about weight gain at older age. Based on the genetic correlation estimates obtained in the present study, selection for increasing daily gain from 8-12 weeks would be expected to result in an increase of body weight at 12 weeks of age. Also, selection for increasing 12-16 weeks daily gain is expected to increase body weight at 16 weeks of age. These findings might indicate the feasibility of including daily gain from 8-12 weeks of age in selection objectives is to improve postweaning growth performance in rabbits.

The magnitude and signs of the unexpected correlations obtained in the present study may be due to the sampling errors. In this respect, Khalil et al. (1986) concluded that bias in genetic correlation estimates may be due to a lack of appropriate correction factors for possible environmental influences and selection.

Estimates of sire transmitting ability (STA)

Sire transmitting ability (STA) estimates were obtained by the procedures of best linear unbiased predictor (BLUP) using restricted maximum likelihood (REML) in estimation of variance components and taking into account relationships among sires (A⁻¹) and BLUP without A⁻¹. Considering all sires, the minimum and maximum estimates of STA for N, Z and G rabbits are presented

in Table 7. The difference (and the mean differences) between minimum and maximum values of STA for both methods of sire evaluation are also illustrated in Table 7. For BLUP using REML with A-1 and BLUP without A-1 in N rabbits, there was a difference being 267 and 312 g for 8-week body weight, respectively. The same trend of the difference between the two evaluation methods was also observed for 12-week body weight (341 and 424 g), 16-week body weight (304 and 691 g), 8-12 week daily gain (17.1 and 19.8 g), 12-16 weeks daily gain (.7 and 4.4 g) and 8-16 weeks daily gain (4.0 and 10.2 g). The difference in estimates of STA for the growth traits of N rabbit were intermediate between lowest estimates for Z rabbits and the highest estimates for G rabbits. For all growth traits across all lines, the largest differences were obtained by BLUP without A-1, while the lowest differences were observed by BLUP with A-1 (Table 7).

Considering the first top 30 to 40 sires for N, Z and G rabbits, it was noticed that the differences between maximum and minimum in STA were smaller than that when considering all sires (Table 7). For all growth traits, the lowest differences in STA of the top sires were recorded by BLUP with A⁻¹. In contrast, the largest estimates were recorded by BLUP without A⁻¹.

Figures given in Table 8 show that percent of sires that are common (CS %) between BLUP with A⁻¹ and BLUP without A⁻¹ for all growth traits ranged from 87 to 97, 80 to 98, and 88 to 98 % in N, Z and G rabbits, respectively. The same top sires in BLUP with A⁻¹ are found in BLUP without A⁻¹. The percentages of sires remaining in the same position (i.e. don't changing their rank) ranged from 7 to 23, from zero to 13 and from 3 to 28 % for N, Z and G rabbits, respectively (Table 8). These results mean that the overall ranking of sires changed much between both methods of sire evaluation.

The criteria for judging the merits of different methods of sire evaluation are the standard errors (SE) of each method (Henderson, 1974 and Raheja, 1992). Estimates of SE for both sire evaluation methods are presented in Table 9. For all growth traits, BLUP with A-1 had the lowest estimates of SE. Including A-1 in BLUP using REML would increase the accuracy of STA estimates (through reduction of predicted error variance) than BLUP without A-1 (Henderson, 1975).

In conclusion, the accuracy in estimating variance components by REML procedure and consequently the more precise ratio of variance (σ^2/σ^2_s) and also adding the relationship coefficient matrix of sires (A⁻¹) created great differences between estimates of STA for the two sire evaluation methods. Therefore, BLUP using REML with A⁻¹ should be used to evaluate sires because it allows a fair comparison between bucks. Sire evaluation is being used extensively in dairy, beef and swine breeding work but little in rabbits. In situation where artificial insemination has been introduced in modern rabbitries, mainly to improve management of rabbitry and the actual development of it dramatically reduces the amount of terminal sires needed in a farm, thus they would be specially selected and cared.

Table 1: Means, standard deviations (SD) and percentages of variation (V %) of postweaning growth traits in the three lines of rabbits.

Trait		Lin	e N			Liz	ne Z			Line	G	
	no.	Mean	SD	V %	80.	Mean	SD	V %	no.	Mean	SD	V %
Body weight (g) :												
8-week	6300	1613	235	12.3	4955	1575	191	10.7	4180	1732	267	12.9
12-week	6300	2615	282	8.9	4955	2394	229	8.8	4180	2856	320	8.8
16-week	390	3715	299	6.9	852	3091	213	6.7	1104	4090	311	6.0
Daily gain (g):			E 81		22	1.000		15				
8-12 weeks	6300	35.8	8.2	19.5	4955	29.3	7.0	22.1	4180	40.2	9.5	19.7
12-16 weeks	390	31.7	7.2	20.5	852	22.5	6.7	28.3	1104	36.6	7.8	18.7
8-16 weeks	390	35.4	5.0	12.7	852	26.3	4.2	15.1	1104	39.9	5.2	10.8

Table 2: Least-squares means, g (LSM), standars errors (SE) and test of significance

of factors affecting growth traits in the line N of rabbits.

OI	racto	rs affe	cting	grow	in tra	its ii	i the i	ine i	NOIR	about				
Independent			В	ody weig	ht (g)						Daily g			
variable		8 weeks		12 wee			16 weeks		8-1 wee		12- wee		8- we	
=	No.	LSM	SE	LSM	SE	No.	LSM	SE	LSM	SE	LSM	SE	LSM	SE
General mean	6300	1697	20	2731	23	390	3730	24	36.9	.8	32.5	.5	35.9	.4
Year of birth significance		***		**			***		8.0				81	,
1987	189	1591	53	2673	60	28	3670	89	38.6	2.2	33.1	1.6	37.0	1.5
1988	603	1756	34	2691	39	35	3984	60	33.4	1.4	36.5	1.3	38.6	1.1
1989	1111	1715	26	2725	29	47	3772	49	36.0	1.0	31.9	1.1	34.5	.9
1990	1374	1705	26	2805	29	68	3748	43	39.3	1.1	31.1	.9	35.5	.7
1991	644	1694	26	2722	30	44	3709	52	36.7	1.1	32.4	1.1	34.4	.9
1992	685	1697	28	2835	31	62	3661	55	40.6	1.1	28.8	1.1	34.9	.9
1993	864	1656	27	2653	31	47	3677	56	35.6	1.1	33.7	1.2	36.3	.9
1994	605	1617	28	2647	32	59	3622	49	36.8	1.2	32.4	1.0	36.2	.9
1995	225	1838	34	2831	39				35.5	1.4	5-6-13 RAPS		1.02.02	
Season of birth														
significance		***		**			n.s.		**		n.		n	.S.
Winter	1741	1685	22	2699	25	93	3795	59	36.2	.9	34.0	1.5	36.8	1.0
Spring	1253	1643	22	2655	25	79	3730	58	36.1	.9	34.3	1.5	36.5	1.0
Summer	1387	1731	21	2770	24	84	3658	48	37.1	.9	30.1	1.2	35.0	.8
Autumn	1919	1726	22	2800	25	134	3738	50	38.4	.9	31.6	1.2	35.4	.9
Parity		***			i i									
significance			41	***			*				*			
1	1330	1602	21	2643	23	22	3638	68	37.2	.8	28.7	1.7	35.0	1.2
2	1672	1699	20	2738	23	71	3780	45	37.1	.8	34.1	1.1	37.5	.8
3	1080	1703	21	2740	24	66	3640	45	37.0	.8	30.2	1.1	34.6	.8
4	811	1674	21	2718	24	71	3649	43	37.3	.9	30.7	1.1	34.6	.8
5	596	1693	21	2749	24	66	3783	46	37.7	.9	33.9	1.1	36.9	.8
6	461	1720	22	2735	25	47	3742	50	36.2	.9	33.1	1.2	36.0	.9
7	169	1712	26	2725	30	25	3800	68	36.1	1.0	34.9	1.7	36.9	1.2
8	141	1725	27	2788	31	22	3809	75	38.0	1.0	34.2	1.9	35.8	1.3
9	40	1740	39	2745	46				35.9	1.4				
Litter size	1	***					110040-							
significance ≤3	115	1767	28	2835	33	1	n.s.		38.1	1.1	n.	5.	n.	S.
4	150	1775	27	2795	31	1			36.4	1.0				
5	211	1722	25	2802	29				38.6	.9			1	
6	408	1710	23	2748	26	1			37.0	.9				
7	636	1714	22	2752	25	15	3695	85	37.1	.9	33.5	2.2	35.7	16
8	787	1689	21	2728	24	36	3768	57	37.1	.9	31.0	1.4	36.2	1.5
9	984	1691	21	2701	24	97	3720	40	36.1	.9	32.8	.9	34.9	
10	1085	1680	21	2719	24	96	3752	40	37.1	.9	32.1	.9	35.9	.7
11	740	1655	21	2668	24	57	3689	47	36.2	.9	100000000000000000000000000000000000000		34.8	.7
12	536	1670	22	2695	25	41	3678	54	36.6	.9	30.4	1.2		.8
13	389	1619	23	2671	26	27	3776	68	37.6	.9	32.7	1.3	35.5	.9
14	259	1666	24	2662	27	21	3763	75	35.5	.9	33.4	1.7	37.5 36.9	1.2
Sex	233	1000	24	2002	21	41	3703	13	33.3	,3	33.9	1.9	30.9	1.3
significance	200	1761	22	2042					70.6					
Male	390	1761	22 20	2842	25				38.6	.9				
Female	5910	1633	20	2620	22				35.3	.8				

* ≤ .05

** < .01

*** ≤ .001

n.s. > .05

Table 3: Least-squares means, g (LSM), standars errors (SE) and test of significance of factors affecting growth traits in the line Z of rabbits.

Independent			В	ody weig	ht (g)			•			Daily ga	in (g)		
variable		8 weeks		12 week			16 weeks		8-1 wes		12-1 wee		8-1 wee	
	No.	LSM	SE	LSM	SE	No.	LSM	SE	LSM	SE	LSM	SE	LSM	SE
General mean	4955	1602	12	2428	13	852	3091	14	29.6	.5	22.4	.4	26.0	.3
Year of birth	-											_		
significance		***		88			n.s.		**		n.s	* C.		
1988	560	1699	43	2437	53	67	3216	131	26.5	1.7	22.5	3.9	25.5	2.5
1989	756	1580	36	2346	44	115	2875	140	27.4	1.4	16.5	4.3	20.9	2.6
1990	576	1558	28	2375	34	97	3009	93	29.1	1.1	22.7	2.8	25.4	1.1
1991	765	1587	29	2488	35	125	3286	110	32.1	1.1	27.8	3.4	31.2	2.
1992	947	1627	27	2458	32	190	3128	95	29.7	1.0	21.9	2.9	26.6	1.
1993	593	1589	23	2411	28	117	3122	68	29.5	.9	25.4	2.1	26.7	1
1994	420	1510	24	2428	29	80	3082	63	32.9	.9	22.8	1.9	27.0	1
1995	338	1662	29	2482	36	61	3012	81	29.5	1.1	19.2	2.5	24.5	1.
Season of birth significance				••			n.s.		n	.s.	n.s	L	n	
Winter	1101	1598	13	2418	16	185	3115	26	29.3	.5	23.1	.8	26.4	
Spring	1371	1576	13	2411	15	248	3062	22	29.9	.5	21.9	.7	26.5	9
Summer	1127	1599	13	2421	15	220	3092	23	29.4	.5	22.4	.7	25.8	
Autumn	1356	1633	14	2463	16	199	3096	28	29.7	.5	22.0	.8	25.3	
Parity significance		***				Γ	n.s.				n.		, n	.s.
1	236	1581	17	2391	20	40	3094	41	28.9	.7	23.2	1.2	25.9	
2	382	1633	15	2433	18	53	3104	36	28.6	.6	22.5	1.1	25.1	
3	259	1608	16	2459	19	56	3120	35	30.5	.6	23.5	1.1	26.5	
4	3358	1598	13	2433	15	561	3080	21	29.9	.5	21.9	.6	26.0	- 0
5	393	1613	15	2444	17	71	3073	31	29.7	.6	20.7	.9	25.9	- 1
6	327	1576	15	2410	18	71	3077	31	29.8	.6	22.3	.9	26.6	
Litter size		***							Τ.	10	n.			
≤5	314	1631	15	2438	18	21	3032	51	28.9	.6	20.4	1.6	24.6	
6	336	1633	15	2481	18	36	3158	39	30.3	.6	22.8	1.2	27.1	
7	715	1640	13	2459	15	95	3134	26	29.3	.5	24.2	.8	27.0	
8	869	1588	13	2409	15	169	3063	21	29.4	.5	22.0	.6	25.6	
9	976	1582	13	2399	15	198	3113	20	29.2	.5	22.8	.6	26.1	
10	839	1587	13	2412	15	165	3105	22	29.5	.5	23.3	.7	26.4	
11	495	1588	14	2413	16	82	3086	28	29.5	.5	21.9	.8	25.7	14
12	411	1563	14	2416	17	86	3041	27	30.5	.6	21.4	.8	25.5	
Sex	-			1	-	1			1				1	_
significance					8	1				88				
	860	1636	13	2477	15	1			30.1	.5	1		1	
Male	1 000													

Table 4: Least-squares means, g (LSM), standars errors (SE) and test of significance of factors affecting growth traits in the line G of rabbits.

Independent	lacto	rs affe	-	lody weig		ш	LIC II	псс	10116	10016	Daily ga	in (g)		
variable		8		12			16		8-	12	12-1		8-1	16
		weeks		weel	ks		weeks		Wa	eks	wee	ks	we	des
	No.	LSM	SE	LSM	SE	No.	LSM	SE	LSM	SE	LSM	SE	LSM	SE
General mean	4180	1773	14	2909	15	1104	4058	19	40.6	.6	37.0	.5	40.7	.4
Year of birth						_								
significance		***		n.s			n.s.		81		n.s		n.	
1988	666	1639	116	2900	130	184	3710	243	45.5	4.1	44.7	6.9	43.7	4.4
1989	322	1630	84	2697	94	97	3649	186	38.4	2.9	36.2	5.2	42.7	3.3
1990	262	1707	68	2943	75	64	4153	127	44.1	2.3	41.9	3.6	45.1	2.3
1991	389	1758	48	2923	53	111	4287	103	41.6	1.7	38.1	2.9	40.9	1.9
1992	570	1742	47	2929	52	216	4322	111	42.4	1.7	37.1	3.2	41.8	2.0
1993	821	1867	61	2962	68	193	4203	148	39.0	2.1	31.3	4.2	35.9	2.7
1994	793	1787	66	2984	74	239	4081	182	42.7	2.4	29.7	5.2	34.8	3.3
1995	357	2057	77	2928	86				30.9	2.7				
Season of birth		1000												
significance	1	***	- 1	***		200	***			•	**	3		
Winter	909	1757	19	2904	21	241	4079	35	41.0	.8	38.3	1.1	41.6	.7
Spring	1105	1704	17	2806	19	246	3916	32	39.4	.7	34.2	.9	39.4	.6
Summer	988	1793	17	2947	19	282	4064	30	41.2	.7	36.3	.8	40.8	.6
Autumn	1178	1837	18	2976	20	335	4173	33	40.7	.7	39.2	.9	41.0	.6
Parity		***												
significance	1	1.1.2.20		n.s			n.s.							
1	1056	1745	15	2901	16	180	4052	27	41.3	.6	36.9	.8	41.3	.5
2	1164	1756	15	2900	16	364	4058	23	40.9	.6	37.9	.6	41.3	.4
3	760	1794	16	2919	17	220	4092	25	40.2	.7	37.5	.7	40.8	.5
5	532	1810	17	2927	18	157	4074	28	39.9	.7	36.8	.8	40.2	.5
	668	1760	16	2894	17	183	4014	27	40.5	.7	35.9	.8	39.9	.5
Litter size significance		***		***							n.i	L.		B::
\$3	302	1785	19	2934	21	67	4087	39	41.0	.8	35.9	1.1	40.7	.7
4	193	1812	21	2989	23	61	4082	39	42.0	.8	36.5	1.1	41.9	. 7
5	296	1821	19	2984	21	88	4101	34	41.6	.8	35.5	.9	40.9	.6
6	295	1809	19	2940	21	88	4125	34	40.4	.8	39.0	.9	41.8	.6
7	454	1767	17	2887	19	108	4083	32	40.1	.7	38.3	.9	40.8	.6
8	518	1768	17	2910	18	166	4046	28	40.8	.7	36.8	.8	40.2	.5
9	559	1749	17	2876	18	140	4073	29	40.3	.7	38.1	.8	41.4	.5
10	614	1759	16	2906	18	171	4078	28	41.0	.7	37.4	.8	41.2	.5
11	436	1743	18	2881	19	91	4025	33	40.7	.7	36.6	.9	39.9	.6
12	291	1734	20	2837	21	72	3950	37	39.4	.8	36.6	1.1	39.9	.7
13	222	1756	21	2846	23	52	3987	43	38.9	.8	36.4	1.2	39.2	.8
Sex														
significance				***					•					
Male	1104	1848	15	3038	16				42.5	.6				
Female	3076	1698	14	2778	14				38.6	.6				

* ≤ .05

****** ≤ .01

100. ≥ ***

n.s. > .05

Table 5: Variance components (o2) and heritability (h2) testimates from Henderson's Method 3 and restricted maximum likelihood (REML considering relationship among sires, A1) for growth traits by line.

Traid	Method			Line N				Line Z			_	Line G	
		n,2	0,3	n,2/n,2	h,2 ± SE	٥,٢	9.3	a, 1/a, 1	σ _e ² σ _e ² /σ _e ² h _e ² ±SE	η., ₁	O. 2	σ_e^2/σ_o^2	h,2 ± SE
Body													
weights:						7							
8-week	ммз	5232	43753	8.36	.43 ± .05	3761	29455	7.83	.45 ± .06	9413	52849	5.61	.61 ± .07
	REML with (A-1)	4683	44862	9.58	.38±.05	4557	29503	6.47	.54 ± .06	13442	52982	3.94	.81 ± .09
12-week	MM3	6718	59534	8.86	.41 ± .05	4633	45375	9.79	.37 ± .05	10352	66008	6.38	.54 ± .07
	REML with (A-1)	6783	60406	8.91	.40 ± .05	5058	45477	8.99	.40 ± .05 15361	15361	66204	4.31	.75 ± .08
16-week	MM3	9943	66046	6.64	.52 ± .23	1568	43332	27.64	.14 ± .09	15686	60061	3.83	.83 ± .13
	REML with (A'1)	8692	67139	7.72	.46 ± .20	1631	43303	26.54	.15 ± .09	19390	61394	3.16	.96±.13
Daily											-		
gains :													
8-12 weeks	ммз	9.3	51.9	5.58	.61 ± .07	5.3	42.7	8.06	.45 ± .06	17.7	64.1	3.62	.86±.09
	REML with (A'1)	1.01	53.3	5.27	.64±.08	6.9	42.8	6.20	.55 ± .07	25.6	64.2	2.51	<u>></u>
12-16 weeks	ММЗ	Ξ	44.5	40.45	.09 ± .22	.9	40.0	44.44	.09 ± .09	11.3	47.9	4.24	.76 ± .12
	REML with (A'1)	۵	45.0	75.00	.05 ± .17	òo	40.1	50.13	.07 ± .08	13.6	48.9	3.59	.87 ± .12
8-16 weeks	MM3	2.9	20.9	7.21	.48 ± .23	1.4	15.3	10.93	.34±.11	5.9	19.2	3.25	.94 ± .13
	REML with (A'1)	2.9	20.8	7.17	.50 ± .20	1.2	13.6	13.00	.29 ± .10	7.2	19.6	2.72	<u>×</u>

 σ_s^2 and σ_e^2 = Components of sire and error variances, respectively. $h_s^2 = h^2$ estimated from sire component.

Table 6 Genetic correlations with standard errors (below diagonal) and phenotypic correlations (above diagonal) estimated by Henderson's Method between the postweaning growth traits in the three lines.

Line	8-Week weight	12-Week weight	16-Week weight	8-12 weeks daily gain	12-16 weeks daily gain	8-16 weeks daily gain
Line N						
8-week body weight		.59**	.39**	32**	15*	35**
12-week body weight	.39 ± .08		.73**	.57**	17**	.32**
16-week body weight	.49 ± .23	.96 ± .09		.46**	.53**	.71**
8-12 weeks daily gain	47 ± .08	.63 ± .06	.78 ± .21		05	.71**
12-16 weeks daily gain	21	58 ± .98	32 ± .61	.35 ± .82		.65**
8-16 weeks daily gain	41 ± .38	.34 ± .25	.59 ± .21	.94 ± .12	.63 ± .49	
Line Z						
8-week body weight		.56**	.27**	29**	.00	45**
12-week body weight	.50 ± .08		.55**	.63**	17**	.23**
16-week body weight	.18 ± .29	.79 ± .23		.21**	.73**	.73**
8-12 weeks daily gain	42 ± .09	.57 ± .07	.38 ± .32		15**	.63**
12-16 weeks daily gain	49 ± .44	28 ± .54	.36 ± .53	.37 ± .50		.68**
8-16 weeks daily gain	81 ± .29	03 ± .27	.44 ± .26	.94 ± .09	.66 ± .27	
Line G						
8-week body weight		.54**	.43**	39**	05	46**
12-week body weight	.29 ± .09		.65**	.55**	26**	.15**
16-week body weight	.39 ± .11	.68 ± .08		.21**	.56**	.60**
8-12 weeks daily gain	57 ± .08	.62 ± .07	.18±.12		21**	.65**
12-16 weeks daily gain	.12 ± .13	20 ± .14	.59 ± .09	27 ± .12		.59**
8-16 weeks daily gain	53± .13	.29 ± .12	.57 ± .09	.75 ± .05	.43 ± .11	34,000

^{* ≤ .05}

^{** ≤ .01}

Table 7: Minimum and maximum values for sire transmitting ability estimated by best linear unbiased predictor in the three lines (BLUP) considering relationship of sires (A1) and BLUP without A1 for postweaning growth traits

Trait and method			Line N	Z				Line Z	Z				Line G		
		والا	All sircs*		Top 30 sires***		≧	All sires		Top 40		<u>A</u>	All sires		Top 40
	Min.	Max.	Diff.	Mean	Diff:	Min.	Max.	Diff.	Mean	Diff.	Min.	Max.	Diff.	Mean	Diff.
				diff.**					diff.					diff.	0.11
8-week weight															
BLUP with A ⁻¹	-117	150	267	2.6	117	-142	Ξ	253	1.9	33	-261	212	473	37	174
'BLUP without A'	-145	167	312	3.0	126	-139	149	308	2.4	110	-271	239	513	4 5	108
12-week weight															
BLUP with A ⁻¹	-154	187	341	3.3	143	-140	140	280	2.2	113	-228	260	488	20	209
BLUP without A'	-187	237	424	4.1	194	-172	210	382	2.9	173	-247	255	502	3.9	215
16-week weight															
BLUP with A.1	-170	134	304	3.0	106	49	50	99	06	43	-292	250	542	4	182
BLUP without A'	-310	381	691	6.8	309	-96	148	244	1.9	133	-326	241	567	4.5	186
8-12 weeks daily gain															
BLUP with A'	-7.9	9.2	17.1	.17	7.9	-3.9	7.6	11.5	.09	6.7	-9.6	11.7	213	17	0
BLUP without A.1	-9.5	10.3	19.8	.19	8.7	4.7	10.7	15.4	.12	9.3	-9.7	11.2	20.9	16	9
12-16 weeks daily gain												l		1	
BLUP with A.1	ů	4	.7	.01	į,	7	1.0	1.7	.01	.9	<u></u>	71	152	12	5.7
BLUP without A.1	-1.9	2.5	4.4	.04	2.0	-1.8	2.6	4.4	.04	2.3	-10.7	7.4	18.1	- i	60
8-16 weeks daily gain														1	1
BLUP with A.1	-1.9	2.1	4.0	.04	.8	-1.4	1.9	3.3	.03	1.6	-5.4	4.6	100	08	3 7
BLUP without A'1	4.7	5.5	10.2	.10	4.4	-2.9	4.2	7.1	.06	3.5	-5.7	4.4	10.1	08	ب ا -

Numbers of sires used for evaluation were 101-103 sires for N line, 120-128 sires for Z line and 126-128 sires for G line.

Mean = difference value divided by number of sires.
 The selected ratio of sires was approximately 30 %.

Table 8: Percentages of common sires (CS %) and remaining in the same position (RS %) in BLUP without considering relationship among sires (A⁻¹) compared with BLUP considering A⁻¹ for postweaning growth traits by line.

Trait	Lin	e N	Lit	ne Z	Lin	e G
	CS %	RS %	CS %	RS %	CS %	RS %
8-week weight	90	23	98	5	95	8
12-week weight	90	20	93	5	88	10
16-week weight	90	13	80	13	90	15
8-12 weeks daily gain	97	17	95	8	98	28
12-16 weeks daily gain	93	10	80 -	10	88	3
8-16 weeks daily gain	87	7	83	0	88	3

Table 9: Standard error of each method of sire evaluation for growth traits by line.

Trait	Li	ne N	L	ine Z	Li	ne G
	BLUP with A-1	BLUP without A ⁻¹	BLUP with A ⁻¹	BLUP without A ⁻¹	BLUP with A-1	BLUP without A ⁻¹
8-week weight	5.6	6.8	4.9	6.2	8.1	8.5
12-week weight	6.9	8.6	5.1	6.8	8.8	9.2
16-week weight	4.8	13.2	1.7	3.9	8.8	9.3
8-12 weeks daily gain	.27	.32	.18	.23	.38	.39
12-16 weeks daily gain	.02	.09	.03	.08	.23	.25
8-16 weeks daily gain	.09	.23	.05	.13	.18	.19

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الملخص العربي

التحليل الوراثي وتقييم الأباء لصفات النمو بعد الفطام في ثلاثة خطوط من الأراتب المرباة تحت ظروف الإنتاج المكثف

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استخدمت بيانات ١٥٤٣٥ أرنب مفطوم من ثلاث خطوط (N. Z. G) ناتجة من ١٩٩٥ أب ومولودة في الفترة ما بين سنة ١٩٩٥ ، ١٩٩٥ في مزرعة إنتاج أنوية السلالات (ZIKA) بألمانيا وذلك لتقدير المقدرة التمريرية للأباء وكذلك تقييم تأثير العوامل الوراثية والبيئية المختلفة على وزن الجسم عند عمر ٨، ١٦، ١٦ أسبوع وكذلك الزيادة اليومية في الوزن خلال الفترات ١٦-١، ١٦-١، ١٦-١، أسبوع. تم مقارنة مكونات التباين وقيم المكافئ الوراثي المقدرة بطريقة 3 Henderson بتلك المقدرة بطريقة معظمة الاحتمال المقيدة مع الأخذ في الإعتبار مقلوب مصفوفة معامل القرابة (٨٠) لصفات النمو بعد الفطام. وقد أظهرت النتائج ما يلي :

كان الخط N متوسط في صفات نموه بين أقل الخطوط (Z) وأعلى الخطوط (G). كانت سنة وموسم الولادة من أهم العوامل الغير الوراثية المؤثرة على وزن الجسم و الزيادة اليومية. كذلك كان ترتيب الولادة مصدرا معنويا للختلاف في معظم صفات

النمو عند أعمار مختلفة. كانت أوزان الجسم و الزيادة اليومية في الوزن للأرانب المولودة في بطون ذات أعداد صغيرة الأثقل حتى عدد معين (حتى 3-0 أرانب للخط N ، V للخط 2 ، 3 للخط 3) ثم قلت بعد ذلك. كما كانت الذكور أتقل معنويا وأسرع في النمو عن الاناث في كل الخطوط.

أوضحت الدراسة أن طريقة REML أدت بصورة عامة الى زيادة فى التباين الأبوى وانخفاض فى تباين الخطأ العشوائى، لذلك قللت طريقة Henderson 3 من قيم المكافئ الوراثى لأنها تجاهلت علاقات القرابة بين الآباء ولهذا فإن التحليل بإستخدام REML والذى يأخذ فى الإعتبار مقلوب مصفوفة القرابة بين الأباء أعطت تقديرات وراثية غير متحيزة وأكثر دقة من طريقة Henderson كانت معظم قيم المكافئ الوراثى لصفات النمو عالية فى كل الخطوط والذى يوضح إمكانية إستخدام الإنتخاب لتحسين هذه الصفات. لمعظم صفات النمو بعد الفطام فى الخطوط الثلاثة، سجل الخط 6 أعلى قيم للمكافئ الوراثى بينما سجل الخط 2 أقل القيم على الرغم أنها كانت قيم معتدله أو عالية.

كانت قيم الإرتباطات الوراثية والمظهرية بين أوزان الجسم عند كل الأعمار موجبة وعالية. كذلك إستخدام صفة الزيادة اليومية في الوزن عند عمر $\Lambda-1$ أسبوع في الإنتخاب يمكن أن يحسن صفات النمو في الأرانب.

تقييم الأباء من خلال تقدير االقيمة التمريرية بواسطة طريقة أحسن التقديرات الخطية الغير متحيزه مع الأخذ في الإعتبار A-1 كانت أفضل من طريقة أحسن التقديرات الخطية الغير متحيزه بدون إستخدام A-1 لأنها تسمح بمقارنة عادلة بين الآباء.