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GENETIC AND PHENOTYPIC RESPONSES ON WOOL PRODUCTION AND FLEECE COMPONENTS IN TWO DIVERGENT LINES SELECTED FOR TOTAL FLEECE WEIGHT IN ANGORA RABBITS

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This paper described a divergent selection experiment for total fleece weight in the French Angora rabbit breed. A high line and a low line were made up in 1993 with 80 females and 10 males each one. From 1994, the renewal after selection was composed each year of 36 females and 5 males, alive at the second harvest in each line. The last experimental year on 2001, 80 females and 20 males in each line were procreated. The selection criterion was the total fleece weight of the does for 3rd and latter harvests but different other wool production traits and fleece components were recorded at each harvest. The aim of this paper was to describe the production traits which have been recorded and the genetic and phenotypic trends observed between the two divergent lines. Genetic values and genetic parameters were estimated with a BLUP applied to an animal model. Heritability of total fleece weight was 0.29. After eight years of a divergent selection experiment, a difference of 3.1 genetic standard deviations on total fleece weight was observed between the two lines. In response to selection, a positive difference of 3.0, 0.7, 0.6 and 0.9 genetic standard deviation were observed for weight of long-angora jarreux quality (WAJ1 with many bristles), weight of long-angora woolly quality (WAW1 with a few bristles), fleece homogeneity and bristle length respectively. No correlated response was observed on down length while negative differences of 0.9, 0.9, 1.1 and 0.4 genetic standard deviations were observed on lock structure, compression and resilience and live bodyweight respectively. Other fleece components such as fibre diameter, proportion of each fibre type and hair follicle

density remain to be determined in this experiment. Such measurements will give more information about the evolution of the structure and the composition of the fleece in response to selection for total fleece weight.

Key words: Angora rabbit, divergent selection, total fleece weight, correlated response, fleece components.

ANALYSIS OF REPRODUCTIVE PERFORMANCES DURING THE FORMATION OF A RABBIT SYNTHETIC STRAIN

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From 1995, a rabbit synthetic strain (called '2666') was formed at INRA for zootechnical purposes by crossing the '2066' strain from INRA and the 'V' strain from the Polytechnical University of Valencia (Spain). The evolution of some reproductive traits and body weight at palpation of the '2666' does was studied from the F1 (first generation cross) to the F4 generation, in comparison with the 'V' does. Furthermore, this evolution was interpreted in terms of Dickerson's crossbreeding parameters. The base strains did not differ significantly for any of the studied traits, either globally or in their direct and maternal genetic value. F1 does exhibited significant individual heterosis for body weight (5.5% of the parental average), pregnancy rate (13.3%), total born (18.3%), born alive (24.4%) and weaned (21.0%) per litter born. Concerning body weight, a significant crossbred superiority over the 'V' line was retained in the F2 but not thereafter. The rate of pregnancy showed no longer crossbred advantage from the F2 on. Concerning litter size traits, the benefit of crossbreeding was maintained until the F4, with however a lower magnitude than in the F1. Body weight and pregnancy rate exhibited maternal heterosis, while litter size did not. Direct epistatic losses were significant for body weight, tended to significance for pregnancy rate but did not affect litter size.

Key words: rabbit, reproduction, synthetic strain, heterosis.

CONSTRUCTION OF AN INTEGRATED GENETIC AND CYTOGENETIC MAP IN THE RABBIT

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Rabbit is an important species for meat and fur in French agriculture as well as a valuable animal model for biomedical research. Since genomic data are still rudimentary in this species, the French National Institute for Agronomic Research (INRA) has launched in 2001 a project to map the rabbit genome. The aim is to produce a genetic map with microsatellite markers distributed every 10 to 20 cM along the

genome and simultaneously to establish the corresponding cytogenetic map to provide the chromosomal position of all the genetic markers. These data will constitute an integrated genetic and cytogenetic map of the rabbit, which should be available in 2004. As demonstrated in other domestic species, this first generation map should help to identify economic traits and contribute to further applications such as marker-assisted selection.

Key words: genetic map, microsatellite, genome, cytogenetic map

STABILITY OF TRANSGENE TRANSMISSION IN THREE GENERATIONS OF TRANSGENIC RABBITS AFTER SINGLE OR DOUBLE PRONUCLEAR MICROINJECTION

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Several problems are commonly encountered with the production of transgenic rabbits: a low pregnancy rate, small litter size, cannibalism, mosaic founders incapable of germ-line transmission, a low transgene transmission rate and uncontrolled expression. One of the requirements for creating lines of transgenic animals creation is stable transgene transmission to offspring. In the present study, we demonstrate the transmission of the heterologous gene mouse WAP-human FVIII into F_1 and F_2 generations. Transgenic founder rabbits were generated by microinjection into a single pronucleus (single microinjection, SM) or into both pronuclei (double microinjection, DM). The rabbits were apparently normal and mating of founders with non-transgenic rabbits yielded litters of normal size (8 ± 0.40). PCR and Southern-blots demonstrated integration of the WAP-hFVIII gene in 35% or 44% of the SM or DM F_1 generation, respectively. Stability of transgene transmission to the F_2 generation was also confirmed (44% or 43%, resp.). Transgenic males and females from F_1 generation were bred to obtain homozygous animals. 73% and 77% of SM and DM offspring tested positive for the transgene. The number of copies integrated into the genome was estimated by Southern blot analysis. Both founders had one copy of the gene, which was transmitted to their transgenic offspring. Our results confirm successful integration and stable germ-line transmission of the WAP-hFVIII hybrid gene in both SM and DM lines and in three rabbit generations. This also indicates that double microinjection does not have any deleterious effects on transgene transgene integration and transmission in rabbits.

Key words: transgenic rabbit, human Factor VIII, transgene integration, transmission

HERITABILITY OF RESISTANCE TO BACTERIAL INFECTION IN COMMERCIAL MEAT RABBIT POPULATIONS

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This study was undertaken to determine if routine observational comments on commercial rabbits, including disease incidence, could be used to identify genetic variation for bacterial infection. In two populations heritability for the infection trait (incidence of bacterial infection) was low but significantly different from zero (0.044±0.010 and 0.034±0.006), when the measurement was treated as a continuous variable. Using threshold models the heritability was higher, in the range of 0.14 to 0.37. The incidence of infection in the populations was 7% (rabbits scored at 10 weeks of age) and 4% (rabbits scored at 9 weeks of age), respectively. There appears to be no significant maternal genetic component for the disease trait. Liveweight was heritable in the two populations (0.180±0.034 and 0.159±0.020, respectively) and showed a significant maternal genetic effect (0.1). The genetic correlation between disease incidence and liveweight was low (-0.13) and could only be estimated in one group. Further studies investigating different statistical approaches are warranted and further work is required to refine the scoring system used and define the optimum age of measurement.

HETEROSIS, DIRECT AND MATERNAL GENETIC EFFECTS ON SEMEN QUALITY TRAITS OF RABBITS

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A complete diallel cross involving two rabbit sire lines (C and R) was carried out to estimate the crossbreeding genetic parameters (direct additive genetic effects, maternal genetic effects and heterosis) of seminal traits. The analysis concerned 2140 ejaculates from 153 males from the 4 groups of bucks. The recorded trait were: pH, ejaculate volume (V), mass motility (Mm), individual motility (Mi), concentration (Cn), total number of spermatozoa per ejaculate (TSE), percentage of sperm viability (Vi), percentage of sperm with acrosome integrity (NAR), percentage of sperm normalcy (Nr), percentage of sperm morphological abnormalities of head (H), neck-midpiece (Nm) and tail (T) and presence of proximal and distal cytoplasmic droplet (Dp, Dd). Estimates of heterosis, direct additive genetic and maternal effects on seminal traits of the lines were obtained from the solutions of the corresponding mixed model by generalized least squares. Main genetic relationships between individuals were taken into account. Differences in direct genetic effects between lines were significative for Cn, TSE, Vi, NAR, Nm and Dp. Those differences were eminent (about

50% of the crude mean) and favourable to line C for Cn and TSE, and unfavourables for Nm and Dp. Differences in Vi and NAR were favourable to line R but lower in magnitude (about 10%). It seems that line C could be superior in traits related with semen production and inferior in semen quality traits. Differences between lines in the maternal genetic effects were observed for V and Cn at the level of signification of 5%. These differences were eminent (14%) and favourable to line C for V and eminent and favourable to line R for Cn (40%). Favourable and significant individual heterosis was observed in pH and Dp at the level of signification of 5%. Heterosis effect was high for Dp (35%) and negligible for pH (1.6%).

Key words: semen, heterosis, direct genetic effects, maternal effects, rabbit

CAN WE SELECT ON WITHIN LITTER HOMOGENEITY FOR RABBIT BIRTH WEIGHT? A DIVERGENT SELECTION EXPERIMENT

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A divergent selection experiment based on homogeneity of birth weight was carried out at the INRA experimental farm of Auzeville. The two lines have been created by selecting breeding does and bucks from the female strain AGP22 bred at the Grimaud Frères Sélection company. This involved a new model incorporating a genotypic value for the mean and a genotypic value for the residual variance. There was a favourable selection response with a difference in residual variance and in within-litter standard deviation of birth weight between the lines in the first two generations of selection. The mortality of kits at birth was significantly lower in the "homogeneous" line (low variability of birth weight), but total number born was lower in this line. The number born alive in the homogeneous line was higher in the first generation but lower in the second one. The selection on the homogeneity of birth weight had no significant influence on other traits

Key words: rabbit, canalisation, birth weight, divergent selection

NEW ZEALAND WHITE RABBITS' BLUP VALUES FOR POST-WEANING INDIVIDUAL BODY WEIGHT UNDER EGYPTIAN CONDITIONS

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Genetic parameters of New Zealand White (NZW) growth traits were estimated, using Multi-Trait Derivative-Free Restricted Maximum Likelihood (DFREML). A total of 962 Individual live body weight at 5 (W5), 8 (W8) and 10 (W10) weeks of age were considered for the evaluation. The animal model analysis included parity (P), sex (S) and year season (YrS) as fixed effects as well as animals and common litter as random effects. Heritabilities of considered body weights were somewhat moderate being 0.23, 0.36 and 0.38 for W5, W8 and W10, respectively. Common litter effects were low

but 10 times higher for weights at earlier ages W5 and W8 (0.007) than that for later ones W10 (0.0007). The ranges for the top 30 % ranked sires were 63 g., 48 g., and 62 g. for W5, W8 and W10, respectively. However, it were 71 g., 57 g. and 70 g. for the top 30 % ranked dams. The product moment correlation coefficient concerning sire breeding value and the spearman correlation coefficient concerning ranks of sire breeding value was lower for coefficients between 5 and 8 weeks compared with the higher and significant ones between 8 and 10 weeks of age. The accuracies ($r_{a\hat{a}}$) of minimum and maximum estimates of predicted breeding vale (PBV) were mostly higher in W8 (71 to 73%) than W5 (60 to 68%) and W10 (58 to 68%).

Key words: breeding values, heritability, correlation

generation had about 80 females and 20 males. Results of the first and second generation of selection were analysed using Bayesian methods. Marginal posterior distributions of all unknowns were estimated by using Gibbs Sampling. Heritabilities of Ovulation rate (OR), number of implanted embryos (IE) and litter size (LS) were 0.50, 0.28 and 0.08 respectively. Genetic correlations between OR and IE and between OR and LS were 0.86 and 0.65 respectively. Response to selection for OR in both generations of selection was 0.97 ova. Correlated response in IE and LS were 0.79 and 0.32 respectively. These results have wide high posterior density intervals, and should be considered as preliminary results. If results are confirmed in further generations, selection for ovulation rate might be an alternative to improve litter size.

Key words: selection, ovulation rate, Bayesian analysis, litter size.

SELECTION FOR OVULATION RATE IN RABBITS. PRELIMINARY RESULTS

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An experiment of selection for ovulation rate was carried out. Animals were derived from a synthetic line first selected for litter size for 12 generations, then for uterine capacity for 11 generations, and then 5 generations in which selection was relaxed. Selection was based on the phenotypic value of ovulation rate with a selection pressure on does of a 30%. Males were selected from litters of does with the highest ovulation rate. Males were selected within sire families in order to reduce inbreeding. Ovulation rate was measured in the second gestation by a laparoscopy, 12 days after mating. Each

GENETIC ANALYSIS FOR MILK YIELD AND COMPONENTS AND MILK CONVERSION RATIO IN CROSSING OF SAUDI RABBITS WITH V-LINE

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Four-year crossbreeding project involving Spanish maternal line called V-line (V) and Saudi Gabali (G) rabbits was carried out to produce six genetic groups of V, G, ½V½G, ½G½V, ¾V¼G and ¾G¼V. Interse matings for genetic groups of ½V½G, ½G½V, ¾V¼G and ¾G¼V were also practiced. Milk yields (MY) at intervals of 0-7 days (MY7), 7-21

days (MY21), 21-28 days (MY28), and 0-28 days (TMY) and milk components (MC) at 14 days of lactation (fat, protein, lactose, ash, and total solids), and milk conversion ratio (kg of litter gain per kg of milk suckled, MCR) were evaluated for 2540 litters of 854 does fathered by 142 sires and mothered by 351 dams. A repeatability animal model was used to estimate linear contrasts and expectations of solutions for the effect of doe genetic groups and to derive the estimate of direct (G^I) and maternal (G^M) additive effects, direct heterosis (H^I), maternal heterosis (H^M) and direct recombination effect (R^I) for different traits under the study. Heritabilities for MY traits and MCR were moderate and ranging from 0.18 to 0.27, while they were low or moderate and ranging from 0.09 to 0.28 for MC. The positive estimates of G^I for MY (5.8-12.6%) and MC (4.0-17.7%) and the negative estimate for MCR (-18.3%) were significantly high and in favour of V-line does. G^M were in favour of V-line dams; being 222 g, 0.67%, 0.63%, and −0.08 for MY21, total solids in milk, fat in milk, and MCR, respectively. All estimates of H^I for MY and MC were positive and most of them were significant ranging from 9.7 to 22.7 % for MY traits (P<0.05–0.001) and 3.2 to 15.8% for MC traits (P<0.05–0.01). Similar to the trend of H^I, the estimates of H^M for MY and MC were positively moderate and ranging from 7.4 to 15.2 % for MY traits and 1.9 to 8.3% for MC. The moderate and negative estimate of heterosis for MCR (−19.2% for H^I and −9.6% for H^M) was also favourable. The ranges in percentages of reduction in direct heterosis were negligible and ranging from 2.2 to 4.4% for MY traits and MCR and -3.4 to −9.6% for MC.

Key words: Crossbreeding, milk yield and components, milk conversion ratio, Animal model.

SELECTION FOR FEED EFFICIENCY IN RABBIT

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A short divergent selection experiment was carried out on residual feed consumption. One step of selection was performed on young male rabbits from a heavy weight line. They were individually caged and measured for weight gain and feed consumption between weaning (30 days) and 65 days of age. The fatness of all the males was estimated by ToBEC measurement at 65 days of age. Their offspring were bred under the same conditions and 120 males were slaughtered at 65 days of age for estimating the correlated response on carcass traits: dressing yield, cutting parts, fatness, ultimate pH and colour. The heritability value estimated for residual feed efficiency was 0.45±0.11, which was of the same order as heritability estimated for average daily gain (0.41±0.13) and higher than heritability estimated for feed conversion ratio (0.27). Residual feed consumption was negatively correlated with hind part percentage (-0.71) and correlated positively with fore part percentage (0.54). The genetic correlations with dressing percentage and carcass fatness were very low. No significant phenotypic differences were found between offspring of high residual feed consumption and low residual feed consumption males, except for hind part percentage which was higher in the low residual feed consumption line.

SEQUENCE VARIATION IN THE RABBIT MAJOR HISTOCOMPATIBILITY COMPLEX *DQA* GENE

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The major histocompatibility complex (*MHC*) genes, especially class II genes, are correlated with the ability of disease resistance and some economic traits in most vertebrates. In this study, we sequenced exon 2 of rabbit *MHC DQA* gene, *RLA-DQA*, in 20 animals raised in China. Sixty-one polymorphisms were observed and 18 haplotypes were defined. Aligning these haplotypes and seven sequences from GenBank, 70 nucleotide polymorphic sites were identified and 24 haplotypes were obtained. Among the 70 polymorphisms, there were 32 transitions, including 20 A/G and 12 C/T, and 32 transversions. At the remaining six polymorphic sites, at least three kinds of nucleotides were observed. On average, *RLA-DQA* exon 2 was composed of 28.1%A, 25.9%T, 23.2%G, and 22.8%C. Among the 24 haplotypes, 41 amino acid (AA) polymorphisms were observed. The rate of nonsynonymous substitution was higher than that of synonymous substitution ($P<0.05$), which means *RLA-DQA* may undergo positive selection. Overall, *RLA-DQA* has a very high degree of polymorphism not only at the nucleotide level, but also at the AA level. Further studies are needed to discover whether these polymorphisms can be used as genetic markers for association studies in the future.

CROSSBREEDING EFFECTS ON CARCASS TRAITS AT 12 WEEKS OF AGE IN PANNON AND DANISH WHITE RABBITS AND THEIR RECIPROCAL CROSSES

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Carcass traits of 105 growing rabbits, which consists of 57 straightbred and 48 crossbred, produced from two purebreds (Pannon White, PW and Danish White, DW) as well as their reciprocal crosses were compared. The experiment was carried out at the rabbit farm of the University of Kaposvar. The aim of the study was to evaluate the crossbreeding effects (i.e. direct, maternal additive and heterotic effect) for carcass traits of rabbits slaughtered at 12 weeks of age. Dressing out percentage based on the ratio of hot carcass (with head, liver, kidneys, heart, lungs, perirenal fat) weight to live weight after 24-hour fasting of PW, DW, PW x DW and DW x PW were: 58.0, 55.9, 58.5 and 57.5%, respectively. Tests of significance revealed that breed group (BG) and sex (S) had no effect on the majority of the carcass traits except on slaughter weight

(P<0.01). No significant differences were found in BG x S interaction for all traits. Breed of sire (SB) and dam (DB) had no influence on all carcass traits investigated except that for SB on the percentage of the head. However, SB x DB had significant effect only on the perirenal fat (P<0.05). Direct heterosis was significant (P<0.05) for perirenal fat, which was negatively signed. Direct and maternal additive effects were almost insignificant on carcass traits disregarding direct additive effect on the percentage of gastrointestinal tract and the head and on dressing out percentage (in favour of PW; P<0.05); as well as the maternal effect (P<0.05) on (kidneys + heart + lungs) in favor of DW. Examining crossbreeding results it could be recommended that the offspring of PW bucks and DW does the dressing out percentage and the total edible parts improved, while the percentage of perirenal and scapular fat decreased compared to purebred rabbits.

Key words: Rabbits, carcass traits, heterosis, direct and maternal additive effect.

BODY MEASUREMENTS AND ITS COEFFICIENT OF CORRELATION WITH THE PERFORMANCE INDEX OF SEXED RABBITS SLAUGHTERED AT DIFFERENT AGES

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Body measurements are important to estimate carcass and body weight. One hundred New Zealand White rabbits were used, fifty males and fifty females. They were slaughtered at 75 and 90 days of age. The experimental design was the randomized blocks in a factorial arrangement 2 x 2, with four treatments and five replications. Both, commercial diet and water, were given *ad libitum*. At 75 and 90 days of age, the animals were weighed and body weight, feed intake and feed: gain ratio were obtained. The body measurements evaluated were: body length and chest, abdominal and thigh circumferences. After a 12 hours fasting the animals were slaughtered and carcasses were also weighed. No differences for body measurements were obtained with respect to sex but slaughter age affected thigh circumference (P<0.001). Body length was negatively correlated (P<0.04) with daily weight gain. Thigh circumference was positively correlated with body weight (P<0.003), daily feed consumption (P<0.003), feed: gain ratio (P<0.003), carcass weight (P<0.003) and negatively correlated with daily weight gain (P<0.0003). It was concluded that the rabbits slaughtered at 90 days showed better meat deposition (higher thigh circumference) than the ones slaughtered at 75 days of age and positive correlation between thigh circumference and body weight, daily ration consumption, feed: gain ratio and carcass weight.

Key words: body measurements, carcass, growing rabbits.

GROWTH TRAITS IN SIMPLE CROSSBREEDING AMONG DAM AND SIRE LINES

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Twenty-five genetic groups were produced following a diallel-crossbreeding scheme among five lines: three dam and two sire lines belonging to two Spanish Research Institutions (UPV and IRTA). A total of 2773 young rabbits from 525 kindlings were controlled in different seasons. Growth traits were evaluated during the fattening period lasting from five to nine weeks. On average, genetic groups coming from lines selected for growth rate were heavier (+57 g at weaning and 311 g at 60 days), had a faster growth rate (+9 g/d) and a realised higher daily feed intake (+12.9 g/d), improving feed conversion ratio (-0.21), than the groups originated from crosses among lines selected for litter size. Crossbreeding parameters were estimated using the Dickerson model. Maternal genetic and heterosis effects were close to 0 or very low. Direct genetic effects mainly regulated expression of these traits.

Key words: Growth, crossbreeding, heterosis, feed efficiency.

DIVERGENT SELECTION FOR UTERINE CAPACITY. EARLY EMBRYO MORTALITY.

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An experiment of divergent selection for uterine capacity was performed during 10 generations and then selection was relaxed until the 18ᵗʰ generation. Early embryo mortality at 25 and 48 hours after mating was studied. A total of 127 intact multiparous females from the 17ᵗʰ generation were slaughtered 25 hours after natural mating, 69 females from the High line and 58 from the Low line. A total of 89 intact nulliparous females from the 18ᵗʰ generation were slaughtered 48 hours after natural mating, 50 females from the High line and 39 from the Low line. Ovulation rate (OR), fertilization rate (FR) and recovery rate (RR) were estimated in both experiments. The embryonic development stage was observed. No differences were found between lines in OR, FR and RR in both experiments. At 25 hours, the percentage of two cell stages *versus* four cell stages was similar in High and Low lines. At 48 hours, a relevant difference of percentage of 8-16 cell *versus* early morulae was found (-9.31%, (P>0)=0.08). Selection for uterine capacity may lead to modification of embryo development at 48 hours after mating, but no differences in embryo survival were found.

Key words: early mortality, rabbit, divergent selection, uterine capacity, Bayesian.

GENETIC PARAMETERS OF FERTILITY IN TWO LINES OF RABBIT OF DIFFERENT APTITUDE

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A Bayesian analysis with a threshold model was performed for fertility defined as a binary trait (1, successful mating, 0, unsuccessful mating) in two populations of rabbit of different reproductive potential: Line P selected for litter size and Line C selected for growth rate. There were 20793 records (86.2% successful) of natural mating in line C from 1983 to 2003 and 17548 records (80.5% successful) in line P, from 1992 to 2003. Data concerned 5388 and 3848 females and 1021 and 685 males in lines C and P. The pedigree included 6409 and 4533 individuals in lines C and P respectively. The binary response was modeled under a probit approach. The model for the latent variable included male and female additive genetic effects, male and female permanent environmental effects and year-season and physiological status of the female as systematic effects. Means (standard deviation) of the estimated marginal posterior distribution (EMPD) of male heritability were 0.013 (0.006) and 0.010 (0.008) in lines C and P respectively and of EMPD of female heritability were 0.056 (0.013) and 0.062 (0.018) in lines C and P. Means of the EMPD of the proportion of the phenotypic variance due to environmental male and female effects were 0.031 (0.007) and 0.128 (0.018) in line C and 0.053 (0.010) and 0.231 (0.024) in line P. Means (posterior standard deviation) of the EMPD of genetic correlations between male and female were 0.733 (0.197) in line C and 0.434 (0.381) in line P. Results indicate that little genetic variation exists for female fertility but not for male fertility and, that genetic control of these traits could be close, but this need to be confirmed. Therefore, it would be possible to improve reproductive performance by including female fertility in a breeding program but response to selection would be very small.

Key words: Bayesian Theory, Fertility, Genetic Parameters, Rabbit, Threshold model.

LACTATION AND GROWTH INTENSITY OF TRANSGENIC RABBITS

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Live weight growth and milk production in selected age categories of transgenic and non-transgenic rabbits were evaluated. The transgenic rabbits originated from descendants of two female founders who were applied the gene construct WAP-hFVIII into the pronucleus by microinjection. The studied animals were kept in standard breeding conditions. On Day 1, 2, 5, 10, 20 and 30 post partum had the transgenic animals higher live weights without statistical significance of differences in arithmetic means for the growth intensity. Higher milk production was noticed with transgenic females on Day 10, 15, 20 and 30 post partum. However, the difference was not statistically significant.

Key words: transgenic rabbits, growth, lactation.

GENETIC VARIABILITY OF THE RESISTANCE FOR THREE TYPES OF ENTEROPATHY IN THE GROWING RABBIT

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This paper described the genetic variability for the resistance to 3 digestive stresses in the growing rabbit: after inoculation of coccidia (trial "coccidia"), with a low dietary fibre level (trial "fibre"), and after experimental reproduction of rabbit epizootic enterocolitis (trial "ERE"). Genetic variability was analysed from a sample of 48 sires, which produced the experimental young rabbits. These animals were weighed and examined on D0, D4, D11, D18, D25 and D32 after weaning (at 30d old). Three clinical patterns were checked : abdominal swelling, diarrhoea and mucus. For each trial, young rabbits without one clinical pattern were used as controls. The threshold daily gain was equal to the control rabbits average daily gain minus two standard deviations. One daily gain was considered to be abnormal when it was below the threshold. Mortality, clinical patterns and growth rate were used to assess individual response to one challenge. Three binary indexes were defined to describe young rabbit individual answer to one challenge. The first one ("Alive") dealt with mortality. The second ("Resilient") and the third ("Tolerant") dealt with mortality and morbidity. Mortality and morbidity indexes were low for "coccidia" trial (61% of alive, 40% of resilient and 20% of tolerant), higher for "fibre" trial (75, 64 and 31%) and medium for "ERE" trial (66, 57 and 33%). Sire effect was significant for each index in the "coccidia" and the "fibre" trials. Sire effect was significant only for the "tolerant" index in the "ERE" trial. Correlations between sire rankings for the 3 indexes of one trial were always highly significant. Correlations between sire rankings were statistically significant between, on the one hand, "resilient" and "tolerant" indexes from "coccidia" and "fibre" trails. They were also statistically significant, on the other hand, between "alive" and "resilient" indexes from the "fibre" trial and "resilient" and "tolerant" indexes from the "ERE" trial. Our results demonstrated that there was a genetic variability for the resistance to 3 different enteropathies.

Key words: genetic resistance, epizootic rabbit enterocolitis, coccidiosis, fibre.

EFFECTS OF THE NAKED GENE ON POSTWEANING PERFORMANCE AND THERMOTOLERANCE CHARACTERS IN FRYER RABBITS

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This investigation quantified the effects of the naked gene on postweaning and thermotolerance characters in rabbit fryers during 42-d growth trials in summer of 2002

in subtropical south Texas. In 1999, a rare naked rabbit was mated to commercial New Zealand White does, resulting in 16 F_1 litters and 113 offspring, all of which had normal fur coats. To expose the recessive naked gene in the homozygous state, F_1 X F_1 *inter se* matings were made between half-siblings to create an F_2 generation. Based on the expected 3:1 phenotypic ratio (furred to naked), in the F_2 generation, 192 rabbits had normal fur coats and 48 rabbits were naked, supporting the single recessive gene hypothesis ($c^2 = 2.94$; P>0.05). Weaned fryers were randomly assigned to growing pens containing either two or three furred or naked non-littermates. Individual fryer traits included initial and final body weights and ADG, as well as respiratory rate and rectal body temperature. Pen traits included feed and water intake. For individual traits, data were blocked for random effects of fraternal-litter and pen (nested within treatment), and fixed effects of treatment (naked and furred groups), age batch, gender, fixed effect interactions, and initial age of fryer (linear covariate). Results revealed (P<0.001) that naked compared to furred fryers had heavier final weights (1996 versus 1784 g) and more rapid ADG (27.3 versus 24.0 g/d). Pens of naked compared to furred fryers, on average, had higher feed intake by 28 g/d per fryer (P<0.001), but pen feed efficiency (total gain/total feed intake) was poorer for naked than for furred rabbits (0.230 and 0.279; P<0.001). Daily water intake was similar (199 and 188 ml), on average, between pens of naked and furred fryers. However, furred compared to naked fryers had a higher free water-to-feed intake ratio (2.13 and 1.72 ml/g; P<0.01). At 1400 hr, naked fryers had lower rectal temperatures (38.9 and 39.7 ºC) and lower respiratory rates (120 and 161 breaths per minute) compared to furred rabbits, respectively. Our results suggest that naked rabbits had better heat tolerance and (or) a higher critical body temperature zone than furred rabbits, and hence better growth performance. This preliminary experiment yielded promising results in favor of naked rabbits, but additional trials are needed to confirm these results.

Key words: fur, growth, rabbits, thermo-regulation, tropical agriculture.

GENETIC COMPONENTS OF LITTER PERFORMANCE IN A DIALLEL CROSS INVOLVING FOUR RABBIT BREEDS

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New Zealand White (NZW), Californian (CA), Chinchilla (CH) and Criollo (CR) rabbits were utilized in a diallel cross to evaluate general and specific combining abilities, as well as maternal and reciprocal effects on litter size and weight at birth and weaning. Data were collected from 66 litters and a total of 502 kits. Statistical analysis was performed by least-squares procedures. Breed differences in general combining ability for litter size indicated that NZW and CA does had better performance at birth and weaning than CH and CR does. Analysis for specific combining ability showed that the best combinations for litter size at both birth and weaning were NZW-CA, NZW-CH and CA-CH. Results of maternal effects showed that litters from NZW and CA does had better performance for litter size and weight at birth and litter weight at weaning than litters from CH and CR does. Differences attributed to reciprocal effects indicated the possibility of an advantage in litter size at birth and

weaning when using NZW does in the mating.

Key words: diallel cross, combining ability, litter traits.

SELECTING HIGH PERFORMANCE RABBITS AT EARLY AGES THROUGH AN STOCHASTIC APPROACH

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A stochastic modeling approach was used to detect at early ages during rabbit growth those individuals which will show better performance. The procedure can be helpful for selection purposes or to check if an animal is growing according to its own pattern. The stochastic model can be based on any known rabbit growth curve but its parameters should be historically chosen according to the breed being raised. In this study five New Zealand White females randomly chosen from different litters were weekly weighed from birth to reproduction age (154 days). A Gompertz growth curve showed best fit to the data. Historical information on New Zealand White and average birth weight from present data were used to define the model $Wt^*=51*\exp(0.113*(1-\exp(-0.026*t))/0.026)$, where Wt^* is the estimated animal weight in g on day t. The stochastic approach is very powerful as it requires the true weight obtained in the last measurement $(Wt-1)$ and provides the expected weight value for age t, $E(Wt)= Wt^*[(Wt-1)/ (W^*t-1)]0.8$. When a rabbit at age t shows real weight $Wt > E(Wt)$ it is an above average animal and can be selected as such. Also, in following the growth of a given animal, when the above inequality shows consistence in sequential ages and then abruptly changes, it is expected that some source (mostly external) affected its growth alerting for intervention.

Key words: growth hazards, stochastic growth model, weight selection

ESTIMATION OF THE CORRELATION BETWEEN LONGEVITY AND LITTER SIZE

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An estimation of the genetic and the environmental correlations between prolificacy (BA and NW) and functional longevity in a population selected for litter size at weaning since 1992 is carried out. The method is only an approximation but suggests that genetically longevity and litter size are not antagonistic objectives in breeding programs, because the genetic correlations are around 0.

Key words: Longevity, Litter size, Correlation

DIRECT AND CORRELATED RESPONSES TO SELECTION FOR DAILY GAIN IN RABBITS

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In a selection experiment for daily gain, direct and correlated responses were estimated, using a cryopreserved population as control. The difference between the selected and control group was 15 generations. The direct response for daily gain was 0.18 g./d. per generation and we did not find correlated response for feed conversion. These results are worse than expected. This could be due to the effect of the special diet used to control the enterocolitis disease.

Key words: selection, response, daily gain

SELECTION OF PANNON WHITE RABBITS BASED ON COMPUTERISED TOMOGRAPHY

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This presentation reviews the selection procedure performed in the last years. From the population (n=12871) with 42.1 g/day average body weight gain between 5 and 10 weeks of age, the rabbits with higher daily weight gain (females: 45.0 g/day /n=1748/, males: 47.6 g/day /n=1179/) were chosen, thereafter CT (computerised tomography) scanning was performed at 10.5 weeks of age. Based on the scans located between the 2nd and 3rd, as well as between the 4th and 5th lumbar vertebrae, the cross-sectional area of the *m. Longissimus dorsi* was measured and the average of the two values was calculated (L value). A linear regression equation between the body weight and L-value was developed, and rabbits with the highest values above the regression line were selected. The L value of the selected animals exceeded the population average by 1 and 1.8 cm^2 in female and male rabbits, respectively. Evaluated with REML the heritability (h2) and common litter effect (c2) of L-value were 0.41 (0.03) and 0.12 (0.01) respectively. Applying BLUP genetic merit of L-value showed an increasing trend for the whole investigation period.

Key words: Rabbits, Pannon White, selection, computerised tomography, weight gain.

GENETIC VARIATION WITHIN AND AMONG FIVE RABBIT POPULATIONS USING MICROSATELLITE MARKERS

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Five microsatellite loci (*Sat3, Sat4, Sat7, Sat8 and Sat12*) were used to analyze the genetic variation among 5 breeds or strains

of domestic rabbit populations (Vc-I Rex rabbit strain (Vc-I), Vc-II Rex rabbit strain(Vc-II), New Zealand White rabbit breed (NZW), Qingzilan rabbit breed (QZL), Japanese White rabbit breed (JAW)). Five microsatellite loci exhibited a total of 20 alleles from the 5 rabbit populations. One private allele was found at Vc Rex population by *Sat4* and *Sat8*, respectively. PIC and heterozygosity had the same tendencies among 5 rabbit populations, and the Vc-II population had the highest value (0.5526, 0.6202), followed by Vc-I population (0.5240, 0.5906), JAW population (0.4932, 0.5374), QZL population (0.4626, 0.5347), and NZW population (0.4515, 0.5261), which suggested that genetic variation was greater in Vc Rex population than in the other three rabbit populations. The result of cluster displayed that the population whose relationship was nearest to Vc-I Rex rabbit population was Vc-II Rex rabbit population, followed by Japanese white rabbit population , QZL rabbit population, and New Zealand White rabbit population was the furthest one to Vc-I Rex rabbit population in relationship, which conformed to the fact of the Vc Rex rabbit breeding history.

Key words: rabbit, microsatellite, genetic, variation.