Breeding and Genetics: Poultry and Small Ruminants

T36 Comparative genomics: The Guinea Fowl satiety center.

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Genetic influence of the mechanisms driving feeding behavior and energy homeostasis in avians has not been fully elucidated; hence there is a paucity of such information in the Guinea Fowl (GF). Recent advances in genomics, proteomics and bioinformatics have made these mechanisms less difficult to evaluate, but assays aimed at developing GF genetic improvement programs continue to lag. The GF has tremendous potential as a viable poultry meat species in the US and globally. Generating genetic information for the GF is essential for its improvement and in comparative mapping of avian species of economic importance. The primary aim of this study was to compile a comprehensive database of genes expressed in GF center of satiety. Messenger RNA was isolated from ventromedial hypothalamus and pituitary of adult GF. Following reverse transcription, cDNAs were cloned into the pBluescript plasmid vector using the Stratagene cDNA Library Construction Kit. Approximately 1000 clones were selectively screened via blue-white selection, restriction digestion and PCR. Positive clones were cycle-sequenced by PCR and analyzed with the ABI PRISM 3100-Avant Genetic Analyzer. A second objective was to comparatively analyze GF gene fragments against homologs from other poultry species. Guinea fowl nucleotide sequences were subjected to sequence homology searches using the megablast option of NCBI's Basic Local Alignment Search Tool. Nucleotide sequence similarity between GF and other avian species averaged 76.5%. Nucleotide sequences exhibiting high homology (~80%) with other avian species averaged 685.6 bases in length and ranged from 293 to 1,025 bases. Nearly 12% of the nucleotide sequences analyzed showed no significant similarity to any available sequence data. Gene fragments generated from this work are currently being used to develop oligonucleotide primers for quantitative PCR and expressed sequence tags for selective breeding.

Key Words: Guinea Fowl genomics, satiety, hypothalamus

T37 Divergent selection for 4-week body weight in Japanese quail: Relationship between blood parameters and carcass characteristics.

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The current study has been carried out to investigate the relationship between blood parameters and carcass characteristics in Japanese quail. Quail lines utilized were 2 lines divergently selected for high (HW) and low (LW) 4-wk body weight following 7 generations and also a control line (C). To investigate quail blood parameters, 15 quail from each line were selected randomly at 42-d of age. Blood samples were taken from the jugular vein just before slaughter and carcasses were measured individually. The plasma cholesterol content of HW line quail were significantly higher than for quail from the LW and C lines. There was a significant correlation (0.99) between serum hematocrit level and breast depth in the HW, LW and control (0.99) lines ($P < 0.01$). There was also a significant correlation between ovary weight and serum triglyceride level (TG) in the HW (0.82) and LW (0.87) lines ($P < 0.01$). Liver weight in the LW line was significantly correlated with TG level (0.82) ($P < 0.01$), and the correlation between testis weight and TG in the LW line (−0.96) was also significant ($P < 0.01$). The results of current study indicated that carcass characteristics and blood parameters of Japanese quail were greatly affected by short-term divergent selection. Thus, to prevent undesirable side effects of selection in this species, like those that have occurred in broilers, we must refine the breeding goal into a broader perspective and consider changes in physiological traits in the breeding goal.

Key Words: quail, divergent selection, blood parameters

T38 Genetic variation in physiological responses following heat stress in laying hens.

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Heat stress (HS), also known as hyperthermia, is a major problem experienced by poultry during high-temperature conditions. The ability to manage the detrimental effects of HS can be attributed to many factors, including genetics. The objective of the present study was to determine the variation of effects that HS poses on the well-being of laying hens. Ninety 28-wk-old White Leghorns of 2 strains were used; a line of individually selected hens for high productivity and survivability, DeKalb XL (DXL), and a line of group-selected hens, kind gentle bird (KGB). Hens were randomly paired, housed by strain and assigned to hot (H) or control (C) treatments for 14 d (mean: C = 24.3°C, H = 32.6°C). Physiological measures were collected at d 8 and 14. Behavior data was collected at d 1, 2, 6, 9, and 13. Compared with controls, H-hens core temperature (CT) was significantly higher at d 8 and 14 ($P < 0.05$). Heterophil:lymphocyte ratios were significantly higher in H-hens at d 14 ($P < 0.05$). H-hens had significantly reduced liver wt (LW) and spleen wt (SW) at d 8 and 14 ($P < 0.05$) and body wt (BW) at d 14 ($P < 0.05$). H-hens tended to have reduced BW at d 8 ($P < 0.10$) and heart wt (HW) at d 14 ($P < 0.10$). H-DXL had significantly reduced LW than H-KGB at wk 1 ($P < 0.05$). Behaviorally, H-hens opened their wings significantly more than C-hens ($P < 0.05$). C-hens did not initiate thermal panting. H-KGB hens exhibited panting behavior significantly more than H-DXL ($P < 0.05$). The data suggest that HS has detrimental effects on the physiology of laying hens. However, differences can be observed in the results of this study due to the genetic basis for variations in heat stress response.

Key Words: heat stress, genetics, laying hen

T39 Genome-wide copy number variation and temporal gene expression analysis in Marek's disease-resistant and -susceptible inbred chickens.

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Viruses that cause cancers are a great threat to human and animal health. Marek's disease (MD) in chickens is a lymphoproliferative disease caused by Marek's disease virus (MDV). The overexpression of Hodgkin's disease antigen in MD makes it an ideal model to study the progression mechanism of Hodgkin's disease in vivo. Three inbred chicken lines (L63, L72 and LM) with different reactions to MDV were used to perform array-based comparative genomic hybridization (CGH) and gene expression microarray experiments at different time points (5dpi, 10dpi and 21dpi) of virus infection, with the objective of comparing copy number variation (CNV) with MDV indicator traits. A total of 43 CNV were found in the 3 chicken lines with the total size ranging from 1.4 Mb in L72 to 1.6 Mb in LM. While only 22% of the sequence found within CNV regions in L63 (MD-resistant) and LM (intermediate in MD-resistance) is unique, about 62% is unique in L72 (MD-susceptible) chickens. Several anti-viral pathways, and particularly the NF-κB pathway, were found activated in the early cytolytic stage (5dpi) in L63 chickens. The array-CGH and gene expression microarray results revealed a CNV loss located on chromosome 4 present in both L63 and LM chickens but absent in L72 chickens that is associated with the expression of a CD8α homolog before and after MDV infection. To our knowledge, this is the first time a CNV loss has been found that might be related to MD-resistance in chickens.

Key Words: copy number variation, microarray, genetics

T40 Broiler breeders with an efficient innate immune response are more resistant to coccidial infections.

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Coccidial infections cost the poultry industry an estimated $600 million in low carcass weights and prophylactic drugs per year. For the past several years we have characterized the innate immune response of 2 broiler breeder lines (A and B) and their F1 reciprocal crosses (C [B sire x A dam] and D [A sire x B dam]) and compared their resistance against Salmonella, Enterococcus, and Campylobacter challenges. In all cases, line A and cross D are more responsive and more resistant than line B and cross C. Now, we want to determine if the trend is also observed following separate challenges with the protozoan parasites, *Eimeria tenella* (ET), *E. maxima* (EM), or *E. acervulina* (EA). Fourteen-day-old chickens from lines A and B and cross C and D were challenged orally with 15–50 × 10^3 ET, 10–40 × 10^3 EM or 25–50 × 10^3 EA oocysts. Birds were sacrificed 6 d post-challenge and the appropriate region of the gut was removed and scored for lesions (ET in the ceca; EM in the mid-gut; EA in the duodenum) and final body weight (BW) compared with non-infected controls. Regardless of the challenge species or dose administered, line A and cross D birds were more resistant to intestinal pathology as demonstrated by lower lesion scores compared with B and C, respectively. As might be expected, the lower lesion scores in line A and cross D chickens were accompanied by higher final BW compared with line B and cross C chickens, thus reducing potential revenue loss associated with low carcass weights in coccidia-infected birds. The results from this study showed that in addition to improved resistance against bacterial infections line A and cross D chickens are also more resistant to coccidial infections compared with line B and cross C birds. Taken together with all of our earlier studies utilizing these lines, an efficient innate immune response protects against a broad range of food-borne and poultry pathogens including costly coccidial infections.

Key Words: genetics, coccidia, innate immunity

T41 Expression of the peptide transporter, PepT1, in chickens from high and low weight-selected lines and their F1 and F2 crosses.

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PepT1, a peptide transporter located in the brush border membrane of the small intestine of chickens, is important in the uptake of amino acids in the form of di- and tri-peptides. Thus, PepT1 plays an important role in growth and feed efficiency. The objective of this study was to determine PepT1 expression and inheritance in the duodenum, jejunum, and ileum of chickens selected for high or low body weight and their F1 and F2 progeny. Parental line chickens selected for 51 generations for high (H) or low (L) 8-week body weight were mated to produce 4 types of progeny. These were parental lines (LxL and HxH) and reciprocal F1 crosses (HxL and LxH). Only males were used in the analysis. On d7 posthatch, LxL chicks had the lowest body weights and the highest levels of PepT1 mRNA in the small intestine, whereas the HxH chicks had the heaviest body weights and lowest levels of PepT1 mRNA. The reciprocal F1 chicks were intermediate in body weight and PepT1 levels. An F2 generation, produced by random matings of LxH and HxL parents, had a greater range in body weights and PepT1 expression levels than the F1 crosses. This 3 generation mating study suggests polygenic inheritance for PepT1 in chickens

Key Words: chicken, PepT1, transporter

T42 Genetic properties of feed utilization efficiency parameters.

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Feed costs constitute about 70% of the total production costs; however, the efficiency of feed utilization has not kept up with the growth potential of today's broilers. Improvement in the efficiency of feed utilization will reduce the amount of feed required for growth, which will directly reduce production cost, increase profitability, and subsequently reduce the amount of manure produced. We estimated genetic parameters of feed conversion ratio (FCR) and residual feed consumption (RFC) in a random mating broiler control population using DFREML and determine nutrient factors that affect both traits. The heritability of FCR and RFC were 0.22 and 0.11, respectively with genetic correlation of 0.72. However, when maternal effects were included in the model, the genetic correlation increased to 0.98, probably suggesting that maternal components influence feed utilization efficiency and as a result both nuclear and mitochondrial genomes are important in deciphering the genetic factors affecting feed utilization efficiency. Among the nutrient factors, it was determined that protein energy and calcium retentions greatly affected feed efficiency.

Key Words: feed efficiency, genetic parameters, chicken

T43 Analysis of ascites susceptibility using genetic markers in commercial broilers.

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Although the ascites syndrome in chickens has been investigated for years, it continues to inflict financial losses within the global poultry industry. It is estimated that annually 5% of the 40 billion world broiler population succumbs to ascites, thus leading to yearly losses of millions of dollars. Efforts to curb the incidence of ascites are typically designed to slow early growth. This limits the bird's ability to show its true genetic potential and impacts later yields. In 1994, lines divergent for susceptibility to ascites were established from a commercial sire line through sibling selection of birds reared at local altitude, after testing sibs reared under simulated high altitude conditions. We used a whole genome SNP array to identify 7 potential regions associated with susceptibility. After 16 generations of selection, the selected lines changed in allele frequency for 2 regions on chromosome 9, as compared with each other and with the line of origin. Changes were consistent with patterns of susceptibility and resistance to ascites. In addition to the research populations, we determined that 2 ascites susceptible commercial lines are also segregating for resistance related alleles in these regions. The data support the predictive nature of these loci, in that the presence of a specific genotype is associated with resistance to ascites, which suggests that one or more genes within these regions might play an important role in ascites development. Future research will include reducing the incidence of ascites in susceptible commercial lines through marker-assisted selection.

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Key Words: ascites, genetic markers

T44 Using quantitative PCR to investigate three candidate genes related to pulmonary hypertension in the chicken. A. A. Al-Rubaye*, N. B. Anthony, G. F. Erf, R. F. Wideman, and D. D. Rhoads, *University of Arkansas*, *Fayetteville*.

Idiopathic pulmonary arterial hypertension syndrome (IPAH) is a disease of humans and chickens that results from chronic high pulmonary arterial pressure. IPAH in broiler chickens results in right-sided congestive heart failure leading to ascites that, if not aggressively treated, will result in death. We have been mapping chicken genes affecting resistance or susceptibility to IPAH. Previously, we identified 2 regions on Gga9 and one on Gga27 that show significant linkage disequilibrium to IPAH in our lines. Within these regions we identified 3 candidate genes that are known to be related to susceptibility to pulmonary hypertension in humans. Those genes are ACE, HTR2B, and AGTR1. We are examining the expression of these 3 genes in chicken IPAH using reverse transcriptase quantitative PCR. Initial analyses have detected significant differences in the expression levels for 2 of the candidate genes in whole blood RNAs. We are expanding the analyses to include increased numbers of samples and a wider range of tissues.

This work was supported by grants from the Arkansas Biosciences Institute and NIH/NHLBI Grant 1R15HL092517 01.

Key Words: QPCR, pulmonary hypertension syndrome, chicken IPAH

T45 Selection of the best model for estimation of genetic parameters for growth traits in Iranian Moghani sheep. N. Ghavi Hossein-Zadeh*[1] and M. Ardalan[2], [1]*Department of Animal Science, Faculty of Agriculture, University of Guilan*, *Rasht, Iran*, [2]*Department of Animal Science, University College of Agriculture and Natural Resources, University of Tehran*, *Karaj, Iran*.

The objective of this study was to estimate the genetic parameters for birth weight (BW), 3 mo weight (3MW), 6 mo weight (6MW), 9 mo weight (9MW), and yearling weight (YW) of Iranian Moghani sheep using restricted maximum likelihood via the MTDFREML program. The data and pedigree information used in this research were collected at Breeding Station of Moghani sheep (Ardebil province, Iran) during 1987–2005. Six different animal models were fitted, differentiated by including or excluding maternal effects, and including or excluding a covariance between maternal and direct genetic effects. The estimates for direct heritability ranged from 0.31 to 0.54, 0.21 to 0.34, 0.13 to 0.25, 0.11 to 0.22 and 0.10 to 0.17 for BW, 3MW, 6MW, 9MW and YW, respectively. These estimates were substantially higher when maternal effects, either genetic or environmental, were ignored in the model. The results of this study show the importance of including maternal genetic and environmental effects when estimating genetic parameters for body weight traits in Moghani sheep.

Key Words: growth traits, genetic parameters, Moghani sheep

T46 Estimates of genetic trends for body weight traits of Moghani sheep obtained by a multivariate animal model analysis. N. Ghavi Hossein-Zadeh*, *Department of Animal Science, Faculty of Agriculture, University of Guilan*, *Guilan, Rasht, Iran*.

The objective of the present study was to estimate genetic changes for body weights at different ages in Moghani sheep. Traits included were birth weight (BW, n = 4208), 3 mo weight (3MW, n = 4175), 6 mo weight (6MW, n = 3138), 9 mo weight (9MW, n = 2244), and yearling weight (YW, n = 1342). The data and pedigree information used in the current research were collected at the Breeding Station of Moghani sheep (Ardebil province, Iran) during 1989–2005. Variance components were estimated from a 5-trait analysis, based on the best model of analysis for each trait, using the MTDFREML program. Level of significance for the inclusion of effects into the model of analysis was declared at $P < 0.05$. The final model included the fixed class effects of year-season (68 levels), sex of lamb and parity of dam, birth type (single, twin, triplet), the linear covariate effect of age of dam (from 2 through 7 years old) and random direct and maternal genetic effects. The most suitable model was determined based on likelihood ratio tests for each trait. Breeding values of individual animals were predicted with Best Linear Unbiased Prediction (BLUP) methodology and obtained from a multivariate animal model analysis and genetic trends were obtained by regressing the means of predicted breeding values on year of birth for each trait. Estimates of direct heritabilities for BW, 3MW, 6MW, 9MW, and YW were 0.29, 0.13, 0.14, 0.10, and 0.31, respectively. Estimates of maternal heritabilities were 0.29 for BW, 0.08 for 3MW, 0.11 for 6MW, 0.06 for 9MW, and 0.10 for YW. Direct genetic trends were positive and significant ($P < 0.05$) for BW, 3MW, 6MW, 9MW and YW and were 1.63, 69.20, 79.38, 66.83 and 110.22 g/year, respectively. Also, maternal genetic trend for BW, 3MW, 6MW, 9MW and YW were positive and significant ($P < 0.05$) and were 2.36, 49.18, 37.33, 17.73 and 9.67 g/year, respectively. The results showed that improvement of body weights of Moghani sheep seems feasible in selection programs.

Key Words: Moghani sheep, growth traits, genetic trend

T47 Association of polymorphisms in the FecB gene with litter size in Wadi sheep. Y. Ren*[1,2], Z. Shen[1,2], M. Li[3], N. Xiao[3], W. Dong[3], and S. Fu[1], [1]*Binzhou Animal Science & Veterinary Medicine Institute*, *Binzhou Shandong, China*, [2]*Research and Development Center of Wadi Sheep Breeding Technology*, *Binzhou Shandong, China*, [3]*Shandong Lvdu Biotechnology Co., Ltd.*, *Binzhou Shandong, China*.

Wadi sheep in the Shandong proving of China are known for fecundity and antireversion. About 20–30% Wadi sheep have 4 nipples, which leads to a tendency for fecundity and high galactosis. The FecB gene, a major gene for fecundity in the Booroola Merino breed, is caused by a 1-base mutation of BMPR-IB and increases litter size by increasing ovulation rate. Polymorphisms within the FecB gene of Wadi sheep and associations with litter size were analyzed by PCR-RFLP to study the fecundity of Wadi sheep on molecular level. This results showed that there was FecB mutation in Wadi sheep that was the same as in Booroola, and the frequencies of 3 genotypes (B/B, B/+, +/+) were 0.29, 0.56 and 0.15, respectively. An association between genotype frequencies and number of nipples was observed. Average litter sizes for the 3 genotypes were 2.81 ± 0.42, 2.49 ± 0.53 and 1.96 ± 0.28, respectively. Statistical analysis showed that litter size of Wadi sheep with B/B and B/+ genotype was significantly greater than that of sheep with the +/+ genotype ($P < 0.01$), but differences between the B/B and B/+ genotype were not significant. In conclusion, the FecB gene could of great interest in the Wadi sheep breed due to its association with fecundity.

Key Words: Wadi sheep, FecB gene, litter size

T48 Inbreeding effects on different weights and population structure of Santa Inês sheep. M. L. Santana Júnior*, V. B. Pedrosa, P. S. Oliveira, J. P. Eler, and J. B. S. Ferraz, *Animal Breeding and Biotechnology Group, Department of Basic Sciences, College of Animal Science and Food Engineering, University of São Paulo, C. Postal 23, 13635-970, Pirassununga, SP, Brazil*.

The aim of this study was to describe the population structure and inbreeding and to quantify its effect for different weights of Santa Inês sheep in Brazil. By this reason, 6,161 production data and 17,097 animals in the pedigree data, of 6 previous generations were utilized to evaluate birth weight (BW), weight at 60 d (W60) and weight at 180 d (W180). The genetic structure analysis of population was realized by the software ENDOG (v.4.6.), resulting in some level of inbreeding for 21.72% of the animals in the pedigree data, with a maximum value of 41.02%, and average of 10.74% for the inbreed individuals. The population average inbreeding was 2.33%, and the average kinship was 0.73%. The ancestral effective number was 156 animals, and the number of population founders was 211 individuals. Parameters related to genetic variability in this population must be monitored to prevent a decrease in genetic progress. The utilization of a program for directed mating, as is presently the case in this flock, is an appropriate alternative to keep the level of inbreeding under control.

Key Words: effective population size, inbreeding, generation interval

T49 Estimates of variances due to direct and maternal effects on birth weight in Moghani sheep.

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Data from a total of 6,758 Moghani lambs were collected from 1995 to 2006 at the Jafar Abad sheep breeding station in the Ardebil province of Iran. Data were analyzed by DFREML using an animal model. The full general model used was as follows: $Y = Xb + Z_a a + Z_m m + Z_p pe + e$. In particular, use of model 1 resulted in high estimates of additive genetic and direct heritability (0.33). Inclusion of maternal effects (models 2, 4 and 5) resulted in much smaller estimates of h^2. Comparing models with likelihood ratio tests showed that model 5 performed significantly better than other models. Based on use of the most appropriate model for birth weight (BW), the estimated ratios of variance components (±SE) were: $h^2 = 0.26\ (\pm\ 0.01)$, $m^2 = 0.09\ (\pm\ 0.009)$, $pe^2 = 0.06(\pm 0.01)$. Maternal effects therefore included heritable components of phenotypic variance that will respond to selection. Although estimates of h^2 also varied between the models with different maternal effect structures, these differences were minor in comparison. It has been suggested that this antagonism will limit the potential for genetic improvement of commercial flocks through artificial selection. The idea that an evolutionary response to selection on birth weight could be similarly constrained through this mechanism is supported by the negative values estimated for rams. In conclusion, there were important maternal genetic effects influencing birth weight in this population.

Table 1. Estimates of (co)variance components, genetic and phenotypic parameters of BW from a univariate analysis

Models	h^2 (±SE)	m^2 (±SE)	pe^2 (±SE)	ram	logL
1	0.33(±0.01)	—	—	—	−796.45
2	0.31(±0.01)	0.22(±0.01)	—	—	−794.68
3	0.31(±0.01)	—	0.29(±0.01)	—	−793.78
4	0.28(±0.01)	0.19(±0.009)	0.02(±0.01)	—	−793.7
5	0.26(±0.01)	0.18(±0.01)	0.12(±0.01)	−0.97	−783.85

h^2: direct heritability; m^2: maternal heritability; pe^2: maternal permanent environmental variance; ram: direct-maternal genetic correlation.

Key Words: Moghani sheep, maternal effects, birth weight

T50 Estimation of additive and non-additive genetic parameters for growth traits of Moghani sheep.

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A total 6,758 records from Moghani lambs were collected from 1995 to 2006 at the Jafar Abad sheep breeding station in the Ardebil province of Iran. Five traits were considered; birth weight (BW),weaning weight (WW), 6-mo weight (6W), 9-mo weight (9W), and yearling weight (YW). Data were analyzed using a single-trait animal model via the DFREML software. The model was: $Y = Xb + Z_a a + Z_m m + Z_p p + e$, where Y is a vector of observations; b is a vector of fixed effects; a is a vector of direct animal genetic effects; m is a vector of maternal genetic effects; p is a vector of maternal permanent environmental effects; e is a vector of residuals, and X, Z_a, Z_m and Z_p are incidence matrices relating records for trait to fixed, direct genetic, maternal genetic, and permanent environmental effects, respectively. Results of the univariate analyses are shown in Table1. Direct heritability for body weight increased after weaning. This study showed important effects of maternal effects on growth traits, which should be considered in genetic evaluations. Direct and maternal heritability estimates obtained in this study indicated that it would be possible to improve growth traits through genetic selection at all ages.

Table 1. Estimates of (co)variance components, genetic and phenotypic parameters of growth traits from a univariate analysis

Trait	h^2 (±SE)	m^2 (±SE)	p^2 (±SE)	$r_{a,m}$
BW	0.26(±0.01)	0.18(±0.02)	0.12(±0.01)	−0.97
WW	0.23(±0.02)	0.16(±0.01)	0.07(±0.03)	−0.95
W6	0.28(±0.07)	0.12(±0.01)	0.06(±0.02)	−0.89
W9	0.33(±0.07)	0.06(±0.02)	0.024(±0.01)	−0.869
YW	0.3(±0.1)	0.02(±0.005)	0.015(±0.008)	−0.79

h2: direct heritability; m2: maternal heritability; p2: maternal permanent environmental variance; ra,m: direct-maternal genetic correlation.

Key Words: Moghani sheep, genetic parameters, growth

T51 Estimation of variance components for reproductive traits of Moghani sheep.

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A total of 3652 records were collected from 1995 to 2006 at the Jafar Abad sheep breeding station in the Ardebil province of Iran. Four traits were measured, including conception rate (CR), litter size (LS), mean litter weight per lamb born and mean litter weight of lambs at weaning. Mixed model methodology was used to analyze all traits using a multiple-trait animal model with repeated records. Covariance components and genetic parameters were estimated using the restricted maximum likelihood method based on a derivative-free algorithm (DFREML). Estimates of direct and maternal heritability, direct-maternal genetic correlation and fraction of variance due to permanent environmental effect of the ewe and ewe-mate, as well as phenotypic variances for each trait are shown in Table1. The low estimates of heritability for LS and CR may be due to the importance of random environmental effects on variability of the observations and due to the categorical expression of the trait. Because the heritability estimate was quite low, improvement of CR by selection would be difficult even though CR has great economic importance. Results showed that all traits were influenced by genetic effects and permanent environmental effects, and to improve these traits one should improve environmental effects in first step. Estimates of genetic variances and heritability are necessary for genetic evaluation of sheep and also for choosing the best selection scheme. Economic weights of traits can be determined to build an advantageous overall selection index.

Table 1. Estimates of (co)variance components, genetic and phenotypic parameters of reproductive traits from a univariate analysis

Traits	Mean ± SD	h^2 (± SE)	m^2 (± SE)	Pe^2 (± SE)	ram
LS	1.4 (± 0.51)	0.08(± 0.01)	0.038(± 0.01)	0.25(± 0.05)	0.33
CR	0.7(± 0.25)	0.03(± 0.01)	—	—	—
LMWLB	4.85(± 0.78)	0.1(± 0.02)	0.03(± 0.02)	0.03(± 0.01)	0.31
LMWLW	22.86(± 5.14)	0.09(± 0.01)	0.05(± 0.01)	—	0.1

Direct (h2) and maternal heritability, direct-maternal genetic correlation (ram), fraction of variance due to permanent environmental (pe2).

Key Words: Moghani sheep, reproduction

T52 Determination of intrinsic tolerance for high dietary nitrate in ewes using hepatic gene expression.

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Ruminants differ in their ability to efficiently reduce nitrate (NO_3^-) to nitrite (NO_2^-). It was hypothesized that these differences may be due to intrinsic differences in ability to metabolize NO_3^-. In a previous study, differentially expressed ($P < 0.05$) hepatic genes (n = 13) were identified in ewes determined as highly tolerant (n = 6) and lowly tolerant (n = 6) to 300 mg of NO_3^-/kg BW administered for an 8-d period. The objective of this study was to determine if those genes were also differentially expressed between highly tolerant and lowly tolerant ewes a priori to NO_3^- treatment, indicating a potential for marker–assisted selection. Thirteen genes involved in metabolism and stress response were identified as differentially expressed ($P < 0.05$) in liver samples from highly tolerant and lowly tolerant ewes after NO_3^- treatment using both 24k bovine oligonucleotide microarray and real–time RT–PCR techniques. Of those genes, 4 were up–regulated ($P \leq 0.05$; *HOPX*, *GPX3*, *ITIH4*, and *HP*), 8 were down-regulated ($P \leq 0.03$; *CYP25A1*, *PFKFB1*, *AOX1*, *ASL*, *SCP2*, *KIK-1*, *FADS2*, and *THRSP*), and *CSAD* tended ($P = 0.07$) to be down–regulated in lowly tolerant ewes compared with highly tolerant ewes. Relative expression of those genes was determined in liver samples collected from the same highly tolerant and lowly tolerant ewes before NO_3^- treatment. Relative expression levels were tested for treatment differences using the GLM procedure in SAS. No differences ($P > 0.05$) in expression before NO_3^- administration were detected, confirming that the changes in expression observed post–treatment were due to the NO_3^- administration. These results also indicated that selection for tolerance to high dietary NO_3^- cannot be made before exposure based on differences in expression of genes involved in metabolism or stress. Instead, differences in microbial populations in the rumen may be key to disparities observed in response to high dietary NO_3^-.

Key Words: nitrate toxicity, gene expression, tolerance

T53 Genetic parameters for growth traits in the progeny of Nubian, French Alpine Saanen, Toggenburgh, and Spanish goats mated naturally to Boer sires.

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Data came from a commercial goat farm at Imperial Valley California. The objectives were to compare the performance of the progeny of goats involving inheritance of Nubian(N), French Alpine (A), Saanen (S) Toggenburgh (T), and Spanish (SP), (n = 160), and to estimate genetic parameters for growth traits. Traits analyzed were weight at birth BWT and weaning WWT, and average daily gain (ADG) from birth to weaning. Separate analysis for each trait used least squares mixed model SAS (1999). The analytical model included: breed of dam, age of dam, sex of the kid, season of parturition as fixed effects; sire × breed of dam interaction and the residual as random. The overall mean values for weight at birth and weaning were: 1.99 and 12.89 kg, respectively. The average values for weight at birth were (2.12 ± 0.66, 2.11 ± 0.56, 2.04 ± 0.55, 1.95 ± 0.63, 2.10 ± 0.55 and 1.98 ± 0.67, 1.97 ± 0.68, 1.93 ± 0.58, 1.83 ± 0.63, 1.96 ± 0.66) for males and females kids, respectively. The average values for weaning weight were (13.99 ± 0.59, 13.29 ± 0.53, 13.25 ± 0.54, 12.67 ± 0.51 and 13.51 ± 0.43, and 12.50 ± 0.59, 12.48 ± 0.50, 11.98 ± 0.58, 12.68 ± 0.56 and 12.60 ± 0.57 kg) for male and female kids, respectively. The estimated ADG from birth to weaning was 181 ± 0.32 g. The average values for daily gain were: 187 ± 0.46 and 175 ± 0.49 g for male and female kids, respectively. Estimates of heritability direct values were ($h^2 = 0.20 \pm 0.67$, $h^2 = 0.15 \pm 0.68$, and $h^2 = 0.25 \pm 0.64$) to BWT, WWT, and ADG, respectively.

Key Words: genetic parameters, growth traits, boer goat