Breeding and Genetics: Functional Traits and Fitness

921   Telomere maintenance mechanisms in normal, immortalized, and transformed chicken cells.   T. H. O'Hare* and M. E. Delany, *Department of Animal Science, University of California, Davis*.

Telomeres protect the ends of linear chromosomes in eukaryotes. A specialized holoenzyme consisting of an RNA and a protein catalytic subunit, telomerase, adds the telomeric TTAGGG repeat to the chromosome ends thus mitigating telomere shortening. A recent study (O'Hare and Delany, 2009) investigated variation within and among the telomeric array profiles of normal, immortalized, and transformed chicken cells. An immortalized chicken embryo fibroblast (CEF) cell line, DF-1, exhibited ~3-fold more telomeric content (17%) as compared with normal chicken cells (5%). Interestingly, DF-1 had been reported to be telomerase-negative (Christman et al., 2005). The current study confirmed that DF-1 cells are telomerase-negative and found that a chemically transformed CEF cell line, OU2, is telomerase-negative. The telomeric profile of this transformed line indicates a content of ~5%. Given their lack of telomerase activity, we hypothesize DF-1 and OU2 are using the alternative lengthening of telomeres (ALT) pathway to maintain or lengthen their telomeres. Gene expression of telomerase components, telomere-regulating, and ALT-related proteins was examined. The expression profiles of DF-1 and OU2 were compared with telomerase-negative mortal CEFs, telomerase-positive virally transformed DT40 cells, and gastrula stage embryos. These results provide evidence supporting the existence of the ALT pathway in DF-1 and OU2 cells.

Key Words: telomere, telomerase, alternative lengthening

922   Genetic analysis of walking ability and mortality in the turkey.   C. D. Quinton[1], B. J. Wood*[1,2], and S. P. Miller[1], [1]*Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, Canada*, [2]*Hybrid Turkeys, Kitchener, Canada*.

Genetic selection for fitness is a potential method to improve overall liveability in the turkey. A method in which fitness can be defined is mortality and the potential to survive to slaughter. In this study the heritability (h^2) was calculated for survival (SURV) to slaughter/maturity (23 weeks) and hip and leg strength (H/L) and their relationship (both phenotypic and genetic) to walking ability (WALK) and bodyweight (BW). The heritabilities of the binary traits were also transformed to a liability scale. Consequently there are heritabilities on both the observed and liability scales. Genetic parameters were estimated with multiple-trait restricted maximum likelihood in ASReml 3.0 using a series of 3-trait animal models. The table shows the results of the analysis with walking score having a moderate heritability similar to body weight. Survival and hip/leg health had lower heritability on the observed scale, but a moderate h^2 on the liability scale. The liability scale heritability estimates were moderate which would predict a good response to selection. All survival traits had high genetic correlations with each other, but negative genetic correlations with weight. Genetic correlations were stronger than corresponding phenotypic correlations. Walking score has good heritability and has high positive genetic correlation with survival, as well as moderate genetic correlations with hip and leg health. As a consequence walking score would be a good indicator trait for selection to improve both survival and hip and leg health.

Table 1. Heritability (h^2), common environment (c^2) and genetic[1] and phenotypic[2] correlations between survival, walking score, hip and leg strength and bodyweight

	SURV[3]	WALK[4]	H/L[5]	BW[6]
h^2 observed	0.166	0.224	0.080	0.248
h^2 liability	0.190		0.174	
c^2	0.034	0.074	0.041	0.350
Correlations				
SURV	-	0.864	0.808	−0.435
WALK	0.670	-	0.913	−0.372
H/L	0.575	0.660	-	−0.366
BW	−0.070	−0.192	−0.090	-

[1]above diagonal, [2]below diagonal, [3]survival to 23 wks, [4]walking score, [5]hip and leg strength, [6]bodyweight.

Key Words: liveability, turkeys, parameter estimation

923   Factors affecting spermatozoa morphology in beef bulls.   C. A. Roberts*, T. W. Geary, M. D. MacNeil, R. C. Waterman, A. J. Roberts, and L. J. Alexander, *USDA-ARS, Fort Keogh Livestock and Range Research Laboratory, Miles City, MT*.

The objective of this study was to evaluate factors affecting sperm morphology of bulls (n = 908) collected at 320 d of age. Bulls were a composite breed (50% Red Angus, 25% Charolais, and 25% Tarentaise) born from 2002 to 2008 to dams fed levels of feed during mid and late gestation that were expected to provide marginal or adequate nutrition while grazing dormant winter forage. After weaning, bulls were fed to appetite (CON) or restricted (REST) to 80% of that consumed by CON on BW basis. Semen samples were collected using an electro-ejaculator and evaluated using standard BSE procedures. Spermatozoa morphology was evaluated by classifying 100 spermatozoa per bull at 400X magnification into the following categories: normal spermatozoa, knobbed acrosome, head defects, distal midpiece reflex, dag defect, bowed midpiece, proximal droplet, distal droplet, coiled principle piece, and bent principle piece. Each morphological trait, along with scrotal circumference (SC), gross motility, and percent progressive motility was analyzed using MTDFREML and pedigree information from 8163 relatives born from 1974 to 2008 to provide heritability estimates. Heritability estimates for these traits were: SC ($h^2 = 0.67$), normal sperm ($h^2 = 0.18$), dag defect ($h^2 = 50$), bowed midpieces ($h^2 = 0.19$), proximal droplets ($h^2 = 0.37$), bent principle pieces ($h^2 = 0.18$), gross motility ($h^2 = 0.20$), and progressive motility ($h^2 = 0.20$). The moderate heritability of percent normal sperm and several of the other sperm defects suggest that selection for improved sperm morphology is possible. Further analysis with MTDFREML determined genetic correlations between the above traits and pre-weaning gain direct, pre-weaning gain maternal, post-weaning gain, and scrotal circumference. Maternal pre-weaning gain was highly correlated with scrotal circumference (r = 0.70 ± 0.24) but pre-weaning gain direct (r = 0.29 ± 0.20) and post-weaning gain (r = 0.01 ± 0.17) were not. Scrotal circumference and post-weaning gain were not highly correlated with morphology and therefore are not good indicators of spermatozoa morphology. Neither in utero nor postweaning diet affected any of the traits measured.

Key Words: bull, spermatozoa morphology, heritability

924 Bayesian QTL inference and gene identification for first service conception rate in Brangus heifers. S. O. Peters[*1,5], K. Kizilkaya[2,4], D. J. Garrick[2], R. L. Fernando[2], J. M. Reecy[2], Z.-L. Hu[2], R. L. Weaber[3], G. A. Silver[1], and M. G. Thomas[1], [1]*New Mexico State University, Las Cruces,* [2]*Iowa State University, Ames,* [3]*University of Missouri, Columbia,* [4]*Adnan Menderes University, Turkey,* [5]*University of Agriculture, Abeokuta, Abeokuta, NGR.*

First service conception (FSC) like many binary fertility traits is of low heritability, but strongly impacts production costs in beef cattle operations. The objectives of this study were to conduct a Bayesian-based whole genome QTL scan for FSC in Brangus (3/8 Brahman x 5/8 Angus) heifers and to identify candidate genes from a hypothalamic transcriptome reference resource. Yearling heifers (n = 830 from 67 sires) were estrous synchronized with progesterone-based protocols, artificially bred, then later palpated for pregnancy status (57.3% FSC rate). Heritability was estimated to be 0.21 ± 0.1. Genotypes for each heifer were obtained from BovineSNP50 Infinium beadchips. Simultaneous association of all SNP with FSC were tested in a GenSel Bayes C analysis using a mixture model that treated SNP effects as random with an assumed fraction 0.001 indicating an association. Fixed effects for analysis of FSC included birth year, calving season, contemporary group, and covariates of yearling age and weight. Model frequency >0.01 was assumed indicative of QTL association. Eight regions on chromosomes 6, 8, 26 and 29 were associated with variation in FSC (model frequency ≥0.03). The strongest evidence of association (model frequency 0.17) was a SNP mapped to position 28.6 Mb on BTA 8. Since the hypothalamus is a regulatory tissue of the reproductive endocrine axis, the transcriptome of this tissue was sequenced using the Illumina Genome Analyzer II (RNA-Seq) and aligned with bovine genome (Ver. 4.0) to evaluate presence and level of expression of potential candidate genes among pre and postpubertal heifers. Several annotations were identified within a 1.5 Mb region flanking this SNP on BTA 8 using Alpheus. Five genes with differential hypothalamic expression were identified and ontology of these genes included neuron function and gene regulation. Cumulatively, results warrant fine mapping this region of chromosome 8 to help determine functionality in regulating FSC.

Key Words: candidate gene, fertility, QTL

925 Impact of sire birth weight potential on birth and weaning traits when mated to virgin heifers. G. K. Mantz* and P. Nyren, *North Dakota State University Central Grasslands Research Extension Center, Streeter.*

The objective of this study was to examine the effect that mating virgin heifers to sires of varying birth weight potential (BWP) has on birth and weaning traits of offspring. In June, 2008, 98 virgin heifers 13 to15 mo of age were stratified by frame score and weight within frame score. Heifers were assigned randomly to 2 treatment groups. Treatments were based on sire BWP: 1) moderate BWP (MBWP) sires - Angus sires with birth weight (EPD between −1.6 and +0.4 kg, and 2) very low BWP (VLBWP) sires - Lowline sires. Pre-calving heifer weights were obtained 18 February 2009. Calves were born March through May of 2009. Birth weights and a calving difficulty (CD) score (1 = unassisted, 2 = hand pull, 3 = jack pull, 4 = Caesarean, 5 = abnormal presentation) were recorded within 24 h of calving. Calf weaning weights and post-calving dam weights were recorded in October of 2009. Weaning weights were adjusted to a constant 205-d weaning age. There was a calf sex by sire BWP interaction for birth weight ($P = 0.01$) and CD score ($P = 0.03$). Bull calves from MBWP sires were heavier at birth than bull calves from VLBWP sires (40vs. 34 kg; $P = 0.0002$) and had a greater CD score (1.7 vs. 1.1; $P = 0.01$). Birth weights did not differ ($P = 0.92$) between heifer calves sired by the MBWP sires (33 kg) and those sired by VLBWP sires (32 kg). All heifer calves from both sire groups were born unassisted (CD = 1). Calf weaning weight was affected ($P < 0.0001$) by sire BWP, and calf sex ($P = 0.01$). Offspring of MBWP sires were heavier at weaning than those of VLBWP sires, 243 and 213 kg, respectively. Steer calves were heavier at weaning (235 kg) than heifer calves (220 kg). Weaning weight for calves from MBWP and VLBWP sires were 217 and 195 kg, respectively. Dams nursing calves of VLBWP sires lost less weight than dams nursing calves of MBWP sires (28 vs. 43 kg; $P = 0.04$). In summary, using VLBWP sires reduced birth weight and calving difficulty in bull calves and reduced dam weight loss. However, calves sired by VLBWP sires weighed less at weaning than calves sired by MBWP sires.

Key Words: birth weight, calving difficulty, heifers

926 Use of random regression models for the genetic analysis of farrowing survival in pigs. C. Y. Chen*[1], I. Misztal[1], S. Tsuruta[1], W. O. Herring[2], J. Holl[2], and M. Culbertson[2], [1]*Department of Animal and Dairy Science, University of Georgia, Athens,* [2]*Smithfield Premium Genetics Group, Rose Hill, NC.*

The objective was to compare estimates of genetic parameters for number of stillborns (NSB) in relation to litter size (LS) using random regression models (RRM). Records of a single Duroc population were obtained from 4 nucleus farms from 2004 to 2008. Data from first parity (P1, n = 6,575) litters and second to fifth parity (P2–5, n = 6,259) litters were analyzed separately. Fixed effects included farm-year-season as contemporary groups, parity (for P2–5 only), and fixed cubic regression coefficients on LS with Legendre polynomials. Random effects were additive genetic and permanent environmental effects (for only P2–5). Heterogeneous residual variances were considered in the models. Legendre polynomials (RRM-L), linear splines (RRM-S), and degree 0 B-splines (RRM-BS) with regressions on LS were applied. Parameter sets used for respective models were quadratic polynomial, knots at LS 5, 9, and 13, and intervals of LS 5–7, 8–10, and 11–13 for P1. For P2–5 the same parameters were linear polynomial, knots at LS 6 and 12, and intervals of LS 5–7 and 8–13. Estimates of genetic parameter were similar with the 3 models. For P1, average heritabilities were 0.14, 0.06, and 0.07 in LS 5, 9, and 13, respectively. For P2–5, heritabilities were 0.18, 0.05, and 0.06 with repeatabilities of 0.19, 0.11, and 0.21. For P1, average genetic correlations between LS 5–9, 5–13, and 9–13 were 0.53, −0.29, and 0.65, respectively. For P2–5, correlations averaged for RRM-L and RRM-S were 0.75, −0.21, and 0.50, respectively. The correlation was 0.66 between LS 5–7 and 8–13 for RRM-BS. Based on the analysis, NSB at low and high LS appear to be different traits although genetic parameters for NSB in first and later parities are similar.

Key Words: litter size, pigs, random regression, stillbirth

927 Effectiveness of genetic predictions of Holstein gestation length and relationship to lactation yield for the subsequent lactation. H. D. Norman*, J. R. Wright, and R. H. Miller, *Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD.*

To determine if genetic evaluations of gestation length (GL) were reliable and repeatable, Holstein bulls used to develop those evaluations were stratified into 7 groups according to predicted transmitting ability (PTA) for service-sire GL based on calvings from 1998 through 2004: ≤ −3.00, −3.00 to −2.01, −2.00 to −1.01, ... 1.00 to 1.99, and ≥ 2.00 d. An independent set of 261,598 first-parity cows later mated to the

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same bulls were grouped by the service-sire PTA GL groups (group size of 8,317 to 73,324 gestations), and their GL were examined to determine effectiveness of PTA GL. The model included fixed effects for service-sire group, conception date, conception date squared, and herd-year. Mean GL for mates by service-sire group (from lowest to highest PTA) were 275.3, 276.4, 277.7, 278.7, 279.6, 280.7, and 281.8 d. Yield in the subsequent lactation was also examined for mates by service-sire group. Least squares differences by service-sire group were –84, –79, –14, 15, 28, 50, and 0 kg for standardized milk yield; –2, –3, –1, 1, 1, 1, and 0 kg for fat yield; and –2, –2, 0, 1, 1, 1, and 0 kg for protein yield. The relationship between PTA for service-sire GL and yield appeared to be curvilinear as yield decreased for the ≥2.0 d PTA group. Phenotypic relationship between GL and standardized yield in the subsequent lactation also was examined using 9 cow GL groups: ≤275, 276, 277, ... 282, and ≥283 d. Group size ranged from 17,493 to 64,876 gestations. The model included fixed effects for GL group, conception date, conception date squared, and herd-year. Least squares differences by GL group were −528, −287, −218, −194, −128, −122, –90, –90, and 0 kg for standardized milk yield; –19, –10, –8, –7, –5, –4, –4, –3, and 0 kg for fat yield, and –11, –6, –4, –3, –2, –2, –2, –2, and 0 kg for protein yield. Cows mated to bulls with PTA for longer service-sire GL and cows with longer GL phenotypes were more productive in the lactation following gestation.

Key Words: gestation length, genetic evaluation, lactation yield

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928   Estimation of genetic parameters for measures of calf survival and health in a population of Holstein dairy calves in New York state.   L. Henderson*[1], F. Miglior[2,3], A. Sewalem[2,3], D. Kelton[1], A. Robinson[4], and K. E. Leslie[1], [1]*Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada, N1G 2W1*, [2]*Guelph Food Research Centre, Agriculture and Agri-Food Canada, Guelph, Ontario, Canada, N1G 5C9*, [3]*Canadian Dairy Network, Guelph, Ontario, Canada, N1K 1E5*, [4]*Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada, N1G 2W1*.

The objectives of this study were to estimate the genetic parameters of calf survival and health for a population of Holstein calves from New York (NY) State, as well as to associate the EBV determined in the current study with traits from on-going genetic evaluations used in Canada and the US. Data were recorded for 7,372 heifer calves at a commercial rearing facility in NY, from arrival at 1 to 7 d of age for the duration of stay at the facility. Performance and disease up to weaning, and mortality before and after weaning, were recorded. Analyzed data were limited to daughters of sires with at least 10 calves originating from farms which had sent at least 5 calves to be raised at the facility. As such, calves from 264 sires and 36 herds were studied using survival analysis and 2-trait model (survival from arrival to weaning and from weaning to exit) for calf survival and 3-trait sire model for calf health (preweaning undifferentiated respiratory disease, umbilical diseases, and bloat). In general, there was increased risk of mortality for calves with very light or heavy weight at arrival, low serum total protein, low weaning weight and for calves born in a difficult parturition. The heritability from the survival analysis was 0.063, where the heritability from the linear model was 0.001 for survival to weaning and 0.036 for survival from weaning to exit. The genetic correlation between the 2 latter traits was 0.58. In the genetic analysis of health traits, the heritability estimates were 0.09 for bovine respiratory disease, 0.14 for umbilical diseases and 0.04 for bloat. The genetic correlation between bovine respiratory disease and umbilical diseases was 0.62. Significant associations between proofs for survival and health traits with proofs for routinely evaluated traits in Canada and the US were found. Results suggest that there are significant differences among Holstein sires for calf survival from weaning to the growing period and for calf health during the preweaning period.

Key Words: calf survival, calf health, multiple-trait model

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929   Estimation of genetic parameters for workability traits.   A. Sewalem*[1,2], F. Miglior[1,2], and G. Kistemaker[2], [1]*1Agriculture and Agri-Food Canada, Guelph Food Research Center, Guelph, ON, Canada*, [2]*Canadian Dairy Network, Guelph, ON, Canada*.

The aim of this study was to estimate the genetic parameters of milking temperament for Canadian Holsteins and to assess the correlation with other traits of economic importance. Cows were evaluated for this trait during milking and given a subjective score based on a 5 point linear scale (1 = Very Nervous, 2 = Nervous, 3 = Average, 4 = Calm and 5 = Very Calm). The phenotypic frequency of each score was 1.45%, 9.80%, 49.20%, 35.43% and 4.13%, respectively. The model included the fixed effects of herd-year, season of calving, age at calving, months in milk and random effects of animal and residual. The estimated additive genetic and residual variances were 0.0042 and 0.0285, respectively. The resulting heritability value was 0.128%. Correlations between bull EBV for milking temperament with EBV for production, type and other traits were calculated for the Holstein breed. Correlations were essentially low for production traits and functional herd life (0.038 - 0.048), favorable for most type traits (0.09 – 0.15) as well as milking speed (0.14) but undesirable for type traits related to feet and legs (−0.02), lactation persistency (−0.07), calving ease (−0.11) and somatic cell score (0.18). Low and undesirable correlations were also observed for most fertility traits (−0.026 to −0.114).

Key Words: milking temperament, variance component estimation, breeding value correlations

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930   Health treatment rates of Holstein cows selected for large versus small body size.   J. C. Becker*, B. J. Heins, G. D. Marx, and L. B. Hansen, *University of Minnesota*, *St. Paul*.

Holsteins selected for large versus small body size since 1966 were evaluated for incidence rates of health treatment from the Northwest Outreach and Research Center, Crookston, of the University of Minnesota. All health treatments were recorded for cows from 1983 to 2005. Treatments were recorded for 12 categories of health disorders. Records were for 544 first lactations, 366 s lactations, and 445 third and greater lactations, and the 3 lactation groups were analyzed separately. A chi-squared test was conducted separately for genetic lines for first, second and third and greater lactations. For first lactation, cows in the small line had significantly ($P < 0.01$) fewer displaced abomasums (5% versus 16%) and significantly ($P < 0.05$) less ketosis (5% versus 9%) than cows in the large line. The small line and large line did not differ significantly for mastitis, locomotion, milk fever, and early reproduction problems during first lactation. For second lactation, cows in the small line had significantly ($P < 0.05$) fewer hoof disorders (15% versus 24%), displaced abomasums (8% versus 2%), and respiratory disorders (0.5% versus 3%) than cows in the large line. The small line and large line did not differ significantly for mastitis, ketosis, milk fever, and early reproduction problems during second lactation. For third and greater lactations, cows in the small line had significantly ($P < 0.01$) fewer hoof disorders (17% versus 38%) than cows in the large line. Cows in the small and the large line did not differ significantly for incidence of mastitis, displaced abomasums, ketosis, milk fever, respiratory disorders, and early reproduction problems during third and greater lactations.

Key Words: body size, health traits, genetics

931   Sequential evaluation of longitudinal conformation data in dairy cows.   N. Gengler*[1,2], S. Vanderick[1], and C. Bastin[1], [1]*University of Liège - Gembloux Agro-Bio Tech*, *Gembloux, Belgium*, [2]*National Fund for Scientific Research, Brussels, Belgium*.

Current genetic evaluation for Holstein type data in the Walloon Region of Belgium is based on a multi-trait animal model for repeated data and missing traits using a transformation based on multiple diagonalization. Currently used data covers 33 traits observed in all lactations if at least one classification was done for a given cow before it was considered mature. A total of 102,875 records were available for first parity and 30,378 records for second or later parities in January 2010. With a total of 117,013 classified cows, the number of repeated records was 16,240, with repetitions within and across lactations. Based on a request from the field and to make better use of available longitudinal data along an age at classification gradient, research was performed to develop an adapted model. In this study a random regression model was developed that was equivalent to a multi-lactation (first vs. later) model allowing repeated classifications inside parity but with some fixed effects spanning across parities. The random regressions were defined as constant and linear regressions on parity number -1. A 2 step approach was developed, for solving and variance components estimation. In this approach, a model based on the current genetic evaluation model modified to host single-trait random regressions was the first step. The second step consisted in the joint multiple-trait analysis of the meta-data (regression coefficients) provided by the first step. The proposed approach has very interesting potential for the analysis of data with large numbers of traits as trait reduction techniques can be integrated in the procedure.

Key Words: type traits, equivalent model, sequential evaluation

932   Fitness of Boer, Kiko, and Spanish does managed on humid, subtropical pasture in central Tennessee.   R. Browning Jr.*[1] and M. L. Leite-Browning[2], [1]*Tennessee State University*, *Nashville*, [2]*Alabama A&M University*, *Huntsville*.

Records for Boer (n = 132), Kiko (n = 92), and Spanish (n = 79) does across 6 yr of production were processed to assess doe fitness traits among meat goat breeds when managed on southeastern US pastures. Does were mated in a complete 3-breed diallel each fall for spring kidding. A total of 1042 doe-yr units were observed with does ranging from 2 to 8 yr of age and managed together in a semi-intensive manner. Herd health records were analyzed for each production year. Does were treated for foot scald and foot rot upon observed lameness. The herd was not vaccinated for foot rot. Breeds differed ($P < 0.01$) for lameness cases treated during the year. Boer required more ($P < 0.01$) treatments for lameness (1.8 ± 0.1 cases/doe) than Kiko (0.6 ± 0.1 cases/doe) or Spanish (0.9 ± 0.1 cases/doe). A larger ($P < 0.01$) proportion of Boer required single ($75 \pm 5\%$) or multiple foot treatments ($49 \pm 4\%$) annually compared with Kiko ($36 \pm 5\%$; $17 \pm 4\%$) or Spanish ($45 \pm 5\%$; $24 \pm 4\%$). Does received a tactical anthelminic treatment at parturition. Individual does presenting clinical symptoms of endoparasitism during the year received need-based treatment. Breeds differed ($P < 0.01$) for need-based anthelmintic treatment. Need-based dewormings were more numerous for Boer (0.8 ± 0.1 cases/doe) than for Kiko (0.4 ± 0.1 cases/doe) or Spanish (0.3 ± 0.1 cases/doe). A larger ($P < 0.01$) proportion of Boer required single ($53 \pm 4\%$) or multiple need-based dewormings ($23 \pm 4\%$) per year compared with Kiko ($26 \pm 4\%$; $4 \pm 3\%$) or Spanish ($23 \pm 3\%$; $7 \pm 2\%$). Fecal egg counts to assess endoparasite loads 3 mo postpartum were higher ($P < 0.01$) for Boer dams (660 eggs/g) than for Spanish dams (362 eggs/g); Kiko dams were intermediate (500 eggs/g). A smaller proportion ($P < 0.01$) of Boer does weaned 3-mo-old kids (49 $\pm 3\%$) and stayed in the herd ($64 \pm 3\%$) annually compared with Kiko ($78 \pm 3\%$, $85 \pm 2\%$) and Spanish does ($77 \pm 3\%$, $84 \pm 2\%$). Significant differences were evident among meat goat breeds for doe fitness under southeastern US pasture conditions.

Key Words: meat goats, breed, fitness

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