684 White blood cell populations in goat kids and lambs during the first four days of life, with special reference to CD4 and CD8. A. Arguello*[1], L. E. Hernandez-Castellano[1], A. Morales-delaNuez[1], I. Moreno-Indias[1], J. Capote[2], and N. Castro[1], *[1]Universidad de Las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Instituto Canario de Investigaciones Agrarias, La Laguna, Tenerife, Spain.*

To investigate the white blood cell populations (including CD4 and CD8) in goat kids and lambs, 10 goat kids (Majorera dairy breed) and 10 lambs (Canaria dairy breed) were used. Blood samples were obtained at birth, and at 2 and 4 d of life in Lithium heparin containers. Immediately after collection, 50 μL of unclothed blood were added with 5 μL of CD4 (FITC) and 5 μL of CD8 (RPE) monoclonal antibodies (Serotec, Dusseldorf, Germany) and the reaction ran for 15 min at room temperature. After that, 50 μL of Optilyse (Beckman Coulter, Brea, CA) were added and the reaction ran for 15 min at room temperature to lyses red blood cells. Subsequently, 150 μL of saline serum were added to clarify the solution. Fifteen minutes later, the samples were redden using an FC500 flow cytometry device (Beckman Coulter, Brea, CA). An ANOVA (with repeated measures) procedure from SAS was used. Two white blood cell populations were observed clearly, lymphocytes plus macrophages (L+M) and polymorphonuclear (PMN), in both species at all tested times. L+M population was higher ($P \leq 0.05$) in goat kids than in lambs at all tested times (75.5, 63.5 and 74.0% in goat kids and 53.2, 45.7 and 59.5%, at birth, 2 and 4 d of life respectively). Concomitantly, the PMN population was greater ($P \leq 0.05$) in lambs than in goat kids. Goat kids CD4 population (expressed as a L+M percentage) was lower ($P \leq 0.05$) than in lambs at all tested times (29.3, 30.4 and 22.6 for goat kids and 53.7, 41.4 and 40.2 for lambs at birth, 2 and 4 d of life, respectively). No significant differences were observed for CD8 between species (ranged from 9.8 to 18.1% of L+M). There was no breed effect on CD4/CD8 ratio but a trend was observed, being goat kid CD4/CD8 ratio lower than lamb ratio (2.7, 2.1 and 2.4 for goat kids and 3.7, 3.0 and 2.8 for lambs at birth, 2 and 4 d of life, respectively). In conclusion, goat kids and lambs are different in the innate immune system during the first days of life.

Key words: goat kid, lamb, CD4 CD8

685 Immune status of goat kids fed cow′s milk with an exogenous source of DHA. I. Moreno-Indias*[1], L. E. Hernández-Castellano[1], A. Morales-delaNuez[1], A. Torres[2], D. Sánchez-Macías[1], N. Castro[1], and A. Argüello[1], *[1]Universidad de las Palmas de Gran Canaria, Arucas, Las Palmas, Spain, [2]Instituto Canario de Ciencias Agrarias, La Laguna, Santa Cruz de Tenerife, Spain.*

As the main role of dairy goat farming is to yield marketable milk, artificial rearing is closely linked to the intensification of these farms. Therefore, the use of milk replacers has been suggested. Classic works did not recommend the use of cow′s milk to feed goat kids, due mainly to problems with diarrhea. Recently, the benefits of the use of omega-3 fatty acids in nutrition such as the docosahexaenoic acid (DHA) have been presented. In this study different diets were supplied to 3 groups of goat kids: goat milk (GM), cow milk (CM) and cow milk with a supplemented source of DHA (DHA-gold) (CM-DHA). Animals were fed ad libitum twice a day. Blood samples were collected from the jugular vein until d 10 of life, and after that, each 5 d until animals weighed 8 kg (animals were weighed twice a week). IgG, IgM, total and alternative pathway complement system activity and chitotriosidase activity were measured to establish the immune status of goat kids. The MIXED procedure of SAS (version 9, SAS Institute Inc., Cary, NC) was used to evaluate the effects of the treatments on immune status of goat kids. When goat kids reached 8 kg, concentrations of IgG were 3.855, 4.002 and 3.662 mg/mL and concentrations of IgM were 0.802, 0.736 and 0.730 mg/mL for GM, CM and CM-DHA, respectively. Differences did not reach significance among treatments. When dairy kids weighed 8 kg, complement system activity did not show significant differences among treatments neither in total (GM: 58.54%, CM: 56.69% and CM-DHA: 55.09%) nor in the alternative pathway (GM: 37.94%, CM: 37.47% and CM-DHA: 34.91%). However, significant differences were found ($P = 0.03$) in the alternative pathway between GM (39.76%) and CM-DHA (23.30%) treatments when goat kids weighed 7 kg, although without continuity in the time. Finally, the chitotriosidase activity in goat kids at 8 kg did not differ significantly among treatments (GM: 1867.67 nmol/mL/h, CM: 1895.83 nmol/mL/h and CM-DHA: 1893.10 nmol/mL/h). In conclusion, CM is a good option to feed goat kids instead GM. However, DHA at this concentration did not show any effect on goat kid immune status.

Key words: DHA, milk replacer, cow milk

686 Effects of feeding sericea lespedeza as a natural anthelmintic for *Haemonchus contortus* in lactating does. J. L. Vest*[1], M. A. Brown[4], J. D. Kohler[1], M. D. Hudson[1], S. R. Nusz[5], J. M. Burke[3], J. E. Miller[2], C. T. Mackown[4], and E. L. Walker[1], *[1]Missouri State University, Springfield, [2]Louisiana State University, Baton Rouge, [3]Dale Bumpers Small Farms Research Center, USDA-ARS, Booneville, AR, [4]Grazinglands Research Laboratory, USDA-ARS, El Reno, OK, [5]Redlands Community College, El Reno, OK.*

In the United States, infection with the gastrointestinal nematode *Haemonchus contortus* is the leading cause of goat mortality. Use of alternative parasite control methods, including forages containing condensed tannins (CT), has been found to reduce the effect of gastrointestinal nematode parasites. During the last 30 d of gestation, 37 Boer-cross does kidding from April to June were randomly assigned to diets of alfalfa (*Medicago sativa*; 21% CP; n = 16) pellets (Alf) or sericea lespedeza (*Lespedeza cuneata*; 16% CP; n = 21) pellets (SL) and allowed to graze on 0.61 ha bermudagrass pasture. Does were fed pellets at a maximum of 3% of BW throughout the study. At parturition, BW and gender of kids was recorded. On d 7, 21, 35, 49, and 63 postkidding, doe fecal samples, BCS, blood samples, and measurements of milk yield and composition were obtained. To account for environmental changes during the 62 d kidding period, does were grouped in 2 kidding periods, early (those kidding from d 1 to d 31) and late (d 32 to d 62 of the trial). The climate during the later kidding period included increased rainfall and high humidity compared with the early period. The later kidding does had greater fecal egg counts (FEC) on d 7, 21, 35 and 49 ($P < 0.003$) and greater packed cell volume (PCV) on d 21, 49, and 63 ($P < 0.05$) compared with early kidding does. SL-fed does had lower FEC ($P < 0.05$) than the Alf does on d 35. On d 63, does with singles had lower FEC ($P \geq 0.03$) and greater PCV levels ($P \geq 0.006$) than does with twins. Doe FAMACHA scores gradually increased from d 7 to d 49 with an improvement by d 63 ($P < 0.0001$). Does with singles tended to have lower FAMACHA scores ($P = 0.08$) and greater BCS ($P = 0.0002$) than does with twins. Does raising twins produced more milk on d 7 and 21 becoming similar to single parity does by d 35 ($P = 0.0001$). Alf-fed, later kidding does had the lowest milk production ($P = 0.0089$). In conclusion, SL decreased FEC at d 35

but not at other times. It is possible the minimal differences in FEC and PCV between alfalfa and SL may have been influenced by treatment differences in crude protein.

Key words: goats, sericea lespedeza, parasite

687 Polymorphisms in the melanocortin-1 receptor (MC1R) gene in Nigerian indigenous goats. M. A. Adefenwa[1], B. Oboh[1], G. O. Williams[1], M. Wheto[2], C. O. N. Ikeobi[2], K. Adekoya[1], M. Okpeku[3], M. De Donato*[4], and I. G. Imumorin[4], *[1]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [2]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [3]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria, [4]Dept of Animal Science, Cornell University, Ithaca, NY.*

Coat color is an adaptive trait in mammals with implications for physiological efficiency. The extension locus, which encodes the melanocortin-1 receptor (MC1R), is known to control the synthesis of the pigment granules, eumelanin and pheomelanin, which in turn affects coat color. Functional mutations is said to cause black coat color while inactivating mutations is said to cause red coat color. There is paucity of information regarding the genetics of coat color in indigenous livestock species in Nigeria and Sub-Saharan Africa. In this study, we examined polymorphisms in the caprine MC1R gene in the 3 major Nigerian goat breeds which exhibit different coat colors: (West African Dwarf, black; Red Sokoto, brown/red; and Sahel, white). We amplified and sequenced a 716 bp fragment spanning part of the coding region of the MC1R gene (716 bp) in 69 Nigerian goats (17 West African Dwarf, 23 Red Sokoto, and 29 Sahel), sampled from across the country, using genomic DNA obtained from whole blood samples. Sequences were aligned using CLUSTALX and DnaSP version 5.10.01 was used for identifying single nucleotide polymorphisms (SNPs). Four single nucleotide polymorphisms were identified: 2 silent mutations (g.T125C and g.G128A) and 2 missense mutations (g.C126G, p.R30G and g.A729C, p.I231L). Our results in this pilot experiment showed no association between coat color and the identified SNPs as none of the variants seem to be fixed in any of the breeds. The SNPs g.T125C, g.G128A and g.C126G were identified in the same set of animals, 7 out of 69, which were cut across the 3 breeds (3 West African Dwarf, 3 Red Sokoto and 1 Sahel). The allele C for the g.A729C polymorphism occurred with a frequency of 0.029. Additional work to genotype these polymorphisms in a larger number of animals for population genetic analysis are in progress.

Key words: MC1R gene, goat, coat color

688 Molecular identification of *Trypanosoma vivax* Infection and physiological indices in Nigerian sheep. G. O. Onasanya[1], M. A. Adefenwa[2], B. O. Agaviezor[3], C. O. N. Ikeobi[1], M. Wheto[1], M. Okpeku[4], A. Yakubu*[5], M. I. Takeet[6], M. De Donato[7], and I. G. Imumorin[7], *[1]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [2]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [3]Dept of Animal Science and Fisheries, University of Port Harcourt, Port Harcourt, Nigeria, [4]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria, [5]Department of Animal Science, Nasarawa State University, Lafia, Nigeria, [6]Dept of Veterinary Microbiology and Parasitology, University of Agriculture, Abeokuta, Nigeria, [7]Dept of Animal Science, Cornell University, Ithaca, NY.*

Trypanosomiasis remains a major challenge to livestock production in endemic areas of Sub-Saharan Africa. Nationwide prevalence of *Trypanosoma vivax* (*T. vivax*) infection was estimated in 4 extant sheep breeds using 161 samples collected from across Nigeria and to ascertain associations of parasite presence with physiological indices. The presence of *T. vivax* was determined by polymerase chain reaction to amplify a 400 bp DNA fragment of the parasite genome. Results showed that 73.9% of sheep sampled were infected with *T. vivax* with geographical locations showing prevalence rates of 73.5% (Southwest), 71.7% (Northwest) 73.5% (Northeast) and 88.0% (Northcentral). Breed prevalence were Balami (85.4%), West African Dwarf (75%), Uda (62.5%) and Yankasa (72.5%). There was a significant ($P < 0.05$) interaction of *T. vivax* and sex status on pulse rate with non-infected females showing higher pulse rates of 129.138 ± 5.57 beats per minute (bpm) compared with infected rams (111.8 ± 5.96 bpm) and infected females (122.6 ± 3.00). Also, non-infected females had higher respiratory rate with 64.4 ± 4.04 bpm compared with infected rams with respiratory rate of 51.217 ± 3.25 bpm. The interaction of *T. vivax* infection and breed on pulse rate was significantly different ($P < 0.5$) between non-infected Balami (159.3 ± 9.98 bpm) compared with infected West African Dwarf (106.7 ± 6.18 bpm) goats. Similarly, respiratory rates differed significantly ($P < 0.05$) between non-infected West African Dwarf (71.6 ± 11.31 bpm), while infected Uda had the lowest respiratory rate (53.560 ± 3.33 bpm). The interaction effect of *T. vivax* infection and sex was also significant on body weight with non-infected males weighing more (39.962 ± 4.43 kg) than infected females. Molecular diagnosis using PCR seem effective and the presence of trypanosome appears to have important implications for physiological efficiency of sheep in Nigeria.

Key words: *Trypanosoma vivax*, Nigeria, sheep

689 Polymorphism in the ovine TNXB gene and association with morphological traits and physiological status in Nigerian indigenous sheep. O. Ajayi[1], M. A. Adefenwa[2,6], B. O. Agaviezor[3,6], C. O. N. Ikeobi[1], M. Wheto[1], M. Okpeku[4], A. Yakubu[5,6], M. De Donato[6], and I. G. Imumorin*[6], *[1]Dept of Animal Breeding and Genetics, University of Agriculture, Abeokuta, Nigeria, [2]Dept of Cell Biology and Genetics, University of Lagos, Lagos, Nigeria, [3]Dept of Animal Science and Fisheries, University of Port Harcourt, Port Harcourt, Nigeria, [4]Dept of Livestock Production, Niger Delta University, Amassoma, Nigeria, [5]Dept of Animal Science, Nasarawa State University, Lafia, Nigeria, [6]Dept of Animal Science, Cornell University, Ithaca, NY.*

The major histocompatibility complex (MHC) plays an important role in the adaptive immune response of vertebrates and tenascin XB (TNXB) localizes to the MHC class III region and encodes a member of the tenascin family of extracellular matrix glycoproteins. The tenascins have anti-adhesive effects and are thought to function in matrix maturation in connective tissues such as blood vessels. Given the role of blood vessel function in adaptive physiological response, we aimed to determine the influence of variation in the ovine TNXB gene on physiological variables in Nigerian indigenous sheep in the hot humid tropics. We sequenced a 450 bp fragment of the ovine TNXB gene in 150 randomly sampled indigenous sheep, comprising 30 West African Dwarf and 40 each of Yankasa, Uda and Balami from 4 geographical zones of Nigeria, and genotyped the identified SNP using PCR-RFLP. The frequencies of genotypes TT, Tt and tt were 40.0%, 48.0% and 12.0%, respectively. While morphological traits did not significantly differ among TNXB genotypes, there were significant ($P < 0.05$) differences for pulse rates in beat per minute (bpm) [129.28 ± 6.64 (tt) versus 111.93 ± 4.05 (TT) versus 110.38 ± 3.82 bpm (Tt), respectively] and in body temperature (35.82 ± 0.65 (tt) versus 37.94 ± 0.40 (TT) versus 38.81 ± 0.370C (Tt); $P < 0.05$, respectively]. Breed x TNXB

genotype and zone x TNXB genotype interaction effects were significant ($P < 0.05$) for heart girth and body temperature, while the interaction effect of breed x sex x TNXB genotype was significant ($P < 0.05$) for body weight, rump height, heart girth and rump width, respectively. Variation in TNXB may be mediated through a possible role in connective tissue biology such as blood vessels which may in turn be a potential genetic marker for heat tolerance traits, as well as for disease resistance when validated in a larger population supported by functional studies.

Key words: Tenascin XB gene, sheep, Nigeria

690 Lean lamb production during the process of grading up to hair sheep genetics. D. K. Aaron*, D. G. Ely, E. Fink, B. T. Burden, M. E. Hoar, M. M. Simpson, and A. K. Lunsford, *University of Kentucky, Lexington.*

The overall objective of a long-term grading-up project was to track changes in production as breed composition of the flock changed from Polypay (PP) to White Dorper (WD). This portion of the project evaluated carcass characteristics of a sample of wether lambs selected for harvest from lamb crops produced from 2003 through 2010. Percentages of WD breeding in harvested lambs were 0 (PP; n = 50), 50 (1/2 WD; n = 50), 75 (3/4 WD; n = 50), 87.5 (7/8 WD; n = 35) and 93.75% or higher (WD; n = 48). Each year lambs were born in April, creep fed on pasture, and weaned at 70 d of age. Lambs were managed postweaning on pasture and supplemented with grain at 2 to 3% BW. Lambs were harvested at a live target weight of 54 kg. Data were analyzed using mixed model procedures. Orthogonal polynomials were used to partition differences among lamb genetic types (0, 50, 75, 87.5 and 93.75% or higher WD). Polypay lambs were youngest at harvest (197 d) and age increased (Linear, $P < 0.01$) as percent WD increased with 93.75% or higher WD lambs being oldest (220 d). Harvest weights decreased as percent WD increased (54.2, 54.3, 53.2, 51.3 and 52.3 kg; Linear, $P < 0.01$). Carcass weights responded quadratically (26.5, 27.4, 27.1, 26.4 and 26.3 kg; $P < 0.01$). Rack weights (1.98, 2.09, 2.25, 2.23 and 2.13 kg) and loin weights (2.38, 2.65, 2.79, 2.84 and 2.72 kg) increased linearly ($P < 0.01$) as percent WD increased. There were no differences in leg weights. Carcasses from 7/8 WD were fattest while carcasses from PP lambs were leanest (Quadratic, $P < 0.01$). Longissimus muscle area was largest for WD and smallest for PP lambs (Linear, $P < 0.01$). Yield grades were lowest for PP and WD lambs (1.8, 2.3, 2.6, 2.9 and 1.8; Cubic, $P < 0.01$). Percent closely trimmed boneless retail cuts increased as percent WD increased (48.3, 48.1, 47.9, 48 and 49.1%; Linear, $P < 0.01$). Results from this project indicate carcasses of percentage WD lambs compare favorably to those of PP lambs for most traits.

Key words: White Dorper, Polypay, carcass characteristics