

# Breeding and Genetics: Small Ruminants, Poultry, and Nontraditional Species

**719 Associations between candidate gene polymorphisms and milk production traits in Alpine goats farmed in Italy.** P. Crepaldi<sup>1</sup>, E. Mlanesi<sup>1</sup>, B. Coizet<sup>1</sup>, L. Nicoloso<sup>1</sup>, P. Fresi<sup>2</sup>, S. Murru<sup>2</sup>, R. Steri<sup>3</sup>, and N. P. P. Macciotta\*<sup>3</sup>, <sup>1</sup>Università di Milano, Milan, Italy, <sup>2</sup>ASSONAPA, Rome, Italy, <sup>3</sup>Università di Sassari, Sassari, Italy.

Milk fat yield and composition have a great economic importance in the goat industry being most of milk destined to cheese processing. The identification of genes associated with these traits could provide useful indications for breeding programs. In this work, an association study between 11 SNP polymorphisms at 3 candidate genes (acetyl-coenzyme A carboxylase, ACACA; stearoyl-CoA desaturase, SCD; lipoprotein lipase, LPL) was carried out on 59 Alpine bucks. Data from 13,331 daily records, for milk, fat, and protein yields (kg/d) and fat and protein contents (%) of 2,220 lactations were recorded on 946 goats, daughters of the 59 bucks. Associations were tested with a mixed linear model that included the fixed effects of flock, date of the test, lactation stage, kidding season, age of the goat at kidding, SNP genotype of the sire and the random effect of the goat. Four SNPs were found to be significantly associated to milk production traits (Bonferroni gene-wide adjusted significance  $P < 0.01$ ). The GC substitution at exon 1 of the LPL locus had the highest effect on milk yield (difference of about 0.6 kg/day between the 2 homozygotes CC and GG, respectively,  $P < 0.01$ ). The CT substitution at exon 45 of the ACACA locus affected milk yield and fat percentage. The deletion at the 3' untranslated region of the SCD locus affected milk, and protein (undelimited homozygotes produced about 16 g/d more than deleted ones) yield and fat percentage. Finally, the CT mutation at exon 5 of the SCD gene was associated to milk yield. These interesting associations should be obviously validated on a larger sample. Moreover, effect on other traits as milk fatty acid composition could be considered in future analyses

**Key Words:** goat, candidate genes, dairy traits

**720 Single nucleotide polymorphisms identified in polygenic traits through the use of the Ovine SNP50 BeadChip.** R. R. Cockrum\*<sup>1</sup>, N. K. Pickering<sup>2</sup>, R. M. Anderson<sup>2</sup>, D. L. Hyndman<sup>2</sup>, M. J. Bixley<sup>2</sup>, K. G. Dodds<sup>2</sup>, R. H. Stobart<sup>1</sup>, J. C. McEwan<sup>2</sup>, and K. M. Cammack<sup>1</sup>, <sup>1</sup>University of Wyoming, Laramie, <sup>2</sup>AgResearch Limited, Mosgiel, New Zealand.

High-density single nucleotide polymorphism (SNP) chips have shown promise in genome wide association studies (GWAS) to target genomic regions that play key roles in traits of economic interest. The objective of this study was to use GWAS to identify SNPs affecting polygenic traits including backfat (BF), loin eye area (LEA), ADG, birth type (BT), and scrotal circumference (SC) in sheep. Phenotypic measurements were collected on rams from 2 separate ram tests (Dual Purpose Ram Test and Blackface Ram Test) at the University of Wyoming Ram Test (n = 328) from 2009 to 2011. Blood was collected via the jugular and DNA was isolated and diluted. Single nucleotide polymorphisms in ram DNA were genotyped using the Ovine SNP50 BeadChip on the Illumina Infinium HD BeadChip Assay. Percentage loci scored per animal and locus, Hardy Weinberg deviations, animal information comparison, replicate sample reproducibility, and unusual allelic ratio analyses were conducted through Genome Studio and R for quality control analysis. A GWAS analysis was conducted in R using the GenABEL package where a polygenic model,  $Y = \mu + G + e$ , where  $\mu$  is the intercept,  $G$  is the polygene, and  $e$  is the random residual, was used to identify SNPs.

The SNP associated with *RXFP2* was used to confirm the accuracy of the polygenic model resulting in a high association ( $P = 9.283^{-04}$ ) with the horn phenotype. There were 11 and 5 SNPs for BF and ADG, respectively, that reached the genome-wide threshold ( $P \leq 9.359^{-04}$ ). Genes associated with SNPs identified in BF include *EPHBA* and *B* family, *ANK* family, *REL*, *XDH*, *RPAIN*, and *FRMPD4*, while only *KLF12* was linked to ADG. Genome-wide threshold was reached ( $P \leq 0.092^{-04}$ ) for BT (i.e., single, twin, or triplet) resulting in 10 SNPs. Genes linked to BT SNPs were *ODZ1*, *ODZ3*, *LTBP3*, and *DSCAM*. The top SNPs for SC and LEA did not reach optimum threshold as in BF, ADG, or BT; however, 3 SNPs for SC and 1 SNP for LEA achieved moderate threshold levels ( $P \leq 0.0003$ ). No genes were associated to SNPs for SC, but one gene, *AAK1*, corresponded to the SNP for LEA. Results indicate that SNPs can be identified for polygenic traits using GWAS. However, further research and validation studies will be required before implementation of marker-assisted selection strategies.

**Key Words:** polygenic, sheep, single nucleotide polymorphism

**721 Genetic parameter estimates for birth weight in three Yemeni indigenous sheep breeds.** S. Al-Shorepy\*<sup>1</sup>, M. Al-Karmah<sup>1</sup>, and Ab. Albial<sup>1</sup>, <sup>1</sup>United Arab Emirates University, Al Ain, United Arab Emirates, <sup>2</sup>Sana'a University, Sana'a, Yemen, <sup>3</sup>Agricultural Research & Extension Authority, Sana'a, Yemen.

Genetic parameters for birth weight were estimated for 3 indigenous Yemeni sheep breeds (White Boni, Barri, and Black Boni breeds), using animal model. Data were analyzed by restricted maximum likelihood (REML) using MTDFREML program. Five different animal models were fitted. Model 1 considered the animal as the only random effect. Models 2 and 3 included in addition to the additive direct effect of the animal, the additive maternal and the permanent maternal environmental effects, respectively. Model 4 fitted both the additive maternal and permanent environmental effects. Model 5 was the same as model 4, except that a covariance between the direct and the maternal additive effects. Estimates of additive direct heritability were 0.19, 0.36, and 0.38 for White Boni, Barri, Black Boni lambs, respectively. Judged by log L, introducing either additive maternal effects (model 2) or permanent environmental effects (model 3) resulted in a similar fitting as compared with model 1 in the 3 breeds. Fitting additive maternal and permanent environmental effects (model 4) resulted in a significantly better fit ( $P < 0.05$ ) compared with models 1, 2, and 3 for White Boni lambs only. Estimates of total heritability ( $h^2t$ ) from model 5 were 0.14, 0.17, and 0.53 for Barri, White Boni and Black Boni lambs, respectively. These results indicate that moderate to high estimates of direct heritability suggest further scope for improvement due to selection for higher birth weight.

**Key Words:** birth weight, direct and maternal effects, Yemeni indigenous sheep breeds

**722 Increased lean growth rate does not extend days to harvest in crossbred lambs.** G. C. Márquez\*<sup>1</sup>, W. Haresign<sup>2</sup>, M. H. Davies<sup>3</sup>, D. R. Notter<sup>1</sup>, R. Roehe<sup>4</sup>, L. Bünger<sup>4</sup>, G. Simm<sup>4</sup>, and R. M. Lewis<sup>1,4</sup>, <sup>1</sup>Virginia Tech, Blacksburg, <sup>2</sup>Aberystwyth University, Aberystwyth, UK, <sup>3</sup>ADAS Rosemaund, Preston Wynn, UK, <sup>4</sup>Scottish Agricultural College, Edinburgh, UK.

A lean growth selection index (LI) was designed for terminal sire sheep in the UK to increase lamb carcass lean weight while decreasing fat at

a constant age end point. The purpose of this study was to investigate if lambs sired by high (leaner) versus low LI rams take longer to reach target harvest condition (fat cover). Data on 6,350 crossbred lambs sired by Charollais, Suffolk and Texel rams were available. From 1999 to 2002, 15 high and 15 low LI sires from each breed were mated to 1,984 crossbred ewes at 3 farms in the UK. Most rams were used for 2 mating seasons, and some were rotated among farms to create genetic links. Lambs were reared on pasture and, from 10 weeks of age, were visually assessed bi-weekly for fat cover until they reached a target condition of 11% subcutaneous fat (estimated) for harvest. The mean days to harvest (DTH) were 180 (SE 1.1) for high LI sires, 176 (SE 1.0) for low LI, 182 (SE 1.2) for Charollais, 182 (SE 1.3) for Suffolk, and 170 (SE 1.3) d for Texel. A semiparametric Cox proportional hazard model was fitted to DTH. The analysis was stratified by lamb rearing type because the hazard for DTH differed for single and twin reared lambs. Fixed effects were sire index, sire breed, dam breed, sex, age of dam, fat class (visual classification of harvest condition), birth year, farm, and birth year-farm interaction. Random effects were sire (considering the relationship matrix among sires) and rearing dam. Likelihood ratio tests indicated that all fixed effects were significant ( $P < 0.001$ ) except sire index ( $P = 0.5$ ) and dam breed ( $P = 0.1$ ). There was no difference in hazard ratio (HR) between lambs sired by high and low index sires, or between lambs sired by Charollais and Suffolk rams ( $P = 0.8$ ). However, Texel-sired lambs had fewer DTH than Suffolk-sired lambs (HR = 1.44,  $P < 0.001$ ). No significant interaction between sire index and breed was found. The HR increased with increasing age of the dam. Heritability of DTH was estimated as 14%. The similar DTH in lambs sired by high as compared with low LI rams is favorable, because it implies that leaner lambs reach acceptable harvest condition without extending their finishing period.

**Key Words:** crossbred lambs, lean index selection, survival analysis

**723 Evaluation of environmental factors affecting the speed of racing camels in the United Arab Emirates.** S. Al-Shorepy,\* S. Al Mansouri, and Z. Al Katheeri, *United Arab Emirates University, Al Ain, United Arab Emirates.*

Camel racing is a deep-rooted traditional sport that finds its origins in the desert culture of the Arabian Peninsula, North Africa, and the Middle East. In United Arab Emirates (UAE), camel racing is very popular and has become a part of tradition and culture. Therefore, the aim of the present study was to evaluate environmental factors affecting speed of racing camels in UAE. The data used in this study were obtained from UAE Camel Race Association, from year 2007 to 2011 and the trait evaluated was racing speed (m/s) for total distance and for the last 1000 m. Five hundred ten races with around 40 camels per race of varying distances were evaluated for which the first 10 winners were determined. The full linear model included the effect of year, age, sex, breed, racetrack, and type. In each race, 3 categories were considered for analysis; fastest 10, fastest 3, and the fastest camels. Overall average speed of the races was 10.40 m/s (SD = 0.37; range: 8.3–13.5 m/s), with a coefficient of variation of 3.6% and the effects included in the analytical model formed  $R^2$  of 85.5%. The average speed for the last 1000 m was 10.87 m/s with maximum speed of 16.1 m/s. Speed significantly ( $P < 0.05$ ) decreased with the age in the 3 categories (fastest 10, fastest 3 and the fastest). Females were significantly ( $P < 0.05$ ) superior to males in the 3 categories evaluated. Similarly, purebred (thoroughbred) camels were faster ( $P < 0.05$ ) than the crossbred camels in the tested categories. The sex by breed interaction had no significant effects on race speed in the 3 categories. Understanding the role of environmental factors in racing camels might assist owners, trainers, and others to optimize the

performance of camels under their care. Moreover, determining these factors is a fundamental step in developing a selection program to improve the racing speed of racing camels.

**Key Words:** racing camels, environmental factors, racing speed

**724 Influence of genomic predictors on yearling sales price and total career earnings in Thoroughbred racehorses.** C. R. Davis\*<sup>1,2</sup>, E. W. Hill<sup>1,2</sup>, and A. G. Fahey<sup>1</sup>, <sup>1</sup>*School of Agriculture and Food Science, University College Dublin, Belfield, Dublin 4, Ireland,* <sup>2</sup>*Equinome Ltd., NovaUCD, Belfield Innovation Park, Belfield, Dublin 4, Ireland.*

Many factors contribute to the yearling sales price (YSP) and total career earnings (TCE) of Thoroughbred horses. The aim of this study was to identify the most influential factors and determine if the addition of genomic information [e.g., genomic predictors (GP) provided by the Equinome Elite Performance Test; www.equinome.com] improves predictions of TCE. Individual, sire, dam, sale and racing information was collected for 256 Thoroughbreds from 4 countries (Ireland, Great Britain, United States, and France). Correlation and regression analyses were performed on the data. TCE had a correlation of 0.23 with GP and 0.15 with YSP. Linear mixed regression analysis identified the main contributing factors to YSP and TCE; the regression model for YSP obtained an  $R^2 = 0.49$  without GP information and an  $R^2 = 0.53$  with GP included. The main factors influencing sales price ( $P < 0.05$ ) were identified as GP, year of sale, parity of the dam, number of winning offspring of the dam, number of races won per crop of foals of the sire and stud fee paid for the covering. The regression model for TCE (in the form of Earnings per start) obtained an  $R^2 = 0.39$  without GP and an  $R^2 = 0.57$  when GP information was included. These data indicate that genomic predictors have a considerable influence on the TCE of a horse. The most influential factors influencing TCE ( $P < 0.05$ ) were GP, month of birth within the year of sale, sex, whether or not the dam was a winner, the number of black type offspring of the dam, parity of the dam and races won per crop of foals of the sire. The results showed GP to have a significant ( $P < 0.05$ ) influence in both models and therefore highlights the contribution that genomic information can have in decision making. This study illustrates that genomic information can enable owners, breeders and trainers to better judge the value of a horse by determining its genetic potential for racing and breeding.

**Key Words:** genomic, performance, regression

**725 Genetic variation study in Pakistani buffalo breeds using microsatellite markers.** T. Hussain\*<sup>1,2</sup>, M. E. Babar<sup>1</sup>, M. Imran<sup>1</sup>, A. Nadeem<sup>1</sup>, A. Ali<sup>1</sup>, R. Saif<sup>1</sup>, A. Wajid<sup>1</sup>, M. De Donato<sup>2,3</sup>, S. O. Peters<sup>2</sup>, and I. G. Imumorin<sup>2</sup>, <sup>1</sup>*Institute of Biochemistry and Biotechnology, University of Veterinary and Animal Sciences, Lahore, Pakistan,* <sup>2</sup>*Dept. Animal Science, Cornell University, Ithaca, NY,* <sup>3</sup>*IIBCA, Universidad de Oriente, Cumana, Venezuela.*

To assess the status of genetic diversity in Pakistani buffalo, 19 microsatellite loci were genotyped to obtain data on 184 DNA samples from all 5 native buffalo breeds (Nili, Ravi, Nili Ravi, Kundhi and Azakheli). All loci showed polymorphism in each breed. The observed number of alleles ranged from 8 (ETH10, ILSTS049, ETH225, CSSM66) to 24 (TGLA227) with a mean value of 13.368 alleles per locus. The effective number of alleles across all loci was as usual lower than the observed values with a mean value of 3.207 alleles per locus. The average observed and expected heterozygosity values across all polymorphic loci in all studied buffalo breeds were estimated to be 0.283 and 0.648

respectively. The overall value for Polymorphic Information Content (PIC) for all markers was 0.56 suggesting their appropriateness for genetic diversity analysis in buffalo. The mean  $F_{is}$ ,  $F_{it}$ , and  $F_{st}$  values were 0.511, 0.570 and 0.120 respectively. The 5 buffalo populations were genetically less diverse as indicated by a small mean  $F_{st}$  value. The average gene flow ( $Nm$ ) indicative of population migration was calculated as 1.817. The Nei's (1972) original measures of genetic distance ( $D_s$ ) revealed ancient divergence of Nili-Ravi and Azakheli ( $D_s = 0.3018$ ) and recent divergence of Nili and Ravi ( $D_s = 0.0468$ ). These estimates of genetic diversity were seen in coincidence with phenotypic differentiation among the studied buffalo breeds. The present study results can facilitate the future researchers interested in further studies in buffalo as well as other livestock breeds of Pakistan.

**Key Words:** genetic diversity, microsatellite markers, buffalo breeds

**726 Analysis of egg production using a random regression model with genomic relationships in layer chickens.** A. Wolc<sup>\*1,2</sup>, J. Arango<sup>3</sup>, P. Settar<sup>3</sup>, J. E. Fulton<sup>3</sup>, N. P. O'Sullivan<sup>3</sup>, R. Preisinger<sup>4</sup>, D. Habier<sup>2</sup>, R. Fernando<sup>2</sup>, D. J. Garrick<sup>2</sup>, and J. C. M. Dekkers<sup>2</sup>, <sup>1</sup>*Poznan University of Life Sciences, Poznan, Poland*, <sup>2</sup>*Iowa State University, Ames*, <sup>3</sup>*Hy-Line International, Dallas Center, IA*, <sup>4</sup>*Lohmann Tierzucht GmbH, Cuxhaven, Germany*.

Random regression models (RRM) can account for the longitudinal nature of egg production which, together with the use of genomic information, are expected to increase accuracy of selection compared with using only mean production and pedigree information. The objective

of this study was to estimate variance components for egg production at various ages in a commercial brown egg layer population using genomic relationship information. A random regression reduced animal model with a marker-based relationship matrix (VanRaden, 2008) was used to estimate genomic breeding values of 3,908 genotyped animals from 6 generations. The first 5 generations were used for training, with predictions validated in generation 6. Daily egg production up to 46 weeks in lay was cumulated into 85,462 bi-weekly records for training, of which 17,570 were recorded on genotyped hens and the remaining on their non-genotyped progeny. The model for bi-weekly records included fifth-order Legendre polynomials nested within hatch-week as fixed effects. Random terms were quadratic polynomials for genetic and permanent environmental components, and residual variances that were uncorrelated and heterogeneous. Models with pedigree based or genomic relationships were used. Estimates of residual variation were very similar for both measures of relationship but the model with genomic relationships estimated a higher proportion of genetic variance. Heritability estimates increased with age up to mid production and decreased thereafter, resulting in average heritability of 0.20 or 0.33 for pedigree or genomic relationships. Predictions of total 46-week egg number and of most biweekly periods were more accurate with genomic than pedigree relationships (correlations with progeny performance of 0.26 vs. 0.16). In conclusion, random regression reduced animal models can be utilized in breeding programs using genomic information, resulting in substantial improvement of accuracy of selection for longitudinal traits. Practical implementation depends on computing and genotyping strategies to minimize costs to make such an approach cost effective.

**Key Words:** egg production, random regression model, GBLUP