Breeding and Genetics: Dairy, Sheep & Goat - Crossbreeding, Inbreeding and Breed Conservation

757   Genetic variation in the threshold of sensitivity to heat stress in Holsteins. J. P. Sánchez*[1], R. Rekaya[2], I. Aguilar[2], and I. Misztal[2,3], [1]*Universidad de León, Campus de Vegazana, León, Spain*, [2]*University of Georgia, Athens*, [3]*Instituto Nacional de Investigación Agropecuaria, Estación Las Brujas, Canelones, Uruguay*.

Past studies in genetics of heat tolerance assumed a fixed threshold in sensitivity to heat stress. The objective of this study was to assess genetic variation in individual variability to that threshold. Data included 379,833 first-parity test day records on 40,986 Holsteins heifers in US, sired by 327 bulls. Inferences were obtained by a Bayesian non-linear hierarchical sire model. Effects in the model included DIM x milking frequency, HYS of the milking day, and two sire effects: the intercept (I_S) and the regression (S_S) on the Temperature-humidity index (THI) above a sire specific threshold (T_S). In the second hierarchical stage the means and (co)variances of I_S, S_S and T_S were estimated using a linear model. The estimated average of the threshold across sires was 22.7(0.20) THI C°, and its variance 4.0(0.74). The marginal posterior mean for the heritability (marginal posterior standard deviation) in the absence of heat stress was 0.083(0.006), and it increased to 0.46(0.047) at 30 THI C°. The DIC indicated a superiority of this model compared to a model where the threshold was fixed for all sires. Genetic variability exists for the threshold of heat stress; however, the threshold can only be well estimated for popular sires. Very fast rise in heritability with increasing THI may be an artifact of a sire model. It would be useful to extend the current methodology to animal models, however, after preliminary analyses, the computing time would be high and convergence could be hard to obtain.

Key Words: Heat Tolerance, Hierarchical Model, Non-Linear Reaction Norm

758   *In situ* goat conservation population and selection for parasite resistance. J. M. Dzakuma*[1], B. M. Johnson[1], N. C. Beckford[1], L. C. Nuti[1], and T. M. Craig[2], [1]*Prairie View A&M University, Prairie View, TX*, [2]*Texas A&M University, College Station*.

In 2002 the International Goat Research Center at Prairie View A&M University obtained animals from 3 goat breeds - the Tennessee Stiff-legged (TS) or Myotonic, the Spanish (SP) and the Boer (BR) - and established them in live populations (*in situ*) for use in a conservation program. Genetic materials are collected and preserved on this population. Simultaneously, we also collect, and preserve germplasm (*ex situ* conservation) from available breeds and strains of goats.

Kids produced from this population are challenged, orally each year, with one large dose of 5000 infective *Haemonchus contortus* larvae per animal to evaluate the impact of management treatments on growth weight (WT), fecal egg count (FEC), blood packed cell volume (PCV) and serum protein levels (SPL). The objective was to compare resistance or tolerance to parasites. The initial experimental design in 2004 included: (1) 32 kids were maintained on pasture as the control; (2) 74 kids challenged and maintained on concrete floors; (3) 74 kids maintained on concrete floors without challenge; and (4) 72 kids were challenged and maintained on pasture. Body weights, fecal and blood samples were collected on day zero to establish initial baseline samples before kids were challenged. Weights and samples were taken weekly for 8 weeks. Statistical analyses were performed using SAS Proc Mixed. Variables were: WT, FEC, PCV and SPL. Sources of variation were: breed, sex, treatment, kid ID, time and all interactions.

Results from the 2004 initial trial indicated that progress could be made by selecting goats, for both high and low tolerance to *Haemonchus*, by selecting from those that are artificially challenged and maintained on pasture. From the 3 breeds used in the initial study, and for FEC (egg/gm) and PCV (%), respectively: BR (485.2±61.6; 25.6±0.4), SP (308.2±53.8; 30.5±0.3) and TS (301.9±40.6; 29.4±0.3). The BR breed appears to be significantly less resistant (P<.02) to the parasite load than the SP and TS that were similar (P>.05). Statistically significant differences were observed for WT and SPL. Results from 2005-2007 (challenged and pastured) followed a similar pattern. Individuals within breed analyses will be presented.

Key Words: Goats Spanish Boer, Tennessee Stiff-Legged, *Haemonchus Contortus*

759   Genetic diversity of US sheep breeds. H. Blackburn*[1], M. Brown[2], S. Wildeus[3], R. Stobart[4], D. Bixby[5], J. Dzakuma[6], S. Ericsson[7], W. Getz[8], N. Cockett[9], D. Matsas[10], C. Welsh[1], S. Spiller[1], and D. Waldron[11], [1]*ARS National Animal Germplasm Program, Ft. Collins, CO*, [2]*ARS Grazing Lands Research, El Reno, OK*, [3]*Virginia State University, Petersburg*, [4]*University of Wyoming, Laramie*, [5]*American Livestock Breeds Conservancy, Pittsboro, NC*, [6]*Prairie View A&M University, Prairie View, TX*, [7]*Sul Ross University, Alpine, TX*, [8]*Fort Valley State University, Fort Valley, GA*, [9]*Utah State University, Logan*, [10]*Tufts University, North Grafton, MA*, [11]*Texas A&M University, San Angelo*.

Understanding the genetic relationships between US sheep breeds is useful in developing conservation strategies and actions. A broad sampling of individual sheep from 28 breeds was performed. Breed types included: fine wool, meat types, long wool, hair, prolific, and fat tailed. Blood and semen samples (n=660) were derived from 222 breeders in 38 states. DNA was extracted from the samples and genotyped using the FAO/ISAG panel of 31 microsatellites, however, based on amplification success only 28 markers were used in the analysis. Genotyping data were analyzed using GENALEX, PHYLIP and STRUCTURE. The following breeds were found to have relatively high inbreeding values: Columbia (0.60), Gulf Coast Native (0.54), Jacob (0.52), and Targhee (0.62) suggesting genetic diversity is an issue for rare breeds and some commercially popular breeds. The average number of alleles per breed ranged from 3.67 (Black Welsh Mountain) to 7.89 (Rambouillet). Private alleles ranged from one to five and were found in 22 breeds. There were six breeds with no private alleles. Of interest were the high frequencies of three private alleles in the Tunis (0.62 and 0.15) and Warhill (0.30) breeds. Nei's genetic distances were computed and ranged from 0.08 for Hampshire:Suffolk to 0.80 for the combinations of Blackbelly Barbados:Black Welsh Mountain, and Hog Island:Tunis. Data were clustered using STRUCTURE assuming 28, 20, 19, and 15 clusters; the assignments from these runs suggest the number of clusters for this dataset is 19. Breeds showing a constant grouping with one another included: Rambouillet:Warhill, Hampshire:Suffolk, Barbados Blackbelly:St Croix, Cotswold:Lincoln, and Columbia:Targhee:Dorset:Polypay. These data provide a baseline for determining the degree of

genetic similarity/dissimilarity between many US sheep breeds. With this information germplasm collection activities can be refined, thereby ensuring that germplasm collections capture the genetic diversity needed to safely conserve sheep populations.

Key Words: Genetic Diversity, Sheep, Conservation

760   Heterogeneity of founder-specific inbreeding depression on birth BW of Ripollesa lambs.   J. Casellas*[1], J. Piedrafita[2], G. Caja[2], and L. Varona[1,3], [1]*Genètica i Millora Animal, IRTA-Lleida, Lleida, Spain*, [2]*Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, Bellaterra, Spain*, [3]*Departamento de Anatomía, Embriología y Genética Animal, Universidad de Zaragoza, Zaragoza, Spain*.

Estimates of inbreeding depression are usually obtained by modeling the overall inbreeding coefficient of each individual, without considering that heterogeneity between founders could be anticipated. Inbreeding has special relevance in local and endangered sheep breeds, whose flocks are characterized by small size, limited genetic connectedness and small number of rams per generation. The objective of this research was to examine heterogeneity in founder-specific inbreeding depression (FSID) effects on lamb birth BW. Data were recorded in the Ripollesa experimental flock of the Universitat Autònoma of Barcelona (Spain), between 1986 and 2007, and included 2,459 birth BW records (3.29 ± 0.02 kg) from 1,634 parturitions and 384 ewes. The operational model accounted for birth type, sex, year of birth, environmental dam effect and infinitesimal genetic effect, as well as FSID effects from 9 founders contributing with more than 50 inbred lambs with phenotypic data. Birth BW was analyzed under a linear animal model solved through Bayesian inference, and each FSID effect was appropriately tested by an empirical Bayes factor (BF; model including the FSID effect against model excluding the FSID effect). Four founders showed null FSID effects with BF ranged between 0.05 and 0.42. The remaining 5 founders showed relevant FSID effects, birth BW being reduced between -8 g (BF = 1.42) and -96 g (BF = 8.80×10^{19}) for each 1% increase in inbreeding. Note that those estimates were obtained from a small range of partial inbreeding coefficients (0% to 10%), and they must be seen with caution outside that range of values. These results revealed a substantial degree of between-founders heterogeneity of FSID effects, where null and negative effects were reported on birth BW of Ripollesa lambs.

Key Words: Birth Weight, Inbreeding Depression, Ripollesa Breed

761   Type appraisal of Holsteins, Jerseys, and reciprocal crosses under two classification systems.   B. G. Cassell*[1], K. M. Olson[1], and A. J. McAllister[2], [1]*Virginia Polytechnic Institute and State University, Blacksburg*, [2]*University of Kentucky, Lexington*.

Holstein appraisers scored Holsteins (HH) and two reciprocal crosses, (HJ and JH with breed of sire first) while Jersey (JJ) appraisers scored JJ, HJ, and JH crosses in the Virginia Tech and Kentucky university dairy herds. Holstein appraisers visited each herd twice scoring 115 HH, HJ, and JH cows. Jersey appraisers visited Virginia Tech twice and Kentucky once scoring 86 JJ, HJ, and JH cows. Fifty four HJ and JH cows were scored on both systems. Only first available appraisals, whether in first or second lactation, were used. Purebreds were compared to crossbreds within the Holstein or Jersey appraisal system using a single score per cow and a fixed model including lactation, age fresh within lactation, station, appraiser within station, days in milk when scored, and breed. Interest was in breed differences. Crossbred cows scored on both systems were analyzed using two scores per cow in a mixed model including random cow within breed, the effects in the previous fixed model, plus appraisal system, station by system, and appraiser nested within station and system. Interest was in system differences. From the fixed analysis, HJ and JH scored significantly lower than HH for final classification (70 and 71 points versus 79), were significantly shorter than HH, with less strength and deeper udders. Front teat placement favored HJ and JH over HH. In the Jersey system, final score was not different for HJ, JH, and JJ breed groups, while crosses were taller than JJ with wider rear udders. Crosses and purebreds were not significantly different in either system for almost all other traits. In the mixed model comparing Holstein and Jersey systems, we observed system differences in final score, dairy form, stature, strength, foot angle, udder depth, and front teat placement. Breed systems assigned similar scores for rump angle, rear udder height and width, udder cleft, and teat length. In general, crossbred conformation was more acceptable to Jersey than to Holstein type standards.

Key Words: Crossbreeding, Dairy, Type Appraisal

762   Montbeliarde-sired crossbred cows compared to pure Holstein cows for production, SCS, days open, and body condition score during their first two lactations.   A. R. Hazel*, B. J. Heins, L. B. Hansen, A. J. Seykora, D. G. Johnson, J. G. Linn, and J. E. Romano, *University of Minnesota, Saint Paul*.

Montbeliarde-sired crossbred (**MX**) cows (n = 83) were compared to pure Holstein cows (n = 61) for 305-d milk, fat, and protein production; SCS; days open (**DO**); and BCS during their first two lactations. Cows were in two research herds of the University of Minnesota and calved from October 2005 to December 2007. Best Prediction was used to determine actual production for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. For DO, cows were required to be at least 250 d in milk and those with greater than 250 d for DO were truncated to 250 d. First and second lactations of cows were analyzed separately. Independent variables for statistical analysis were the fixed effects of herd, season (fall or spring) nested within herd, breed group, and two-breed (Montbeliarde × Holstein) vs. three-breed (Montbeliarde × Jersey/Holstein) crossbred nested within breed group. Age in months at calving and days in milk were also covariates for BCS. The MX and pure Holstein cows were not significantly different for fat plus protein production during first lactation (493 kg vs. 502 kg, respectively) and second lactation (617 kg vs. 618 kg, respectively). Also, MX cows (2.74) were not significantly different from pure Holstein cows (2.66) for SCS during first lactation; however, MX cows (1.53) had significantly ($P < 0.01$) lower SCS than Holstein cows (2.51) during second lactation. During first lactation, MX cows (121 d) had significantly ($P < 0.01$) fewer days open (40 d) than pure Holstein cows (161 d). The MX cows carried significantly ($P < 0.01$) more body condition than pure Holstein cows during both first lactation (3.22 vs. 2.77, respectively) and second lactation (3.27 vs. 2.65, respectively).

Key Words: Crossbreeding, Heterosis, Montbeliarde

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763   Jersey × Holstein crossbred cows compared to pure Holstein cows for production, SCS, days open, body condition score, and udder measurements during the first three lactations. B. J. Heins*, A. R. Hazel, L. B. Hansen, A. J. Seykora, D. G. Johnson, J. G. Linn, and J. E. Romano, *University of Minnesota*, *Saint Paul*.

Jersey × Holstein crossbred (**J×H**, n = 76) cows were compared to pure Holstein (n = 73) cows for 305-d milk, fat, and protein production; SCS; days open (**DO**); BCS; and udder measurements during the first three lactations. Cows were in two research herds of the University of Minnesota and calved from September 2003 to June 2007. Best Prediction was used to determine actual production for 305-d lactations with adjustment for age at calving, and records less than 305 d were projected to 305 d. For DO, cows were required to be at least 250 d in milk and those with greater than 250 d for DO were truncated to 250 d. Independent variables for statistical analysis were the fixed effects of herd, season (fall or spring) nested within herd, and breed group. During first lactation, J×H (497 kg) and pure Holstein (515 kg) cows were not significantly different for fat plus protein production. However, during second (577 kg vs. 608 kg) and third (598 kg vs. 641 kg) lactations, J×H cows were significantly ($P < 0.01$) lower for fat plus protein production than pure Holstein cows. The J×H cows were not significantly different from pure Holstein cows for SCS during first and second lactations; however, J×H cows (4.00) had significantly ($P < 0.05$) higher SCS than pure Holstein cows (3.20) during third lactation. The J×H cows tended ($P < 0.10$) to have fewer days open than pure Holstein cows (127 d vs. 150 d) in first lactation and had significantly ($P < 0.01$) fewer days open than pure Holstein cows (130 d vs. 162 d) in second lactation. For BCS, J×H cows had significantly ($P < 0.05$) greater body condition (2.80 vs. 2.71 and 2.96 vs. 2.85) than pure Holstein cows in first and second lactations, respectively. For udder measurements, J×H cows had significantly ($P < 0.01$) less udder clearance than pure Holstein cows in first (47.7 cm vs. 54.6 cm) and second (41.7 cm vs. 50.2 cm) lactations. Furthermore, J×H cows had significantly ($P < 0.01$) greater distance between front teats in first (15.8 cm vs. 14.0 cm) and second (17.0 cm vs. 14.7 cm) lactation than pure Holstein cows.

Key Words: Crossbreeding, Heterosis, Jersey

764   Number of services per conception, estimated calving interval and lactation length in New Zealand and Mexican Holstein cows in Torreon, Coahuila, Mexico, Case study. T. B. Garcia-Peniche*[1] and A. Aranda-Munguia[2], [1]*Instituto Nacional de Investigaciones Forestales Agricolas y Pecuarias*, *Paso del Toro, Veracruz, Mexico*, [2]*Establo La Montaña*, *Torreon, Coahuila, Mexico*.

This work compares calving interval (CI), empty time (Emp), number of services per conception (NuIns), and lactation length (TotDIM) in Holstein cows from 3 origins (breedtyp): imported as pregnant heifers from New Zealand (NZ), born in Mexico, from New Zealand dams (d_NZ) or from American parentage (d_EUA). All the cows were in the same herd in an intensively managed, confined dairy in Torreon, Coahuila, Mexico. Data were obtained from 15 test days from March 2007 to January 2008. Records from 1657 dry cows (73% NZ, 20.6% d_EUA and 6.4% d_NZ) provided information about totDIM, as well as days pregnant (days_preg) and days dry (dd). Assuming a pregnancy length of 283 d, the time that the cows are expected to remain dry can be calculated from 283 d minus the reported days_preg. Thus, CI was estimated as: { [(283-days_preg) + dd] + TotDIM }, and EMP = CI-283. The NuIns were directly obtained from the records of 2006 pregnant

cows in production (68% NZ, 8.4% d_NZ, and 20.6% d_EUA). No interaction was found between breedtyp with either lactation number (1 to 3) or season of conception, yet the models were adjusted for those effects. The data were analyzed using SAS® 9.1. Calving interval, EMP and totDIM were analyzed with the MIXED procedure, while NuIns was assumed to follow a poisson distribution and analyzed with the GENMOD procedure. Total time that the cows remained dry was also analyzed, but no differences for breedtyp were found. There were no significant differences between d_EUA and d_NZ for CI, TotDIM and EMP, as the Table shows. The expected NuIns values have the Wald 95% confidence lower and upper limits between parentheses, and the letters a and b show that no significant Chi-square difference was found between NZ and d_EUA. The total time that the cow remains dry is a trait derived from management and showed no breedtyp difference, however, results show that the longer CI in NZ comes both from longer lactations (totDIM) and more difficulties in achieving pregnancies (larger EMP and NuIns) in this study.

Table 1. Calving interval (CI), empty time (EMP), lactation length (totDIM), and number of services per conception (NuIns) in New Zealand (NZ) and Mexican (d_NZ and d_EUA) Holstein cows

Origin	CI (d)	EMP (d)	totDIM (d)	NuINs
NZ	418.3 ± 4.7 a	135.3 ± 4.7 a	332.5 ± 4.3 a	3 (2.67 - 3.36) a
d_NZ	383.2 ± 10.1 b	100.2 ± 10.0 b	297.2 ± 9.2 b	2.5 (2.16-2.99) b
d_EUA	382.0 ± 7.2 b	99.0 ± 7.2 b	297.8 ± 6.6 b	2.9 (2.73–3.03) a

d_NZ are daughters of New Zealand dams, d_EUA are cows with American parentage

Key Words: Fertility, Lactation Length, Mexican Dairies

765   Puberty and conception in Holsteins, Jerseys and reciprocal crossbred heifers. W. J. Silvia*[1], K. G. Hall[2], C. M. Williams[3], A. J. McAllister[1], B. G. Cassell[2], and S. P. Washburn[3], [1]*University of Kentucky*, *Lexington*, [2]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [3]*North Carolina State University*, *Raleigh*.

Reproductive performance was compared in purebred Holstein (HH, n=54), Jersey (JJ, n=35) and reciprocal crossbred heifers (HJ, n=45 and JH, n=37; sire breed first) from 3 research herds. Blood samples were collected at weekly intervals beginning at approximately 8 mo of age for quantification of progesterone. Age at puberty was defined as difference in days between birth and the first date on which a significant increase in progesterone was observed. Heifers were bred by artificial insemination following visual detection of estrus beginning at 15 mo of age. The number of services required for each heifer to become pregnant was recorded. Age at first service and age at conception were also determined. Genetic group comparisons for quantitative variables were made using a fixed model with additive, maternal, and heterotic genetic effects partitioned. Effects of herd, season of birth (win:Jan-Mar, spr:Apr-Jun, sum:Jul-Sept, fall:Oct-Dec) and year of birth (2003-2006) were also included in the model. Percentages of heifers requiring 2 or fewer services to conceive were compared among breed groups by logistic regression with additive, maternal, and heterotic effects partitioned. Age at puberty differed across breed groups with significant additive and heterosis effects: LSMEANS: HH = 349 ± 11.2 d; HJ = 315 ±11.0

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d; JH = 304 ± 11.7 d; and JJ = 300 ± 10.8 d. Also, proportions of heifers pregnant after 2 services differed by breed group with significant heterosis: HH = 83.6%; HJ = 91.7%; JH = 91.1%; JJ = 66.7%. Trends for heterosis were observed for number of services (P = 0.10) and for age at conception (P = 0.07). There were no effects of genetic group on age at first service, service interval, or total breeding period. In conclusion, beneficial heterotic effects were observed on age at puberty and percentage of heifers conceiving to 1 or 2 services.

Key Words: Puberty, Conception, Crossbred

766 Production, conformation, health, and fertility of backcross Holstein × Jersey cattle and their Holstein contemporaries. K. A. Weigel*, P. C. Hoffman, C. Maltecca, and T. J. Halbach, *University of Wisconsin, Madison*.

Since 2003, lactating Holstein cows in the University of Wisconsin herd have been randomly mated to Holstein young sires or F1 Jersey × Holstein young sires, resulting in an experimental population of 75% Holstein × 25% Jersey females and a control population of pure Holstein females. Age at first calving tended to be lower in crossbred cows (N = 64) than in Holstein cows (N = 98) (721 d vs. 731 d; P < 0.10), and crossbred cows weighed less at first calving (562 kg vs. 601 kg; P < 0.01). Crossbred cows had higher dystocia scores at first calving than Holsteins (2.27 vs. 1.73; P < 0.01), despite the fact that their calves were lighter (37.6 kg vs. 40.5 kg; P < 0.01). In first lactation, average daily milk yield of crossbreds was lower than that of Holsteins (26.3 kg vs. 29.4 kg; P < 0.01), as was peak daily milk yield (31.0 kg vs. 35.1 kg; P < 0.01) and total 305-d milk yield (7647 kg vs. 8737 kg; P < 0.01), but protein percentage of crossbreds was higher (3.12 vs. 3.00; P < 0.05). On a 50-point scale, crossbred cows had shorter stature (21.2 vs. 35.2; P < 0.01), more sloped rumps (32.3 vs. 28.0; P < 0.05), narrower rumps (24.0 vs. 30.2; P < 0.01), and longer teats (22.1 vs. 17.7; P < 0.01) and tended to have deeper udders (21.9 vs. 24.5; P < 0.10) than Holsteins. Milking duration tended to be longer in crossbreds than in Holsteins (5.2 min vs. 4.9 min; P < 0.10). Differences between breeds in fat percentage, somatic cell score, body condition score, and other linear type traits were not statistically significant (P < 0.10), nor were differences in days open, services per conception, or the incidence of mastitis, lameness, retained placenta, ketosis, or respiratory disease.

Key Words: Crossbreeding, Production, Conformation

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