

Breeding and Genetics: Crossbreeding

430 Application of a crossbred model reveals additional genetic variation in reproduction traits of commercial females. S. Bloemhof^{1,2}, E. F. Knol¹, A. Kause², and I. Misztal³, ¹*IPG, Institute for Pig Genetics B.V., Beuningen, the Netherlands*, ²*Animal Breeding and Genomics Centre, Wageningen University, Wageningen, the Netherlands*, ³*Department of Animal and Dairy Science, University of Georgia, Athens*.

The objective of our study was to estimate genetic parameters for litter size and farrowing rate in a data set of 2 pure lines and the corresponding crossbreds. Data were obtained from the TOPIGS database and included 91,461 cycle records from 23,432 sows on 33 farms in Spain and Portugal collected from 2003 to 2008. Sows originated from two lines, namely Yorkshire (D) and Large White (I), and from their crosses (DI). Traits studied were litter size (1 to 29) and farrowing rate (0 or 1). Litter size was analyzed using a linear animal model and farrowing rate was analyzed using a threshold model. Both models included fixed effects of parity and number of inseminations, and random effects of herd-year-month, service sire, permanent environment, and the additive animal effect. Within-line and crossbred variance components were estimated via Gibbs sampling. Within-line heritability estimates for litter size were 0.05±0.01 for line D, 0.11±0.01 for line I, and 0.08±0.02 for line DI. Heritability estimates for litter size, obtained from the crossbred model, were 0.06±0.01 for line D, 0.11±0.01 for line I, and 0.14±0.03 for line DI. Genetic correlations for litter size were 0.81±0.15 between line D and line DI, and 0.85±0.06 between line I and line DI. Within line heritability estimates for farrowing rate were 0.06±0.01 for line D, 0.07±0.01 for line I, and 0.02±0.01 for line DI. Heritability estimates for farrowing rate, obtained from the crossbred model, were 0.07±0.01 for line D, 0.07±0.01 for line I, and 0.10±0.04 for line DI. Genetic correlations for farrowing rate were 0.57±0.57 between line D and line DI, and 0.50±0.25 between line I and line DI.

Estimates for genetic variation in litter size almost doubled (0.76 to 1.36) and for farrowing rate more than quadrupled (0.02 to 0.12) when pure line data were added to the crossbred dataset. Genetic correlations between pure line and crossbred data were (considerably) less than unity. These results indicate that pig breeders are advised to introduce crossbred data in their routine evaluations to increase genetic progress at commercial level.

Key Words: pig breeding, crossbred model, reproduction

431 Genetics-nutrition interactions influencing wool spinning fineness in Australian crossbred sheep. A. E. O. Malau-Aduli* and B. Holman, *School of Agricultural Science/TIAR, University of Tasmania, Hobart, Tasmania 7001, Australia*.

Our objective in this study was to investigate the interactions between sire genetics, supplement and gender on spinning fineness (SF) in crossbred sheep either grazing or supplemented with dietary protein. Correlations between SF and other wool traits were also investigated. We utilized 5 sires (Texel, Coopworth, White Suffolk, East-Friesian and Dorset) and mated them with 500 Merino ewes at a ratio of 1:100 in individual paddocks. Five hundred of the F1 progeny were raised on rye grass until weaning at 12 weeks of age. Forty of the weaners with initial BW range of 23–31 kg (average of 27 ± 3.2 kg) were subjected to a supplementary feeding trial that lasted for 6 weeks. They were randomly assigned to 4 treatment groups in a 5 × 2 × 2 × 2 factorial experimental design representing 5 sire breeds, 2 supplementary feeds (canola and

lupins), 2 feeding levels (1 and 2% BW) and 2 sexes (ewes and wethers). SF of the wool was commercially measured at the Australian Wool Testing Authority. The data were statistically analyzed in SAS using MIXED models procedures with sire fitted as a random effect, while sire breed, supplement, level of supplementation and gender and their interactions were fitted as fixed effects. We found highly significant interactions between sire breed × level of feeding ($P < 0.0043$) and sire breed × gender ($P < 0.019$) on SF that ranged from 22.7 ± 0.16 microns in White Suffolk-sired progeny to 25.1 ± 0.21 in East-Friesian crosses. Coopworth-sired sheep supplemented with either canola or lupins at 1% BW recorded the highest spinning fineness. There were significant correlations between SF and wool fiber diameter (0.93), CV of fiber diameter (-0.40), wool curvature (-0.12) and wool yield (0.10). We concluded that the significant interactions between sire genetics and nutrition would impact on choices sheep farmers make in selecting sires and supplementary feeding levels to achieve desirable spinning fineness in their crossbreds. The correlations between spinning fineness and other wool traits should be taken into account when designing breeding programmes.

Key Words: spinning fineness, wool, sheep

432 Effects of index selection and sire breed on crossbred lamb growth and finishing. G. C. Márquez¹, W. Haresign², M. H. Davies³, R. Roehe⁴, L. Bünger⁴, G. Simm⁴, and R. M. Lewis^{1,4}, ¹*Virginia Polytechnic Institute and State University, Blacksburg*, ²*Aberystwyth University, Wales, UK*, ³*ADAS Rosemaund, Preston Wynne, England, UK*, ⁴*Scottish Agricultural College, Edinburgh, Scotland, UK*.

A lean growth index (LGI) was developed in the UK for terminal sire sheep to increase carcass lean weight keeping fat constant. High and low LGI rams were progeny tested to evaluate the effectiveness of the LGI in improving growth and carcass of their crossbred progeny reared commercially. From 1999 to 2002, Charollais (CH), Suffolk (SF) and Texel (TX) rams were selected for high or low LGI score, differing 5 SD on average. Across years, 15 high and 15 low LGI sires from each breed (90 total) were mated to 4,800 crossbred ewes at 3 farms in the UK. Most rams were used for 2 mating seasons, with some rotated among farms to create genetic links. Live weight of 6,515 lambs was recorded at birth (BWT), 5 weeks (5WK), 10 weeks (10WK), and finishing (FWT) at approximately 11% subcutaneous fat. Data were analyzed with a mixed model in SAS to investigate effects of sire index and breed on body weight and finish age (FAGE). Fixed effects were sire index and breed, their interaction, sex, dam breed, dam age, birth-rearing rank, farm and year, and their interaction. Covariates were d within lambing season for BWT, age for 5WK and 10WK, and subcutaneous fat percentage for FAGE and FWT. Rearing dam and residual were fitted as random effects. Lambs from high vs. low LGI sires were 0.07 ± 0.017, 0.3 ± 0.06, 0.4 ± 0.08, and 1.1 ± 0.1 kg heavier at BWT, 5WK, 10WK, and FWT, respectively. The SF sired lambs were heavier at BWT, 10WK and FWT ($P < 0.05$), while SF and TX lambs were heavier than CH lambs at 5WK ($P < 0.01$). High and low LGI sires did not differ for FAGE ($P > 0.1$), and TX sired lambs finished faster ($P < 0.01$). Birth-rearing rank influenced FAGE ($P < 0.01$): single born and reared lambs finished at 119 ± 1.9 d, multiple born, single reared at 154 d ± 2.1 d, and multiple born and reared at 189 ± 1.1 d. Multiple born and reared lambs from high LGI sires required 2.5 ± 1.2 more d to finish, with breed differences persisting. Selection of sires on LGI produced lambs that were heavier at all ages, and at finish. Irrespective of sire LGI, lambs reared

as singles took the same time to finish but offspring of high LGI lambs sires reared as multiples finished significantly later.

Key Words: sheep, selection index

433 Inclusion of the inbreeding coefficient into models for genetic evaluation of dairy cattle. C. A. García-Munguía, A. Ruíz-Flores*, R. Núñez-Domínguez, R. Ramírez-Vlaverde, and R. López-Ordaz, *Universidad Autónoma Chapingo, Chapingo, México, México.*

The objective was to evaluate the effect of the inclusion of the inbreeding coefficient (F) into the models to predict breeding values (BV) of Jersey (J) and Brown Swiss (BS) Mexican dairy cattle. In J the conventional model that included the fixed effect of herd-year-season, and the random genetic additive, permanent environmental, and residual effects; was compared with an alternative model that additionally included F. In BS the models also included the linear covariable of upgrading level, and the linear and quadratic covariables of age of cow at calving. The traits analyzed in J were milk (MY), fat and protein yields per lactation, and the percentages of fat and protein (%P) in milk. In BS only MY was studied. The analyses were done using an animal model and the MTDFREML program. The pedigrees for J and BS included 21,026 and 101,861 animals. Several criteria to compare the results from the alternative models were used. The effect of the inclusion of F into the models depended on the criterion of comparison and the trait. The most notorious change was for the BV for %P in J; the BV for the other traits remained essentially the same with the 2 models in both breeds. The percentage of coincidence among the top 100 sires evaluated with the 2 models ranged from 90 to 98% for all traits. The regression coefficients of BV and their accuracies from the conventional model on the BV and their accuracies from the alternative model ranged from 0.96 to 1.10, and from 1.00 to 1.01, respectively. For the 2 alternative models, the variance components and h^2 estimates were essentially the same. The results suggest that inclusion of F into the models to evaluate genetically Jersey and Brown Swiss Mexican dairy cattle is not necessary.

Key Words: inbreeding coefficient, genetic evaluation, Brown Swiss

434 Jersey-sired and Montbeliarde-sired crossbred heifers compared to pure Holstein heifers for survival and fertility from birth to first parturition. A. R. Hazel*, L. B. Hansen, B. J. Heins, A. J. Seykora, D. G. Johnson, and J. G. Linn, *University of Minnesota, St. Paul.*

Jersey x Holstein crossbred (JH) heifers (n = 91) were compared with pure Holstein (HO) heifers (n = 87). Also, Montbeliarde x Holstein crossbred (MH) heifers (n = 66) and Montbeliarde/(Jersey x Holstein) crossbred ((MJH) heifers (n = 101) were compared with HO heifers (n = 188) for survival to 90d, 365d, and to first parturition; days to first service; first service conception rate; interval from first to last service; number of services; age at conception; and gestation interval to first calving. The heifers were born at 2 research facilities of the University of Minnesota, and JH and HO contemporary heifers were born from September 2001 to June 2003, and MH, MJH and contemporary HO heifers were born from September 2003 to May 2008. JH heifers were mated to Montbeliarde AI sires, MH heifers were mated to Jersey AI sires, and MJH and HO heifers were mated to HO AI sires. Independent variables for all traits included breed group. Also, 2-breed versus 3-breed crossbreds nested within breed group was an independent variable for the MO crossbreds. Additionally, effects of location and year of birth were considered. JH and HO heifers did not differ significantly for survival to 90d, 365d, or to first parturition. MH (94.2%) and MJH (94.2%) were similar to HO (91.3%) heifers for survival to 90d. For survival to 365d

and to parturition, MH and MJH were similar to HO heifers. Age at first breeding tended ($P < 0.07$) to be less for JH (437d) compared with HO (445d) heifers. MJH (429d) were significantly ($P < 0.05$) younger at first breeding than HO (440d) heifers. For first service conception rate, MH (63.5%) were significantly higher than HOL (48.4%) heifers. Age at conception was significantly ($P < 0.05$) less for JH (462d) than HO (484) heifers. MJH were significantly ($P < 0.01$) younger at conception than HO heifers (457 d versus 480 d). The MH heifers, carrying Jersey-sired calves, and the MJH heifers, carrying HO-sired calves, had longer ($P < 0.01$) gestation length than pure HO heifers (280 d versus 278 d, respectively).

Key Words: crossbreeding, survival, Montbeliarde

435 Productivity over five lactations of Normande, Montbeliarde, and Scandinavian Red crossbreds compared to pure Holsteins in commercial dairies in California. B. J. Heins* and L. B. Hansen, *University of Minnesota, Saint Paul.*

Normande (NM) x Holstein (HO) crossbreds (n = 245), Montbeliarde (MO) x HO crossbreds (n = 494), and Scandinavian Red (SR) x HO crossbred (n = 328) cows were compared with pure HO (n = 380) cows for 305-d milk, fat, and protein production and SCS during their first 5 lactations. Cows were housed in 7 commercial dairies in California and calved from June 2002 to January 2009. All HO sires and HO maternal grandsires of all cows were required to have a code assigned by the National Association of Animal Breeders to assure they were sired by AI bulls. The SR was a mixture of Swedish Red and Norwegian Red. Best Prediction was used to calculate actual production (milk, fat, and protein) for 305-d lactations. Adjustment was made for age at calving and milking frequency, and records less than 305 d were projected to 305 d. Independent variables for statistical analysis were the fixed effects of parity, herd-year-season (4-mo seasons within the 7 herds) nested within parity, the genetic level of HO maternal grandsire (linear), genetic group, parity nested within genetic group, and cow within genetic group, which was a random effect. During first lactation, the SR x HO (637 kg) cows were not significantly different from the pure HO (646 kg) cows for fat plus protein production; however, the NM x HO (597kg) cows and the MO x HO (623 kg) cows had significantly ($P < 0.05$) lower fat plus protein production than pure HO cows. Pure HO cows were significantly ($P < 0.05$) higher for fat plus protein than all crossbred cows during second and third lactation. Pure HO (808 kg) cows had significantly ($P < 0.05$) greater fat plus protein than NM x HO (723 kg) and SR x HO (774 kg) cows during fourth lactation. The MO x HO and SR x HO cows were not significantly different from pure HO cows for fat plus protein production during fifth lactation. Pure HO cows and all crossbred cows were not significantly different for SCS for first to fourth lactation, however, during fifth lactation the NM x HO (3.70), MO x HO (3.46), and SR x HO (3.74) cows had significantly ($P < 0.05$) less SCS than pure HO (4.14) cows.

Key Words: crossbreeding, heterosis, production

436 Death rates, survival rates to 5th lactation, and profitability of Normande, Montbeliarde, and Scandinavian Red crossbreds compared to pure Holsteins. B. J. Heins* and L. B. Hansen, *University of Minnesota, Saint Paul.*

Normande (NM) x Holstein (HO) crossbreds (n = 251), Montbeliarde (MO) x HO crossbreds (n = 503), and Scandinavian Red (SR) x HO crossbred (n = 321) cows were compared with pure HO (n = 416) cows for death rate and survival to calving a second, third, fourth, and fifth time. Cows were housed in 6 commercial dairies in California and

calved from June 2002 to January 2009. All HO sires and HO maternal grandsires of cows were required to have a code assigned by the National Association of Animal Breeders to assure they were sired by AI bulls. The SR was a mixture of Swedish Red and Norwegian Red. All cows had the opportunity to calve at least 3 times. Four cows (2 HO and 2 SR) did not have the opportunity to calve a fourth time, and 71 cows (10 HO, 4 NM × HO, 33 MO × HO, and 24 SR × HO) cows did not have the opportunity to calve a fifth time. A chi-squared test was conducted for all traits. Ten of 1,075 crossbred cows (0.9%) died before first observation for milk recording, however, 15 of 416 pure HO (3.6%) died before first observation for milk recording. Pure HO (5.3%) cows had significantly ($P < 0.05$) higher death rate on farm than NM × HO (1.2%) cows, MO × HO (2.0%) cows, and SR × HO (1.6%) cows during the first 305-d of first lactation. All crossbred groups had ($P < 0.01$) significantly more cows calving a second, third, fourth, and fifth time than pure HO cows. For pure HO cows, 77% calved a second time; 59% calved a third time, 35% calved a 4 time, and 18% calved a fifth time. Percentage of cows calving a second, third, fourth, and fifth time for NM × HO (88%, 70%, 51%, 28%) cows, MO × HO (88%, 70%, 52%, 32%) cows, and SR × HO (86%, 69%, 50%, 28%) cows were significantly higher than pure HO cows in all cases.

Key Words: crossbreeding, heterosis, reproduction

437 Production, reproduction, health and growth traits in backcross Holstein x Jersey and their Holstein contemporaries. D. W. Bjelland*, N. M. Esser, K. A. Weigel, and P. C. Hoffman, *University of Wisconsin, Madison*.

A total of 172 purebred Holsteins and 177 backcross Holstein x Jersey dairy cattle were compared for production, reproduction, health, and growth traits. These animals were born between 2003 and 2006 and were housed in the University of Wisconsin - Madison experimental herd. All animals had Holstein dams, which had been mated to either Holstein sires to produce purebred Holsteins or Jersey × Holstein crossbred sires to produce the backcross animals. Traits were analyzed using a linear mixed model with effects of season of birth, age of dam, pen number as a heifer, sire, birth year of sire, and days in milk. Holsteins had significantly ($P < 0.05$) greater 305-d milk yield (9230 vs. 8311 kg), 305-d mature equivalent milk yield (10836 vs. 9632 kg), peak daily milk yield (35 vs. 32 kg), total milk yield (8913 vs. 7682 kg), and total protein yield (284 vs. 267 kg) compared with the crossbreds. Days open (152 vs. 162 d), services per conception as a heifer (1.43 vs. 1.40) or first parity cow (1.70 vs. 2.03) did not differ, but the proportion of first parity births with calving ease score ≥ 3 was significantly less in Holsteins than in crossbreds (11 vs. 32%). Health traits included incidence of scours and respiratory problems as a heifer and incidence of mastitis, feet problems and injury during first lactation. Holsteins had a significantly

higher incidence of injury (39 vs. 22%) and scours (30 vs. 23%) and a lower incidence of respiratory problems (5 vs. 18%). Holsteins were significantly heavier (630 vs. 559kg), with greater hip height (145 vs. 139 cm), body length (167 vs. 163 cm), heart girth (205 vs. 198 cm), and hip width (55 vs. 53 cm) at 22 mo of age. Results of this study suggest that backcross Holstein × Jersey have decreased production but fail to demonstrate an advantage in health and reproduction when compared with purebred Holsteins.

Key Words: crossbreeding, backcross, Jersey

438 Multibreed genomic evaluation of dairy cattle. K. M. Olson*¹ and P. M. VanRaden², ¹*Virginia Polytechnic Institute and State University, Blacksburg*, ²*Animal Improvement Programs Laboratory, ARS, USDA, Beltsville, MD*.

Multibreed models are currently used in traditional USDA dairy cattle genetic evaluations of yield and health traits, but within-breed models are used in genomic evaluations. Multibreed genomic models were developed and tested using all 19,686 genotyped bulls included in the official August 2009 USDA genomic evaluation. The data were divided into training and validation sets. The training data set were comprised of bulls that were proven (had daughter information) as of November 2004 and totaled 5,331, 1,361, and 506 Holstein, Jersey, and Brown Swiss, respectively. The validation data set had 2,477 Holstein, 410 Jersey, and 182 Brown Swiss bulls that were unproven (no daughter information) in November 2004 and proven by August 2009. A common set of 43,385 single nucleotide polymorphisms (SNP) were used for all breeds. Three methods of multibreed evaluation were investigated. Method 1 estimated SNP effects separately within-breed and was tested by multiple regressions to predict daughter deviations of bulls of another breed. Method 2 estimated a common set of SNP effects from combined genotypes and phenotypes of all breeds. Method 3 solved for correlated SNP effects within each breed estimated jointly using a multitrait model. Multiple regressions were used to test across-breed genomic predicted transmitting ability (GPTA) with within-breed GPTA and parent average (PA). A few effects were significant with method 1, mostly for Jerseys and Holsteins, but estimates were small compared with within-breed GPTA and PA. Across-breed GPTA from method 2 were significant for certain traits in some breeds; correlations between within-breed GPTA and across-breed GPTA ranged between 0.91 and 0.93. Results from method 3 were significant and adjusted coefficient of determination for protein yield (the only trait tested for method 3) were highest of all methods for all breeds. However, compared with the current within-breed genomic model, method 3 increased the adjusted coefficient of determination by only 0.0097, 0.0042, and 0.0017 for Brown Swiss, Jerseys, and Holsteins, respectively.

Key Words: dairy cattle, genomic evaluation, multibreed