

514 Developing a competitive research program and securing tenure as a new faculty hire. B. W. Hess*, *University of Wyoming, Laramie.*

Developing a competitive research program and securing tenure can be a daunting task for a new faculty hire. There is no special formula that suits all; however, the task may be less daunting if one considers several principles that are common among those who have trudged down the path leading to success. The following nouns are offered as examples of key elements to developing a competitive research program and securing tenure: Courage; Confidence; Compatibility; Consistency; Collaboration; Colleagues; and Commitment. Embarking on a career in academia certainly requires courage. A new faculty hire must face many new challenges and guard against being deflected from a major career hurdle. Building a research program that garners support hinges upon one's ability to convince those whom are in a position to make decisions that the program possesses the prowess required for success. The trick is to strike a balance between exuding sufficient confidence without exaggerating capabilities. Furthermore, it is critical to research

topics that are compatible with one's training and interests. Focusing on strengths will naturally generate consistency and lead to the ability to maintain a research program. Although independent research is of utmost importance, collaboration with others may be necessary to realize a program's full potential. Colleagues can provide invaluable insight and lend expertise that enhances the program's competitive advantage. It is prudent to welcome the advice of those who have completed the journey successfully. Additionally, because procurement of funds to support a research program is inherently essential, commitment to pursuing all possible mechanisms of funding is critical. Presenting and publishing results also demonstrates commitment to establishing a reputation necessary to maintain a competitive research program and securing tenure. The level of commitment required to accomplish these goals supersedes the tangibles; a commitment to those who are engaged in the research is also required. Practicing some or all of the seven "Cs" may help a new faculty hire develop and maintain a competitive research program and attain tenure.

Key Words: research, tenure, success

Breeding and Genetics: Beef Cattle & Sheep Breeding

515 Genotype by region and season interactions for postweaning gain in beef cattle. J. L. Williams*¹, M. Lukaszewicz^{1,2}, I. Misztal¹, and J. K. Bertrand¹, ¹*University of Georgia, Athens,* ²*Institute of Genetics and Animal Breeding, Polish Academy of Sciences, Jastrzebiec, Poland.*

The objective of this study was to determine if sires perform consistently across different environments and calving seasons in the US. Data and pedigree information were provided by the American Angus Association. A preliminary bivariate analysis containing yearling contemporary group as the sole fixed effect was conducted for postweaning gain in the Southeast (SE) and in the Northwest (NW) as these regions are perceived as opposite extremes in climate. In a second analysis, gains in these two regions were further divided based on season of birth (spring and fall) and fit in a four trait model with fixed effects as previously mentioned. Spring records included 6304 and 37129 observations in SE and NW, respectively. Fall records consisted of 38987 and 5800 observations in the SE and NW, respectively. Heritability estimates from the first analysis were 0.20 ± 0.01 and 0.27 ± 0.01 for gain in SE and NW, respectively. The genetic correlation between the two regions was 0.79 ± 0.02 . Heritability estimates from the second analysis were 0.25 ± 0.04 and 0.18 ± 0.02 for spring and fall gain in SE and 0.26 ± 0.02 and 0.16 ± 0.03 for spring and fall gain in NW, respectively. Genetic correlations between NW and SE were 0.56 ± 0.15 and 0.76 ± 0.07 for spring and fall, respectively. Correlations between spring and fall were 0.85 ± 0.06 and 0.57 ± 0.11 for SE and NW, respectively. The genetic correlation between spring in NW and fall in SE was 0.58 ± 0.08 and that between fall in NW and spring in the SE was 0.44 ± 0.17 . Sires may perform differently across both seasons and regions suggesting it may be better for producers to select bulls based on performance in the calving season utilized in their production region. Subsequent analyses will be performed on weaning weight to determine if strong selection at weaning is leading to low correlations in postweaning gain.

Key Words: Angus, genotype by environment, postweaning gain

516 Estimation of genetic parameters for mature weight in Angus cattle. R. B. Costa*¹, I. Misztal¹, J. K. Bertrand¹, and S. Northcutt², ¹*University of Georgia, Athens,* ²*American Angus Association, St. Joseph, MO.*

The objective of this study was to estimate genetic parameters for weight of up to 5 years in Angus and to investigate options for including mature weight (MW) as a trait in a genetic evaluation. Data were obtained from American Angus Association. Only female records in herds with at least 500 animals and with > 10% of animals with weights at ≥ 2 years were included. Traits in the analysis included weaning weight (WW, $n=81,525$), yearling weight (YW, $n=62,721$), and weights measured from 2 to 5 years of age (MW2, $n=15,927$, MW3, $n=12,404$, MW4, $n=9,805$, MW5, $n=7,546$). Genetic parameters were estimated using a multiple-trait animal model with fixed effects of contemporary group and linear effect of (actual age - standard age), both in days (205, 365, 730, 1,095, 1,460, and 1,825 for WW, YW, MW2, MW3, MW4, and MW5, respectively). The random effects were animal direct, maternal, and maternal permanent environment. Estimates of direct variances were 298, 563, 925, 1221, 1406, and 1402; maternal variances were 167, 153, 123, 136, 167, and 110; the variances of maternal permanent environment were 124, 120, 61, 69, 103, and 134; and residual variances were 258, 608, 829, 1016, 1017, and 1202 for WW, YW, MW2, MW3, MW4, and MW5, respectively. For the direct effect, the genetic correlation of WW and YW was 0.84 and of WW and MW ranged from 0.66 (WWxMW4) to 0.72 (WWxMW2). The genetic correlations of YW and MW ranged from 0.77 (YWxMW5) and 0.85 (YWxMW2). Among MW2, MW3, MW4, and MW5, the genetic correlations were ≥ 0.98 . Correlations between maternal effects ranged from 0.52 (WWxMW4) and 0.95 (WWxYW). Regarding only MW, the correlation between maternal effects ranged from 0.54 (MW4xMW5) to 0.94 (MW2xMW3). Variability of maternal effects at MW may be an artifact due to low heritabilities and low number of records. A genetic evaluation for mature weight may include MW2, with weights at higher ages accommodated by variance adjustments to the scale of MW2.

Key Words: mature weight, growth, multiple-trait

517 Rate of maturing and proportion of mature body weight at puberty of crossbred cows. H. C. Freetly* and L. A. Kuehn, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Cows born (1999 – 2000) resulting from AI breeding Hereford (n = 58), Angus (n = 61), Red Angus (n = 70), Simmental (n = 74), Limousin (n = 80), Charolais (n = 74), or Gelbvieh (n = 78) bulls to Angus (A; n = 69), Hereford (H; n = 173), or MARC III composite (M; n = 253) cows were weighed 6 times as calves and then twice a year as cows through 7 years of age. Body condition scores (BCS; 1 through 9 scale) and BW were collected at the beginning of breeding and then again in 4 mo. Cow BW was standardized to a BCS of 6 by allowing ± 45 kg BW/BCS different than 6. Individual growth curves of BW on age (wk) were fit with the nonlinear function $f(\text{age}) = A - Be^{kx_{\text{age}}}$ using the Gauss-Newton iterations to minimize error sum-of-squares. Proportion of mature weight reached at puberty (n = 459) was solved for age at puberty with $f(\text{age}) = 1 - (B/A)e^{kx_{\text{age}}}$. Sire and dam breed effects were tested with a model including sire breed (S), dam breed (D), birth year (Y), S x D, S x Y, and D x Y. Sire nested within S, was treated as a random effect. There was no S x D interaction for k ($P = 0.49$), B/A ($P = 0.21$), and maturity at puberty ($P = 0.61$). Main effects for S differed for k ($P = 0.01$), B/A ($P = 0.04$), and tended to differ for maturity at puberty ($P = 0.09$). Main effects for D differed for k ($P < 0.001$; H -0.01308 ± 0.00024 , A -0.01426 ± 0.00015 , M -0.01365 ± 0.00013), and for maturity at puberty ($P < 0.001$; H 0.523 ± 0.007 , A 0.542 ± 0.004 , M 0.523 ± 0.003), but not for B/A ($P = 0.88$). There were S x Y ($P = 0.005$), and D x Y ($P = 0.02$) interactions for k, and S x Y ($P = 0.006$), and D x Y ($P = 0.02$) interactions for B/A.

Table 1. Sire breed means and standard errors

Breed	k	B/A	Maturity at puberty
Hereford	-0.01244 ± 0.00034	0.9135 ± 0.0035	0.508 ± 0.011
Angus	-0.01382 ± 0.00029	0.9123 ± 0.0030	0.529 ± 0.007
Red Angus	-0.01397 ± 0.00030	0.9075 ± 0.0031	0.532 ± 0.008
Simmental	-0.01396 ± 0.00030	0.9099 ± 0.0031	0.532 ± 0.008
Limousin	-0.01362 ± 0.00027	0.9178 ± 0.0027	0.545 ± 0.007
Charolais	-0.01393 ± 0.00027	0.9200 ± 0.0027	0.538 ± 0.007
Gelbvieh	-0.01390 ± 0.00027	0.9132 ± 0.0028	0.521 ± 0.007

Key Words: cow, maturity, puberty

518 Breed comparison of post partum ovarian activity in cows. C. Disenhaus*¹, E. Cutullic¹, F. Blanc², and J. Agabriel³, ¹INRA UMR1080 Dairy Production, Rennes, France, ²ENITAC, Lempdes, France, ³INRA UR1213 Unité de recherches sur les herbivores, Saint-Genès-Champagnelle France.

Recent references about postpartum ovarian activity are available only in Holstein cows. The aim of the study is to compare post partum (pp) ovarian activity in Charolaise (beef, CH), Normande (dual purpose, NO) and Holstein (dairy, H) cows. A data set including 367 progesterone profiles established between 2006 and 2008 was used (CH: N=125; NO: N=106; H: N=136). Twice a day, cows were or milked (NO and H) or suckled (CH). The onset of luteal activity (C-LA), length of normal estrous cycles and characterization of the pp activity were determined. Breed and parity effects were analyzed. The resumption of ovarian activity was slower in CH breed than in others (Table 1; $P < 0.01$). At 50 days pp, more H than NO cows ($P < 0.05$) were still inactive. In all breeds, C-LA 50d were lower for primiparous cows than for multiparous (CH:

50% vs.74%; $P < 0.01$; NO: 84% vs.100%; $P < 0.05$; H: 70% vs. 84%; $P < 0.01$). Once estrous cycles have been established, CH cows showed good further cyclic activity without any abnormal cycles. In agreement with the literature, the main cycle abnormality was prolonged luteal phase (PLP). 23% of H-cows showed PLP vs. 8% of NO cows ($P < 0.01$). Duration of cycles seemed to be related to breed milk potential. Normal cycles were longer for H than for NO cows (22.6 ± 2.3 vs. 21.4 ± 2.1 days, N= 136 and 155; $P < 0.001$) with a median value of 23 vs. 21 days. Cycles were shorter for CH than for NO cows (20.2 ± 2.2 vs. 21.4 ± 2.1 days, N=77 and 155; $P < 0.05$) with the same 21 days median value. In conclusion, pp ovarian activity impairment seems to explain partially poor reproductive performances in H breed.

Table 1. Breed effect on resumption of ovarian activity: cumulative percentage of cows which have achieved C-LA at 30 day pp (C-LA 30d) or 50 day pp (C-LA 50d).

Breed*	N	C-LA 30d (%)	C-LA 50d(%)
CH	125	32 ^a	68 ^a
NO	106	63 ^b	92 ^b
H	136	57 ^b	79 ^c

*Values within column with different superscripts differ significantly (a≠b, b≠c, $P < 0.01$; a≠c, $P < 0.05$)

Key Words: ovarian activity, cows, breed

519 Prediction of wool fibre diameter from protein and metabolisable energy digestibility coefficients in crossbred sheep. A. E. O. Malau-Aduli*, R. E. Walker, and W. C. Bignell, *University of Tasmania, Hobart, Tasmania 7001, Australia.*

Our objective in this study was to investigate the interactions between sire breed and supplement on digestibility and to ascertain its accuracy in predicting wool fibre diameter. Forty first-cross Merino weaner sheep sired by Texel, Coopworth, White Suffolk, East-Friesian and Dorset sires with initial BW range of 22.9 and 31.3 kg (average of 26.8 ± 3.2 kg) were randomly assigned to four treatment groups in a $5 \times 2 \times 2 \times 2$ factorial experimental design representing 5 sire breeds, 2 supplementary feeds (canola and lupins), 2 feeding levels (1 and 2% of bodyweight) and 2 sexes (ewes and wethers). The feeding trial lasted for six weeks with an initial 3-week adjustment period and the last 7 days for faecal collection. Factorial ANOVA with orthogonal contrasts in SAS was used for statistical analysis to test for the interactions between sire breed and supplement on digestibility and wool fibre diameter. Our results demonstrated that sire breed \times level of feeding interactions significantly influenced digestibility ($P < 0.01$) whereby Coopworth-sired sheep supplemented at 1% of their body weight recorded the highest ME and N digestibility of 54% and 67% compared to 42% and 62% respectively, in their counterparts fed at 2% of body weight. There was a highly significant ($P < 0.01$) effect of type of supplement \times level of feeding interaction on wool fibre diameter at the end of the trial because sheep fed canola supplements at 1% of body weight had finer wool (22.1 microns) than their 2%-fed counterparts (25.4 microns). Regression of wool fibre diameter on digestibility revealed very poor prediction accuracy ($R^2 = 0.0087-0.169$). We concluded that sire breed variation in digestibility is unlikely to be a useful predictor of genetic merit for wool fibre diameter in first cross sheep under the same management.

Key Words: digestibility, wool, fibre diameter

520 Wool quality and growth traits of Tasmanian pasture-fed crossbred lambs and relationships with plasma metabolites. A. E. O. Malau-Aduli*, C. F. Ranson, and C. W. Bignell, *University of Tasmania, Hobart, Tasmania 7001, Australia.*

Wool quality, growth and plasma metabolite traits of 500 F₁ progeny from Merino dams sired by 5 ram breeds were investigated to study the influences of sire breed, sex and their interactions with plasma metabolites aimed at dual-purpose crossbreeding options. Coopworth, Texel and White Suffolk sired progeny had significantly ($P < 0.05$) heavier weaning weights (WWT) and average daily gains (ADG) than those sired by Dorset or East-Friesian rams. Coopworth-sired sheep had the highest WWT (31.3 ± 1.7 Kg) and East-Friesian sired sheep the lowest (22.9 ± 3.1 Kg) with ADG ranging from 0.15 kg/day in East-Friesian to 0.23 Kg/day in Texel and White Suffolk sire breeds. Highly significant ($P < 0.01$) sex by sire breed interaction were evident; Coopworth-sired ewe lambs had the highest WWT and ADG (34 Kg, 0.27 Kg/day) and Dorset-sired ewe lambs the least (22 kg, 0.15 Kg/day). Greasy fleece weight ranged from a minimum of 964 g to a maximum of 1303 g in Dorset and Coopworth-sired lambs respectively, with Coopworth and Texel sire breeds having significantly heavier ($P < 0.05$) fleece weights than either Dorset, White Suffolk or East-Friesian. Texel-sired sheep had significantly larger ($P < 0.05$) micron fibre diameter ($23.4 \mu\text{m}$) than the $21 \mu\text{m}$ recorded in White Suffolks and East-Friesians. There were also highly significant differences ($P < 0.01$) between sire breeds in staple length (range 50-68 mm) and staple strength (range 39-52 Nktx), with males having finer fibre diameter (21 vs $23 \mu\text{m}$) and shorter staple length (55 vs 60 mm). Regardless of sire breed or gender, blood plasma metabolites were well within the normal range. A strong, positive and significant phenotypic correlation of 0.72 existed between marking and weaning weights. There were no significant correlations between the wool quality and growth traits, essentially implying that producers can select for finer wool without compromising growth. Coopworth x Merino first cross was the overall best performing sheep breed studied because of its heavier liveweight, faster daily gain, heavy fleece weight and a comparatively lower micron fibre diameter than the other crossbreds.

Key Words: Tasmanian crossbreds, wool quality, plasma metabolites

521 Bayesian estimation of genetic parameters for body weight traits and litter size of Moghani sheep using Gibbs sampling. N. Ghavi Hossein-Zadeh*^{1,2}, ¹University of Tehran, Karaj, Iran, ²University of Guilan, Rasht, Iran.

The objective of the present study was to estimate genetic parameters for body weights at different ages and litter size in Moghani sheep. Traits were included birth weight (BW), 3 months weight (3MW), 6 months weight (6MW), 9 months weight (9MW), yearling weight (YW) and litter size (LS). Data and pedigree information used in this research were collected at Breeding Station of Moghani sheep (Ardebil, Iran) during 1987–2005. Linear and threshold animal models with additive genetic, maternal genetic, maternal permanent environmental and residual effects were implemented by Gibbs sampling methodology. A single Gibbs sampling with 100,000 rounds was generated by the MTGSAM program. The posterior means of genetic parameters were estimated based on the 900 samples that were left after elimination of 10,000 rounds in the burn-in period and 100 rounds of each thinning interval. Posterior means of direct heritability estimates for BW, 3MW, 6MW, 9MW, YW and LS were 0.29, 0.13, 0.14, 0.10, 0.31 and 0.10, respectively. Posterior mean estimates of maternal heritabilities were 0.29 for BW, 0.08 for 3MW, 0.11 for 6MW, 0.06 for 9MW, 0.10 for YW and 0.17 for LS. All the posterior mean of phenotypic correlation estimates among body weight traits at different ages were positive and changed from 0.08 to 0.68. But, the estimates of phenotypic correlations between litter size and body weights were negative and ranged from -0.69 to -0.08. A moderate negative direct genetic correlation has been estimated for 9MW-YW, but the estimates of direct genetic correlation between other body weight traits were positive and ranged from 0.08 to 0.88. But, there were negative medium to high direct genetic correlations between body weights at different ages and litter size, ranging from -0.92 to -0.28. Thus, selection for increased growth or LS may have a negative genetic effect on the other trait. The medium to high negative estimates of direct-maternal correlations for body weight traits or litter size suggest that it would be difficult to jointly improve direct and maternal growth ability for Moghani sheep.

Key Words: Bayesian inference, Moghani sheep, body weight

Dairy Foods: Dairy Foods/Microbiology

522 Molecular and technological characterization of lactic acid bacteria isolated from the Egyptian white pickled cheese. M. El Soda*, M. Mohammed, S. Anwar, and S. Awad, *Department of Dairy Science, Faculty of Agriculture, Alexandria University, Alexandria, Egypt.*

Egyptian white pickled cheese samples were collected from different areas in Egypt. One hundred isolates obtained from the cheese samples were identified using repetitive genomic element-PCR (Rep-PCR) fingerprinting. The identified isolates were tested for efficiency of biomass production and separation, acidifying activity, autolytic, aminopeptidase and antagonistic activities and exopolysaccharide production. The obtained results revealed that *Enterococcus faecium*, *Enterococcus faecalis*, *Lactobacillus paracasei* subsp. *paracasei*, *Lactobacillus plantarum* and *Lactobacillus delbrueckii* subsp. *lactis* were the predominant species in Egyptian white pickled cheese. Fifteen percent of *Lactobacillus* and 2% of *Enterococcus* isolates showed fast acidifying activity. Aminopeptidase and autolytic properties were generally higher for *Lactobacillus* strains when compared to the enterococci. Among the lactobacilli, *Lactobacillus paracasei* subsp. *paracasei* was the highest in aminopeptidase activity and autolytic properties. Antagonistic activity was detected in 70% of *Lactobacillus* and 30% of *Enterococcus*

isolates. Two strains of *Lactobacillus paracasei* subsp. *paracasei* and one of *Lactobacillus plantarum* were capable of producing exopolysaccharides in milk.

Key Words: Rep-PCR, Egyptian white pickled cheese, lactic acid bacteria

523 Physiological and transcriptional response of *Lactobacillus casei* ATCC 334 to acid stress. R. Thompson*¹, V. Deibel^{2,3}, J. Steele², and J. Broadbent¹, ¹Utah State University, Logan, ²University of Wisconsin, Madison, ³TracMicro, Madison, WI.

Lactobacillus casei is used as a starter culture in fermented foods, as a probiotic, and in the industrial production of lactic acid. *Lb. casei* produces lactic acid as a major end product of carbohydrate fermentation, which acidifies the environment. Cell survival in acidic environments is critical to industrial application of *Lb. casei*, so a fundamental knowledge of cellular physiology during acid stress may reveal strategies to enhance its industrial performance. Here, we investigated the effect of acid adaptation of *Lb. casei* ATCC 334 on viability during acid chal-