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

515 Genotype by region and season interactions for postweaning gain in beef cattle. J. L. Williams*, 1 M. Lukaszewicz*, 2 I. Misztal*, and J. K. Bertrand*, 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


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, 1,211, 1,406, and 1,402; maternal variances were 167, 153, 123, 136, 117, and 110; the variances of maternal permanent environment were 124, 120, 61, 69, 103, and 134; and residual variances were 258, 608, 829, 1,016, 1,017, and 1,202 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

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(age) = A – Be^ke_age. Sire and dam breed effects were tested with a model including sire breed (S), dam breed (D), breed of first calf (B/A), and year (Y), S x D interaction for k, and S x Y (P<0.001; H 0.523 ± 0.007, A 0.542 ± 0.004, P<0.001). Main effects for D differed for k (P<0.01), B/A (P<0.04), and tended to differ for maturity at puberty (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 ± 0.00113), 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.


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 either 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: 498 J. Anim. Sci. Vol. 87, E-Suppl. 2/J. Dairy Sci. Vol. 92, E-Suppl. 1
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 (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±1.7Kg) and East-Friesian sired sheep the lowest (22.9±3.1Kg) with ADG ranging from 0.15Kg/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 (34Kg, 0.27 Kg/day) and Dorset-sired ewe lambs the least (22Kg, 0.15 Kg/day). Greasy fleece weight ranged from a minimum of 964g to a maximum of 1303g 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 μm) than the 21μm recorded in White Suffolks and East-Friesians. There were also highly significant differences (P<0.01) between sire breeds in staple length (range 50–68mm) and staple strength (range 39–52Nktex), with males having finer fibre diameter (21 vs 23μm) and shorter staple length (55 vs 60mm). 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 activity. Aminopeptidase and autolytic properties were generally higher for lactic acid bacteria, enterococci and lactic acid lactobacilli, 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*, V. Deibel1, J. Steele2, and J. Broadbent1, 1Utah State University, Logan, 2University of Wisconsin, Madison, UTAC MICRO, Madison, WI.

Lactobacillus casei was 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, as 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-