625 Development and validation of SNP markers comprising the IGENITY® profile for carcass traits and ADG in beef cattle. B. W. Woodward* and J. D. Nkrumah, *Merial Ltd., Duluth, GA*.

Genomic markers have been used for several years to provide producers with an early prediction of differences in genetic potential in their animals. Discovery research at many institutions has allowed for rapid expansion of these panels to include larger numbers of markers in more genes to explain more variation in traits of economic importance. This abstract presents the results of panels of markers developed by IGENITY® for beef carcass traits and feedlot ADG. The initial step involved single marker analyses using an allele substitution mixed model in a population of 1,367 cattle. Compound covariate prediction methods were used along with single marker associations to develop panels of markers associated with each trait. Molecular breeding values (MBV) were computed and tested in independent populations, one internal and the other external, as part of a National Beef Cattle Evaluation Consortium validation process. Data used for internal and external validation of the MBV for each trait included 1,104 hd and 1,354 hd, respectively. All 3 data sets are comprised of purebred and crossbred steers and heifers with known sire and sire breed, representing at least 15 Bos taurus and Bos indicus breeds but with considerable Angus influence. All cattle were fed in commercial feedlots in the Midwest; however, they were born on cattle operations in eight states. All regressions of MBV on phenotype in the internal and external validations were highly significant for backfat, marbling score, quality grade (percent Choice or better), ribeye area, yield grade, and ADG. P-values for these traits from the internal validation regressions were 1.7×10^{-5}, 1.0×10^{-8}, 2.0×10^{-8}, 1.7×10^{-3}, 3.0×10^{-4}, and 2.4×10^{-2}, respectively; and external validation p-values were 2.2×10^{-4}, 5.0×10^{-8}, 9.2×10^{-5}, 4.7×10^{-4}, 1.5×10^{-6}, and 6.7×10^{-5}, respectively. Therefore, these results from internal and external analyses of independent populations support concluding these IGENITY trait panels are validated and can be used to predict differences in genetic potential for these traits in cattle.

Key Words: beef carcass traits, ADG, SNP

626 High-density SNP scan of production and product quality traits in beef cattle. R. M. Thallman*, W. M. Snelling, M. F. Allan, C. L. Ferrell, H. C. Freetly, T. G. Jenkins, T. L. Wheeler, S. D. Shackelford, D. A. King, L. A. Kuehn, J. W. Keele, and G. L. Bennett, *USDA, ARS, USMARC, Clay Center, NE*.

Genotypes from the BovineSNP50 BeadChip (50K)were obtained on animals derived from 150 AI sires from seven breeds (22 sires per breed; Angus, Charolais, Gelbvieh, Hereford, Limousin, Red Angus, and Simmental) as either progeny (F_1; 590 steers) or grandprogeny (F_1 x F_1 = F_1^2; 1,306 steers and 707 females). Single SNP associations were conducted for each of the 44,163 SNP with minor allele frequency > 0.05 in the F_1^2 generation. Records analyzed included birth weight (BWT), weaning weight (WWT) and postweaning gain (PWG) of 2,540 to 2,578 F_1 and F_1^2 steers and heifers; hot carcass weight (HCW), fat thickness (FT), ribeye area (REA), marbling score(MARB) and 14 d Warner-Bratzler shear force(WBS) of 1,667 to 1,693 F_1 and F_1^2 steers; and residual feed intake (RFI) and flight speed (FLS) of 1,187 to 1,192 F_1^2 steers. Models included fixed effects for additive substitution effect of the SNP as well as sex, age of dam, contemporary group (year-season-location), covariates for calf breed composition and heterosis, and random direct additive polygenic effects. Models for BWT, WWT, and PWG also included fixed dam SNP substitution effects, covariates for dam breed composition and heterosis, and random maternal additive polygenic and permanent environment effects. The number of SNP nominally significant at $P < 0.001$ and the false discovery rate (FDR), respectively, for each trait were BWT: 638, 0.07, WWT: 273, 0.16, WWT - maternal: 376, 0.12, PWG: 670, 0.07, PWG - maternal: 717, 0.06, FT: 115, 0.38, REA: 120, 0.37, MARB: 113, 0.39, HCW: 166, 0.27, WBS: 48, 0.92, RFI: 116, 0.38, and FLS: 51, 0.87. The number of SNP nominally significant at $P < 0.0001$ and their FDR, respectively, were BWT: 308, 0.01, WWT: 103, 0.04, WWT - maternal: 79, 0.06, PWG: 226, 0.02 and PWG - maternal: 192, 0.02. For FT, REA, MARB, HCW, and RFI, 29-37% of SNP significant at $P < 0.001$ are expected to be spurious. Many SNP could be identified with high confidence ($0.01 < FDR < 0.06$) for BWT, WWT, and PWG, the traits for which the greatest number of 50K genotypes and phenotypes were available. Only 7-16% of the many additional SNP significant for these traits at $P < 0.001$ are expected to be spurious associations.

Key Words: beef cattle

627 Whole genome candidate gene approaches to identifying gene SNP markers influencing fat deposition and carcass merit in beef cattle. C. Li*[1,2], M. Vinsky[1], R. Crews[3], E. Okine[2], S. S. Moore[2], and D. H. Crews Jr.[2,4], [1]*Agriculture and Agri-Food Canada, Lacombe Research Centre, Lacombe, AB, Canada*, [2]*Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB, Canada*, [3]*Agriculture and Agri-Food Canada, Lethbridge Research Centre, Lethbridge, AB, Canada*, [4]*Colorado State University, Fort Collins*.

Identification of DNA markers that affect quantitative traits is the first step towards successful implementation of marker assisted selection in order to improve the traits of economic importance. Single nucleotide polymorphisms (SNP) within a gene are of particular importance for association analyses of quantitative traits as they may be the causal allelic determinants that contribute to phenotypic variation. The aim of this study was a genome-wide identification of gene-specific SNP markers that are associated with fat deposition and carcass merit in beef cattle. The candidate genes were chosen based on their chromosomal locations within or in close proximity to reported quantitative trait loci (QTL) for fat deposition in cattle and(or) their possible function and involvement in fat metabolism, and a panel of 1536 SNPs in 418 candidate genes spanning 25 bovine autosomes was developed. The gene-specific SNPs were genotyped on 1027 steers from three unrelated beef cattle populations including 456 Hybrid, 313 Angus and 258 Charolais steers. Marker association analyses were carried out separately for each population on seven fat deposition and carcass merit traits including ultrasound backfat thickness, average daily gain of ultrasound backfat thickness during feedlot test, carcass average backfat, lean meat yield, carcass marbling score, carcass rib-eye area, and hot carcass weight. Single SNP marker association analyses identified a panel of between 18 to 53 SNP markers that were significantly associated with each trait of each population at a $P<0.05$. Comparison of the SNP markers across the three populations for a similar phenotypic trait identified common SNP markers as well as SNP markers specific to each population. These results will facilitate the development of breed-specific SNP panels for genetic improvement of carcass merit in the three populations.

Key Words: candidate gene association, single nucleotide polymorphisms (SNP), fat deposition and carcass merit in beef cattle

628 Association of single nucleotide polymorphisms in the CAST gene associated with longissimus tenderness in beef cattle. E. Casas*, T. L. Wheeler, S. D. Shackelford, G. L. Bennett, and T. P. L. Smith, *USDA, ARS U.S. Meat Animal Research Center, Clay Center, NE*.

The objective was to assess the association of single nucleotide polymorphisms (SNP) developed on the CAST gene, with longissimus tenderness. Forty one SNP were identified in the CAST gene and assays were developed. Markers were scattered throughout the gene. These markers, in conjunction with a commercially available SNP, were evaluated in a *Bos taurus* population (n = 556) that included crossbred animals derived from Hereford, Angus, Red Angus, Limousin, Charolais, Gelbvieh, and Simmental sires. The trait evaluated was longissimus tenderness measured as Warner-Bratzler shear force (kg). Of the 41 SNP developed, 21 were significantly ($P < 0.05$) associated with longissimus tenderness. The minor allele frequency (MAF) of the commercially available marker in this population was 0.20. Eleven of the 21 SNP, significantly associated with longissimus tenderness, had an average MAF = 0.366. The other 10 SNP significantly associated with longissimus tenderness, had an average MAF = 0.183. The 11 SNP with an average MAF = 0.366 had an additive effect. Animals homozygous for the allele with the lowest frequency had tougher longissimus than animals homozygous for the alternate allele. The average significance for these 11 SNP was $P = 0.032$. The commercially available marker had a dominant effect, where heterozygous animals had similar longissimus tenderness as homozygous animals with the MAF allele. These two groups of animals had tougher longissimus than those homozygous for the alternate allele ($P = 0.001$). The 10 SNP with an average MAF = 0.183 showed similar performance in longissimus tenderness as the commercially available marker. The average significance for these 10 SNP was $P = 0.004$. When evaluated in additional populations and their effects validated, these markers could be used as alternate candidates to characterize variation of longissimus tenderness in beef cattle.

Key Words: beef cattle, calpastatin, tenderness

629 Reproductive responses of dairy cows to supplemental fat. J. D. Ferguson[1], D. W. Remsburg*[1], E. Block[2], and Z. Wu[1], [1]*University of Pennsylvania, New Bolton Center, Kennett Square*, [2]*Arm and Hammer Animal Nutrition Group, Church & Dwight Co. Inc., Princeton, NJ.*

Measurements of reproduction function in cows fed supplemental fat were taken. Twenty-one multiparous Holsteins were fed a control diet (CO), a diet added with saturated fat (SF), or a diet added with a fat source high in linoleic acid and enriched with n-3 fatty acids (UF) (Megalac-R®, Church & Dwight Co., Inc.) beginning 3 wk prior to parturition and continuing for 16 wk after parturition. The supplemented diets were formed by adding fat sources to the control diet to provide 1% supplemental fat before parturition and 2.5% supplemental fat after parturition, resulting in higher NEL content. All cows were inseminated 80 to 86 DIM following estrous synchronization using the PreSynch-OvSynch protocol beginning 43 to 49 d postpartum. Blood samples were taken every 2 to 3 d beginning 2 d prior to breeding and continuing for 3 wk after breeding. The concentration of PGFM in blood plasma after breeding was lowest for UF ($P < 0.05$). There was no difference ($P > 0.05$) among treatments in the means for the concentration of progesterone, insulin, or IGF-1, but significant and non-significant interactions between dietary treatment and sampling day were observed in these analyses, showing some increased concentrations with supplemental fat. Dietary supplementation with linoleic and n-3 fatty acids may improve reproduction by increasing progesterone postpartum and decreasing $PGF_{2\alpha}$ in plasma during early pregnancy. *Research supported by Church & Dwight Co. Inc.*

Table 1.

Item	CO	SF	UF	SEM	Fat[1]	Fat source[1]
Progesterone (ng/mL)	5.0	5.7	5.2	1.0	0.73	0.75
PGFM (pg/mL)	582	704	391	83	0.73	0.03
Insulin (µg/mL)	0.7	1.0	0.8	0.2	0.49	0.38[a]
IGF-1 (ng/mL)	124	126	154	19	0.52	0.34

[1]*P* for difference between CO and SF plus UF, and between SF and UF. [a]Treatment and measuring day interaction ($P < 0.05$).

Key Words: reproduction, progesterone, fat

630 Differential gene expression in Suffolk ewes exposed to subacute dietary nitrate. R. C. Cockrum*[1], K. J. Austin[1], P. A. Ludden[1], J. F. Taylor[2], J. W. Kim[2], S. C. Fahrenkrug[3], J. R. Garbe[3], and K. M. Cammack[1], [1]*University of Wyoming, Laramie*, [2]*University of Missouri, Columbia*, [3]*University of Minnesota, St. Paul*.

Accumulation of nitrite (NO_2^-), by high dietary nitrate (NO_3^-) consumption in ruminants, leads to formation of methemoglobin, resulting in toxicity symptoms. Our objective was to identify genes differentially expressed in ewes identified as highly tolerant and lowly tolerant to subacute dietary NO_3^-. Purebred Suffolk ewes were administered a control supplement (n = 8) or a potassium nitrate supplement (300 mg KNO_3/kg BW daily; n = 47) for 8 d. Liver biopsies were conducted prior to (d 0) and on the last day (d 8) of treatment to collect tissue for gene expression analyses. Coefficients of variation (CV) indicated that supplement intake was more variable among NO_3^- treated ewes (CV = 59.3%) than among control ewes (CV = 13.6%). Among NO_3^- treated ewes, ewes highly tolerant (n = 6) and lowly tolerant (n = 6) to elevated dietary NO_3^- were identified based on individual performance and toxicity symptoms. Genes identified by microarray analysis and confirmed by real-time RT-PCR as differentially expressed between lowly tolerant and highly tolerant NO_3^- treated ewes included cytochrome P450 family 25, subfamily A, polypeptide 1, transcript variant 1 (CYP26A1); glutathione peroxidase 3 (GPX3); homeobox (HOP); fatty acid desaturase 2 (FADS2); thyroid hormone responsive gene (SPOT14); and cysteine sulfinate decarboxylase (CSD). Relative expression of CYP26A1, FADS2, and SPOT14 genes was downregulated ($P < 0.02$) in lowly tolerant ewes compared to highly tolerant ewes; furthermore, relative gene expression of CSD tended to be downregulated ($P = 0.07$) in lowly tolerant ewes compared to highly tolerant ewes. In contrast, relative expression of GPX3 and HOP genes was upregulated ($P < 0.05$) in lowly tolerant ewes compared to highly tolerant ewes. These results indicate that ewes identified as lowly tolerant and highly tolerant to subacute levels of NO_3^- varied in performance and hepatic gene expression. Identification of genes correlated to response to subacute dietary NO_3^- may allow producers to identify lowly tolerant animals and employ alternative management strategies for those individuals.

Key Words: gene expression, nitrate, toxicity

631 Effects of high-sulfur water on growth performance and gene expression of steers fed forage-based diets. K. L. Kessler*[1], K. C. Olson[2], C. L. Wright[2], K. J. Austin[1], K. McInnerney[3], P. S. Johnson[2], and K. M. Cammack[1], [1]*University of Wyoming, Laramie*, [2]*South Dakota State University, Brookings*, [3]*University of Montana, Bozeman*.

Sulfur-induced polioencephalomalacia (PEM), a neurological disorder affecting ruminants, is frequently associated with consumption of

high-S water. The objective of this study was to determine the effects of high-S water on performance and hepatic gene expression of steers. A secondary objective was to determine if clinoptilolite, a clay mineral high in cation-exchange capacity, ameliorates the effects of high-S water consumption. Yearling steers (n = 96; 318.2 ± 2.1 kg BW) were randomly assigned to one of four treatments for a 77 d period: low-S water control (566 mg kg^{-1} sulfate), high-S water (3,651 mg kg^{-1} sulfate), or high-S water plus clinoptilolite supplemented at either 2.5% or 5.0% of diet DM. Feed and water consumption were measured daily, and all steers were weighed on d -2, -1, 29, 53, 76, and 77. Liver biopsies were performed on all steers after the treatment period. Morbidity and mortality were higher ($P = 0.0014$) in steers receiving high-S water. No differences in animal health were observed among clinoptilolite levels, suggesting clinoptilolite is ineffective in negating the effects of high-S water consumption. Dry matter intake was lower ($P = 0.074$) in steers consuming high-S water regardless of clinoptilolite level; no differences in ADG were observed. Microarray analyses of hepatic tissues from selected control steers (n = 6) and healthy high-S water treated steers (0% clinoptilolite; n = 6) revealed that 264 genes were upregulated ($P < 0.05$) and 102 were downregulated ($P < 0.05$) due to high-S water treatment. Real-time RT-PCR confirmed numerical downregulation of aldo-ketoreductase family 1, major histocompatabiltity complex (MHC) class II DQA, transforming growth factor β, MHC class I heavy chain and amyloid-beta genes, and numerical upregulation of inhibin beta A, integrin β 2, MHC class I heavy chain, MHC class II DQB in high-S water treated steers compared to control steers. Results from this study suggest that administration of high-S water alters hepatic gene expression, which may explain the reduced performance associated with high-S water.

Key Words: sulfur, polioencephalomalacia, gene expression

632 Development and independent validation of SNP markers comprising the IGENITY® profile for feed intake and efficiency in indicus-influenced beef cattle. B. W. Woodward*[1], J. D. Nkrumah[1], P. A. Lancaster[2], G. E. Carstens[2], and D. J. Johnston[3], [1]*Merial Limited, Duluth, GA*, [2]*Texas A&M University, College Station*, [3]*University of New England, Armidale, NSW, Australia*.

Recent improvements in individual intake measurement technology have enabled producers and researchers to more accurately record intake (DMI) for calculation of feed efficiency, e.g., residual feed intake (RFI). These data are used to study the genome with the goal of finding molecular markers that are associated with these key economic traits. The objectives of this study were to 1) confirm SNP marker associations with feed efficiency traits discovered in a research program, 2) develop panels of the most informative markers, and 3) validate these panels in multiple resource populations. Single marker analyses using an allele substitution mixed model in a population of 464 purebred Brangus heifers with individual intake data (70 d) confirmed a number of the associations reported by discovery scientists. Panels of markers associated with each trait were developed and used to compute molecular breeding values (MBV) using compound covariate prediction methods along with single marker associations. These panels were evaluated in a combined analysis of two Beef CRC populations as part of a National Beef Cattle Evaluation Consortium validation process. Data used for testing the MBV included 1,270 hd of Santa Gertrudis, Belmont Red, and composite cattle based on Brahman, Senepol, and Belmont Red from the Beef CRC in Australia. Steers and heifers in these datasets had individual daily feed intake (DFI) recorded for an average of 60 and 71 d, respectively. Positive regression coefficients between MBV and phenotypes were found in the combined population analysis - RFI, P = 0.005 and DFI, P = 0.02. It is concluded that these DNA marker panels are validated (P < .05) and can be used to predict differences in genetic potential for feed intake and efficiency in indicus-influenced animals and for developing marker-based EPD.

Key Words: feed efficiency, SNP, indicus-influenced beef cattle

634 Effects of single nucleotide polymorphisms in stearoyl CoA desaturase and fatty acid synthase on milk yield, composition, and fatty acid profile in lactating Holstein cows. L. Clark*, S. Moore, and M. Oba, *University of Alberta, Edmonton, AB, Canada*.

The objective of this study was to determine the effect of single nucleotide polymorphisms (SNP) in the stearoyl CoA desaturase (SCD) gene and the fatty acid synthase (FASN) gene on milk yield, composition, and fatty acid profile. A SNP in SCD found on the fifth exon of chromosome 26, which encodes an amino acid change from alanine to valine, and a SNP in FASN located in the thioesterase domain (TE) of chromosome 26, which encodes an amino acid change from threonine to alanine were evaluated in this study. Milk samples were collected from 215 lactating dairy cows at a commercial dairy farm. The distribution of genotypes was $111AA_S$, $85AV_S$, and $19VV_S$ cows for SCD, and $35AA_F$, $89AG_F$, and $91GG_F$ cows for FASN. Cows in one group were fed a diet containing 30.8% NDF, 18.0% CP, and 4.7% fat, and those in the other group were fed a diet containing 29.5% NDF, 18.2% CP, and 4.5% fat. The effects of SCD and FASN on milk composition and fatty acid profile were analyzed separately using the mixed procedure of SAS 9.1 with the fixed effects of genotype, stage of lactation, parity and their interactions, and the random effect of group. Milk yield and composition were not affected by SCD genotype. Fatty acid profile was affected by SCD where the ratio of C14:1 to C14:0 was greater for AA_S cows than both AV_S and VV_S cows (0.085 vs. 0.070; $P < 0.0001$), indicating greater activity of the desaturase enzyme for AA_S cows. However, the SCD genotype did not affect CLA concentration in milk fat, averaging 0.54%. For FASN genotype, GG_F cows had greater yields of milk (28.1 vs. 25.4 kg/d), milk fat (0.84 vs. 0.69 kg/d), and lactose (1.23 vs. 1.08 kg/d) than AG_F cows ($P < 0.04$), but fatty acid profile was not affected by FASN genotype. These results indicate that the genotype of SCD and FASN can affect milk and milk component production.

Key Words: SNP, stearoyl CoA desaturase (SCD), fatty acid synthase (FASN)

635 Genetic regulation of milk β-carotene content. S. D. Berry*[1], S. R. Davis[1], E. M. Beattie[1], N. L. Thomas[1], A. K. Burrett[1], H. E. Ward[1], A. M. Stanfield[1], M . Biswas[1], A. E. Ankersmit-Udy[1], J. L. Barnett[1], Y. van der Does[2], A. H. K. MacGibbon[2], R. J. Spelman[3], K. Lehnert[1], R. G. Snell[1], [1]*Vialactia Biosciences, Auckland, New Zealand*, [2]*Fonterra Research Center, Palmerston North, New Zealand*, [3]*LIC, Hamilton, New Zealand*.

Selection of cattle for milk β-carotene content, if genetically determined, could alter milk fat color, and produce β-carotene enriched milks. We identified QTL regions for milk β-carotene content on BTA15, BTA17, and BTA18 in a Friesian-Jersey crossbred herd (n~850) derived from six F1 bulls. This lead to the identification of three candidate genes: β-carotene oxygenase 2 (BCO2, on BTA15); scavenger receptor class B, member 1 (SCARB1, on BTA17); and β-carotene oxygenase 1 (BCMO1, on BTA18). For each gene, the coding regions were sequenced, along

with approximately 2kb of 5′ sequence. For BCO2, an A>G mutation was discovered in exon three, 240bp from the translation initiation site. The A allele creates a premature stop codon resulting in a putative truncated protein of 79 amino acids (compared to the wild-type protein of 530 amino acids), in the three F1 sires heterozygous for this mutation. BCO2 cows homozygous for the stop mutation produced milk with 78% and 55% more β-carotene than homozygous (GG) and heterozygous (AG) wild type animals, respectively. In BCMO1, three polymorphisms were discovered (one in the 5′ region of the gene, one in exon 6 causing a G>R amino acid change, and one in exon 7 causing a N>D amino acid change. The most striking of these, N341D, resulted in a 32% increase in milk β-carotene. In SCARB1, one polymorphism was discovered, in the 5′ regulatory region (-321 bp relative to the +1 translation start site), which resulted in a 10% increase in milk β-carotene content. The results establish important physiological roles for BCO2, BCMO1 and SCARB1 in bovine β-carotene metabolism, and consequently the regulation of milk β-carotene content. Thus, milk fat color may be decreased or increased, using genetic selection, for specific industrial applications, including the production of bovine milk enriched for β-carotene to alleviate vitamin A deficiency in humans.

Key Words: β-carotene, β-carotene oxygenase, milk fat color

636 Analysis of quantitative trait loci affecting female fertility and twinning rate in Israeli Holsteins on chromosome 7. J. I. Weller*[1], G. Glick[1], M. Golik[1], E. Ezra[2], Y. Zeron[3], E. Seroussi[1], and M. Ron[1], [1]*ARO, The Volcani Center, Bet Dagan, Israel*, [2]*Israle Cattle Breeders Association, Caesaria, Israel*, [3]*Sion, Shikmim, Israel*.

Female fertility and twinning rate were analyzed by the multitrait animal model with parities 1 through 5 considered correlated traits. Fertility was scored as the inverse of the number of inseminations to conception at each parity. Negative genetic correlations between all combinations of parities 1 through 3 between twinning rate and fertility were found by multitrait REML analysis. We have previously reported the existence of QTL affecting these traits segregating on BTA7. The objective of this study was to test if the overall genetic relationship between these two traits was maintained at the level of individual genes on BTA7 affecting the traits. In the preliminary analysis, 288 Israeli Holstein bulls were genotyped by the BovineSNP50 BeadChip (Illumina, Inc.). After edits there were 1752 valid SNPs on chromosome 7. Three hundred to 600 bulls were genotyped for an additional 225 SNPs on the first half of the chromosome. Significance of SNP effects on both traits was tested by a linear model that included the effects of allele and the bulls' birth year on the bulls' genetic evaluations. There were a total of 27 SNPs that were significant for both traits ($p<0.05$). The effects were located in three major clusters, between physical positions 14 and 52 Mbp (Build 4.0). Assuming independent association among the 27 effects, 4.9 significant effects were expected by chance, giving a false discovery rate of 0.18. Of these 27 SNPs the effects associated with the two traits were in opposite directions in all but 4 SNPs ($p<0.001$). Thus it can be concluded that the observed negative genetic correlation is due to specific quantitative trait loci with effects in opposite directions on twinning rate and female fertility.

Key Words: female fertility, genomic selection, twinning rate

Contemporary and Emerging Issues: Joint with Extension Education: Science-Based Approaches to Address Consumer Concerns with the Processing and Marketing of Animal Products

637 Effects of cattle production practices on environmental quality. F. M. Mitloehner*, *University of California, Davis*.

A recent United Nations report suggested that global livestock production is a significant threat to environmental quality, contributing to levels of greenhouse gas emissions that exceed those from all transportation sources. Furthermore, the report states that livestock is a major factor in degradation of air quality and surface and ground water resources. Indeed, livestock production in industrialized countries has consolidated, while at the same time production efficiencies per animal are at their near optimum. Over the last few decades, both beef and dairy production systems have dramatically improved efficiencies. For example, over the last 50 years, dairies have quadrupled milk output per lactation. This improvement in efficiencies per animal has considerably reduced the environmental impact per unit of production (milk or meat). However, in several regions of the industrialized world, cattle production has also spatially concentrated. A sustainable future in animal agriculture will require that the output of the cattle system will match the capacity of crops and soils to utilize these nutrients and that alternative uses of manure for fuel and energy production will be implemented. The ultimate goal must be to minimize unwanted nutrient losses to air and water while providing a growing human population with safe and nutritious food. Several recent papers have used a Life Cycle Assessment (LCA) to investigate the impacts of the entire milk- or meat chain on carbon footprint or energy use. To assess and compare production practices for their potential of releasing pollutants to air and water, a second, more comprehensive bio-geochemical modeling effort is required, often referred to as Process-based Modeling (PBM). Comparisons of cattle production systems like conventional versus organic or the use of production techniques with respect to effects on carbon footprint or pollutant contributions, will be feasible in the near future as numerous research teams are working on such assessment tools. These life cycle and emission prediction modeling tools will bring us closer to design and optimize sustainable production systems in animal agriculture.

Key Words: cattle, environmental impact, modelling

638 Effect of farm production practices on ruminant-derived foods: Fatty acid profile, product quality and human health outcomes. A. L. Lock*[1], J. Kraft[1], A. M. O'Donnell[2], and D. E. Bauman[2], [1]*University of Vermont, Burlington*, [2]*Cornell University, Ithaca, NY*.

There is increased consumer interest in the link between diet and health. A major focus of this has been the recognition that certain dietary fatty acids (FA) can impact human health. Related to this is the recent inter-