Destruction of aquaculture and rice fields support a strong argument that livestock are among the few options for fast recovery. Poultry, cattle and goats among others were the most popular species before the quake. The paper is advocating a participatory approach and integration of the existing network of university alumni in Indonesia. The concept is build on the assumption that sustainable agricultural development requires well adapted livestock for re-stocking. Risk sensitive development of livestock production system is of key strategic importance and includes capacity building and training of farmers as well as stakeholder participation. The masterplan consists of a comprehensive 5-years plan of action ranging from introducing specific husbandry practices to reestablishing the livestock population through local breeds of the preferred species. The challenge offers opportunities for global partnerships.

Acknowledgements: The authors thank the postgraduate students of the Indonesian-German student association and the partners of the Faculty of Animal Science of IPB, Bogor, Indonesia for substantial input.

Key Words: Livestock Development, Disaster Management, Indonesia

Lactation Biology

593 Evidence of a role of prolactin in mediating photoperiodic effects during the dry period. H. M. Crawford*[1], J. L. Dauderman[1], D. E. Morin[1], T. B. McFadden[2], and G. E. Dahl[1], [1]*University of Illinois*, *Urbana*, [2]*University of Vermont*, *Burlington*.

Short day photoperiod (SDPP) during the dry period increases milk production in the subsequent lactation relative to long day photoperiod (LDPP). In addition we have observed that SDPP improves immune function during the transition compared with LDPP. Our hypothesis is that mammary and immune responses under SDPP result from increased prolactin (PRL) sensitivity. In the present study our objective was to determine if exogenous PRL administered to cows on a SDPP would cause production and immune responses to be similar to those of cows on LDPP. To test this we assigned 24 multiparous Holstein cows to one of three treatments during their dry period: LDPP (16L:8D), SDPP (8L:16D), and SDPP+PRL (SDPP and recombinant bovine PRL). In the SDPP+PRL group, 12mg/d of PRL was continuously delivered via subcutaneous osmotic minipump for the last 30 days of pregnancy to match circulating concentrations of the LDPP cows, yet maintain other photoperiod factors consistent with SDPP. During the dry period, weekly blood samples were taken to quantify PRL concentrations. Treatments ended at calving when all cows were moved to an ambient photoperiod and milked two times daily for the entire lactation. SDPP+PRL cows calved 5.5 d earlier than SDPP and LDPP cows (P<0.11), resulting in 21 d of PRL treatment prior to calving. DMI as a percentage of body weight did not differ between LDPP and SDPP for weeks -8 to -4, but for weeks -3 to 0 DMI was greater in SDPP cows than SDPP+PRL cows, but SDPP+PRL did not differ from LDPP. The periparturient PRL surge was 26.4, 29.5, and 36.3ng/mL for SDPP, SDPP+PRL, and LDPP. Milk production was inversely related to the periparturient PRL surge. Milk production through 120 d of lactation averaged 42.0, 39.5, and 35.8 kg/d for SDPP, SDPP+PRL and LDPP cows (P<0.04). There were no differences among groups in postpartum BW or DMI, or prepartum BW. These results support the concept that circulating PRL during the dry period is inversely related to subsequent milk yield.

Key Words: Dry Period, Prolactin, Photoperiod

594 Lactational effects of the dry off period in dairy goats. A. A. K. Salama, G. Caja*, X. Such, E. Albanell, and R. Casals, *Universitat Autònoma de Barcelona*, *Bellaterra, Spain*.

Seventeen Murciano-Granadina multiparous dairy goats, milked once daily throughout lactation, were used to study the effects of the dry off period on the following lactation. Goats were impregnated at 210 DIM and assigned to two experimental groups at 300 DIM. Treatments were: 1) **D56**, dried off for 56 d before the expected kidding (n = 9); and, 2) **ND**, not dried (n = 8). Milk yield was recorded weekly during the preceding (561 ± 22 L/goat) and the following lactation. Five goats (63%) in the ND group dried off spontaneously at d 27 ± 4 before kidding and were considered as a separate group (**D27**; n = 5). Kids were weighed at parturition and removed before sucking. Colostrum samples were taken for milk components and IgG analysis. Mammary biopsies were taken at 280 DIM in the preceding lactation, d 7 after drying off (D56 group only), and d 49 in the following lactation (all groups). Apoptotic and proliferating cells were detected immunohistochemically by TUNEL and PCNA assays, respectively. Litter size (2.25 kids/goat) did not vary between groups, but ND kids had lower birth weight (1.7 kg; $P < 0.05$) than D56 (2.1 kg) and D27 (2.2 kg). Colostrum of ND goats contained lower IgG (5.6 mg/ml; $P < 0.001$) than D56 (42.4 mg/mL) and D27 (32.9 mg/mL) goats. In the following lactation (210 DIM), ND goats produced less milk (1.66 L/d; $P < 0.05$) than D56 (2.32 L/d) and D27 (2.45 L/d) goats. Comparing d 280 (late lactation) with d 7 after dry off (involution) in D56 goats, an increase in apoptosis (0.51 to 1.75%; $P < 0.06$) and proliferation (2.09 to 7.12% $P < 0.05$) of the mammary tissue was observed. At d 49 of the following lactation there were no differences between groups in apoptosis (0.71, 0.68 and 0.65%) or proliferation indices (2.95, 1.37 and 2.48%) for D56, D27 and ND, respectively. These results indicate that the length of the dry off period (27 or 56 d) did not affect mammary cell turnover in the following lactation. Omitting the dry period reduced colostrum quality and milk yield in dairy goats. Goats which spontaneously dried off for approximately one month were as productive as the goats that dried off for approximately two months.

Key Words: Apoptosis, Mammary Involution, Milking Frequency

595 Effects of milking interval on hourly milk secretion rate in goats. G. Pulina*, S. Fancellu, G. Battacone, and A. Nudda, *University of Sassari*, *Sassari, Italy*.

The effects of milking interval on secretion rate of milk, fat, protein, casein, lactose and fatty acids (FA) in dairy goats were investigated. Twenty Saanen lactating goats in mid lactation were used in a 4x4 Latin Square experimental design with 5 replications. Goats were allocated in four milking interval treatments: 3, 6, 12 and 24 hours after receiving at the morning milking (0 hr), i.v injection of 1 IU of oxytocin to remove residual milk. The goats were machine milked and stripped by hand. Milk yields were recorded and milk samples were collected at each milking. A regular twice daily milking (12 hr interval) was restored between each experimental period. The hourly secretion rates of milk, fat, protein, casein, lactose and FA were calculated. The hourly secretion rates of milk and lactose decreased up to 3 hr (P<0.05). The fat content is the milk component mostly affected by prolonged milking interval, decreasing linearly as milking intervals increased. The hourly secretion rate of FA does not seem to have a defined trend.

Secretion rate (g/hr) with different milking intervals

Milking Interval (hr)	Milk	Fat	Protein	Casein	Lactose
3	99 a	3.5 a	2.8	1.9	4.5 a
6	84 b	3.2 ab	2.5	1.7	3.8 b
12	87 b	3.0 bc	2.5	1.8	4.0 ab
24	82 b	2.4 c	2.4	1.7	3.7 b
P	0.013	0.002	0.063	0.110	0.022
P	0.013	0.002	0.063	0.110	0.022

a,b,c P£0.05

Acknowledgements: Research funded by FISR project (MIUR and MIPAF).

Key Words: Dairy Goat, Milking Interval, Milk Secretion Rate

596 Induced lactation in 15-month-old heifers: production, health and survival. R. S. Kensinger*, A. L. Magliaro, R. Graboski, P. R. Tozer, M. L. O'Connor, and L. D. Muller, *Pennsylvania State University*, *University Park*.

The costs of raising replacement heifers are large and significantly impact dairy farm profitability. The present study determined the health and productivity of Holstein heifers (n = 31) induced into lactation at 15 mo of age (BW of 427 ± 41 kg), as well as their lactational response to treatment with somatotropin (bST). Heifers were given daily sc injections of estradiol-17B and progesterone (75 and 250 ug/kg/d, respectively) on treatment d 1-7, and milking commenced on d 18. On d 25 ± 7 of lactation heifers were randomly assigned to control or bST treatment groups, and milk production was compared over the next 70 d (d 25-94 of lactation). After d 94 all heifers were treated with bST. Milk yields increased gradually and peaked at 22.7 kg/d at d 175 of lactation. Milk protein, fat and lactose averaged 17.9, 1.2 and 2.3 % on day 1 of milking and changed to 3.6, 4.6 and 5.1 %, respectively, by day 21 of milking. Milk yield of heifers treated with bST (17.9 kg/d) was greater than that of controls (15.6 kg/d) from d 25-94, but composition was not affected. Heifers induced into lactation averaged 301 DIM and produced 5,329 kg milk with 3.68 % fat and 3.35 % protein while gaining an average of 0.7 kg BW/d. Induced heifers conceived with 1.81 services/conception, averaged 102 d open, and had their first calving at 27.9 mo of age. Induced heifers were compared to a similar aged peer group (n = 31) that was not induced. Induced animals were older at first calving than peers (24.5 mo). Body condition scores at calving and calving ease scores were similar between the groups, but % calf mortality was lower for induced heifers. Survival analysis after 76 mo indicated that induced heifers left the herd at an earlier age but had a similar productive life compared to peers. Young heifers induced into lactation were healthy, grew normally, produced reasonable amounts of milk with normal composition, had good reproductive performance, and had similar productive lives relative to conventionally raised heifers.

Key Words: Induced Lactation, bST, Heifer

597 Leptin alters albumin synthesis in the bovine mammary gland. Y Feuermann[1,2], S. J. Mabjeesh[2], and A Shamay*[1], [1]*Agriculture Research Organisation The Volcani center*, *Bet Dagan Israel*, [2]*The Hebrew University of Jerusalem*, *Rehovot, Israel*.

At the late 70th Phillippy and McCarthy had published a work named "Multi-origins of milk serum albumin in the lactating goat" this work showed the first evidence that albumin can be synthesized by the mammary gland in ruminants. Lately we have established the fact that albumin is synthesized in the bovine mammary gland by performing de novo synthesis of albumin in bovine mammary gland primary explants culture. We showed that albumin synthesis is altered by mastitis in the bovine mammary gland. Albumin is a 68-kDa multifunction protein that can regulate a number of physiological functions. Some publications demonstrated the anti-apoptotic effect of albumin in cell system such as human endothelial cell line and murine peritoneal macrophages. The extensive lactation performance of the "modern cow", due to advance genetic selection is accompanied with advanced apoptotic process. Resent studies in our lab established the ability of leptin to up regulate lactation performance in bovine. Our findings that albumin is synthesized by the mammary gland and the effect of leptin on the bovine mammary gland, led us to investigate the relationship between leptin, lactation and albumin. We found that leptin can up regulate mRNA expression of albumin in bovine mammary gland explants and we also demonstrated the same effect on albumin secretion (preformed by western blot). The results showed that leptin can up regulate the expression and secretion of albumin in the bovine mammary gland explants but the up regulation is more significant when leptin was introduced together with prolactin. Based on this finding we examined the effect of leptin combined with prolactin on proliferation and other cell maintenance parameters, the results showed the same trend.

Key Words: Leptin, Albumin, Mammary Gland

598 Effects of continuous milking (CM) and prostaglandin E_2 (PGE_2,) on mammary gene expression in dairy cows. E. L. Annen*[1], P. C. Gentry[1], R. Sprissler[1], D. L. Hadsell[2], A. V. Capuco[3], and R. J. Collier[1], [1]*University of Arizona*, *Tucson*, [2]*Baylor College of Medicine*, *Huston, TX*, [3]*USDA-ARS*, *Beltsville, MD*.

First and second lactation cows (n=8) were utilized in a half udder model in which one half was dry 60 d (CTL) and the other half CM. Udder halves (n=16) were assigned a postpartum (PT) treatment of + or - PGE_2 (875 µg) by intramammary infusion at calving and 72 h PT. Tissue samples were obtained at 3 and 7 d after milk stasis of the CTL udder half and at 2 and 4 d PT. In CTL halves, mammary epithelial cell (MEC) growth was greater at 7 d of milk stasis and apoptosis was elevated at 3 and 7 d of milk stasis. PT MEC growth was increased in CM halves, but apoptosis was similar in CM and CTL tissue. PT milk yield was reduced in CM halves. Milk yield and MEC turnover was unaffected by PGE_2. RNA pools were created for prepartum (PP) and PT timepoints for each udder half. We evaluated expression of adenosine 5′-triphosphate binding cassette 1 (ABC1, stem cell marker), α-lactalbumin (α-lac, lactose synthesis) bax (apoptosis), bcl_2 (survival), CCAT/enhancer binding protein-β (CEBP-β, mammary growth); insulin-like growth factor binding protein 5 (IGFBP5, apoptosis); kinase inhibitor protein p27 (p27, cell cycle arrest). The housekeeping gene, 18S, was not changed by any of the treatments or interactions. PGE_2 did not alter gene expression. Involution of PP CTL tissue was associated with decreased ($P < 0.02$) α-lac expression, and increased expression of bax ($P < 0.05$) and IGFBP5 ($P = 0.07$) compared to lactating CM tissue. ABC1, CEBP-β, cyclin D1, p27, and bcl_2 expression were not changed in CM vs. CTL tissue. In PT tissue, α-lac expression was similar in CM and CTL tissue and ABC1 and IGFBP5 expression were increased ($P < 0.05$) in CTL tissue compared to CM tissue. Results demonstrate MEC apoptosis during involution of CTL tissue was regulated by bax and IGFBP5. Results for PT expression of IGFBP5 and ABC1 warrant further investigation on the role of IGFBP5 in PP apoptosis in CTL tissue and the role of the dry period on ABC1 expression and mammary stem cell renewal.

Key Words: Continuous Milking, Gene Expression

599 Effects of continuous milking (CM) and bovine somatotropin (bST) on mammary gene expression in primiparous cows. E. L. Annen*[1], P. C. Gentry[1], R. Sprissler[1], D. L. Hadsell[2], A. V. Capuco[3], and R. J. Collier[1], [1]*University of Arizona*, *Tucson*, [2]*Baylor College of Medicine*, *Huston, TX*, [3]*USDA-ARS*, *Beltsville, MD*.

Primiparous cows (n=8) were used in a half udder model in which one half was dry 60 d (CTL) and the other half was CM. Cows were assigned to + (n=4) or - bST (n=4) treatment. Tissue was sampled at 20 and 8 d prepartum (PP) and 1, 7, and 20 d postpartum (PT). Mammary epithelial cell (MEC) proliferation was increased PP compared to PT timepoints, but was 50% lower in CM tissue vs. CTL tissue at d -8. MEC apoptosis was elevated through d 7 PP in CTL tissue, but only to d 1 in PP CM tissue. Milk yield was reduced 53% in CM halves.

MEC turnover and PP milk yield was not altered by bST. Real-time RT-PCR analysis of genes regulating cell turnover or milk synthesis included: adenosine 5′-triphosphate binding cassette 1 (ABC1, stem cell marker), α-lactalbumin (α-lac, lactose synthesis) bax (apoptosis), bcl_2 (survival), CCAT/enhancer binding protein-β (CEBP-β, mammary growth); insulin-like growth factor binding protein 5 (IGFBP5, apoptosis); kinase inhibitor protein p27 (p27, cell cycle arrest). RNA pools were created for PP and PT timepoints for each udder half. Expression of 18S (housekeeping gene) was not changed ($P > 0.10$) by dry period length (DP) or bST. We failed to detect an effect of bST on expression of any of the genes evaluated. PP α-lac expression was increased 27-fold in CM tissue compared to CTL. During the PT period, α-lac expression was similar between CM and CTL tissue. ABC1, p27, bax, and IGFBP5 were not affected ($P > 0.1$) by DP treatment (CTL vs. CM) or gestation status (PP vs. PT). Cyclin D1 and CEBP-β expression were greater ($P < 0.03$) during the PP period than PT period, but were not affected by DP length. Expression of bcl_2 was increased ($P < 0.05$) 2.6-fold in PP tissue compared to PT tissue. Results indicate that late-gestation mammary development may be regulated by CEBP-β, cyclin D1, and bcl_2. Differences in milk yield and morphology between CM and CTL tissue were not represented in expression of genes evaluated in this study.

Key Words: Continuous Milking, Gene Expression

600 Effects of heat stress on morphology and gene expression of bovine mammary epithelial cells (BMEC) in collagen gel culture. C. Stiening[1], J. Hoying[1], M. Ben Abdallah[1], P. Coussens[2], and R. Collier*[1], [1]*University of Arizona*, *Tucson*, [2]*Michigan State University*, *East Lansing*.

Primary BMEC embedded in collagen gels were cultured at 37C (thermal neutral: TN) for seven days in a serum-free medium; a subset were then exposed to thermal stress (TS) at 41.5C for up to 24 hr. Growth was estimated by fluorometric DNA quantification at -24, 0, 8, 16 and 24 hr relative to TS initiation. Over the 48 hr period, net growth was unchanged in TS cultures, compared to a 4-fold increase in TN cultures. Analysis of Hsp70 (inducible) gene expression by RT PCR over the first 24 hr was used to determine temporal pattern of the TS response. Relative Hsp70 transcript levels remained low at 0, 15, 30 and 60 minutes of TS. A dramatic up-regulation occurred between 1 and 2 hr, and peaked between 2 and 4 hr; expression levels returned to near baseline by 8 hr. Replicate samples were collected at 1, 2 and 4 hr from both TS and TN cultures for global gene expression analysis using the NBFGC bovine cDNA microarray from MSU. Over 400 genes were identified as differentially expressed in TS BMEC. Genes involved in trafficking (ligatin) and remodeling (cofilin), as well as TS-responsive genes (HSPs, CLK1, BAG3) were among the most significant up-regulated genes. Downregulated genes included those involved in glycolysis (PFKs), peptide metabolism (DNPEP), and cell morphology (S100A1 and utrophin). Also of interest were a large number of differentially expressed genes related to G-protein signaling. Confocal microscopy of collagen whole mounts stained with phalloidin and Hoechst dye 33258 indicated a dramatic reduction of the prominent, complex networks of stellate-like ductal structures in TN to small, spherical masses within 24 hr of TS. Together, these data suggest an acute shift in intracellular trafficking and gene expression, including a down-regulation of biosynthesis and up-regulation of stress-response genes, leading in part, to a dramatic remodeling of the cytoskeleton following TS.

Key Words: Heat Stress, Mammary, Microarray

601 A proteomic approach to evaluate the effects of body weight and plane of nutrition on protein expression profiles of mammary gland extracts from Holstein heifers. K. M. Daniels*[1], K. E. Webb, Jr.[1], M. L. McGilliard[1], M. J. Meyer[2], M. E. Van Amburgh[2], and R. M. Akers[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*Cornell University*, *Ithaca, NY*.

Biochemical and cellular mechanisms governing alterations in heifer udder development are poorly understood relative to prepubertal feeding and animal performance. Mammary development in dairy heifers was characterized with the use of proteomics, which is the study of the complete set of translated proteins in a biological sample. A 2 x 2 factorial experiment generated two-dimensional protein maps of mammary tissue extracts from heifers (n = 24) that were reared on one of two dietary treatments (Moderate (M) 650 g/d or High (H) 950 g/d of daily gain) and slaughtered at one of two body weights (BW, 200 or 350 kg). Cytosolic mammary gland extracts were prepared from frozen mammary parenchyma and used in two-dimensional PAGE analysis. Proteome maps of extracts were constructed using PDQuest software. Densities of 820 total protein spots were analyzed using the Mixed Procedure of SAS. Selected individual proteins were identified by changes in profiles of expression in response to increased BW and/or dietary treatment. Dietary treatment differed the expression of 131 protein spots; the expression of 108 spots differed by heifer BW. The 22 most significant spots were excised and submitted for mass spectrometry analyses. Returned protein names and accession numbers were used in NCBI database searches to obtain information on the identified proteins. For example, one of the proteins that differed by dietary treatment, transferrin, a binding protein (BP) of insulin-like growth factor BP-3, was identified via these methods. Possible roles of this and other proteins in mammary development were described. Validation assays are ongoing. Proteomic approaches are effective for the identification of proteins involved in bovine mammary development.

Key Words: Heifer, Mammary, Proteome

602 Inhibitory activity of bovine milk fat globule membrane against sialic acid-dependent and -independent strains of rotavirus. K. Ochonicky*[1], S. Donovan[1], T. Kuhlenschmidt[1], R. Jimenez-Flores[2], and M. Kuhlenschmidt[1], [1]*University of Illinois*, *Urbana*, [2]*Dairy Products Technology Center*, *San Luis Obispo, CA*.

Milk fat is encapsulated in a milk fat globule membrane (MFGM) that has associated with it glycoproteins, complex carbohydrates and bioactive lipids. Rotavirus (RV) is the most common cause of diarrhea in human infants and also affects calves and piglets, with the greatest incidence at weaning. Anti-RV activity of human and bovine MFGM occurs in vitro and has been attributed primarily to its glycoprotein (lactadherin) and complex carbohydrate (MUC1) components. In the present study, the anti-RV activity of an organic extract of bovine MFGM was tested. MFGM enriched in polar lipids was prepared from buttermilk (MFGM-B) and cheese whey (MFGM-C) by microfiltration and supercritical fluid extraction and lipid extracted using the Svennerholm method. Whole MFGM and the organic extract were compared against sialic acid dependent (porcine OSU) and sialic acid independent (human Wa) RV strains in MA-104 cells using a virus focus forming infectivity (FFU) assay. Dose dependent anti-RV activity was observed for whole MFGM-B and MFGM-C against both Wa and OSU RV strains ($P<0.05$). The % inhibition of OSU was greater ($P<0.05$) than Wa for both MFGM-B (94 ± 7.6 vs. 50 ± 2.8) and MFGM-C (79 ± 8.5 vs. 67 ± 3.5). The primary mechanism of RV inhibition by whole MFGM may be related to its protein and carbohydrate components, as these differed between MFGM-B and MFGM-C. The MFGM lipid extracts from both sources inhibited infectivity of OSU RV to a similar degree and in a dose dependent manner dependent (53 - 87% inhibition) ($P<0.05$). In contrast, lipid extracts were less effective inhibitors of Wa strain RV. In summary, whole MFGM was more effective against sialic acid dependent RV and differed between buttermilk and cheese whey sources. MFGM lipid extracts inhibited sialic acid dependent RV independent of MFGM source. These data suggest that whole MFGM and lipids isolated from MFGM inhibit RV by different mechanisms.

Key Words: Milk, Fat Globule Membrane, Rotavirus

603 Inhibitory effects of human and porcine milk oligosaccharides on sialic acid dependent and sialic acid independent strains of rotavirus. K. Ochonicky*, S. Donovan, T. Kuhlenschmidt, and M. Kuhlenschmidt, *University of Illinois*, *Urbana*.

Milk oligosaccharides have been proposed to protect the neonate from intestinal pathogens. We have shown that porcine colostrum and milk contain 1.5 and

0.5 mg/ml of oligosaccharides (PMO), of which 50% is sialyllactose. Some strains for rotavirus (RV) require sialic acid for binding to enterocytes, thus we hypothesized that PMO would inhibit RV infectivity. To test this hypothesis, oligosaccharides were purified from defatted human milk (HMO), pig colostrum collected during parturition, and pig milk collected 3-10 days post-parturition by gel filtration. Samples were further subjected to protein A affinity chromatography to remove immunoglobulins. HMO and PMO were analyzed by HPAE chromatography on Dionex PA100 columns and found to yield distinctive oligosaccharide profiles. Purified HMO and PMO were assessed for their ability to inhibit infection of cultured MA-104 cells by human sialic acid independent RV (Wa strain) or porcine sialic acid dependent RV (OSU strain) using a focus forming unit assay. PMO and HMO were studied in a dose-dependent manner and data were expressed as the oligosaccharide dose required to inhibit RV infectivity by 50% compared to control. Approximately 1.32 mg/ml of purified HMO inhibited OSU strain RV infection by 50% ($P<0.05$), but did not inhibit infection by Wa strain RV. Similarly, 1.5 mg/ml of purified PMO from colostrum inhibited ($P<0.05$) infection by the OSU strain RV by 50%. In contrast, 2.5 mg/ml of purified PMO from mature milk was required to achieve a 50% inhibition ($P<0.05$) of OSU strain RV infectivity. No consistent inhibition of Wa strain RV by PMO was observed. In summary, a higher dose of mature milk PMO was required for an equivalent degree of RV inhibition obtained with HMO or colostral PMO. These data imply that changes in the PMO composition from colostrum to mature milk may confer differential protection from RV. Additional fractionation of PMO is ongoing and should yield isolated structures for further comparison.

Key Words: Milk, Oligosaccharides, Rotavirus

604 Glucose and histidine affect the phosphorylation state of translation initiation factor 2 in the bovine mammary gland in vivo. C. A. Toerien*, D. R. Trout, and J. P. Cant, *University of Guelph*, *Guelph, ON, Canada*.

In eukaryotic cells, nutrients activate the cell signalling cascades that regulate protein synthesis at the level of translation. Eukaryotic translation initiation factor (eIF) 2 is a major control point in translation initiation. Phosphorylation of the α subunit inactivates eIF2 and impairs ribosome loading onto mRNA. To identify nutrients that regulate eIF2 in the mammary gland, Holstein cows were fasted to decrease protein synthesis before re-supplying nutrients. In a 6x6 Latin Square design, cows (initial: 69±4 DIM; 43.4±0.5 kg milk/d) were subjected every 14 d to a 31-h fast. For the last 9 h of the fast, cows were infused iv with EAA+Glc (positive control), Glc, Met+Lys, His, Leu, or saline (Sal; negative control). Milk production response to infusion was calculated from milk produced in the front quarters between +1 and +7 h of the 9-h infusion. At +9 h, an approximately 1.5-g biopsy sample of mammary tissue was harvested from a hindquarter (HQ). In successive periods, HQs were alternated so that each HQ was allowed 28 d to recover. Relative to Sal, infusion of EAA+Glc and Glc increased ($P<0.05$) total protein yield by 40% and 36% respectively. The effect of His on protein yield equalled 52% of the effect of EAA+Glc, which is far greater than its 5% proportion in the EAA of the EAA+Glc infusate. The stimulatory effect of EAA+Glc, Glc and His on protein yield was accompanied by a dephosphorylation of eIF2α. Although infused in a smaller proportion of EAA+Glc, His elicited a similar level of eIF2α dephosphorylation to that of Glc. In conclusion, glucose and His, but not Met+Lys or Leu, regulate the phosphorylation state of eIF2α in the bovine mammary gland.

Phosphorylation of eIF2a

	Treatment (LSmeans±SE)					
Item	Sal	EAA+Glc	Glc	Met+Lys	His	Leu
Milk protein, g/6h	59^{a}±2.8	82^{b}±3.3	80^{bc}±3.2	67^{abc}±3.2	71^{abc}±3.2	61^{ac}±3
eIF2a(P), %*	99±11	73±10	49±12	95±12	51±11	84±12
eIF2a, %*	101±14	105±14	110±16	111±16	99.4±14	128±16
eIF2a(P), %†	22.6^{a}±2.4	11.5^{b}±2.4	8.6^{b}±2.7	13.4^{ab}±2.7	8.5^{b}±2.4	13.2^{ab}±2.7
Inclusion, %y			100	19.8	5	17.3

[a,b,c] Significance ($P<0.05$); * of Sal when Sal was set to 100; † of total eIF2a; y of EAA+Glc infusate

Key Words: Milk Protein Regulation, Translation Initiation Factors, Nutrients

Physiology and Endocrinology: Effects of Maternal Nutrient Supply on Embryonic and Fetal Development and Postnatal Performance

605 Effects of maternal metabolic state and intra-uterine crowding on embryonic survival and fetal development in swine. G. Foxcroft*, J. Barry, W. Dixon, S. Novak, M. Vinsky, E. Putman, S. Town, G. Murdoch, A. Wellen, S. Terletski, and J. Patterson, *University of Alberta*, *Edmonton, AB, Canada*.

Maternal metabolic state has important effects on embryonic survival in the pig. A switch towards a less positive energy balance in the cyclic gilt, and increased tissue catabolism in the lactating and weaned sow, produce detrimental effects on embryonic survival. Endocrine and metabolic profiling during follicular development and use of in vitro maturation and fertilization techniques, suggest that both the follicle and the enclosed oocyte can be nutritionally imprinted. Inherent deficiencies in oocyte maturation are a primary cause of poor embryonic survival, increasing variability in fertilization rate and early embryonic development. Embryonic development is further confounded by adverse effects of metabolic state on steroid-dependent changes in secretory function of both the oviduct and uterus. Dynamic changes in the pattern of prenatal loss may also affect fetal development through naturally occurring intra-uterine crowding. Studies of commercial dam-line sows, suggest that selection for litter size has indirectly increased ovulation rates in higher parity females (>30 ovulations), and increased the number of conceptuses surviving to the post-implantation period. Increased uterine crowding around day 30 of gestation decreases placental size in all surviving conceptuses. In prolific Meishan sows, increased uterine crowding also reduces placental weight, but this is partly compensated by increased placental vascularity. In contrast, in white-line sows, such compensatory changers in placental efficiency are not evident and uterine crowding results in intra-uterine growth retardation (IUGR) and a decrease in the number of secondary muscle fibers in the fetus. Available evidence suggests that these effects on prenatal development will have significant negative effects on postnatal growth.

Key Words: Swine, Preantral Survival, Uterine Crowding

606 Pre-gestational ewe management systems alter the impacts of early maternal undernutrition on fetal growth and offspring quality. S. Ford*[1], M. Du[1], B. Hess[1], and P. Nathanielsz[2], [1]*University of Wyoming*, *Laramie*, [2]*University of Texas*, *San Antonio*.

This study investigated if the management system a ewe was selected under alters the impacts of maternal undernutrition on fetal growth and offspring quality. Range ewes normally experiencing limited nutrition from Baggs, WY (Baggs ewes) maintained normal fetal weights when subjected to nutrient restriction (50% NRC requirements; NR) from day 28 to 78 of gestation. In contrast, ewes of similar breeding from the University of Wyoming flock (UW ewes), selected to a sedentary lifestyle and above adequate nutrition, exhibited a 30% decrease in fetal weight, under the same NR. The growth restricted fetuses of UW ewes exhibited bilateral cardiac ventricular hypertrophy, reduced kidney nephron numbers, and fewer secondary myofibers and smaller fasciculi in skeletal muscle than fetuses from control fed (100% NRC requirements; CF) UW ewes. The ability of NR Baggs ewes to maintain normal fetal weights was linked to an early placentomal conversion from Type A to more efficient Types B, C, or D by