677 Inhibitory effect of unsaturated fatty acids on *de novo* fatty acid synthesis in bovine mammary epithelial cells. J. W. McFadden*, I. K. Mullarky, and B. A. Corl, *Virginia Polytechnic Institute and State University*, *Blacksburg*.

In vitro, unsaturated fatty acids (UFA) inhibit lipid synthesis in rat hepatocytes as well as goat and bovine mammary epithelial cells. A bovine mammary epithelial cell line (BME-UV) was used to determine the effect of saturated, monounsaturated, and polyunsaturated fatty acids (PUFA) on *de novo* fatty acid synthesis. Cells were grown to confluence in DMEM supplemented with 10% serum. Serum or increasing incubation time reduced radiolabeled acetate incorporation into lipids (pmol/μg DNA). Addition of insulin (0.1 μg/ml) and prolactin (1.5 μg/ml) serum-free media enhanced acetate incorporation (22%). Subsequent experiments included BME-UV cells cultured in the presence of hormones with BSA-complexed fatty acid in the absence of serum for 24 h starting at confluency. Treatment with 50 μM oleic acid, linoleic acid (LA), *cis*-9, *trans*-11 conjugated linoleic acid (CLA), or *trans*-10, *cis*-12 CLA resulted in 40 to 50% reductions in acetate incorporation. A minor increase (14%) in acetate incorporation was observed with 50 μM stearic acid (SA) treatment. Fatty acid synthase mRNA was reduced by 29, 9, and 22% for the LA, *cis*-9, *trans*-11 CLA, and *trans*-10, *cis*-12 CLA treatments, respectively. Acetyl-CoA carboxylase mRNA expression remained unaffected by treatment. Expression of peroxisome proliferator activated receptor-γ and liver X receptor (LXR)-α mRNA were unaffected by treatment; however, significant reductions in sterol response element-binding protein (SREBP)-1 mRNA and protein were observed for all PUFA treatments. Cells incubated with a LXR agonist, T0901317, resulted in enhanced acetate incorporation (21% at 1 μM). Incubating BME-UV cells with LXR agonist rescued the suppressive effect of UFA on lipid synthesis. Presence of a LXR agonist had no effect on acetate incorporation in SA treated BME-UV cells. These results suggest, *in vitro*, that UFA decrease BME-UV cell lipid synthesis by inhibiting the expression of SREBP-1 and this effect may be mediated by suppressing LXR activity.

Key Words: LXR, SREBP-1, Unsaturated Fatty Acids

678 Lipogenic gene expression in MAC-T cells is affected differently by fatty acids and enhanced by PPAR-gamma activation. A. K. G. Kadegowda*[1], M. Bionaz[2], L. S. Piperova[1], R. A. Erdman[1], and J. J. Loor[2], [1]*University of Maryland*, *College Park*, [2]*University of Illinois*, *Urbana*.

Recent work has focused on trans10,cis12-CLA (t10c12CLA) and its effect on mammary lipogenic gene expression, while the effects of other fatty acids (FA) remain ill-defined. Objectives were to test individual FA effects on mRNA expression via qPCR of 19 genes with roles in de novo synthesis (ACACA, FASN), FA uptake (LPL, CD36), intracellular FA transport (FABP3, FABP4), desaturation (SCD), triacylglycerol synthesis (AGPAT6, DGAT1, GPAM, LPIN1), transcriptional regulation (SREBF1, SREBF2, INSIG1, THRSP), and nuclear receptor signaling (PPARG). A PPARG-specific agonist (Rosiglitazone, ROSI) was used to assess the role of this nuclear receptor on mammary lipogenesis. Lipid droplet (LD) formation was quantified with Oil Red O staining. MAC-T cells were cultured in triplicate for 12 h with 50 Î¼M ROSI or 100 Î¼M t10-18:1, t10c12CLA, 16:0, 18:0, c9-18:1, 20:5, or ethanol (control). All FA increased ($P < 0.05$) CD36 expression (~770%) and, except for 16:0 and 18:0, decreased LPL (~150%) and FABP3 (~200%) relative to control. 16:0 and 18:0 elicited greater mRNA of FABP3 (+500%) and FABP4 (+160%) over control. Responses common to 16:0 and 18:0 included greater THRSP (~90%), INSIG1 (~200%), AGPAT6 (~150%), DGAT1 (~60%), and LPIN1 (~90%), coupled with greater LD formation with 16:0. T10-18:1 and t10c12CLA reduced expression of ACACA (~60%), FASN (~50%), SCD (~240%), and LPIN1 (~30%). SREBF1 was lower with t10c12-CLA (~200%), c9-18:1 (150%), and EPA (~140%) over control. C9-18:1 and EPA also decreased ACACA (~40%) and SCD (~300%). No effects were observed for PPARG but ROSI upregulated by >40% ACACA, FASN, SCD, LPIN1, AGPAT6, DGAT1, SREBF1, SREBF2, and INSIG1 without changes in LD formation over control. Results showed that FA regulate mammary lipogenic gene expression to different extents. Further, PPAR-gamma activation of de novo lipogenesis coupled with exogenous FA availability might play a role in regulating milk fat synthesis.

Key Words: Mammary Cells, Gene Expression, Fatty Acids

679 Comparative MammOmics™ of milk fat synthesis in *Mus musculus* vs. *Bos taurus*. M. Bionaz* and J. J. Loor, *University of Illinois*, *Urbana*.

A sequenced genome and low cost are at the root of the preferential use of the mouse to study genome-wide mechanisms of mammary function. Whether mammary tissue from mouse and cow share similar gene expression patterns remains to be determined. We propose that the degree of similarity in relative % mRNA abundance coupled with temporal responses in both species is indicative of the importance of a gene in the process of mammary lipid and protein synthesis. Our objective was to compare temporal patterns and relative % mRNA abundance of lipid synthesis-related genes in mammary tissue from mice (FVB and C57B1) and Holstein cows during pregnancy and lactation. Published mouse mammary microarray data (>20,000 genes) and our bovine qPCR data were used in this comparison. Murine data encompassed pregnancy to 9-10 d post-partum, and bovine the last 30 d pre-partum through late lactation. With few exceptions, mouse strains had similar relative % mRNA abundance and temporal patterns across selected genes. Overall, mouse mammary had proportionally lower relative % mRNA abundance of *CD36*, *GPAM*, *AGPAT6*, *INSIG1*, and *LASS2* and larger % mRNA abundance of *ACSL1*, *ACBP*, *FADS1*, *OXCT1*, *SREBF1*, and *THRSP* compared with cow. Genes characterizing mammary tissue of both species included *ABCG2*, *ACSS1*, *ACSL1*, *FABP3*, *FASN*, *SCD*, *BTN1A1*, *XDH*, *OXCT1*, *LPIN1*, *SREBF1*, and *PPARGC1A*. In contrast, we observed lower up-regulation of genes involved in uptake of fatty acids (FA) from blood (e.g., *LPL*, *CD36*, and *VLDLR*) and desaturation (e.g., *SCD*) in murine vs. bovine. Thus, it appears that FA uptake from blood, relative to *SREBF1*/*THRSP*-regulated de novo FA synthesis (e.g., *FASN*), and delta-9 desaturation are more relevant processes in the cow. Intracellular FA trafficking also appears more important in bovine mammary as suggested by larger up-regulation of *FABP3*. Comparative analysis revealed unexpected findings such as down-regulation of

GPAM in lactating murine mammary. Murine mammary data might be partly confounded by the greater amount of adipocytes during pregnancy and the beginning of lactation. Care should be taken when inferring phenomena in bovine mammary using murine data.

Key Words: Genomics, Lactation, Metabolism

680 SREBP1 and Spot14 are acutely down-regulated in mammary tissue during abomasal infusion of *trans*-10, *cis*-12 conjugated linoleic acid (CLA) in the dairy cow. K. J. Harvatine*, Y. R. Boisclair, and D. E. Bauman, *Cornell University*, *Ithaca, NY*.

Trans-10, *cis*-12 CLA is a potent inhibitor of milk fat synthesis in the dairy cow. We have previously reported down-regulation of the mammary mRNA expression of sterol response element binding protein 1 (SREBP1), SREBP1 regulatory proteins, SREBP-regulated enzymes and thyroid hormone responsive spot 14 (S14) during chronic CLA- and diet-induced milk fat depression (MFD). This provides strong evidence for a central role of the transcription factor SREBP and the nuclear protein S14 in the regulation of milk fat synthesis. To distinguish between primary mechanisms regulating milk fat synthesis and secondary adaptations to the reduction in milk fat, we conducted a time-course experiment. An initial priming dose of 7.5 g of CLA was given at time-zero followed by steady state abomasal infusion of 2.5 g every 4 h for 36 h, and then by 3.75 g every 6 h until 120 h. In a separate previously reported experiment we characterized at high resolution the temporal production response to an identical infusion protocol by milking every 4 h with the aid of oxytocin. In the production experiment, milk fat percent progressively decreased over the first 24 h, although the ratio of *de novo* and preformed fatty acids was not modified until after 24-30 h. In the current experiment, mammary biopsies from 9 cows were obtained at -48, 12, 30, and 120 h relative to initiation of CLA infusion. Expression of fatty acid synthase and lipoprotein lipase were decreased at 30 and 120 h compared to control. Expression of SREBP1 and S14 were also decreased at 30 h and 120 h compared to control. Time course analysis during MFD demonstrates that CLA down-regulates master transcriptional regulators of lipid synthesis and their dependent enzymes during the onset of MFD. This provides additional support for SREBP1 and S14 as primary central regulators of MFD.

681 PPAR-gamma activation and trans10,cis12-CLA affect gene expression profiles and intracellular lipid droplet formation and secretion to different extents in MAC-T cells. A. K. G. Kadegowda*[1], M. Bionaz[2], R. E. Everts[2], H. A. Lewin[2], L. S. Piperova[1], R. A. Erdman[1], and J. J. Loor[2], [1]*University of Maryland*, *College Park*, [2]*University of Illinois*, *Urbana*.

We showed previously that PPAR-gamma activation induces lipogenic gene expression in MAC-T cells. To examine effects of PPAR-gamma activation on large-scale gene expression profiles, RNA from MAC-T cells cultured in triplicate for 12 h with 50 micro molar rosiglitazone (ROSI; PPAR-gamma agonist), 100 micro molar t10c12CLA (CLA; negative control), or ethanol (control) were hybridized to an annotated 13,257 bovine oligonucleotide (70-mers) microarray in a dye-swap design (i.e., 18 microarrays). Lipid droplet (LD) formation was quantified with Oil Red O staining and concentrations of triacylglycerol (TG) and glucose in culture media measured by commercial kits. ANOVA identified 769 differentially expressed ($P<0.05$) genes due to treatment. Relative to control, CLA uniquely increased expression by ≥ 1.5-fold of 47 genes associated with lipid transport (e.g., ADFP, VLDLR) and cellular proliferation (e.g., IGFBP3, SPP1), and decreased expression of 45 genes associated with TG synthesis (e.g., SCD, IDH1, FABP3) and cholesterol synthesis/transport (e.g., HMGCS, LDLR). Similarly, ROSI distinctively affected expression of 32 genes associated with amino acid (e.g., CTH, SLC7A1) and glucose metabolism (PCK2, PFKFB2), and decreased expression of 35 genes associated with cell morphology (e.g., MCAM, WPIF1, ACTN2). CLA resulted in substantially greater LD (350%) accumulation and 3.6-fold more TG in culture media compared with control. ROSI resulted in 1.6-fold more TG in culture media than control, and also lowered glucose relative to control or CLA. Responses to ROSI or CLA for several genes previously measured by qPCR (e.g., LPIN1, FASN, FABP3, SCD) on the same RNA were confirmed. The suggested increase in glucose utilization inferred by microarray data due to ROSI also was confirmed. Paradoxically, CLA promoted intracellular TG accumulation and secretion into culture media via mechanisms that remain to be determined.

Key Words: Genomics, Mammary Cell, PPAR-Gamma

682 *Trans*-10, *cis*-12 conjugated linoleic acid (CLA) induces a dose-dependent reduction in milk fat synthesis in C57BL6J mice. K. J. Harvatine*, M. M. Robblee, Y. R. Boisclair, and D. E. Bauman, *Cornell University*, *Ithaca, NY*.

Inhibition of milk fat synthesis by fatty acid intermediates originating from rumen biohydrogenation (e.g. *trans*- 10, *cis*- 12 CLA) has been extensively studied in the cow. Inhibition of milk fat synthesis by CLA has also been investigated in rodent models, but a dose response has never been reported. We determined the dose dependent effect of *trans*-10, *cis*- 12 CLA on milk fat synthesis using 24 wild type C57BLJ mice. Starting at 6-8 d of lactation, dams nursing 6-7 pups received daily doses of water (control) or 6, 18, or 54 mg/d of CLA for 5 d. CLA was orally administered in three equal doses. CLA caused a linear decrease in dam feed intake (up to -27%) and pup growth rate (up to -49%). Milk fat percent was progressively decreased up to 20% with the 18 mg/d dose, but the 54 mg dose did not differ from control. All CLA treatments caused a decrease in the concentration of short and medium chain fatty acids in milk fat similar to milk fat depression (MFD) in the dairy cow. In agreement, mammary tissue lipogenesis measured by in vitro tissue incorporation of C14 glucose into fatty acids was decreased at the 18 and 54 mg/d doses. Finally, gene expression was analyzed by real-time PCR for the control and 18 mg/d treatments. Expression of SREBP1, S14, and FASN was decreased by CLA treatment compared to control. We have previously reported decreased expression of SREBP1 and S14 during diet- and CLA-induced MFD in the dairy cow. Overall these data show that MFD can be experimentally induced in the mouse with 18 mg/d of *trans*- 10, *cis*- 12 CLA, although higher doses may cause a more generalized inhibition of milk synthesis. We conclude that the mouse can serve as an experimental model to investigate functional mechanisms mediating the effect of CLA on milk fat synthesis.

Key Words: Milk Fat, Mouse, CLA

683 MammOmics™ in *Sus scrofa*: Uncovering genomic adaptations underlying mammary development during pregnancy and lactation. S. Tramontana[1,2], W. L. Hurley[2], M. Bionaz*[2], A. Sharma[2], D. E. Graugnard[2], E. A. Cutler[2], R. E. Everts[2], P. Ajmone-Marsan[1], S. L. Rodriguez-Zas[2], and J. J. Loor[2], [1]*Università Cattolica del Sacro Cuore*, *Piacenza, Italy*, [2]*University of Illinois*, *Urbana*.

Elucidating genes controlling growth, development, and metabolism of swine mammary glands can reveal potential metabolic or signaling pathways that might help improve efficiency of milk synthesis. A swine microarray consisting of 13,263 oligonucleotides (70 mer) was used for transcript profiling of mammary tissue from 4-5 sows at -34, -14, -4, 0, 7, 14, 21, and 28 d relative to parturition. Annotation of the microarray was based on similarity searches using BLASTN and TBLASTX against human, mouse, and pig UniGene databases, the human genome, and pig TIGR. Cy3- and Cy5-labelled cDNA from mammary tissue and a reference standard were used for hybridizations. ANOVA (false discovery rate ≤ 0.10) identified 2,664 differentially expressed genes (DEG) due to physiological state. Gene network/pathway analysis revealed that cell growth and proliferation (n = 548 genes) and cell signaling (n = 612) were among the most affected molecular functions due to physiological state in DEG. A clear switch in metabolic state of mammary gland from pregnancy to lactation was apparent, with up-regulation of genes involved in milk component synthesis (e.g., *LALBA*, *CSN3*, *BTN1A1*) and concomitant down-regulation of genes involved in catabolism and energy production (e.g., *ACOX1*, *NDUFA4*). Peak of lactation (21 d) was characterized by the largest number of DEG with ≥1.5-fold expression (714 up-regulated, 791 down-regulated) relative to late pregnancy (-34 d). A total of 110 transcription regulators with ≥1.5-fold in at least one time point relative to -34 d were identified via gene network analysis. Among these, 14 (e.g., *RARB*, *TP53BP1*) had ≥3-fold up-regulation during lactation relative to pregnancy. The imminent onset of lactation elicited tremendous adaptations in mammary gene expression, including many novel molecular functions. Differential expression of novel transcription regulators might help explain long-term adaptations in mammary gland development and function.

Key Words: Genomics, Sow, Lactogenesis

684 Mammary fat pad but not parenchyma is affected by diet in pre-weaned Holstein heifers. K. M. Daniels*[1], S. R. Hill[1], K. F. Knowlton[1], R. E. James[1], M. L. McGilliard[1], A. V. Capuco[2], and R. M. Akers[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*USDA-Agricultural Research Service*, *Beltsville, MD*.

Overfeeding prepubertal heifers may impair mammary parenchymal growth and reduce milk production, but dietary impacts in pre-weaned calves are unknown. This study was to evaluate effects of milk replacer (MR) composition on mass and composition of mammary parenchyma and fat pad (MFP). Twenty-four newborn heifers were fed one of four MR diets (n=6/diet): CON (20% CP, 21% fat MR fed at 441 g DM/d), HPLF (28% CP, 20% fat MR fed at 951 g DM/d), HPHF (27% CP, 28% fat MR fed at 951 g DM/d), and HPHF+ (27% CP, 28% fat MR fed at 1431 g DM/d). Water and starter (20% CP, 1.43% fat) were offered ad libitum. Animals were sacrificed and tissues were harvested on d 63 for analysis of protein, lipid, and DNA. Total mammary gland mass was lowest in CON (CON vs. others; 150 vs. 284 ± 30 g). Increased feeding (HPHF vs. HPHF+; 288 vs. 379 ± 30 g) as well as addition of fat to an isonitrogenous diet (HPLF vs. HPHF; 185 vs. 288 ± 30 g) increased gland mass. Parenchymal mass (CON, HPLF, HPHF, and HPHF+: 9.2, 11.7, 15.5, 15.1 ± 3.3 g) was not affected by diet nor was parenchymal composition, or concentrations of protein (4.2 ± 0.30%), lipid (13.8 ± 2.2%), and DNA (0.21 ± 0.02%). However, MFP was markedly affected by diet; MFP mass (CON vs. others; 140 vs. 270 ± 30 g) and total MFP lipid (37 vs. 144 ± 25 g) were lowest in CON, whereas total DNA content did not differ (60 vs. 54 ± 12 mg). Added fat increased MFP mass (173 vs. 273 ± 30 g), tended to increase total MFP lipid (64 vs. 132 ± 25 g), but decreased total MFP DNA (84 vs. 42 ± 12 mg). Increased intake of HPHF increased MFP mass (273 vs. 364 ± 30 g) and MFP lipid (132 vs. 234 ± 22 g), but did not affect MFP DNA (42 vs. 37 ± 11 mg). Total protein in MFP was unaffected by diet, but protein concentration of MFP was highest in CON (CON vs. others; 20 vs. 11 ± 3 mg/g MFP). Added fat decreased MFP protein concentration (20 vs. 9 ± 3 mg/g), and increased intake of HPHF had no effect on MFP protein concentration (9 vs. 6 ± 3 mg/g). In conclusion, diet had no effect on mammary parenchyma, but MFP mass and composition were affected. Implications with respect to future milk production remain to be determined.

Key Words: Heifer, Mammary, Milk Replacer

685 Hormone interactions modulate mammary growth, morphogenesis and local IGF expression in peripubertal gilts. K. C. Horigan[1], J. F. Trott[1,2], and R. C. Hovey*[1,2], [1]*University of Vermont*, *Burlington*, [2]*University of California*, *Davis*.

Development of the mammary glands is coordinately regulated by hormone interactions during postnatal development. While responses by the mammary gland to the ovarian hormones estrogen (E) and progesterone (P) and pituitary-derived prolactin (PRL) have been characterized across various species, their combined effects have received limited investigation. We therefore determined the individual and combined effects of E, P and PRL on mammary gland growth, morphogenesis and hormone receptor expression in sham-operated and ovariectomized (OVX) peripubertal miniature swine (n=36). Females received bromocriptine (Bromo) for 9d after OVX surgery to suppress endogenous PRL. Thereafter females received daily injections comprising all possible combinations (n=4/group) of E, P and/or haloperidol (HAL, to induce PRL secretion) for 5d. Sham-operated females received saline only. The incidence of cells proliferating (BrDU-positive) and expressing E and P receptors (ER and PR) was determined immunohistochemically. Total RNA from mammary glands was analyzed for IGF-I and IGFBP-3 expression by qRT-PCR. OVX plus Bromo blocked proliferation relative to that in Sham controls (P<.05) while it was restored by exogenous E. Hal alone failed to stimulate proliferation but positively interacted (P<.001) with the effects of E, where maximum proliferation was induced by E+P+Hal. The incidence of ER-positive cells was less when E, P and Hal were administered in combination compared to the individual hormone effects. While E increased PR incidence, this effect was blunted by treatment with P and/or Hal. Expression of IGF-I mRNA in the mammary glands was unaffected by ovariectomy but increased in response to E or Hal. Conversely, E and E+Hal suppressed IGFBP-3 levels, supporting the potential for local modulation of IGF bioavailability. These findings provide important details about the interactive effects of ovarian and pituitary hormones on mammary growth in swine.

Key Words: Mammary Growth, Prolactin, Estrogen and Progesterone

686 Possible involvement of connective rissue growth factor (CTGF) in insulin-like growth factor-I (IGF1) stimulation of proliferation of bovine mammary epithelial cells. Y. Zhou[1], A. V. Capuco[2], and H. Jiang*[1], [1]*Virginia Polytechnic Institute and State University*, *Blacksburg*, [2]*USDA-ARS*, *Beltsville, MD*.

IGF1 plays an important role in mammary gland development and lactation in part by stimulating proliferation of the milk-producing epithelial cells. In this work, we used the bovine mammary epithelial cell line MAC-T as a model to study the mechanism by which IGF1 stimulates proliferation of the mammary epithelial cells. A microarray analysis revealed that 155 transcripts were up- or down-regulated at least twofold by IGF1 in MAC-T cells ($P < 0.05$). Among the most significantly down-regulated genes was CTGF, a secretory protein that has both proliferative and apoptotic effects, depending on cell type, and also a low-affinity binding protein of IGF1. Quantitative PCR confirmed IGF1 regulation of CTGF and eight other mRNAs in MAC-T cells. Using selective inhibitors of signaling pathways from the IGF1 receptor (IGF1R), it was found that IGF1 suppressed CTGF mRNA in MAC-T cells through the phosphatidylinositol 3-kinase pathway. Administration of growth hormone (GH), a major stimulator of IGF1 production in vivo, decreased mammary expression of CTGF mRNA in cows ($P = 0.07$). However, GH had no effect on CTGF mRNA expression in MAC-T cells, suggesting that IGF1 mediates the reduced expression of CTGF mRNA in the mammary gland. In the absence of IGF1, CTGF stimulated proliferation of MAC-T cells ($P < 0.05$), but in combination with IGF1 it attenuated the stimulation of IGF1 on proliferation of MAC-T cells ($P < 0.05$), and the attenuation was reversed by excess IGF1 ($P < 0.05$). Western blotting analyses indicated that despite being an IGF1 binding protein, CTGF did not affect IGF1-induced phosphorylation of IGF1R or total IGF1R expression in MAC-T cells, indicating that CTGF attenuation of IGF1-stimulated proliferation of MAC-T cells is not mediated by decreasing the ability of IGF1 to activate IGF1R or by decreasing IGF1R expression. Overall, these results suggest a novel biochemical and functional relationship between CTGF and IGF1 in the bovine mammary gland, where IGF1 may inhibit CTGF expression to reduce the attenuating effect of CTGF on IGF1 stimulation of epithelial cell proliferation.

Key Words: IGF1, CTGF, mRNA

687 Stromal changes in the bovine mammary gland during involution and mammogenesis. L. De Vries*, M. VandeHaar, T. Casey, T. Petzke, H. Dover, J. Liesman, and K. Plaut, *Michigan State University*, *East Lansing*.

The bovine mammary gland undergoes extensive remodeling during involution and mammogenesis between lactations. Changes in mammary epithelium have been well characterized during the dry period, but few studies in dairy cattle have characterized changes in stromal tissue. We hypothesized that stromal fibroblasts are activated and the amount of fibronectin is increased during the dry period to promote remodeling of the mammary gland for the subsequent lactation. Our objective was to determine if changes occur in the number of activated fibroblasts, the percent stromal area, and the expression of fibronectin in the stroma during involution and mammogenesis. Tissue was biopsied from 7 Holstein cows at 4 time points: late lactation, 7 d after dry-off, and at 21 d and 7 d before expected calving date. Smooth muscle α-actin, which is an indicator of activated fibroblasts, and fibronectin were measured by immunohistochemistry with image analysis software. Overall morphology of biopsied tissues was typical of involution and mammogenesis within each cow. The number of activated fibroblasts was similar for the first three time points but tended to increase from 20% to 33% of total fibroblasts between the last two time points (P=0.04). The intralobular stromal area decreased relative to the lumen and epithelial area from 48% to 32% between the last two time points (P<0.01). Fibronectin expression did not significantly change across time points (P>0.2). Based on these preliminary data, we suggest that fibroblast activation may indeed be important for stromal remodeling and that the major changes in the stroma occur in the late stages of the dry period.
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Key Words: Mammogenesis, Involution, Mammary Gland