a limited amount of data suggest that forages may be a reasonable source of alpha-linolenic acid (C18:3). However, the FA composition of different forages is not well described. The objective of this study was to characterize the FA composition of several grass and legume hays commonly fed to horses. Different sources of each of the following 5 hays were examined: timothy (n=8), orchardgrass (n=6), Coastal bermudagrass (n=10), alfalfa (n=8) and perennial peanut (n=6). Hays were analyzed for FA composition, total fat, crude protein, NDF and ADF. Data were analyzed by ANOVA to compare differences between individual hay varieties, grass vs. legume hays and warm- vs. cool-season grass hays. Across all hays, C18:3 made up the greatest ($P<0.01$) portion of the total fat content of hay (39.1±1.9 g/100 g fat), followed by C16:0 (23.8±0.9 g/100 g fat) and C18:2 (21.2±0.9 g/100 g fat). Other FA detected in all hays included C18:0, 18:1, 20:0, 22:1 and 24:1, each ranging from 0.02 to 4.1 g/100 g fat. Grass hays tended to contain a higher ($P<0.10$) proportion of C18:0 than legume hays, but no other differences in FA content were detected between these hays. The total fat content of legume hays (6.9±0.6%) was higher ($P<0.05$) than that observed for grass hays (3.8±0.3%), suggesting that while the FA composition of legume hays does not differ greatly from grass hays, legume hays may provide a greater total quantity of C18:3. Warm-season grass hay tended to be higher ($P<0.10$) in C16:0 and C18:0 and lower ($P<0.10$) in C18:3 than cool-season grass hays. Individual grass hay varieties did not differ in total fat content. Across all hays, a negative correlation was found between C18:3 and ADF content ($r=-0.58$; $P<0.05$), which indicates n-3 FA content of hay may decline when forage is harvested for hay at a more mature stage. Ultimately, consumption of commonly available hays of good to moderate quality will result in a greater intake of n-3 FA (C18:3) over omega-6 FA, regardless of the type of hay.

Key Words: Omega-3 Fatty Acids, Alpha-Linolenic Acid, Forage

64 Effect of season, forage maturity and grazing on the fatty acid composition of bahiagrass pasture. L. K. Warren* and J. Kivipelto, *University of Florida*, *Gainesville*.

Although low in total fat, a limited amount of data suggest forage may serve as a significant source of alpha-linolenic acid (C18:3) in equine diets. However, the fatty acid (FA) composition of common pasture forages has not been widely described. The objectives of this study were to characterize the FA composition of bahiagrass pasture selected by grazing horses and to determine the effect of season and cumulative growth on pasture FA composition. Over a 24-mo period, 3 replicates of each of 3 types of pasture samples were obtained at 1-mo intervals: grasses on or near areas where there was recent evidence of grazing by horses (GRAZE), grasses obtained from the same plots each month (MONTH), and grasses obtained from different plots each month that were allowed to accumulate up to 12 mo of growth (ACCUM). Both MONTH and ACCUM samples were obtained from areas on pasture that were restricted from grazing. MONTH was used to assess change in FA composition for new growth occurring in each 1-mo interval. ACCUM was used to determine changes in FA content as pasture forage grew and matured. All samples were obtained from an 8.1-ha, mixed-cultivar bahiagrass (*Paspalum notatum*) pasture that continually housed the same 6 mature geldings. Differences in FA content between sample types and with season were determined by ANOVA. On average pasture contained 4.1±0.2% total fat. Across all months and sample types, C18:3 made up the largest proportion of the total fat in forage ($P<0.01$), followed by C16:0 ($P<0.01$) and C18:2 ($P<0.01$). Other FA detected in pasture included C17:0, 18:0, 18:1, 20:0, 22:1 and 24:1, each ranging from 0.1 to 5 g/100 g fat. On average C18:3 was higher ($P<0.01$) in GRAZE (56.4±2.2 g/100 g fat) and MONTH (54.7±2.3 g/100 g fat) than ACCUM (39.8±4.2 g/100 g fat), whereas C18:2 made up a greater ($P<0.01$) proportion of the fat in ACCUM (21.5±1.1 g/100 g fat) compared to GRAZE (15.2±0.6 g/100 g fat) and MONTH (16.8±0.6 g/100 g fat). Season ($P<0.05$) affected C18:3 and C18:2 content of MONTH and ACCUM samples, with higher levels observed from April to July. ACCUM samples contained higher ($P<0.01$) C17:0, 18:0, 18:1 and 20:0 than GRAZE and MONTH, indicating a rise in these FA as bahiagrass pasture matures.

Key Words: Alpha-linolenic acid, Omega-3 fatty acids, Warm-season forage

Immunology - Livestock and Poultry I

65 An initial evaluation of the pathogenesis of Turkey-origin avian reovirus in poults. C. Stephens*[1], M. Pantin-Jackwood[2], E. Spackman[2], and J. M. Day[2], [1]*University of Georgia*, *Athens*, [2]*Southeast Poultry Research Labs, USDA*, *Athens, GA*.

Enteric disease causes poor performance in turkey flocks and, consequently, production losses in the industry. The pathogenesis of enteric viruses is not well understood and needs to be studied to further understand the nature of enteric disease. A virus isolated in 2003 from the intestines of poorly performing commercial turkeys in North Carolina (NC/SEP-R44/03) was selected for this study. In a previous study, this virus induced both humoral and cell-mediated immunosuppression in two-day-old poults. Three-week-old Broad Breasted White turkeys were inoculated by oral gavage with NC/SEP-R44/03, and the sham inoculated birds were inoculated with sterile phosphate buffered saline. Both the sham inoculated birds and the infected birds were weighed at days 0, 9, and 16 days post inoculation (DPI) to evaluate body weights. At 8 and 15 days PI, ten sham birds and 10 inoculated birds were selected to study the cutaneous basophil hypersensitivity (CBH) response; a measure of cell-mediated immunity. Another 20 birds were selected to study the humoral immune response by evaluating their antibody titers to Newcastle disease vaccine. Serum was collected from these birds at 21 and 42 DPI, and the antibody titers were determined by ELISA and were compared between the sham inoculated birds and the virus inoculated birds. Poults were periodically necropsied and examined for clinical signs of enteric disease. The spleen, bursa, and thymus were collected for histopathological analysis. No clear differences between the treatment groups in bodyweight, CBH response, and antibody response were observed; however, gross lesions consistent with enteric disease were observed at 8 and 15 days PI. Gross lesions included gas-filled, fluid filled intestines with undigested feed, and ceca with frothy contents. Enlarged bursas of fabricius with bursal 'cores' were also observed. In conclusion, older turkeys, in contrast with younger turkeys, do not appear to suffer immunosuppression with reovirus; however, enteric disease is observed.

Key Words: Turkey, Reovirus, Pathogenesis

66 Characters and functions of anterior pituitary progenitor cells that are identified by a novel monoclonal antibody. Y. Nagai*, H. Aso, H. Ogasawara, S. Tanaka, K. Watanabe, S. Ohwada, and T. Yamaguchi, *Laboratory of Functional Morphology, Graduate School of Agricultural Science, Tohoku University*, *Sendai, Japan*.

In anterior pituitary gland, inflammatory mediators such as cytokines modulate the cell function through immuno-endocrine pathway. Our previous study showed that proinflammatory cytokine, IL-18 was localized in the cell layer of Rathke′s pouch that has been proposed to embody stem/progenitor cell compartment in the anterior pituitary gland of cattle. We established a stem/progenitor cell line (BAPC-1) from the anterior pituitary gland. BAPC-1 expressed the mRNA of stem/progenitor cell-associated factors and inflammatory cytokines including IL-1, IL-6, IL-8, IL-12 and IL-18. However, the nature and behavior of anterior pituitary progenitor cells remains unclear. The present study was conducted to produce monoclonal antibodies (mAbs) specific for the membrane protein of BAPC-1 and to detail anterior pituitary progenitor cells. It was revealed that the mAbs termed 12B strongly reacted with BAPC-1 and recognized 4Ig-B7-H3 molecule, which is a costimulatory molecule and a negative regulator in T-cell activation. The 12B-immunoreactive cells (12B-ir cells) were localized around the Rathke′s pouch in young and adult cows. However, the number of 12B-ir cells was less in adult cows compared with young cows. The 12B-ir cells were also observed around the pars tuberalis, which lie closely to median eminence and have blood supply via the primary portal plexus in anterior pituitary gland. In the intermediate lobe, 12B-ir cells were sporadically observed around the Rathke′s pouch in both cows. The 12B-ir cells corresponded with the cells immunoreactive for IL-18 around the Rathke′s pouch. Thus, 12B was available to detect anterior pituitary progenitor cells. These results suggest that anterior pituitary progenitor cells are localized in the layer of Rathke′s pouch and function as immunomodulatory cells.

Key Words: Anterior Pituitary, Stem/Progenitor, Immunomodulator

67 Effect of photoperiod on immune function in broiler chickens. S. Dalal*, K. Schwean-Lardner, B. Laarveld, H. L. Classen, and A. G. Van Kessel, *University of Saskatchewan*, *Saskatoon, SK, CANADA*.

Three experiments were conducted to investigate the effect of lighting program on immunity in broiler chickens. In experiment 1, 560 day-old male chicks were placed in 8 rooms (70 birds/pen) on used litter and assigned to 14, 17, 20 or 23 hours continuous light. Sixteen chickens were selected from one pen in each room and intraperitoneally administered 400 μg of lipopolysaccharide (LPS) in 1ml saline or saline every second day for 10 days beginning at day 17. Experiment 2 was a replicate experiment except that LPS or saline were administered beginning at 27 days of age. Weight gain during LPS administration and relative organ weight at the end of LPS administration were recorded. In experiment 3, 6264 day-old chickens were placed on fresh litter in one of 9 rooms at a housing density of 30 kg/m^2 and assigned to one of 3 lighting programs including intermittent (15h light: 3.5h dark: 2h light:3.5h dark), 17h light:7h dark (17L) and 23h light:1dark (23L). One bird was selected from each pen per room and administered (i.m.) on days 10 and 21 a commercial *E.coli* (K88) vaccine (0.2 mL/bird). On day 39, antibody titre was assayed in serum and heterophil phagocytic and free radical production was assayed in whole blood. LPS administration reduced ($P < 0.001$) weight gain in experiment 1 and increased ($P< 0.05$) relative liver and spleen weight in experiment 1 and 2. No interaction was found between lighting program and response to LPS. In Experiment 3, serum anti-K88 titre was highest ($P<0.05$) in birds on a 1 hour dark period compared with birds on other lighting treatments ($P<0.05$). Blood phagocytic activity was highest ($P<0.05$) in birds exposed to a 7 hour continuous dark period compared to an intermittent 7 hour dark period or a 1 h dark period. We conclude that lighting program did not markedly influence the magnitude of the inflammatory response to LPS. Short dark exposure appeared to support the highest serum antibody response, whereas a long continuous dark exposure supported the highest whole blood phagocytic activity.

Key Words: Lighting Program, Broiler, Immune Function

68 Gene expression profiling in heterophils from *Salmonella*-resistant and -susceptible chicken lines using a chicken 44K Agilent microarray. H. I. Chiang*[1], C. L. Swaggerty[2], M. H. Kogut[2], X. Y. Li[1], and H. Zhou[1], [1]*Texas A&M University*, *College Station*, [2]*United States Department of Agriculture*, *College Station, TX*.

Large-scale expression profiling is a promising tool for ascribing complex biological function and interactions between genes with available genomic sequence data. To determine the transcriptional response to *Salmonella* enterica serovar Enteritidis (SE) infection, a newly developed chicken 44K Agilent array was used to analyze RNA of heterophils from SE-resistant (line A) and SE-susceptible chickens (line B), treated with in vitro infection of SE (I) or non-SE medium (N). A dual-color balanced design was used to provide a direct comparison between SE-infected and non-infected groups (A-I vs. A-N, B-I vs. B-N) and between line A and line B (A-N vs. B-N, A-I vs. B-I). Each comparison includes four biological replicates with a dye swap. The medium signal intensity was normalized using locally weighted linear regression (LOWESS) method, and followed by a mixed model analyses using SAS program. The results indicated that: for the comparisons of SE infection with non-infection, 3096 genes in line A and 3312 genes in line B were differentially expressed ($P < 0.05$), while 67 and 56 genes were related to immune function, respectively. In the comparison of lineage (line A and line B) difference, 4377 genes in the non-infected and 4333 genes in the infected groups showed differential expression ($P < 0.05$), whereas 71 genes and 69 genes were immunologically related, respectively. Interestingly, more differentially expressed genes were identified in the comparison of the lineage difference than in the comparison of SE infected to non-infected group, however, there were more genes that achieved a 4-fold change (up- or down-regulated) in the latter comparison. The results discovered in the present study have laid a solid foundation to elucidate cellular and molecular mechanisms of SE infection in chickens.

Key Words: Chicken, Microarray, Salmonella

69 Relationship between growth performance and immuno-competence measurements in broiler strains under high ambient temperatures. M. M. Fathi*, A. Galal, S. A. El-Safty, and S. S. Al-Rishan, *Faculty of Agric., Ain Shams Univ.*, *Cairo, Egypt*.

An experiment was conducted to quantify the growth performance and immunological parameters of broiler strains under high ambient temperatures. Three different genetic strains of broiler chicks (125 Hubbard, 125 Ross and 125 Arbor Acres) were reared under similar managerial, environmental and hygienic conditions during summer

season of Egypt. The high and low ambient temperatures recorded during the experimental period were 33 and 28C, respectively. The birds were weighed weekly. Feed consumption and feed conversion ratio were determined on a week basis. At 4 weeks of age, 20 birds from each strain were randomly assigned to determine cell mediated response and relative weight of lymphoid organs. Also, at 5 weeks of age, 5 birds from each strain were randomly taken to determine the phagocytic ability. The results of the current study revealed that the Ross broiler chicks had significantly heavier body weight than that of Hubbard chicks. However, the Arbor Acres broiler chicks were intermediated. There were no significant differences among strains for feed consumption, feed conversion ratio and rectal temperature. With respect to cutaneous basophil hypersensitivity (CBH) response, it could be observed that the Hubbard strain had a greater dermal swelling response to phytohemagglutinin-P (PHA-P) followed by Ross one when compared to Arbor Acres strain at 72 hours post injection. Also, the Arbor Acres strain exhibited greater bursa and spleen (as a percentage of live body weight) compared to the remaining strains. On the other hand, the Ross strain showed smaller relative weight of thymus compared to the other strains. Concerning the phagocytic activity, the Ross strain had significantly lower level of carbon particles in their blood circulation as compared to Hubbard and Arbor Acres chicks. We concluded that although there was no significant difference for productive performance traits among strains, the Ross broiler chicks strain is hyper responder to phytohemagglutinin-P (PHA-P), had a better phagocytic ability and lower mortality rate compared to other strains.

Key Words: Broiler Strains, Immunocompetence, Growth Performance

70 The feather as an *in vivo* test tube for tissue immune responses. G. F. Erf*, B. Lockhart, K. Bateman, R. Finley, and O. T. Bowen, *University of Arkansas*, *Fayetteville*.

While the blood serves as an excellent window into humoral immune activity, it is much more difficult to monitor and assess qualitative and quantitative aspects of tissue immune responses. To determine the presence of cell-mediated immunity (CMI) to an antigen (Ag) *in vivo*, the Ag is injected into the wattle, wing-web or toe-web and the swelling response (SR) measured over a 12 to 72h period. However, the SR does not provide direct information on Ag-induced immune activities. Through our work on autoimmune loss of feather pigment cells (vitiligo) in Smyth line chickens, we have studied CMI extensively and noted that growing feathers, like other integumental tissues, are immunologically active sites. For our vitiligo studies we used growing feathers (5-10 mm living pulp) for histology, immunohistochemistry, cell isolation and gene-expression studies. Considering that the growing feather is a defined, accessible, living unit that can easily be removed for down-stream analyses, we examined the suitability of feathers for study of *in vivo* tissue immune responses. In Study 1, growing feathers of 12-wk-old roosters were injected with LPS, PHA, or vehicle. The feathers were collected 6h later. Histological examination revealed infiltration of heterophils, and heterophils, macrophages and lymphocytes, when LPS and PHA were injected, respectively. Vehicle injection was not associated with leukocyte infiltration. To test Ag-specific CMI, *Mycobacterium butyricum* was injected into feathers of *M. butyricum*-sensitized and -unsensitized chickens. Feathers were collected 4, 24, 48, and 72h later. Conventional histology and immunohistochemistry revealed leukocyte infiltration profiles in feathers identical to those reported previously for wattle tissue. Therefore, the feather is highly suitable for monitoring and assessing various aspects of CMI in an individual bird. Knowledge gained by studying tissue immune responses *in vivo* will find direct application in the design of vaccines and strategies to optimize immune system development and function.

Key Words: Cell-mediated Immunity, LPS, PHA

71 Risk factors for avian developmental immunotoxicity (DIT): potential role of sex, hormone status, and age. R. R. Dietert*, *Cornell University*, *Ithaca, NY*.

Recent research has suggested that the developing immune system is far more sensitive to environmental modulation than that of the fully-mature adult. Both quantitative differences in dose-response sensitivity as well as qualitative differences in the nature and extent of environmentally-induced immune alterations have been linked to the age of exposure. But a surprising observation is that age alone may not be the only risk factor warranting consideration. The sex of the embryo and hormone balance at the time of exposure may also help to determine subsequent immunotoxicity and as a result, later-life health risk. In fact, differential immunotoxic risk based on sex may be even greater in early life than in the adult. Even in cases where there is not necessarily a dose-sensitivity difference between the sexes, the nature of immunotoxic alterations may differ among the sexes. Hormone alteration at the time of exposure seems to influence risk even when the toxicant is not a potent endocrine-disruptor. Additionally, immune impairment may not be readily apparent until post-hatch stress and/or disease challenges occur. As a result, unpredicted post-hatch immune responses, particularly when they are restricted to a subpopulation, may not be readily identified in term of early-life cause/later-life effect. For this reason, it is important to recognize the potential for differential sex-determined and hormone-influenced immunomodulatory responses following both intended (vaccine and/or adjuvant exposures in poultry) and unintended in ovo exposure. This presentation will review recent results in birds concerning heavy metals, and other toxicants relative to early life-insult and subsequent immunotoxic risk. Supported by USDA Grant Regional Project NE-1016.

Key Words: Developmental Immunotoxicity (DIT), Avian, Risk Factors

72 Antibody response against bovine red blood cells in major histocompatibility (*B*) complex recombinant *R13*. N. G. Wilkinson[1], L. M. Yates[2], R. T. Kopulos[2], W. E. Briles[2], and R. L. Taylor, Jr.*[1], [1]*University of New Hampshire*, *Durham*, [2]*Northern Illinois University*, *DeKalb*.

Recombination within the chicken major histocompatibility complex (MHC) has enabled more precise identification of genes controlling immune responses. Chicken MHC genes that are closely linked on chromosome 16 include *B-F*, MHC class I; *B-L*, MHC class II; and *B-G*, MHC class IV. Six congenic lines, each containing a single unique MHC recombinant, achieved 99.9% genetic uniformity through ten backcross generations to inbred Line UCD 003 genotype *B17B17*. Recombinant *R13* (*BF17-BG23*), arose in a single male from the tenth backcross generation for *R1* (*BF24-BG23*). An additional backcross to the Line UCD 003 background increased the number of *R13*

individuals. This new recombinant was tested for antibody production against the T-dependent antigen, bovine RBC (BRBC). Fifty-one progeny segregating for *R13R13* (n = 10), *R13B17* (n = 26), and *B17B17* (n = 15) genotypes were produced by a single *R13B17* male mated to five *R13B17* dams. One mL of 2.5% bovine BRBC was injected intravenously into all genotypes at 4 and 11 weeks of age to stimulate primary and secondary immune responses, respectively. Blood samples were collected 7 days post-injection. Serum total and mercaptoethanol (ME)-resistant antibodies against BRBC were measured by microtiter methods. Titers were expressed as the $\log_2$ of the reciprocal of the highest dilution giving visible agglutination. The least squares ANOVA used to evaluate all primary and secondary antibody titers included hatch and *B* genotype as main effects. Significant means were separated by Fisher's Protected LSD at $P < 0.05$. *R13R13* chickens had significantly lower primary total and ME-resistant antibodies than did the *R13B17* and *B17B17* genotypes. Secondary total and ME-resistant antibodies were significantly lower in *R13R13* chickens compared with *R13B17* but not *B17B17* chickens. Gene differences generated through recombination impacted the antibody response of *R13* compared with *B17*. Secondary antibody titers were not substantially higher than the primary titers suggesting that the memory response had waned in the 7 week interval between injections.

Key Words: Immunity, Recombination, Antibody

Graduate Student Paper Competition: National ADSA Dairy Foods Division

73 Use of HTST pasteurization combined with other nonthermal processes to improve fluid milk shelf life. Z. P. Caplan* and D. M. Barbano, *Cornell University*, *Ithaca, NY*.

Our objective was to develop a process using minimum HTST pasteurization in combination with other nonthermal processes to achieve 60 to 90 days of fluid milk shelf life at 6°C. Microfiltration of raw skim milk and different methods of reducing the total bacteria count of milk fat sources for production of 2% milk were evaluated. Microfiltration (MF) and HTST pasteurization were used to reduce total bacteria, spores, and coliforms in 2% milk made from MF skim milk and various milk fat sources. Raw skim milk was microfiltered at 51°C using a Tetra Alcross M7 Pilot Plant equipped with a ceramic Membralox membrane (pore size: 1.4 micron). MF skim milk plus 3 different milk fat sources were heated to 51°C, and pumped, by weight, into separate containers of MF skim milk to create different 2% milks. These milks were compared to a MF skim milk control without fat added. Each 2% milk was homogenized at 500/2500 psi before undergoing HTST processing (73°C, 15 sec). Total bacteria counts of raw and pasteurized MF skim milks, and pasteurized 2% milks, were determined with most probable number and standard plate count (SPC) methods. Average (n=4) raw skim milk SPC was reduced from 1690 cfu/mL to 0.13 cfu/mL by MF, and further reduced to 0.08 cfu/mL by HTST processing, demonstrating an average 4.3 log reduction from the raw skim milk count due to the combination of MF and HTST. The SPC for all of the pasteurized 2% milks averaged <100 cfu/mL. The pasteurized MF skim milk and pasteurized 2% milks were then stored at 6°C, and the SPC was determined weekly over a 90 d period using a Foss Bactoscan™ FC. Different fat sources did not have a large impact on shelf life. Across 3 replicates, 9 of 9 one liter containers of the pasteurized MF skim milk, and 23 of 27 one liter containers of the pasteurized 2% milks, remained below 20,000 cfu/mL at 70 d. Minimum HTST pasteurization combined with other nonthermal processes was used to successfully extend refrigerated fluid milk shelf life beyond 60 d at 6°C.

Key Words: Microfiltration, Shelf Life, HTST

74 Manufacture of pasteurized process cheese spread from milk concentrated by microfiltration. H. Somni*, V. V. Mistry, K. Muthukumarappan, and K. R. Nauth, *Midwest Dairy Foods Research Center, South Dakota State University*, *Brookings*.

The objective was to replace base cheese in pasteurized process cheese (PC) spread making with microfiltered (MF) milk. Earlier studies focused on PC manufacture from ultrafiltered (UF) milk. With microfiltration, milk proteins are fractionated and offer unique opportunities in process cheese making. Raw skim milk was microfiltered using 0.1µm membrane to approximately 5.7X casein concentration (MFC). Casein in the MFC was 95, 94 and 77% of true protein, total protein and total solids, respectively. MFC was used to substitute base Swiss cheese in PC spread formulations at 33% (T1), 66% (T2) and 100% (T3) by weight of cheese. Total solids, fat, and salt were targeted to 59, 21.5, and 1.5%, respectively, and pH at 5.75. Control (C) was made from Swiss cheese without any substitution. Swiss cheese flavor concentrate was added at 0, 0, 1.85 and 3.5 % levels to C, T1, T2 and T3, respectively. The cheese spread was pasteurized at 71°C for 2 min. The treatments were replicated three times using a randomized block design. Cheeses were analyzed for composition, sensory and rheological properties. Spreadability was measured as percent increase in area after 2.5 and 5.0 min at 25°C. Means were compared using PROC GLM procedure of SAS at p=0.05. With increase in the level of MFC in the spreads, total protein decreased and minerals increased significantly. Control differed from treatments and had minimum viscosity. The bulk and elastic moduli differed for the treatments but did not correlate to level of MFC. A panel of seven expert judges rated T1 above C and the difference was significant for overall flavor, body and texture, and overall acceptability on 1-9 scale (9-liked most and 1-extreme dislike). Substitution of base Swiss cheese with MFC significantly affected rheological properties of the PC spread. This could be because of differences in the protein and minerals levels within the treatments. Thus, microfiltration offers opportunities for developing spreads with consistency and acceptable quality.

Key Words: Microfiltration, Process Cheese Spread

75 Effect of different stabilizers on the textural and rheological properties of cream cheese. M. Brighenti*[1], S. Govindasamy-Lucey[2], J. J. Jaeggi[2], M. E. Johnson[2], and J. A. Lucey[1], [1]*University of Wisconsin*, *Madison*, [2]*Wisconsin Center for Dairy Research*, *Madison, WI*.

Stabilizers are added during cream cheese manufacture to help prevent syneresis during storage. The objective of this study was to determine the impact of different stabilizers on the texture and rheology of cream