in 650 herds from 969 sires for Ayrshire, 33,548 heifers in 815 herds from 932 sires for Jersey. Functional longevity was defined as the number of days from the first calving to culling or death or censoring. Reproduction traits were calving ease (unassisted, easy pull, hard pull or surgery), calf size (small, medium or large), stillbirth (dead or alive within 24-h of calving), non return rate (unsuccessful or successful), number of services and days from first service to conception. The statistical model included the effects of stage of lactation, season of production, the annual change in herd size, type of milk recording supervision, age at first calving, effects of milk, fat and protein yields calculated as within herd-year-parity deviations, herd-year-season of calving, each fertility trait and sire. The relative culling rate was calculated for animals in each class after accounting for the above-mentioned effects. The result showed that heifers that require hard pull, producing large calf size and dead calves were more likely to be culled compared to the average group in each breed. For instance, heifers producing dead calves were 35% and 14% times more likely to be culled compared heifers producing live calves in Ayrshire and Jersey, respectively. In all breeds, as number of services increased there was a trend toward higher risk of culling among heifers. The relative risk ratio for heifers that required greater than 120 days from first service to conception were 1.35 (Ayrshires) and 1.25 (Jersey) times more likely to be culled compared to heifers that did conceive with the first insemination.

Key Words: Functional longevity, Reproduction traits, Canadian dairy breeds

348 Factors that impact longevity of Holsteins in the United States. H. D. Norman* and J. R. Wright, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA*, *Beltsville, MD*.

Region, herd size, inbreeding, and performance were examined to determine their impact on longevity of 8 million US Holsteins from 1980 through 2005. Seven geographical regions (5 to 9 states each) were defined. Ten inbreeding groups were defined based on percentage of inbreeding: 0, 0.1 to 1.0, 1.1 to 2.0, 2.1 to 3.0, 3.1 to 4.0, 4.1 to 5.0, 5.1 to 7.0, 7.1 to 10.0, 10.1 to 15.0, and >15.0. Seven herd-size groups were defined: <50, 51 to 100, 101 to 200, 201 to 500, 501 to 1,000, 1,001 to 2,000, and >2,000 cows. Cows were excluded if sold for dairy purposes or if the herd discontinued testing during productive herdlife of the cow. Time restraints were imposed so that cows had an opportunity to survive to parity 8. Differences in number of calvings for the most recent year with complete data were notable between regions; number of calvings ranged from 2.59 (Southeast) to 2.92 (Northeast). Differences based on herd size were smaller; number of calvings ranged from 2.75 (101 to 200 cows and >2000 cows) to 2.83 (<50 cows and 501 to 1,000 cows). Inbreeding coefficients have increased over time, and inbreeding had a large impact on number of calvings and productive herdlife. For the latest year with survival opportunity, mean number of calvings decreased with increasing inbreeding from 2.97 calvings at 0% inbreeding to 2.53 calvings at >10% inbreeding. First-parity yield traits (milk, protein, and fat) had greater impact on cow longevity than did region or herd size. For terminal records, lactations were shortest for cows with mastitis or high somatic cell score (197 d) or that died (200 d) and longest for cows with reproductive problems (389 d). Cows that were culled after early parities had longer lactations than those culled after later parities. As cows aged, fewer were sold because of low yield or poor reproduction, and more died or were culled because of mastitis and high somatic cell score.

Key Words: Culling, Longevity, Survival

349 Health, immune function, and survival of calves from Holstein dams and Holstein or crossbred Jersey x Holstein sires. C. Maltecca*, K. Weigel, H. Khatib, V. Schutzkus, and P. Hoffman, *University of Wisconsin*, *Madison*.

Differences in birth weight, calving ease, serum protein level, serum IgG level, fecal consistency score, respiratory disease score, and perinatal and pre-weaning survival were evaluated in calves resulting from the random mating of lactating Holstein cows to young Holstein sires (N = 74) or young F1 Jersey x Holstein sires (N = 7). Calves from Holstein sires (N = 99) were 1.9 kg heavier than calves from crossbred sires (N = 211), leading to greater likelihood of an assisted calving (estimated odds ratio of 1.24). Furthermore, mean serum protein level at 24 to 72 hr of age was significantly higher ($P < 0.01$) for calves from crossbred sires than for calves from purebred sires, as was mean serum IgG level ($P < 0.05$), suggesting an improvement in the attainment of passive immunity among crossbred calves. Rates of perinatal survival, as measured by stillbirths and calves that died by 24 hr of age, and pre-weaning survival, as measured by deaths that occurred between 24 hr and 6 wk of age, were also significantly higher ($P < 0.05$) among calves from crossbred sires, as compared with calves from Holstein sires. Mean fecal consistency scores from birth to 7 d of age and average number of days with scours also tended to be lower ($P < 0.10$) among calves from crossbred sires. No differences were observed in the incidence or severity of respiratory disease. Results of this study suggest that the introduction of Jersey genes into Holstein herds via crossbreeding may lead to a reduction in calving problems and improvements in calf health, immune function, and survival. Future studies should address other traits related to dairy farm profitability, including milk composition, female fertility, longevity, feed efficiency, and resistance to infectious and metabolic diseases.

Key Words: Health, Immune function, Calves

Dairy Foods: Chemistry and Microbiology

350 Effect of EPA and DHA fortification on the oxidation stability of caprine milk infant formula analogue. C. O. Maduko*[1], Y. W. Park[2], and C. Akoh[1], [1]*University of Georgia*, *Athens*, [2]*Fort Valley State University*, *Fort Valley, GA*.

Eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA) are polyunsaturated fatty acids (PUFA) that are present in human milk and infant formulas, and required for proper growth and healthy brain development of infants. Oxidation alters the nutritional quality of PUFA due to their high unsaturation and produces toxic compounds, which may cause the milk unacceptable for consumption. Some standard methods can determine oxidative deterioration of PUFA, which include peroxide value (primary oxidative products) and P-anisidine value (secondary oxidative products). The objective of this study was to determine the effect of EPA and DHA fortification on the oxidation rate of caprine milk infant formula analogue. Skim goat milk was modified for two preparations: coconut, safflower and soybean

oils in the ratio of 2.5:1.1:0.8 (VGM), and coconut, safflower, soybean and menhaden fish oils in the ratio of 2.1:1.1:0.8:0.4 (FOGM). Both fortifications were made to contain 4.4g fat/100ml milk. Lecithin (0.5g/100ml) was added to both preparations before homogenization, freeze-drying and storage in airtight containers at room temperature for 6 weeks. A subsample from each batch was reconstituted every 14 days by dissolving 12.5 g dried sample in 87.5 g water, and then extracted for lipids. Peroxide value (POV) and P-Anisidine value (P-Anv) were determined for each subsample and TOTOX value was calculated as 2POV + P-Anv. For VGM samples, the respective ranges of POV, P-Anv and TOTOX were: 2.55-3.55, 0.60-2.06 and 3.55-9.16, while for FOGM samples the corresponding ranges for the three parameters were: 5.55-5.90, 12.0-18.38 and 23.1-29.8 for the 6 weeks storage period. The oxidation values for VGM were significantly ($P<0.05$) lower than those of FOGM. Although there may be a greater risk of oxidation for EPA and DHA fortified infant formulas, the study revealed that oxidative rate could be reduced significantly by use of antioxidants as well as low temperature storage treatment.

Key Words: EPA and DHA fortification, Oxidative stability, Infant milk analogue

351 Identification and putative proteolytic origin of some major water-soluble peptides produced during ripening of Ragusano cheese. C. Pediliggieri[1], T. M. Carnemolla[1], V. Gagnaire[2], D. Mollé[2], V. Fallico[1], S. Carpino[1], G. Licitra[1,3], and S. Lortal*[2], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*UMR Science et Technologie du Lait et de L'Oeuf*, *Rennes Cedex, France*, [3]*D.A.C.P.A. Catania University*, *Catania, Italy.*

Raw milk was collected from two farms of the Hyblean region sited on mountain level (ML) and sea level (SL). Raw milk was transformed in Ragusano cheese at the CoRFiLaC experimental cheese plant. The extent of proteolysis was estimated by soluble nitrogen at pH 4.6 and at 12%TCA; respectively 20.57 ± 2.25 and 17.52 ± 2.97 % for ML cheeses; 25.74 ± 2.21 and 21.37 ± 2.77% for SL cheeses after 210 days of ripening. Cheeses after stretching (0 days), as well as 120 days and 210 days aged cheeses were analyzed by RP-HPLC and the peptides further identified by tandem mass spectrometry. RP-HPLC profiles were similar for ML and SL after stretching and exhibited slight differences during ripening. After stretching, 224 peptides were successfully identified: 163 peptides arising from β-casein, 45 from αs1-casein and 16 from αs2-casein. Some peptides were common between ML and SL: 21% out of the β-casein peptides, 29 out of the αs1-casein and 56% out of the αs2-casein. Protein splitting corresponding to plasmin and cathepsin D, cell envelope proteinase of lactic acid bacteria and peptidase activities were observed. After 120 and 210 days of ripening most of these peptides were hydrolyzed. As observed in other cheese varieties, phosphopeptides were more resistant and can be found till the end of ripening like peptides from the N-terminal part of the β-and αs1 caseins. Some peptides like the fragment αs2 CN (100-115)(105-114)(153-162) and β (11-28)(29-52)(193-206) and α s1 (1-9)(14-23)(83-93), were released in cheese after manufacture and remained after 210 days of ripening; this suggested that these peptides might be used as markers of cheese age. These results showed that the raw milk origin and its variable bacterial ecosystem might lead to a certain modulation of the general proteolysis pathway. However, many identical peptides were also found indicating the importance of the process.

Key Words: Ragusano cheese, LC/MS-MS, Peptides

352 Measurement of ionic calcium in milk by molecular probes and front face fluorescence spectroscopy. R. R. Gangidi* and L. E. Metzger, *MN-SD Dairy Research Center, University of Minnesota*, *St. Paul*.

Ionic calcium influences the visco-elastic properties of the milk and other dairy products. Molecular probes, such as Fluo-5N, have the potential to be used to determine the ionic calcium content in milk. However, Fluo-5N was designed to measure calcium ions in the range of 1 to 1000μM at a physiological pH of 7.0, whereas the typical calcium ion concentration of milk is in the range of 2.5 to 3mM. The objective of the current study is to develop a simple calibration to measure calcium ion in milk with Fluo-5N and fluorescence spectroscopy. The calcium concentration of a milk sample was adjusted to various ranges by addition of 7.3 and 14.5mM of disodium-EDTA or 2mM of $CaCl_2$. Additionally a control milk sample without added EDTA or $CaCl_2$ was also used in the study. The pH of all the samples is adjusted to 6.6-6.7. After addition of EDTA or $CaCl_2$, the milk concentration was 80% in all samples. Fluo-5N (2.62μM) was added to the samples and thoroughly mixed. Fluorescence spectra (excitation at 470nm, and emission from 500-560nm) were collected on each sample before and after addition of the probe. The spectra of each sample prior to probe addition was used as the background and subtracted from the spectra collected from each sample after probe addition. The entire experiment was subsequently repeated with two additional milk samples. The fluorescence intensity at 519nm of each sample was correlated ($R^2 = 0.84$) to the logarithmic calcium ion concentration determined using a calcium ion selective electrode. These results indicate that the ionic calcium content of milk can be determined with Fluo-5N and fluorescence spectroscopy. The molecular probes, with further modifications, may also be used to measure ionic calcium in other dairy products.

Key Words: Calcium ion, Molecular probes, Ion selective electrode

353 Effect of mountain and sea level pasture on Conjugated Linoleic Acid content in plasma and milk. S. La Terra*[1], S. Carpino[1], S. Banni[2], M. Manenti[1], M. Caccamo[1], and G. Licitra[1,3], [1]*CorFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*Cagliari University*, *Cagliari Italy*, [3]*D.A.C.P.A Catania University*, *Catania, Italy*.

Total CLA in plasma and CLA isomers on bovine milk were studied in four groups of cows from two different located farms. Three groups of cows, from a mountain level (ML) farm, fed at 3 different levels of pasture. Group 1 fed TMR (ML0) no pasture; group 2 fed TMR supplemented with 30% DM of pasture (ML30), and group 3 fed TMR supplemented with 70% DM of pasture (ML70). The fourth group of cows, from a farm sited on sea level (SL), fed with TMR supplemented with 30% DM of pasture (SL30). Cattle breed, lactation days and milk production level were similar for all the 4 groups of cows. Blood from the jugular vein and milk samples were collected at the same time during the afternoon milking. Samples were transported to the lab and stored at -80°C. The experiment was repeated three times. The effect of pasture in the diet was significant ($P<0.01$) for CLA concentration in plasma. CLA level increased with the percentage of pasture in the diet: 1.17 (nmoli/mg fat) in the ML0, 2.07 (nmoli/mg fat) in the ML30, and 2.70 (nmoli/mg fat) in the ML70 treatment. In milk samples the comparison of amounts of the total CLA was significant ($P<0.01$) and was higher than the plasma samples: 10.41 nmoli/mg fat, 11.75 nmoli/mg fat and 15.26 nmoli/mg fat respectively. Milk isomers showed statistically different concentrations related to the percentage of pasture in the diet and in the different date of sampling. Isomers

trans 12 trans 14, trans 10 cis 12, cis 9 trans 11 and cis 10 cis 11 increased (P<0.01) with the percentage of pasture in the diet and the concentration of trans 11-trans 13, trans 10-trans 12, cis 11-trans 13, and cis 7-trans 9, and cis 9-cis 11 isomers increased linearly with time (P<0.01). The comparison of the level altitude (ML30 vs SL30) had no impact for total CLA in plasma and milk samples. Isomers trans 9 trans 11 (0.19 vs 0.11 nmoli/mg fat), and cis 10 cis 12 (18 vs 101 nmoli/mg fat) of the milk had a significative impact (P<0.01), and cis 9 trans 11 increased with time.

Key Words: Mountain and sea level pasture, CLA, Plasma and milk

354 Immunobiotic lactic acid bacteria induce immune responses in immature gut-associated lymphoid tissues via Toll-like receptors 2 and 9. H. Kitazawa*, M. Tohno, T. Shimosato, H. Aso, Y. Kawai, and T. Saito, *Graduate School of Agricultural Science, Tohoku University*, *Sendai, Japan*.

Studies comparing the composition of intestinal microflora in allergic and nonallergic infants have suggested a relationship between intestinal microflora and the development of allergies; however, the molecular mechanisms by which immature gut-associated lymphoid tissues (GALT) of newborns recognize microbial molecules have been unclear. Our laboratory has focused on the specific effectors on immunobiotics, probiotic bacteria, such as lactic acid bacteria, that promote health by activating intestinal immunity. Here, we investigated the expression patterns of Toll-like receptor (TLR) 2 and 9, which are receptors for bacterial components, and the immune responses induced by their ligands in the immature GALT of presuckling newborn swine. We found that TLR2 and 9 mRNAs are expressed at higher levels in ileal Peyer's patches (Pps) and mesenteric lymph nodes (MLNs) than in the duodenum, jejunum and ileum. We confirmed that the TLR2 and 9 proteins were also highly expressed and that their ligands were preferentially recognized by TLR2- or TLR9-expressing cells in the ileal Pps and MLNs. Zymosan, CpG2006, and lactic acid bacteria promoted mitogenesis and the production of multiple cytokines in the MLNs and ileal Pps. In addition, double immunostaining for cytokeratin 18 and either TLR2 or TLR9 revealed that both TLR2 and 9 are strongly expressed in the columnar membranous cells. Interestingly, although the apical membrane of the columnar membranous cells strongly expressed TLR2 protein and preferentially recognized zymosan, both TLR2 expression on the apical membrane and TLR2-mediated zymosan binding were negligible in neighboring enterocytes. These results indicate that TLR2 and 9 allow ileal Pps and MLNs to respond to a variety of bacterial components immediately after birth, thereby providing newborns with a host defense system. Understanding the functional role of TLR2 and 9 in the immature GALT should also aid the development of oral vaccines and immunobiotic foods that specifically target immune responses in the GALT.

Key Words: Immunobiotics, Toll-like receptor 2 and 9, Gut-associated lymphoid tissues

355 Microbiological safety of Ragusano cheese through traditional farmhouse manufacturing: A preliminary study. G. Licitra*[1,2], A. Fiori[1], M. Manenti[1], S. La Terra[1], P. Campo[1], and S. Carpino[1], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*D.A.C.P.A. Catania University*, *Catania, Italy*.

Ragusano is a raw milk pasta-filata cheese produced in the south-eastern region of Sicily at farmhouse level using natural rennet and traditional wooden tools. The cheese manufacturing process involves two rounds of cooking, stretching of the overnight-ripened curd, moulding, brining and aging. Slight differences in the manufacturing process among producers lead to different flavor and texture of the final product. In an attempt to define the key steps of the process that lead to a safe cheese, we monitored the production of PDO Ragusano cheese in five farms. During each of three subsequent days, two blocks of Ragusano were produced per farm, for an overall count of thirty blocks of cheese. Chemical and microbiological analysis were performed on milk, production intermediates and different sections (sub-rind, intermediate, and core) of cheese aged for 2, 3 and 4 months. Results point to the importance of the second cooking of the curd as a key step in establishing the necessary conditions for a fast acidification. In fact, in the only farm where this step takes place for 10 minutes only (as opposed to an average length of 150 minutes), acidification of the curd appears to be noticeably slower, with a concomitant higher susceptibility to contamination. Manufacturing conditions proved to be very effective in causing death of the small number of *Staphylococcus aureus* cells found as contaminants of raw milk. No contaminations by *Listeria monocytogenes*, *Salmonellae* and *Escherichia coli* were detected at any stage of the process. On the other hand, after 2 months from manufacturing already, cheeses showed water activity levels which are hardly compatible with growth of the above mentioned pathogens, and which decreased further with subsequent aging. Our results show that the cheese-making technology of Ragusano guarantees high levels of microbiological safety as long as good practices are mantained throughout the entire process. The high temperatures used for cooking and stretching the curd, fast acidification, low aw values and high salt content contribute to make Ragusano a hostile environment for the growth of pathogens.

Key Words: Ragusano cheese, Safety, Traditional

356 Development of a new evaluation system for the selection of probiotic lactic acid bacteria (LAB) with specific adhesion to human blood type A-antigen of intestinal mucosa. H. Uchida*[1], H. Kinoshita[1], Y. Kawai[1], H. Kitazawa[1], K. Miura[2], K. Shiiba[2], A. Horii[2], K. Kimura[3], N. Taketomo[3], M. Oda[3], T. Yajima[3], and T. Saito[1], [1]*Graduate School of Agricultural Science, Tohoku University*, *Sendai, Miyagi, Japan*, [2]*Graduate School of Medicine, Tohoku University*, *Sendai, Miyagi, Japan*, [3]*Meiji Dairies Corporation*, *Odawara, Kanagawa, Japan*.

A new evaluation system for selecting probiotic lactic acid bacteria (LAB) with activity for specific adhesion to human colonic mucin by recognizing differences in ABO-blood type was established. Sixteen strains that showed strong adhesion to human blood type-A antigen [GalNAc-α-1-3 (Fuc-α-1-2) Gal-] of intestinal mucosa were selected from 237 probiotic strains with a biosensor BIACORE, by surface plasmon resonance (SPR). Similarly, sixteen and eleven strains were selected with strong activity to human B-antigen [Gal-α-1-3 (Fuc-α-1-2) Gal-] and H-antigen [Fuc-α-1-2 Gal-], respectively. Because there is a lot of population of human blood type-A in Japan (40%), we experimented the LAB recognizing human A-antigen for further evaluation. The adherence of the SLPs (surface layer proteins) prepared from the selected strains towards human A-antigen was reevaluated by BIACORE and the *L. brevis* strains revealed strong adhesion to the A-antigen. The SLP from *L. brevis* strain OLL2772 showed a single band at ca. 48 kDa using SDS-PAGE analysis and it had a very high adherence to the human A-antigen as shown using an anti-A lectin blocking technique. A partial N-terminal sequence of the band showed high homology to a S-layer protein of *L. brevis* ATCC 8287^T . There are few reports of LAB recognizing human blood type antigens in

comparison to those showing the adhesion of LAB to the human intestine. The new assay system will be useful for the selection of probiotic candidates in future construction of functional foods including yogurt.

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Key Words: Lactic acid bacteria (LAB), Adhesion, Human blood type-A

357 Identification of the microflora in the complete Ragusano cheese processing from milk produced at two different farm locations. G. Licitra[1,2], S. Parayre[3], H. Falentin[3], S. Carpino[1], V. Fallico[1], C. Pediliggieri[1], and S. Lortal*[3], [1]*CoRFiLaC, Regione Siciliana*, *Ragusa, Italy*, [2]*D.A.C.P.A. Catania University*, *Catania, Italy*, [3]*UMR Science et Technologie du Lait et de L'Oeuf*, *Rennes Cedex, France*.

Raw milk was collected in two farms of the Hyblean region sited on mountain level (ML) and sea level (SL). Raw milk was transformed in Ragusano cheese, using two different wood vats 'tina' at the CoRFiLaC experimental cheese plant. Milk, curd before and after cooking, stretching and cheeses (4 and 7 months aged) were analyzed by PCR–TTGE and enumeration microbiology. In addition the biofilm of the vats 'tina' was studied before putting milk in it. The total count for the raw milk samples from ML farm and SL was respectively 6 10^4 and 2.3 10^5.Using universal primers PCR–TTGE revealed many differences between the raw milk profiles, excepted few common bands identified as *S. thermophilus*, *L. lactis*, *L. delbruecki*, and *E. faecium*. Other various species detected were *Lactobacillus helveticus*, *Propionibacterium freudenreichii*, *Staphylococcus xylosus*, *Lactobacillus plantarum*. 'Tina' exhibited different biofilms: the 'tina' for ML milk was colonized by two clearly predominant species: *S. thermophilus*and *L. delbrueckii* whereas the one used for SL milk exhibited at least 5 different bands, *S. thermophilus* being predominant. By numeration, the count of Enterococcus and Lactic acid bacteria increased (0,5 to 1 log) when milk was transferred in the 'tina'. In both cases (ML–SL), the stretching step induced a simplification of the profiles and 3 of 5 dominant species only were detected by TTGE trough the entire process of ripening. At this stage and whatever the milk origin the profiles were rather similar. Classical numeration confirmed the presence of predominant viable thermophilic lactic acid bacteria growing until stretching and decreasing until the end of the ripening. In conclusion, the cheese making process of Ragusano cheese (pH and temperature, mainly during stretching) has a major role in selecting predominant natural microflora. The exact role of the tina in inoculating the milk has to be further explored.

Key Words: Ragusano cheese, PCR–TTGE, Microbiology

358 Rheological properties of rennet-induced milk gels made from milk protein concentrate solutions with different ratios of A_s-: β-casein. J. A. O'Mahony*[1,2], P. L. H. McSweeney[1], and J. A. Lucey[2], [1]*University College*, *Cork, Ireland*, [2]*University of Wisconsin*, *Madison*.

The rheological properties of rennet-induced milk gels made from milk protein concentrate (MPC) solutions with α_s- (i.e., α_{s1}- + α_{s2}-):β-casein ratios of 1.00:0.80 (MPC A), 1.00:0.70 (MPC B) or 1.00:0.87 (MPC C), each having identical concentrations of total casein (2.5%), were studied using dynamic low amplitude oscillatory rheometry. The ratio of α_s-:β-casein had no significant ($P > 0.05$) effect on rennet coagulation time. Storage modulus (G′; index of firmness), measured 30 min after addition of rennet, decreased with increasing ratio of α_s-:β-casein. Storage modulus for gels made using each of the three MPC solutions reached plateau values ~200 min after addition of rennet, with the plateau value of G′ decreasing significantly ($P < 0.05$) as relative concentration of β-casein increased in the MPC solutions. There were no significant ($P > 0.05$) differences in the frequency dependence of G′ in the frequency range 0.001 to 1 Hz between gels made using any of the three MPC solutions. On shearing the gels at a rate of 0.01 s^{-1}, the value for apparent yield stress and apparent yield strain increased significantly ($P < 0.05$) as relative concentration of α_s-casein increased in the MPC solutions. Thus, the ratio of α_s-:β-casein influenced the small and large deformation rheological properties of rennet-induced milk gels.

Key Words: Casein, Rennet, Rheology

Dairy Foods: Production Meets Processing: A Vital Link for High Quality Dairy Foods

359 Production meets processing: A vital link for high quality dairy foods. S. A. Rankin*[1], S. P. Washburn[2], B. Luth[3], G. Licitra[4], S. Carpino[4], and P. Kindstedt[5], [1]*University of Wisconsin*, *Madison*, [2]*North Carolina State University*, *Raleigh*, [3]*Tillamook County Creamery Association*, *Tillamook, OR*, [4]*CoRFiLaC*, *Regione Siciliana, Ragusa, Italy*, [5]*University of Vermont*, *Burlington*.

The American Dairy Science Association has a strong heritage of facilitating cutting edge research in the areas of milk production and milk processing. However, few research programs or symposia highlight the findings and benefits of research that involves both disciplines working in complement. The ADSA annual meeting provides a unique opportunity where researchers from both disciplines are present. This symposium is designed to present work linking the production of raw milk with the quality and safety of finished dairy foods. Symposium presenters will discuss collaborative research models, benefits and challenges of conducting such work.

Key Words: Production, Processing