

Ability of the supplementation protocol to augment ICE expression may, in part, explain ability of the product to stimulate neutrophil IL1B synthesis in immunosuppressed sheep. The microarray study also revealed up-regulation ( $P < 0.05$ ) of IL8R. This implies that the product may sensitize neutrophils to pathogen signaling during the peri-parturient period. Finally, we examined ability of a nutritional product to affect immune function during shipping. Shipping is a stressful event and methods to augment immunity during this time are needed. The nutritional product augmented ( $P < 0.05$ ) indexes of innate immunity (neutrophil IL8R and L-selectin) in neutrophils of cattle and sheep during shipping stress.

**Key Words:** Immunity, Nutrition, OmniGen-AF

**338 Cumulative physiological events influence the inflammatory response of the bovine udder to E.coli infections during the transition period.** C. Burvenich\*<sup>1</sup>, M. Kehrl<sup>2</sup>, M. Paape<sup>3</sup>, D. Bannerman<sup>2</sup>, and J. Lippolis<sup>2</sup>, <sup>1</sup>*Ghent University, Faculty of Veterinary Medicine, Milk secretion and mastitis research center, Merelbeke, Belgium*, <sup>2</sup>*Periparturient Diseases of Cattle Research Unit, USDA, ARS, Ames, IA*, <sup>3</sup>*Bovine Functional Genomics Laboratory, U.S. Department of Agriculture, Agricultural Research Service, Beltsville, MD*.

A high proportion of cows with intramammary coliform infections at parturition display signs of severe inflammation and develop systemic complications and sepsis during the first 60-70 days of lactation. In the lactating bovine mammary gland, the innate immune system plays a critical role in the host response to infection and the eventual outcome of mastitis. Since the beginning of the 1990's, research on bovine mammary innate defense mechanisms in connection with the pathogenesis of coliform mastitis has increased significantly. There is no doubt that the viable neutrophil in the cisterns and ducts is a key factor in the protection of the mammary gland. However, in the bovine udder the protective role by the neutrophil seems to be influenced by a cumulation of physiological events occurring during the transition period. During the last 30 years most efforts have been focused on diapedesis, phagocytosis and killing by neutrophils, one of the most important components of the efferent innate arm. How these functions modulate the clinical outcome of coliform mastitis and how they are influenced by hormones and metabolism have also been the subject of intensive research. The study of the afferent (sensing) arm of innate immunity that enables host recognition of a diverse array of pathogens is a new area of interest and differences in the ability of the immune system to detect the presence of a pathogen may vary depending on stage of lactation and influence the inflammatory response.

**Key Words:** Mastitis, Escherichia coli, Innate immunity

## Breeding and Genetics: Genetic Fitness

**339 Stillbirth (co)variance components for a sire-maternal grandsire threshold model.** J. Cole\*, G. Wiggans, P. VanRaden, and R. Miller, *Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*.

with pure maternal effects. Economic values of sire and MGS effects for stillbirth are less than for calving ease, and all four traits may be combined into a calving index.

**Key Words:** Stillbirth, (Co)variance components, Threshold model

(Co)variance components for stillbirth in US Holsteins were estimated under a sire-maternal grandsire threshold model using subsets of data from the national calving ease database, which includes over 7 million calving records with associated stillbirth scores. Stillbirth was coded as a binomial trait indicating whether or not the calf was alive 48 h postpartum; 10.8% of calves born to heifers were stillborn, versus 4.8% of calves born to cows. Records were selected from calves with sire and maternal grandsire (MGS) among the 2600 most-frequently appearing bulls (2578 distinct sires and 2586 distinct MGS). Herd-years were required to contain at least 20 records and only single births were used. After edits, the dataset included 2,083,979 calving records from 5765 herds and 33,304 herd-years. Six sample datasets of approximately 250,000 records each were created by randomly selecting herd codes. Quasi-REML and Gibbs sampling approaches were used to estimate (co)variance components from each sample. The model included fixed year-season, parity-sex, birth year group of sire, and birth year group of MGS effects and random herd-year, sire, MGS, and residual effects. Quasi-REML point estimates fell within the corresponding Gibbs sampling 95% confidence intervals for all samples, indicating good agreement between the two estimation procedures. Marginal posterior means (and standard deviations) averaged 0.0085 (0.0015), 0.0181 (0.0020), 0.0872 (0.0538), and 0.00410 (0.0001) for sire, MGS, and herd-year variances and the sire- MGS covariance, respectively. Mean direct and MGS heritabilities were 0.030 (0.003) and 0.058 (0.003), respectively, and the genetic correlation between direct and MGS effects was 0.331 (0.079). Heritability estimates were lower than some literature results, but the genetic correlation between direct and MGS effects was larger than previous estimated correlations of direct

**340 Genetic parameters for calf vigor in the Montana Line 4 inbred Hereford herd.** J. M. Rumph\*<sup>1</sup>, D. D. Kress<sup>1</sup>, K. C. Davis<sup>1</sup>, D. C. Anderson<sup>1,2</sup>, H. C. Van Wagoner<sup>3</sup>, and D. L. Boss<sup>2</sup>, <sup>1</sup>*Montana State University, Bozeman*, <sup>2</sup>*Montana State University, Northern Agricultural Experiment Station, Havre*, <sup>3</sup>*Montana State University, Bair Ranch, Martinsdale*.

Records for 510 Hereford calves produced in the Line 4 Hereford herd at the Northern Agricultural Research Center (NARC) in Havre, Montana from 1997 to 2004 were analyzed to determine the genetic parameters associated with calf vigor. This herd is descended from the Miles City Line 1 Hereford herd and has been a closed herd in Havre since 1963. Inbreeding is increasing in this herd at an average rate of 0.7% per year and animals born in 2004 had an average inbreeding coefficient of 36.5%. Since 1995, selection in this herd has been based on single trait selection for yearling scrotal circumference adjusted for age of dam. For calf vigor, the model included fixed effects of year, age of dam, sex, calving ease score, and the linear and quadratic covariates of day of birth and birth weight. Random effects included were direct genetic, maternal genetic, direct-maternal correlation, and the proportion of variance attributed to maternal permanent environmental effects. Estimates of the genetic parameters were 0.14, -0.23, 0.06, and 0.00 for direct heritability, direct-maternal correlation, maternal heritability, and proportion of variance attributed to maternal permanent environmental effects, respectively. Genetic trends in this data for both direct and maternal breeding values are not significant for animals born from 1993 through 2004 which includes many of

the dams of the calves in this dataset. Calf vigor is a moderately heritable trait that does not appear to be affected by selection for scrotal circumference or the increasing level of inbreeding in this population.

**Key Words:** Calf vigor, Inbreeding, Scrotal circumference

**341 Genetic parameters for rear legs/rear view in Brown Swiss cattle.** G. R. Wiggans<sup>1</sup>, L. L. M. Thornton\*<sup>1</sup>, and R. R. Neitzel<sup>2</sup>, <sup>1</sup>*Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD*, <sup>2</sup>*Brown Swiss Association, Beloit, WI*.

Genetic parameters for rear legs/rear view (RLRV) and the 15 current linear type traits in Brown Swiss cattle were estimated. Appraisers record linear traits on a 1 to 9 scale. Reported scores were multiplied by 5 to make them compatible with earlier scores that were on a 1 to 50 scale. The Brown Swiss Association began scoring RLRV in 2004 so only two years of data with all traits recorded were available. These 7,511 records were on 6,896 cows in 375 herds. Pedigree data included 14,168 ancestors and seven unknown parent groups, each including four years of birth. The model included fixed effects for herd appraisal date, and age within parity effects, and random effects animal, permanent environment, and error. The multitrait analysis for the 16 linear type traits used canonical transformation, multiple diagonalization with the F-G algorithm and the expectation-maximization REML algorithm. Heritabilities ranged from 0.073 for RLRV to 0.438 for stature. They averaged 0.046 lower for the 15 currently evaluated traits and ranged from 0.114 lower for teat placement to 0.030 higher for udder height. Strength and udder width had heritability 0.102, the lowest of the currently evaluated traits. The highest genetic correlations for RLRV with the other traits were 0.55 with udder width, 0.47 with strength, and 0.35 with thurl width. The most negative correlation was -0.15 with rear legs side view. The lower heritabilities may reflect the short period of data collection and change in parameters over time. The trait RLRV has the lowest heritability and relatively high correlations with several other traits, but may still be useful in the type program because of the importance of locomotion traits. It is likely to be included in the feet and legs composite. This would affect net merit values.

**Key Words:** Locomotion, Type traits, Genetic evaluation

**342 Quantifying the impact of multiple independent heterozygous loci on survival.** H. A. Adams\* and R. D. Shanks, *University of Illinois, Urbana*.

The objective was to quantify the impact multiple independent heterozygous loci have on the survival of progeny of a bull. A simulation was created to demonstrate the impact of changes in inbreeding (%F), number of heterozygous loci (HeL), and total number of loci (TL), on the amount of survival reduction. Homozygous recessive alleles were assumed to be lethal. All heterozygotes were considered carriers of a lethal defect. Other simulation components included calf mortality rate (%CM) and total survival reduction of the bull (%TSR). Calf mortality was calculated as a function of inbreeding. Total survival reduction was calculated as %CM\*(HeL / TL). Results were based on three scenarios: (1) fixed %F and HeL with changing TL, (2) fixed %F and TL with changing HeL, and (3) fixed HeL and TL with changing %F. In the first scenario, inbreeding was set to a value of 5.1%, the

average inbreeding percentage of cows born in 2005. The variable HeL was fixed at 2. Increasing the number of loci decreased the amount of total survival reduction for a fixed number of defects per bull. For bulls with 5, 50, and 500 loci influencing a trait, bull survival was reduced by 5.1%, 0.51% and 0.051% respectively. Offspring of a bull with a greater number of loci had a greater chance of homozygosity of favorable alleles among the loci, and their chance for survival increased. The second scenario fixed %F at 5.1%, and TL at 15. As heterozygosity increased, %TSR increased. Bulls with 1, 5, and 10 HeL out of 15 TL had a total survival reduction of 0.85%, 4.25%, and 8.5%, respectively. The final scenario fixed TL at 4 and HeL at 2, or heterozygosity fixed at 50%. Bulls with inbreeding percentages of 1, 3 and 5 had a total survival reduction of 1.25%, 3.75% and 6.25% respectively. This scenario showed a negative impact of inbreeding on survival regardless of the genotype of the individual. Greatest survival was associated with more loci influencing survival, few heterozygous loci and low inbreeding.

**Key Words:** Inbreeding, Survival, Heterozygosity

**343 Mapping quantitative trait loci affecting calves immune function and birth weight in a Holstein x (Holstein x Jersey) backcross population.** C. Maltecca\*, H. Khatib, V. R. Schutzkus, and K. A. Weigel, *University of Wisconsin, Madison*.

Calf birth size and health status are related, and they both influence the ability of the adult animal to avoid culling. Health problems from which an animal appears to recover early in life can in fact impair its productivity later. Objective of the study was to identify molecular markers associated with traits related to calf size and immune function. A resource population consisting of 250 backcross calves (118 females, 132 males) was created via backcross matings, in which lactating Holstein cows were randomly selected from the University of Wisconsin – Madison herd and randomly mated to 7 young F1 Holstein x Jersey sires to produce ¾ Holstein : ¼ Jersey offspring. Calves were measured for weight immediately after birth (mean 38.52 kg ± 2.21kg) and their immune function was evaluated through total serum protein level and serum IgG levels. Serum was harvested from jugular vein between 24 and 78 hours of age. Total serum protein level (mean 5.03 g/100ml ± 0.06 g/100ml) was measured using a refractometer, while serum IgG level (mean 1053.55 mg/dl ± 345.12 mg/dl) was determined by radial immunodiffusion assay. Results from a whole genome scan are discussed. 182 microsatellites markers were chosen among 270 after sires genotyping. Sires heterozygosity were of 62.83%, 62.76%, 62.10%, 63.49%, 58.53%, 65.32% and 57.36%, for sire one to seven respectively. Spacing between markers ranged from 3.4 cM to 32.85 cM with an average of 15.93 cM. Average number of markers per chromosome was 7.06 with a minimum of 4 and a maximum of 11. Analysis was carried out through selective genotyping in which the top and bottom 20% of the population were included. Phenotypic averages for the upper tail were 6.57 g/100ml, 2648 mg/dl and 46.55 kg for total serum protein, IgG protein level and birth weight respectively. Phenotypic averages for the lower tail were 3.49 g/100ml, 448.64 mg/dl and 34.45 kg for total serum protein, IgG protein level and birth weight respectively.

**Key Words:** Bovine, Quantitative trait loci, Immune function

**344 Genetic parameters of cortisol and creatinine in pigs as indicators for behavioral and nutritional disorders.** H. N. Kadarmideen<sup>\*1</sup>, S. Gebert<sup>2</sup>, and C. Wenk<sup>2</sup>, <sup>1</sup>*Statistical Animal Genetics, Institute of Animal Science, Federal Institute of Technology (ETH), Zurich, Switzerland*, <sup>2</sup>*Nutritional Biology, Institute of Animal Science, Federal Institute of Technology (ETH), Zurich, Switzerland*.

This study reports results from the genetic analysis of pig populations that were under 20 year selection experiment in the experimental animal research station of ETH Zurich, Switzerland. The overall aim of this experiment was to study the possible differences of the activity of *hypothalamo-pituitary-adrenal axis* in two lines of Large White pigs, which had differences in response (Cortisol and Creatinine levels) to various stress stimuli. Pigs were also recorded for urinary excretion of cortisol and creatinine and their ratio in 24-h periods. The ratio between cortisol and creatinine represents protein metabolism. The main dataset had 417 animals. Pedigrees for these pigs contained a total of 483 animals. The data were analyzed by residual maximum likelihood approach, implemented by ASReml software. The statistical model for genetic analysis of cortisol (CRT), creatinine (CRE) and their ratio: CRT-CRE (CCR) included effects of year, weight, urine output and feed intake and direct genetic value of animals. Multiple-trait animal models were used to estimate variance and covariance components and subsequently heritabilities ( $h^2$ ) and all correlations. The weight, sex and feed intake significantly affected all traits. The  $h^2$  (s.e.) of CRT, CRE and CCR were 0.40 (0.02), 0.39 (0.03) and 0.17 (0.01), respectively, which show strong genetic control and inheritance patterns. The genetic and phenotypic correlations (with s.e.) were: CRT-CRE: 0.07 (0.04) and 0.05 (0.01), CRE-CCR: 0.26 (0.01) and 0.08 (0.01) and CRT-CCR: 0.28 (0.01) and 0.11 (0.01). These results show common co-inheritance patterns as well as environmental conditions that increase (genetic merit for) cortisol and creatinine levels. Results suggest that these indicator traits can be used in genetic selection for physiologically and metabolically stable and healthy pigs in national pig breeding programs. These results will also have strong implications for human diseases such as obesity and diabetes.

**Key Words:** Genetics, Cortisol, Pigs

**345 Success of rebreeding given first parity calving ease scores in Canadian Charolais cattle.** M. L. Spangler<sup>\*</sup>, R. Rekaya, and J. K. Bertrand, *The University of Georgia, Athens*.

Field data from Canadian Charolais herds were used to investigate the genetic relationship between calving ease (CE) scored from 1 to 3 and rebreeding within a 90 day opportunity period post partum (R90). Data were analyzed using a bivariate threshold model where CE was treated as categorical and R90 as binary. At the liability scale, the linear mixed model included herd, yr, and month of mating as fixed effects; unrelated service sire, additive animal and residual as random effects; and linear and quadratic effects of age at mating as covariates. The model for R90 included the CE score as a covariable in order to account for the recursive relationship between both traits. For females who were bred via artificial insemination (AI) in the second parity the conception date and thus the success or failure of rebreeding within the opportunity period is known. For natural service mating data, an average gestation length (GL) and standard deviation (SD), by sex, derived from AI records was used to determine the approximate date of conception. Females who have delayed conceptions create added expenses in the form of increased labor, breeding costs, extended calving seasons, and lighter weaning weights. Therefore, the current study had two main objectives: 1) Estimate genetic parameters for

CE and R90 and 2) to determine if calving difficulty as a first calf heifer had a negative impact on the ability to conceive within a 90 day period post partum. The results indicated, in general, a decrease in reproductive performance with the increase in calving difficulties. Although the difference was minimal between cows scored 1 (no calving problems) and 2 (some assistance or mal presentation), it was significant for cows with calving score of 3 (hard pull or surgery). In fact, cows with CE scores of 2 and 3 have a 3% and 11% less chance of getting pregnant compared with cows with a CE score of 1. The small difference in R90 between cows with CE scores of 1 and 2 could be due in part to the subjective nature of calving ease scoring and the lack of clear boundaries between both classes.

**Key Words:** Beef cattle, Calving ease, Recursive function

**346 Conception rates trend of Holsteins in South-East USA.** C. Huang<sup>\*1</sup>, S. Tsuruta<sup>1</sup>, I. Misztal<sup>1</sup>, T. J. Lawlor<sup>2</sup>, and J. S. Clay<sup>3</sup>, <sup>1</sup>*University of Georgia, Athens*, <sup>2</sup>*Holstein Association USA Inc., Brattleboro, VT*, <sup>3</sup>*Dairy Records Management System, Raleigh, NC*.

The purpose of this study was to estimate trends in conception rate (CR) of Holsteins. Data were obtained from Dairy Records Management Systems in Raleigh, NC. Raw data includes 13,533,978 services from 1988 to 2004 in 10 states: VA, KY, NC, SC, TN, GA, FL, AL, MS, LA, TX. Edits removed services with missing cow ID, birth date, calving date, and service date and retained services with days to service after calving between 21 and 250 d in the first parity and born between 1985 and 1999. Edits also removed data from FL because trends calculated with FL data were different from the remaining states. After these edits, there were 1,582,209 services for 765,652 cows. After elimination of censored lactations, there were 776,470 services of 388,028 cows with confirmed next calving. Analyses used SAS PROC GLM. The model included the effects of birth year (1985-89, 1990-94, 1995-99), service at DIM interval group, milk production level during the first 3 test days ( $< \text{Mean}-\text{SD}$ ,  $\text{Mean} \pm \text{SD}$ ,  $> \text{Mean} + \text{SD}$ ), service month, service type (only natural insemination, only artificial insemination and both for all service) and two-way interactions. For AI services, the average CR decreased from 55% in 1985-89 to 46% in 1995-99. Considering the month of service, the smallest decrease was 5% in January and the steepest decrease was 15% in June. High performing cows had CR about 3% lower. For cows born in 1995-99, CR was 28% at 50 DIM, increased to 40% at 125 DIM, and again to 55% at 250 DIM. Estimated CR of natural bulls was 10% higher, which may be due to incomplete and inaccurate recording of natural service. Fertility of Holsteins declined over time. Only a fraction of that decline can be attributed to increased milk yield in the first 100 days. The length of declined CR in the summer is increased indicating deterioration of heat tolerance over time. The deterioration in CR over time can be offset by extending the voluntary waiting period by 75-100 d.

**Key Words:** Conception rate, Fertility, Holstein

**347 Relationship between reproduction traits and functional longevity in Canadian dairy breeds.** A. Sewalem<sup>\*1,2</sup>, G. Kistemaker<sup>2</sup>, F. Miglior<sup>1,2</sup>, and B. Van Doormaal<sup>2</sup>, <sup>1</sup>*Agriculture and Agri-Food Canada - Dairy and Swine Research and Development Centre, Lennoxville, QC, Canada*, <sup>2</sup>*Canadian Dairy Network, Guelph, ON, Canada*.

The aim of this study was to assess the relationship between reproduction traits and functional survival of Canadian dairy breeds using a Weibull proportional hazard model. Data consisted of 47,949 heifers

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.**

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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 herd life 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 herd life. 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.**

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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.**

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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