T28 Relationship between calpastatin gene polymorphism and beef cattle growth, carcass and meat quality traits. L. Suguisawa, A. A. Souza*, H. N. Oliveira, A. C. Silveira, and R. A. Cury, *São Paulo State University*, *Brazil*.

The Calpastatin polymorphism was associated with performance and meat quality traits, by Chung et al. (2001) methodology, in 300 bullocks. To validate this finding, we looked at a group of animals (126 Angus Nellore, 10 Angus, 18 Brangus, 24 Simmental Nellore, 12 Simental, 11 Simbrasil, 17 Santa Gertrudes Nellore, 18 Brown Swiss x Nelore, 12 Canchim, 16 Brahman Nellore and 36 Nellore). The animals were weaned at 7 months old at the creep-feeding and raised at the feedlot system for 120 days. The animals were harvested with 450 kg live weight, 3 millimeters of ultrasound fat thickness and 12-15 months old age. The gene polymorphism was analyzed by PCR-RFLP. The animals were classified at three genotypes forms: AA, AB and BB. The higher frequency of AA genotype was from Angus Cattle. Nevertheless, the higher frequency of BB genotype was from Nellore and Brahman Nellore cattle. The genotypes effects on traits were analyzed by General Linear Model of SAS and the Least Square Means of the genotypes were compared by Tukey test. The model included genotype, genetic group x year of feedlot x ranch and interactions. The collected growth traits were: initial and final live weight, average daily gain, ultrasound ribeye area, ultrasound fat thickness and ultrasound rump fat thickness. The collected carcass and meat traits were: dressing percentage, hot carcass weight, carcass ribeye area, carcass fat thickness and warner bratzler shear force. Because almost all genetics groups of this research were Zebu crossbreed, these animals could have high Calpastatin quantity. Despite of that, there were not found any relationship between any Calpastatin genotypes and all traits evaluated. The lack of effects of this Calpastatin gene polymorphism indicates that this polymorphism could not be used as a selection tool for improving Animal Breeding.

References:

CHUNG, H.Y.; DAVIS, M.E.; HINES, H.C.; Genetic variants detected by PCR-RFLP in intron VI of the bovine calpastatin gene. **Animal Genetics**, v. 32, p. 40-53, 2001.

Key Words: Calpastatin gene, Meat quality, Cattle growth

T29 Corn oil or Corn grain supplementation to forage-finished steers. IV. Effects on gene expression of lipogenic enzymes in the s.c. adipose tissue. E. Pavan*[1,2], S. Joseph[1], K. Robbins[1], S. Duckett[3], and R. Rekaya[1], [1]*University of Georgia*, *Athens*, [2]*INTA*, *Balcarce, Bs. As., Arg.*, [3]*Clemson University*, *Clemson, SC*.

Samples of s.c. fat were obtained from 28 Angus steers after slaughter to determine the effect of energy supplementation of steers grazing tall fescue pastures. Steers (n = 8/ treatment; 289 ± 3.8 kg) were supplemented with either corn grain (0.52% BW; PC) or soybean hulls plus corn oil (0.45% BW + 0.10% corn oil; PO). Negative (pasture only; P) and positive (85% concentrate/15% roughage; C) controls were also included in the study. RNA was extracted from the s.c. adipose tissue using TRIzol reagent (Gibco Invitrogen Corp.). RNA from each treatment was pooled (10 µg/steer) and five replicates from the same RNA pool were used for microarray hybridization. GeneChip Bovine Genome array (Affymetrix) was used for hybridization of the extracted mRNA's according to the Affymetrix protocol. The data was normalized and analyzed using a simple linear (ANOVA) model. Treatments effects were compared using non-orthogonal contrasts between all possible comparisons, the Benjamini and Hochberg method of false discovery rate (FDR) was used to control the experimentwise error rate. Genes were identified as being differntially expressed using a FDR of 0.05. At a FDR of 0.01 a total of 89, 39 and 1133 genes were detected to be differently expressed between P and PO, P or C, respectively, 757 and 113 between C and PO or PC, and 183 between PO and PC. Lipoprotein lipase was differently ($P < 0.01$) expressed between PO and C and acetyl-coA carboxilase ($P < 0.01$) between P and C. Fatty acid synthase was differently expressed ($P < 0.01$) between C and either P or PO. Stearoyl-coA desaturase was differently expressed ($P < 0.01$) between PC and P, C or PO and between C and P, whereas did not differ (FDR > 0.05) between PO and either P or C. The gene encoding the soluble form of isocitrate dehydrogenase was differently expressed ($P < 0.01$) between PO and P, PC and C as well among C and either PC or P. The expression of glycerol phosphate acyltransferase differ ($P < 0.01$) between all comparison evaluated. Gene expression of the adipocyte lipogenic enzymes from beef steers may be manipulated through diet.

Key Words: Bovine, Lipogenic enzymes, Gene expression

Companion Animals: Nutrition & Health

T30 Identification of canine markers related to obesity. R. Yamka* and K. Friesen, *Hill's Pet Nutrition, Inc.*, *Topeka, KS*.

Thirty lean and thirty obese neutered/spayed beagles (average age = 7.5 ± 0.7 years) were identified for this study. Fifty percent of the dogs were female (15 lean and 15 obese) and fifty percent were male (15 lean and 15 obese) in order to determine if gender played a role in marker differences. Animals were weighed, given a body condition score (1=lean, 3=ideal and 5=obese) and a blood sample was drawn. Average body condition scores were 4.7 and 2.5 for the obese and lean groups, respectively. Average body weights were 17.3 ± 0.4 and 11.2 ± 0.4 kg for the obese and lean groups, respectively. Serum was analyzed for chemistry screens, obesity markers, thyroid markers and arthritis markers. The obese group had higher levels of alkaline phosphatase ($P = 0.04$), cholesterol ($P = 0.04$), triglycerides ($P = 0.06$), total protein ($P < 0.01$), albumin ($P < 0.01$), thyroxine ($P = 0.05$), calcium ($P < 0.01$), phosphorous ($P = 0.04$), glucose ($P < 0.01$), insulin ($P < 0.01$), insulin like growth factor-1 ($P < 0.01$), low density lipoprotein ($P < 0.01$), leptin ($P < 0.01$) and type 2 cartilage synthesis ($P < 0.01$). The obese group had lower levels of creatinine ($P = 0.01$), serum urea nitrogen ($P < 0.01$), chloride ($P < 0.01$) and obese males had lower levels of testosterone ($P = 0.04$). These data indicate that obesity is directly related to other disease states in dogs (i.e. dyslipidemia, arthritis and diabetes). Thus, managing obesity through weight loss and/or calorie restriction may alleviate or prevent the differences observed between lean and obese blood markers.

Key Words: Canine, Obesity, Marker

T31 Identification of feline markers related to obesity. R. Yamka* and K. Friesen, *Hill's Pet Nutrition, Inc.*, *Topeka, KS*.

Thirty lean and thirty obese domestic short hair cats (average age = 7.4 ± 0.5 years) were utilized for this the study. Animals were weighed, given a body condition score (1=lean, 3=ideal and 5=obese) and a

blood sample was drawn. Average body condition scores were 4.2 and 2.5 for the obese and lean groups, respectively. Average body weights were 5.8 ± 0.2 and 3.2 ± 0.2 kg for the obese and lean groups, respectively. Serum was analyzed for chemistry screens, obesity markers, thyroid markers and arthritis markers. The obese group had higher levels of alkaline phosphatase ($P = 0.07$), triglycerides ($P = 0.05$), total protein ($P < 0.01$), albumin ($P < 0.01$), potassium ($P = 0.03$), magnesium ($P < 0.01$), sodium: potassium ($P = 0.02$), glucose ($P = 0.02$), leptin ($P < 0.01$) and thyroxine ($P = 0.02$). The obese group had lower levels of thyroid stimulating hormone ($P = 0.02$) and ghrelin ($P = 0.06$). These data indicate that obesity is closely related to other disease states in cats (i.e. dyslipidemia, diabetes and hyperthyroidism). Management of obesity may prevent the early onset of other diseases in cats.

Key Words: Feline, Obesity, Markers

T32 Impact of age on gene expression profiles of canine brain tissue. K. Swanson*, C. Apanavicius, B. Vester, and N. Kirby, *University of Illinois*, *Urbana*.

Many anatomical changes occur in brain tissue of aged dogs, many of which are correlated with decreased cognitive function. Factors responsible for these changes are largely unknown. To identify genes and biological pathways altered due to old age, gene expression profiles of brain tissue from healthy young adult and geriatric dogs were compared. Six geriatric (11 yr-old at baseline) and 6 weanling (8 wk-old at baseline) female beagles were randomly assigned to one of two diets and fed for 12 months: 1) Animal-protein based diet (APB; 28% protein, 23% fat, and 5% fiber); or 2) Plant-protein based diet (PPB; 26% protein, 11% fat, and 15% fiber). RNA was isolated from cerebral cortex tissue using Trizol and hybridized to Affymetrix GeneChip Canine Genome Arrays as per manufacturer'$s instructions. Following array normalization, data were analyzed using the mixed models procedure of SAS. Transcripts having a $P < 0.05$ (following a false discovery rate adjustment) and > 1.5-fold change were considered significantly different among groups. 286 transcripts (corresponding to 74 up-regulated and 28 down-regulated genes) were differentially expressed in old vs. young dogs consuming the APB diet. Old vs. young dogs consuming the PPB diet had 281 differentially expressed transcripts (54 up-regulated and 44 down-regulated genes). Old dogs on both diets tended to have expression profiles indicative of inflammation, oxidative stress, or acute phase response. Genes associated with neuropeptide signaling (e.g., somatostatin, corticotropin-releasing hormone, neuropeptide Y, etc.) were also decreased in old dogs. The current study has identified numerous genes and pathways altered in aged brain tissue. These results may be used for future experiments focused on preventing or treating age-related cognitive decline via dietary intervention. This research was funded in part by the National Center for Supercomputing Applications and the University of Illinois, under the auspices of the NCSA/UIUC Faculty Fellows Program, and by Pyxis Genomics, Inc.

Key Words: Canine, Aging, Microarray

T33 Age impacts skeletal muscle gene expression profiles of young adult and geriatric dogs fed either an animal- or plant-protein based diet. L. Karr-Lilienthal*, C. Apanavicius, B. Vester, and K. Swanson, *University of Illinois*, *Urbana*.

Aging is associated with loss of muscle mass and increased oxidative damage, both having significant health implications. The objective of this study was to measure gene expression differences in skeletal muscle of young adult and geriatric dogs. Six geriatric (11 yr-old at baseline) and 6 weanling (8 wk-old at baseline) female beagles were randomly assigned to one of two diets: Animal-protein based (APB; 28% protein, 23% fat, and 5% fiber) or Plant-protein based (PPB; 26% protein, 11% fat, and 15% fiber) for 12 months. RNA, isolated from skeletal muscle samples using Trizol, was hybridized to Affymetrix GeneChip Canine Genome Arrays as per manufacturer's instructions. Following microarray normalization, data were analyzed using the mixed models procedure of SAS. Transcripts having a $P < 0.05$ (following a false discovery rate adjustment) and > 1.5-fold change were considered different among groups. Gene expression changes were noted in old dogs fed either APB (205 transcripts, corresponding to 115 identified genes) or PPB (415 transcripts; 216 identified genes). Regardless of diet, old dogs had decreased expression of genes associated with carbohydrate metabolism compared with young dogs. Old vs. young dogs fed APB had increased expression of genes associated with immunity and stress response and decreased expression of genes associated with energy and lipid metabolism and muscle contraction. While more genes were differentially expressed in dogs fed PPB, the responses were mixed. Increased expression of genes associated with signal transduction and nucleotide metabolism was noted. Overall, aging increased expression of stress response genes and decreased those associated with energy metabolism, many of which were most prominent in dogs fed APB. This research was funded in part by the National Center for Supercomputing Applications and the University of Illinois, under the auspices of the NCSA/UIUC Faculty Fellows Program, and by Pyxis Genomics, Inc.

Key Words: Canine, Aging, Microarray

T34 Diet impacts colonic gene expression profiles of young adult and geriatric dogs fed either an animal- or plant-protein based diet. B. Vester*, C. Apanavicius, L. Karr-Lilienthal, and K. Swanson, *University of Illinois*, *Urbana*.

We have previously reported diet-related differences in intestinal morphology and fermentative end product concentrations in geriatric and young dogs. Mechanisms responsible for these differences however are unknown. Thus, the objective of this study was to measure gene expression differences in the proximal colon of healthy young adult and geriatric dogs consuming two distinct dog foods. Six geriatric (11 yr-old at baseline) and 6 weanling (8 wk-old at baseline) female beagles were randomly assigned to one of two diets for 12 months: animal-protein based (APB; 28% protein, 23% fat, and 5% fiber) or plant-protein based (PPB; 26% protein, 11% fat, and 15% fiber]. RNA was isolated from colon samples using Trizol and hybridized to Affymetrix GeneChip Canine Genome Arrays. Following normalization, data were analyzed using the mixed models procedure of SAS. Transcripts having a $P < 0.05$ and > 1.5-fold change were considered different among groups. Diet manipulated gene expression in both young adult (144 transcripts) and geriatric dogs (166 transcripts). Colonic tissue of young dogs fed APB had a higher metabolic activity, with genes associated with carbohydrate metabolism being expressed in greater quantities than young dogs fed PPB. Sodium potassium transporters were increased in young dogs fed APB while unchanged in old dogs. Genes associated with neurotransmitter degradation (MAOA and MAOB) were decreased in old dogs and increased in young dogs fed APB. Dipeptidyl peptidase IV, a gene involved in the break-down of GLP-1 was increased in young dogs fed APB. This research was funded in part by the National Center for Supercomputing Applications and the University of Illinois, under the auspices of the NCSA/UIUC Faculty Fellows Program, and by Pyxis Genomics, Inc.

T35 Screening of epitopes of canine enteropathogenic viruses for the production of IgY. S.-E. Woo*[1], S.-O. Shin[1], J.-W. Kim[2], A.-R. Lee[2], S.-O. Shin[2], and S.-Y. Yang[1], [1]*Danbiotech. Inc*, *Cheonan, Chungnam, Rep. of Korea*, [2]*Dankook University*, *Cheonan, Chungnam, Rep. of Korea*.

This study was carried out for the screening of epitope region of canine enteropathogenic viruses (CPV, CCV, CAV and CRV) for the production of IgY (egg yolk immunoglobulins). VP2, a part of the CPV (canine parvovirus) capsid protein, was expressed into 7 segments (pCPV2a through pCPV2g) with glutathione S-transferase fused pGEX 4T. The expressed proteins were immunoblotted with sera of CPV infected dog. It was revealed that the most immunoreactive regions were CPV2d, CPV2e and CPVsf. Results of neutralization test using rabbit antiserum, anti-CPV2e showed the highest neutralizing activity against CPV protein. CCV (canine coronavirus) spike protein was expressed into 6 segments (pCCVsa ~ pCCVsf) with pMAL vector. For the screening of epitope of CCV, the heterologous antisera against the 6 segments and spike protein were tested for neutralizing effect against CCV. CAV (canine adenovirus) fiber protein was expressed into 7 segments (pCAVfa~pCAVfg) with expression vector. For the screening of epitope of CAV, the heterologous antisera against the 7 segments and fiber protein were tested for neutralizing effect against CAV. CRV (canine rotavirus) VP4 was expressed into 9 segments (pCRVva~pCRVvi). For the screening of epitope of CRV, the heterologous antisera against the 9 segments and VP4 were tested for neutralizing effect against CRV. Selected epitopes of 4 viruses were expressed and immunized to laying hens for the production of specific IgY. All the antibody titers were detected after two weeks of immunization and reached the highest level (100,000~500,000) at 6 weeks after immunization, in general.

Key Words: IgY, Canine parvovirus, Canine coronavirus

T36 Comparison of yeast culture and brewers dried yeast as palatability enhancers in dry cat food. J. W. Jones*[1], B. Leiner[1], and H. M. Sullivan[2], [1]*Western Yeast Company*, *Chillicothe, IL*, [2]*New Mexico State University*, *Las Cruces*.

Brewer's dried yeast is the preferred additive for increasing palatability in cat rations in the pet food industry. In this study, yeast culture (the dried product composed of yeast and the media on which it was grown) and brewers dried yeast (the dried non-fermentative, non-extracted yeast resulting as a byproduct from the brewing of beer and ale) were offered to cats to determine palatability preference. Yeast culture and brewer's dry yeast was included in a 32% protein, 20% fat cat food and offered to a panel of cats on two consecutive days. Twenty adult domestic long and short-haired cats with a median age of six were randomly assigned to the panel. Cats were housed at a commercial nutrition laboratory. The yeast products were added to the diets, prior to extrusion, at 1.25% of the ration dry matter. One hundred fifty grams of each ration was offered to the cats and bowl position was reversed daily to prevent 'left-right' bias. The brewer's dry yeast was approached first on 19 of 40 occasions, but only consumed first on 10 of those 40 occasions. Total daily consumption was not statistically different between the two yeast products with the yeast culture ration consumed an average of 22.25 ± 13.4 g day and the brewers yeast ration 27.05 ± 13.7 grams per day. Cats tended to consume more of the yeast culture ration per kg of body weight (P = 0.08). The brewer's dry yeast ration was consumed at 5.6 ± 2.55 g/kg of body weight and yeast culture ration at 7.58 ± 4.24 g/kg. Additionally, the yeast culture was preferred by 11 of the 20 cats based on total consumption. Total daily consumption averaged 445.5 g for the brewer's dry yeast ration and 541 g for the yeast culture ration. In conclusion, there was no statistical difference between intake of cat food containing brewer's dry yeast and yeast culture, however, intake per kg of body weight tended to be higher for yeast culture.

Key Words: Feline, Nutrition, Yeast

T37 Characterization of strains of *Lactobacillus reuteri* as potential probiotics for dogs. S. McCoy* and S. E. Gilliland, *Oklahoma State University*, *Stillwater*.

Because of the need to control pathogenic microorganisms in the intestinal tract of dogs, there is interest in using probiotics such as species of *Lactobacillus* as dietary supplements. For successful use, the *Lactobacillus* species should be of canine intestinal origin since this species exhibits host specificity. Serial dilutions of freshly voided dog feces (from various breeds owned by laboratory personnel or their friends) were plated on Lactobacillus Selection (LBS) agar to isolate the cultures. Isolates were identified based on Gram stain, Catalase test, and fermentation patterns using API 50 CH kits. All potential isolates were compared for bile resistance based on relative ability to grow in broth containing 0.3% Oxgall, and for the ability to inhibit *Salmonella* Typhimurium in associative broth cultures. Of the lactobacilli isolated, Lactobacillus reuteri was the dominant species. We found variations among isolates of *L. reuteri* with respect to bile tolerance. There also were variations in the ability to inhibit growth of *S.* Typhimurium. The inhibition by *L. reuteri* may have been caused by the production of the anti-microbial substance, reuterin. Comparisons of the amount of reuterin produced were made and the isolate of *L. reuteri* that produced the most reuterin (X-18) also caused the greatest inhibition of *S.* Typhimurium Further research has been done using isolate X-18 to determine stability of the chosen culture during frozen storage of pet food. After 35 days of frozen storage in pet food, there was approximately one-half log cycle decrease in CFU/gram of pet food. Stability during frozen storage is necessary for successful commercial adaptation of a culture for use as a probiotic in frozen dog food.

Key Words: Lactobacillus, Probiotics, Dogs

T38 Genetic differentation by restriction fragment length polymorphism (RFLPs) in isolates of Giardia spp. in humans and dogs. S. C. Cota-Guajardo*[1], S. M. Gaxiola[1], J. J. Portillo[1], F. Juarez[1], and S. Velarde[2], [1]*FMVZ-Universidad Autonoma de Sinaloa*, *Culiacan, Sinaloa, Mexico*, [2]*Hospital Infantil Federico Gomez*, *Distrito Federal, Mexico*.

Giardia spp is considerate one of the ancient eukaryotes. Its importance as a causative pathogen of diarrhea in humans has been mentioned by the World Health Organization (WHO).There is also information about the importance of *Giardia* spp as a causative diarea agent in dogs. Its zoonotic potential has been established using molecluar biology, discovering strains that can affect both humans and dogs. In order to differentiate Giardia spp. found in dog and human feces utilizing PCR techniques and Restriction Fragment Length Polimorphism (RFLPs) in the β-giardin gene, stool samples from dogs of different ages, breeds and both sexes from were collected in Culiacan, Sinaloa, in Mexico; likewise stool samples of children from 45 days to 3 years old, both sexes, were collected from two child care centers located in the above mentioned city. Stool samples from adults and children from the same city were also collected. The samples were analyzed using the zinc

sulfate flotation technique. Samples in which *Giardia* ssp cysts were present were considered positive. PCR of the β-giardin gene was performed on 40 positive samples each of humans and dogs, obtaining 24 and 20 amplified of each origin respectively. RFLPs were obtained by digesting the amplified with *Hae III* nuclease in two percent agarose gels. Regarding the obtained RFLPs of each species, it was possible to demonstrate the existence of two different strains of *Giardia* ssp., of which one of them had the same pattern for both humans and dogs. It is concluded that, in Culiacan, Sinaloa, Mexico, humans and dogs share at least one causative diarrhea strain of *Giardia* ssp., suggesting the possibility of cross-transmission.

Key Words: *Giardia*, PCR technique, β-giardin gene

T39 Presence of eggs Toxocara spp. in soil of public parks in Culican, Sinaloa. M. C. Rubio Robles*, S. M. Gaxiola camacho, N. Castro del Campo, B. N. Verduzco, and M. N. López, *Universidad Autonoma de Sinaloa*, *Culiacan, Sinaloa, México*.

Toxocariasis is a zoonotic infection caused by the parasitic Toxocara spp. commonly found in the intestine of dogs and cats. Disseminated for defecate in parks and public areas. Toxocariasis can result in a condition known as visceral and or ocular larval migrans, which is associated with inflammation of body organs and or the central nervous system. Symptoms of which are caused by the movement of the worms through the body, include fever, coughing, asthma, or pneumonia. Toxocariasis most often occurs in children, who often play or eat (pica)dirt that potentially is contaminated with Toxocara spp. eggs. The eggs of Toxocara spp. are extremely resistant to adverse environmental conditions, capable of surviving in soil for many months. The objective of the work was to determine the presence of eggs of Toxocara spp. in the soil of the children play area in public parks of the city of Culiacan, Sinaloa. Egg presence was determined by means 291 soil samplings in 23 public parks of the city. Established by random stratified samplings, and collecting soil samples using the technique of double W; We took surface soil scraping of 100 grams of earth for each sample and deposited it in previously identified plastic bags. The samples were later transferred to the laboratory of parasitology of the FMVZ-UAS to be analyzed by means of the sedimentation and flotation techniques. The samples indicate that of the 23 parks analyzed 13 (54%) contained eggs of Toxocara spp.; We conclude that the contamination with eggs of Toxocara spp.; shows up in a percentage in the area of children play areas in the public parks of the city of Culiacan, Sinaloa. Knowing the danger this parasite represents for the public health, indicates to us the risk to which are exposing especially our children, mainly if they frequently use these recreation places. Therefore the necessity arises of implementing control strategies and education for the prevention of the infections by fecal origin in public parks.

Key Words: Toxocara, Public parks, Parasites

Dairy Foods: Chemistry and Microbiology

T40 Partition coefficients for toxic agents in multiple phase foods: Separation of raw whole milk. J. E. Schlesser*[1], J. E Jablonski[1], and P. Mariappagoudar[2], [1]*FDA, National Center for Food Safety*, *Summit, IL*, [2]*Illinois Institute of Technology, National Center for Food Safety*, *Summit, IL*.

Contamination of milk with toxic compounds may be accidental or intentional. Since milk consists of skim milk and cream phases, it is of interest to determine into which phase the toxin will partition. Aconitine, nicotine and strychnine were chosen as model toxin contaminants. An HPLC method for analysis of aconitine, nicotine, strychnine from milk products was developed. Sample clean up techniques consisted of liquid-liquid partitioning (hexane/water-acetonitrile), solid phase extraction (OASIS HLB), and manipulation of pH of sample to avoid volatility and hydrolysis losses. Analysis was conducted with an HPLC with dual band UV detector. Nicotine and strychnine levels were measured at 260nm and aconitine at 232nm. Centrifugation of whole milk was used to simulate commercial separation. Whole milk was placed into 50 ml centrifuge tubes, spun for 30 minutes at 2000 x g and 5°C. Skim milk from tubes were decanted and mixed. Cream layer adhering to the side of bottles was dissolved and mixed together. The mixed samples were used for fat testing or if spiked, for testing of toxins. Centrifugations were conducted at 30 minutes and 5 days after spiking to simulate contamination in the plant and on the farm, respectively. Mean recoveries for the three analytes in skim milk, whole milk and cream ranged from 72.1% to 89.2%. Centrifugation of 3.25% whole milk resulted in a fat content of 39.5% and 0.07% for cream and skim milk respectively. Whole milk was spiked with 1 ppm of each of the three toxins. Aconitine, nicotine and strychnine were found in both cream and skim milk streams. Initial partition coefficient for aconitine was 0.769 in cream, and increased to 1.121 by day 5. Initial partition coefficient for nicotine was 0.49 in cream, and increased to 0.761 by day 5. Initial partition coefficient for strychnine was 1.064 in cream, and increased to 1.135 by day 5. Between day 0 and day 5, partition coefficients for the toxic compounds in skim milk decreased.

Key Words: Aconitine, Nicotine, Strychnine

T41 Modelling of the high-pressure and temperature induced pH change in whey protein isolate solutions. H. Hernández-Sánchez*[1], J. O. Rodiles-López[1], M. E. Jaramillo-Flores[1], and G. V. Barbosa-Cánovas[2], [1]*Depto. Grads. Alimentos, Escuela Nacional de Ciencias Biologicas, Instituto Politecnico Nacional*, *Mexico, DF, Mexico*, [2]*Washington State University*, *Pullman*.

High hydrostatic pressures (HHP) can lead to greater ionization in certain biological systems resulting in a temporary decrease in pH while under pressure. It has been reported that in some cases, the HHP-induced denaturation of whey proteins is decreased when the pH during the treatment is less than 7. The objective of this study was to evaluate and model the effect of high hydrostatic pressure and temperature on the final pH of whey protein isolate (WPI) solutions. WPI solutions at a concentration of 5% (w/v) were treated with HHP of 200, 400 and 600 MPa at different temperatures (25, 40 and 55°C)