598 Quality attributes of lightly salted sweet cream butter in the North Carolina marketplace. A.P. Hansen* and M.D. Keziah, *North Carolina State University.*

Approximately 300 samples of sweet cream butter were obtained from local stores in North Carolina and nearby states. The samples were collected over a three-year period and analyzed for flavor. This evaluation was conducted with 15 trained dairy judges according to ADSA protocol. The variation in quality and uniformity was quite different across brands. The color of the butter went from whitish to yellow in color depending on if it was winter butter or summer butter. The flavors identified in the National Brands were coarse and slight feed but they were consistently good month after month. The store brands tend to have many more flavor defects. Going from the most to the least they were as follows: old cream, high salt, neutralizer, storage, flat, coarse, acid, scorched and oxidized. The store brands also had slight coarse and slight feed as the national brands and some store brands were consistently better than other store brands. In most cases, it was related to the price of the butter.

Key Words: Butter, Marketplace, Quality

599 Characterization of volatile nutty flavor compounds in Cheddar cheese. M.A. Drake*[1], Y.K. Avsar[2], Y. Karagul-Yuceer[1], and K.R. Cadwallader[3], [1]*North Carolina State University,* [2]*Mustafa Kemal University,* [3]*University of Illinois.*

Cheese flavor is the one of the most important criteria in determining consumer choice and acceptance. Cheddar cheese flavor ideally is composed of sulfur and nutty flavors. The aim of the present study was to characterize the volatile compounds responsible for nutty flavors in Cheddar cheese.

Cheddar cheeses (1-3 years old) were screened for nutty flavor by a descriptive sensory analysis panel (n=7). Samples with and without nutty flavor (4 cheeses each) were selected and analyzed for volatile aroma compounds. Cheeses were grated and extracted with diethyl ether containing internal standards (2-methyl-3-heptanone and 2-methylpentatonic acid). Volatiles were isolated by high vacuum distillation. Volatile extracts were separated into acidic and basic/neutral fractions, which were then analyzed by gas chromatography-olfactometry (GCO). Identification of odor active compounds was carried out by comparison of GC-MS data, retention indices and odor properties against reference standards.

Results showed that the compounds found in the neutral/basic phase, 2-acetyl-1-pyrroline and 2-acetyl-2-thiazoline (popcorn/nutty/roasted), 2-isopropyl-3-methoxy pyrazine (earthy), 3-(methylthio)propanal (bolied potato), 2,3-butanedione (buttery), trimetylpyrazine (nutty/dirty) and δ-decalactone (sweet/fatty) were the most odor-active compounds and their intensities were higher in nutty cheeses. Volatile fatty acids including acetic, propionic, pentanoic and butanoic acids were found in acid fractions of both nutty cheese and not nutty cheeses. The data obtained in this study will be used for better understanding Cheddar cheese flavor and for identification of the chemical pathways for the formation of these compounds.

Key Words: Cheddar Cheese, Flavor, Nutty Flavor

Food Safety
Foodborne Pathogens

600 Acid resistance status of *Escherichia coli* O157 in bovine feces as shed from naturally contaminated cattle. E. D. Berry* and G. A. Barkocy-Gallagher, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE.*

Exposure to low pH and acids in the bovine gastrointestinal (GI) tract may result in the induced acid resistance of *E. coli* O157. Because bovine feces are a source of carcass contamination, and acid tolerance of bacteria can affect the efficacy of decontamination procedures, the acid resistance of this organism as shed from cattle was determined. The objectives of this study were to examine the capacity of naturally-occurring *E. coli* O157 shed in bovine feces to survive exposure to low pH and to assess the relative acid resistance status of *E. coli* O157 as shed from cattle. Fecal grab samples and freshly-dropped feces were collected randomly from cattle in the MARC feedlot from August through October in 2000 and 2001. Initial numbers of *E. coli* O157 and numbers following exposure to pH 2.5 for 6 h were determined in fecal slurries, using a most probable number-immunomagnetic separation procedure. Isolates were confirmed as *E. coli* O157 and genotyped by pulsed-field gel electrophoresis. Fifteen positive fecal samples containing at least four distinct genotypes were obtained. Initial populations ranged from 0.99 to 4.86 $\log_{10}$ CFU/g, and log reductions following acid challenge ranged from 0.68 to 3.21 $\log_{10}$ CFU/g. For each unique isolate, acid resistance was determined in vitro for cells both in mid-log and stationary phases of growth, cultured with and without glucose (acid-adapted [AA] and nonacid-adapted [NA], respectively), by exposing the cells to the same acid challenge as the fecal slurries. Stationary phase cells were resistant to the acid challenge; generally, reductions of AA cells were <0.20 $\log_{10}$ CFU/g and NA cells were <0.60 $\log_{10}$ CFU/g. Log reductions of all mid-log phase cells were >4.00 $\log_{10}$ CFU/g and many populations were reduced below detectable levels. Comparison of the in vivo and in vitro acid resistance data indicates that residence in the bovine GI tract does not result in the development of extreme acid resistance of *E. coli* O157.

Key Words: *E. coli* O157, Acid Resistance, Cattle

601 Effect of preconditioning and distance of transport on shedding of *Escherichia coli* and *E. coli* O157:H7 by calves destined for feedlot. S.J. Bach*[1], T.A. McAllister[1], G.J. Mears[1], A.L. Schaefer[2], and K.S. SchwartzkopfGenswein[3], [1]*Agriculture and Agri-Food Canada, Lethbridge, AB,* [2]*Agriculture and Agri-Food Canada, Lacombe, AB,* [3]*Alberta Agriculture, Food and Rural Development, Lethbridge, AB.*

The effects of stressors (weaning, transport) on shedding of total *Escherichia coli* and *E. coli* O157:H7 were investigated using 174 range steer calves (80 Angus; 94 Charolais) blocked by breed and birth date and assigned to 4 treatments. The calves were preconditioned (P) or not (NP), and transported by commercial cattle liner for 15 h (long haul, L) or 3 h (short haul, S). Preconditioning comprised vaccinating 29 d prior and weaning 13 d prior to hauling; NP calves were weaned 1 d prior to transport (no vaccination). The NP calves were also penned (water only) for 24 h, followed by a second (2-h) haul. This simulated transport from ranch to feedlot for P calves; and from ranch to auction to feedlot for NP calves. Following transport, calves were allotted to 16 feedlot pens. Fecal samples were collected at weaning, day of transport, day of feedlot arrival, twice in the first week, and on d 7, 14, 21 and 28 for enumeration of *E. coli* Biotype 1, and culturing for *E. coli* O157:H7 (+ or -). Higher levels ($P<0.005$) of *E. coli* were shed by NP-L calves than by P-L, NP-S or P-S calves at weaning, on day of arrival at the feedlot, and after 1, 7 and 21 d. Repeated measures analysis revealed the same was true over the entire experimental period ($P<0.005$). No calves were positive for *E. coli* O157:H7 prior to transport. Chi-square analysis revealed that after transport, more ($P<0.005$) calves were positive for *E. coli* O157:H7 in the NP-L group than in P-L, NP-S or P-S. Holding facilities or the feedlot may have served as source of infection, fostered by intensive association of animals during transport and relocation. Lack of preconditioning coupled with long-haul transport increased fecal shedding of *E. coli* and *E. coli* O157:H7 by calves following transport. Management strategies to reduce stress-associated shedding of *E. coli* O157:H7 may include preconditioning.

Key Words: Cattle Transport, *E. coli* O157:H7, Fecal Shedding

602 Intervention to reduce fecal shedding of enterohemorrhagic *Escherichia coli* O157:H7 in naturally infected cattle using neomycin sulfate. R.O. Elder*[1], J.E. Keen[2], T.E. Wittum[3], T.R. Callaway[1], T.S. Edrington[1], R.C. Anderson[1], and D.J. Nisbet[1], [1]*USDA/SPARC, College Station, TX,* [2]*USDA/MARC, Clay Center, NE,* [3]*Ohio State University, Columbus, OH.*

Cattle are implicated as the major reservoir of enterohemorrhagic *Escherichia coli* (EHEC) such as EHEC O157:H7. To date effective preharvest strategies to reduce the number of EHEC O157:H7 positive cattle entering the food supply is limited or nonexistent. Mechanisms for short-term treatment of cattle, prior to slaughter, which eliminate or reduce the level of shedding of EHEC, can greatly impact the number of food borne outbreaks associated with EHEC. Using naturally infected EHEC O157:H7 positive cattle (n = 32) we tested and found that oral administration of neomycin sulfate at therapeutic doses reduces fecal shedding of EHEC O157:H7, to non-detectable levels compared to controls ($P < 0.05$), and lowers total numbers of generic *E. coli* ($P < 0.05$) in treated animals. Administration of neomycin sulfate reduced concentrations of *E. coli* O157:H7 24 hrs post treatment and lowered their levels beyond detection limits 72 hrs post treatment. Also, total generic *E. coli* concentrations in these cattle were also dramatically reduced 72 hrs post treatment. By day 7 post treatment generic *E. coli* levels returned to pretreatment levels, however, animals remained negative for EHEC O157:H7. These data show neomycin sulfate is an effective intervention that will reduce the risk of EHEC O157 from entering the food supply. This short-term intervention is amendable to current livestock production systems prior to cattle processing at a minimal cost.

Key Words: EHEC O157, Intervention, Food safety

603 Effect of co-mingling stress on fecal shedding of *Salmonella typhimurium* by early weaned piglets. T. R. Callaway*[1], J. L. Morrow[2], T. S. Edrington[1], K. J. Genovese[1], R. O. Elder[1], J. W. Dailey[2], R. C. Anderson[1], and D. J. Nisbet, [1]*Agricultural Research Service/USDA, Food and Feed Safety Research Unit, College Station, TX,* [2]*Agricultural Research Service/USDA, Livestock Issues Research Unit, Lubbock, TX.*

Weaned pigs are often transported to grower facilities and may be comingled without regard to farm of origin. This study was designed to determine the effect of mixing stress on intestinal populations of *Salmonella typhimurium* in SEW pigs. Piglets (7 d old; n = 28) were separated into 4 groups (2 control and 2 mixed groups). One pig from each group of 7 was challenged with 3 x 10^9 CFU of *S. typhimurium* via oral gavage. In the mixed groups, one piglet each day for 5 days was swapped between the two mixed groups, to simulate mixing stress; control groups were not mixed. Behavior of all 4 groups was recorded continuously. Groups indicated significant ($P < 0.01$) behavioral differences; mixed pigs devoted significantly less time to eating ($P < 0.02$), to rooting ($P < 0.01$) and performed less agonistic behavior ($P < 0.01$), indicating that the mixed groups were indeed stressed. Fecal swabs were enriched each day to qualitatively monitor shedding of *S. typhimurium*; each day more mixed pigs ($P < 0.05$) shed *Salmonella* than did control groups. After necropsy, rectal populations of *Salmonella* in mixed pigs were significantly ($P < 0.05$) greater than in control pigs but cecal *Salmonella* populations were unaffected by mixing. When tissues from the tonsils, ileo-cecal lymph node, cecum and rectum were enriched for *Salmonella*, the mixed group demonstrated more ($P < 0.05$) *Salmonella*-positive tonsils and lymph nodes than did control pigs. Results suggest that mixing groups of pigs from different farms can cause social stress that may increase their susceptibility to *S. typhimurium*.

Key Words: *Salmonella typhimurium*, Stress, Fecal shedding

604 The prevalence of multiple antibiotic-resistant *Salmonella* recovered from swine at a slaughter facility. F. M. Wallace*[1], L. Wonderling[1], P. J. Fedorka-Cray[2], A. Oser[3], R. Pearce[4], J. Call[1], M. L. Tamplin[1], I. F. Feder[1], L. Yoder[3], and J.B. Luchansky[1], [1]*USDA-ARS Wyndmoor, Pa.,* [2]*USDA-ARS Athens, Ga.,* [3]*Hatfield , Pa.,* [4]*National Food Center, Castleknock, Dublin, Ireland.*

Carcass (100) and fecal (60) samples were collected from swine at slaughter on 10 days over a 30-day period. Seventy-four percent of carcasses and 35% of fecal samples were positive for *Salmonella*. The 582 *Salmonella* isolates obtained were analyzed by ribotyping and PFGE, as well as for susceptibility to a panel of 17 antimicrobials used in the National Antimicrobial Resistance Monitoring System program. The majority (85%) of the isolates displayed PFGE profile types "F", "B", and "I". Ribotyping suggested that isolates displaying profiles F and I were most likely S. Typhimurium, whereas isolates displaying profile B were most likely S. Derby. When tested for antimicrobial susceptibility, a majority (85%) of the isolates exhibited resistance to antimicrobials with a wide variety of susceptibility patterns. Interestingly, multiple isolates obtained from the same sample generally displayed different resistance profiles, indicating that testing multiple isolates may be important during routine susceptibility studies. Of the 203 isolates displaying profile B, 167 (82%) were resistant to only tetracycline, sulfamethoxazole, and streptomycin. Among the 85 profile I isolates, 56 (66%) were resistant to at least ampicillin, kanamycin, streptomycin, sulfamethoxazole, and tetracycline (AKSSuT). Among the 206 profile F isolates, 199 (97%) displayed resistance to at least ampicillin, chloramphenicol, streptomycin, sulfamethoxazole, and tetracycline (ACSSuT), while 28 of these 199 isolates were also resistant to amoxicillin/clauvulanic acid. Further characterization of the profile F isolates by serotyping and phage typing will enable identification of those isolates that may be *S.*Typhimurium DT104. These data confirm that multiple antibiotic-resistant *Salmonella* are prevalent in swine feces/carcass samples collected at a slaughter facility.

Key Words: Swine, *Salmonella*, Antimicrobial Resistance

605 Characterization of farm management practices that contribute to number and type of gram-negative bacteria in bulk tank milk. N. V. Hedge*, R. Butchko, C. Hampton, A. A. Sawant, and B. M. Jayarao, *The Pennsylvania State University, University Park, PA, USA.*

In this study, four bulk tank milk (BTM) samples were collected at intervals of 15 days from each of the 126 dairy herds that participated in the study. The BTM samples were examined for; 1) Somatic cells (BTSCC), 2) Standard plate count (SPC), 3) Preliminary incubation count (PIC), 4) Laboratory pasteurization count (LPC), 5) *Staphylococcus aureus* (SA) count, 6) Coagulase negative staphylococcal (CNS) count, 7) Streptococci and streptococci-like organisms (SSLO) count, 8) Coliform count (CC), and 9) Gram-negative non-coliform (NC) count. Coliforms were detected in 89 of 126 (70.6%) of BTM samples. Counts ranged from 0 to 4,130 cfu/ml (mean, 159 cfu/ml). Gram-negative non coliform bacteria were observed in 83 of 126 (65.8 %) of BTM samples. Counts ranged from 0 to 15,475 cfu/ml (mean, 838 cfu/ml). A total of 369 isolates from 121 BTM samples were examined to species level; 369 isolates belonged to 38 different bacterial species. Coliforms and NC accounted for 64.5 and 35.5% of the total isolates, respectively. *Escherichia coli* was isolated from 44 of 126 (34.9%) of bulk tank milk, of which 6 of 44 (13.6%) BTM samples had *E. coli* that encoded for shiga toxin 2, while one isolate (1 BTM sample) encoded for both shiga toxin 1 and 2. *Escherichia coli* 0157:H7 was not detected in BTM. Coliform counts (> 50 cfu/ml) and NC (> 200 cfu/ml) were significantly associated with high SPC (> 5,000 cfu/ml) and PIC (> 20,000 cfu/ml). A critical review of farm management practices using a self-administered questionnaire followed by consultations with dairy producers strongly indicated that; 1) Use of bedding material other than sand, newspaper in particular can contribute to high NC count in BTM, 2) Most of the dairy producers (92%) who practiced fore-stripping, had none to very low (<50 cfu/ml) CC, and 3) Dairy producers who pre-rinsed their milking system before milking using an acid sanitizer had none to very low counts of CC or NC or both in BTM.

Key Words: Bulk tank milk, Coliforms, Management practices

606 Pasteurization effects on *Mycobacterium paratuberculosis*, *E. coli* 0157:H7, *Salmonella sp.*, *Listeria monocytogenes*, and *Staphylococcus aureus*. L. Green*, S. Godden, and J. Feirtag, *University of Minnesota, St. Paul, MN.*

The objectives of this study were to evaluate the efficacy of on-farm commercial pasteurization units and the effectiveness in which they destroy *Mycobacterium paratuberculosis*, *E. coli* 0157:H7, *Salmonella sp.*, *Listeria monocytogenes*, and *Staphylococcus aureus* in saleable bulk tank milk inoculated with a low (between 10^2 and 10^3 CFU/ml) and a high inoculum (between 10^5 and 10^6 CFU/ml). The pasteurizers (batch/vat and continuous-flow) used in this study were made for on-farm commercial use. Bulk tank milk was obtained from the University of Minnesota

campus farm. Milk was put into the respective pasteurizers and inoculated with the appropriate level of pathogens. The pasteurizers were heated to the specific time and temperatures: 145F for 30 minutes for the batch/vat pasteurizer and 161F for 15 seconds for the continuous-flow pasteurizer. Pre- and post-pasteurization (0, 24, and 48 h) samples were taken from each of the triplicate runs performed for each of the two pasteurizers. The milk samples were plated onto selective media for each pathogen and incubated at 37C for the appropriate time. All of the post-pasteurization samples showed no growth for *E. coli* 0157:H7, *Salmonella sp.*, *Listeria monocytogenes*, and *Staphylococcus aureus*. The HEYM Mycobactin J slants from the milk samples for the *Mycobacterium paratuberculosis* are in week 5 of incubation. From the results obtained, pasteurization with both on-farm units (batch/vat and continuous flow) was shown to destroy *E. coli* 0157:H7, *Salmonella sp.*, *Listeria monocytogenes*, and *Staphylococcus aureus* effectively. Because it will take 16 weeks to determine a true negative for *M. paratuberculosis*, results are still pending.

Key Words: Pasteurization, *Mycobacterium paratuberculosis*, Commerical pasteurizers

607 Detection comparison of *L. monocytogenes* in yogurt and cold pack cheese using enzyme-linked immunofluorescent assays. T. M. Silk* and C. W. Donnelly, *University of Vermont, Burlington, Vermont, USA*.

Recent outbreaks of *Listeria monocytogenes* have been attributed to low levels of contamination in food products. Rapid detection methods should be sensitive and accurate at reporting the presence of this pathogen in food. In the current study, two commercially available enzyme-linked immunofluorescent assays (ELIFAs), specific for *Listeria* spp., were used for the detection of *L. monocytogenes* in yogurt and cold-pack cheese. Food products naturally contaminated, and inoculated with *L. monocytogenes* at various inoculation levels ranging from 3.0 - 0.007 MPN/g were tested. Ten to twenty replicate samples were analyzed for each inoculation level. Detection results were compared with those obtained using the current U. S. Food and Drug Administration Bacteriological Analytical Manual (BAM) method for *Listeria* detection in food. One of the ELIFAs, lacking a secondary enrichment step, performed very poorly in comparison to the BAM method. Detection agreement values decreased as inoculation levels decreased. In food products inoculated with fractional positive levels of *L. monocytogenes*, ELIFA performance produced false negative rates approaching 100% whereas the BAM method did not produce false negative rates higher than 10%. Further cultural analysis of enrichment used for ELIFAs subsequently yielded positive *L. monocytogenes* results, indicating that the enrichment used for ELIFAs may not have increased target cell levels to those needed to elicit a positive response. The inability of the enrichment to increase *Listeria* levels may be attributed to an increased acriflavine level, which may result in a failure of these procedures to recover low levels of or injured *Listeria*, which can exist in acidic foods or those containing preservatives. Better enrichment protocols focused on the recovery of low level, or injured cell populations may increase the sensitivity of detection, ultimately improving the safety of dairy foods.

Key Words: *Listeria monocytogenes*, Detection, Enzyme-linked immunofluorescent assay

Growth and Development

608 Effect of differences in pattern of prepubertal growth on response to realimentation: Relationships to reproductive development. John Klindt*, J.T. Yen, and R. K. Christenson, *USDA, ARS, U.S. Meat Animal Research Center, Clay Center, NE*.

Our previous work (Klindt et al., 2001, J. Anim. Sci. 79:2513) showed an inverse relationship between feed consumed during development and feed consumed during breeding in gilts subjected to feed restriction during development, 1/2 to 7/8 ad lib, and given ad libitum access to feed during breeding. Age at first estrus was least in the 1/2 ad lib gilts, possibly due to increased feed consumption during breeding. The current study sought to replicate the feed intakes of gilts in the previous study and measure the effect on physiological responses. Crossbred white gilts, 90.3 ± 0.5 d of age, 38.2 ± 0.7 kg BW, were assigned to receive 1/2, 5/8, 3/4, or 7/8 of calculated ad libitum feed intake (24 gilts/dietary treatment, TRT) for 12 wk. After the restriction period, all gilts were fed quantities of feed similar to those consumed by similar gilts given ad libitum access to feed in group pens previously. During realimentation, ADFI was 3.03 ± 0.06, 2.76 ± 0.08, 2.40 ± 0.07, and 2.31 ± 0.08 kg/d by gilts in the 1/2, 5/8, 3/4, and 7/8 TRT groups, respectively. On d 0, 7, 14, and 21 of realimentation, gilts were slaughtered and wts of offal and carcass components were recorded. Blood samples were collected from the gilts during the last wk of the restriction period and during realimentation for assay of serum urea, glucose, insulin, and IGF-I. Urea, glucose, insulin, and IGF-I were influenced ($P < 0.03$) by the interaction of TRT×wk of realimentation. Slaughter and carcass wts were influenced ($P < 0.01$) by the main effects of TRT and wk. Of the offal components, only liver and small intestine were influenced ($P < 0.02$) by TRT×wk. It is concluded that increased feed intake by the more severely restricted gilts during the early part of breeding/realimentation period allowed those gilts to exhibit compensatory gains, had effect on liver and small intestine wts, and stimulated acceleration of onset of first estrus in the most severely restricted gilts.

Key Words: Gilts, Puberty, Growth

609 The effect of carbohydrate source on intestinal morphology of weaned pigs. M.A.M. Spreeuwenberg*[1], J.M.A.J. Verdonk[2], M.W.A. Verstegen[3], and A.C. Beynen[4], [1]*Nutreco, Boxmeer,* [2]*IDTNO, Lelystad,* [3]*Wageningen University,* [4]*Utrecht University, The Netherlands*.

Epithelial cells need energy to maintain gut integrity as measured with histology. It is hypothesised that with increasing the number of glucose molecules bound together, glucose availability and thereby gut integrity decreases: glucose > lactose > starch. A total of 42 newly weaned barrows (26 ± 0.8 d of age, 7.8 ± 1.0 kg) was used. On the day before weaning (d -1) all pigs were weighed and assigned to 7 experimental groups (n=6). The groups differed in diet and day of dissection. On the day of weaning (d 0), dissection was performed on 1 group. The remaining groups were fed 1 of 3 diets in which glucose, lactose or starch were iso-energetically exchanged, supplying 24% of the energy. The animals received a liquid diet (meal: water = 2:1) based on net energy requirement for maintenance (M, kcal = $78 \times BW^{0.75}$). Energy offered to the pigs increased from 0.5×M at d 0, 1.0×M at d 1, 1.5×M at d 2, 2.0×M from d 3-9. At d 0, 3 and 10 selected pigs were weighed and euthanized. Tissue samples for histology were taken at 0.5 m (prox.) and 3.5 m (mid) distal of the ligament of Treitz. Dry matter intake, body weight gain, villus height and crypt depth did not differ between diets. Dry matter intake was 59 28.0 g/pig/d from d 0-3, 173 ± 67.0 from d 3-7 and 257 ± 33.1 from d 7-10. At d 3, villus height was decreased compared to d 0. At d 10, villus height reached pre weaning levels for the lactose diet at the prox and for all diets at the mid small intestine. Crypt depth was increased at d 10 compared to d 0 and 3. It was concluded that dietary carbohydrate source does not affect intestinal morphology.

Day		0	3			10			
Diet			glucose	lactose	starch	glucose	lactose	starch	SEM
Villus height (μm)	prox[1]	394^{a}	274^{bc}	278^{c}	272^{bc}	315^{b}	360^{ab}	298^{b}	32.5
	mid[1]	337^{a}	236^{bc}	200^{c}	252^{bc}	293^{ab}	304^{a}	311^{ab}	32.4
Crypt depth (μm)	prox[2]	166^{a}	175^{a}	188^{a}	185^{a}	288^{b}	291^{b}	2 88^{b}	14.6
	mid[2]	157^{a}	172^{a}	193^{a}	179^{a}	254^{b}	252^{b}	256^{b}	15.6

different letters within a row differ: 1, $P<0.10$; 2, $P<0.05$. Comparisons: between diets within day and between days for the same diet.

Key Words: pig, morphology, small intestine