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Enhancing the Pork Meat Quality Value Chain

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Background: Unexplained and uncontrolled variations in the meat quality of pork decreases returns for the whole Ontario pork industry. Without consistent quality that meets the demands of consumers, it is difficult to build consumer confidence in premium quality pork products. This variability comes from many factors, and their interactions. This project aims to understand these, and create strategies to optimize quality.

Objectives:

1. Identify the variability in pork meat quality produced in Ontario.
2. Systematically evaluate behavioural, nutritional and genetic interactions contributing to this variability.
3. Investigate basic mechanisms whereby these factors impact on quality through proteomics, genomics and the biochemical conversion of muscle to meat.
4. Identify management strategies to improve the quality of pork produced in Ontario

Experimental Procedures: To date, data have been collected on 23 occasions from 20 farms with a total of 672 pigs sampled. For each farm, genetic, management, nutrition and behaviour information were collected, and 24 pigs were identified and individually marked for tracking from farm through processing. At the plant, video records were used to quantify behaviour during handling, with blood samples collected for analyses of stress parameters. Temperature and pH were recorded over the first 48 hours in the ham and loin. Selected tissue samples were collected at 1.5 hours postmortem and analysed for gene expression and enzyme biochemistry. Loin and ham samples were also sent to U of G Meats Lab for subjective evaluation of meat quality (colour, marbling, firmness, wetness) and objective determination of colour ($L^* a^* b^*$ scale), pH, drip loss and Warner-Bratzler shear force (an instrumental measure of tenderness).

Results to date:

Average values and ranges for meat quality measures in the loin across animals analysed to date (*Similar patterns are seen in hams*)

Variable*	Mean	Min	Max	SE
Measures on the loin (longissimus muscle)				
pH Loin (initial)	6.12	5.45	6.60	0.01
pH Loin (final)	5.67	5.29	6.27	0.01
Colour Loin (L^*)	44.81	35.47	54.35	0.23
Drip loss Loin (%)	7.42	2.69	12.54	0.14
Shear force Loin	4.21	2.08	7.66	0.13

*Optimal final pH is between 5.5 and 6.2 with lower values tending toward PSE and higher values tending toward DFD. Normal range for colour (L^* -value) is between 47 and 53. Higher numbers indicate lighter meat. Ideally, drip loss should be around 2.5-3%.

Take home message: As in other pig production systems in the world, large variability occurs in key aspects of Ontario pork meat quality. This variability represents opportunities to improve consistency and overall -quality of pork meat produced in Ontario.

Acknowledgments: The authors would like to thank Ontario Pork and NSERC for their financial support.

Enhancing the Pork Meat Quality Value Chain: Role of Calpains in drip loss

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Background:

Unexplained and uncontrolled variations in the meat quality of pork decreases returns for the whole Ontario pork industry. As part of a larger survey of the factors affecting end-product quality, we have specifically identified variations in the activity in the calpain system, enzymes known to be active in the post-mortem tenderization process. Here we report a subset of the data, specifically relating calpain activity in ham and loin muscles immediately post mortem to drip loss and shear force. This data has been reported in a recent conference paper (Purslow et al, 2006).

Experimental Procedures:

Subsamples of longissimus and semimembranosus muscles taken immediately post-mortem were snap-frozen in liquid nitrogen and subsequently stored at -80°C. Following analysis of the meat quality results, a sub-set of 65 loin and ham samples representatively spanning the range of drip loss and shear force values obtained were selected for measurement of net calpain-1 (micro-calpain) and calpain-2 (milli-calpain) activity by zymography, based upon the methods of Melody et al.(2004). Four repeats of each activity determination were conducted per muscle sample. Internal controls of calpain-1 and -2 were used in each zymogram and the activity in each sample related to mg of pure enzyme standard. Statistical analysis of simple correlations and partial correlations (with one controlled variable) were performed using SPSS.

Results to date:

Drip loss ranged from 2.61% to 12.54% across both loin and ham samples. There was no significant correlation between cooked meat shear force for either ham or loin and calpain activity in this study. Fig. 1 shows the correlation between the % drip loss and calpain-1 (micro-calpain) activity of all ham and loin samples in the sub-set studied to date. There is a clear negative relationship; higher calpain-1 activity is correlated to lower drip loss. This negative correlation is highly significant ($0.01 < p < 0.02$).

Take home messages:

Consistent with the implications from previous studies, degradation of cytoskeletal proteins by calpain reduces drip loss in pork meat. Manipulating calpain activity in muscle represents a means to enhance pork meat quality.

Acknowledgments

The authors would like to thank Ontario Pork, NSERC and OMAFRA for support of this research.

Mechanisms affecting pork meat quality in protein-restricted versus total feed-restricted dietary regimes

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Background: Recent studies show that compensatory growth occurs in finisher pigs following periods of both total feed intake and protein intake restriction during the grower phase of production. These dietary regimes can lead to greater feed efficiency and in some cases leaner carcasses. It appears that protein restriction versus total feed restriction may have very different effects on promoting activity of the calpain system, involved in meat quality development post-mortem. We have recently started to measure the impact that protein restriction, total feed restriction, or a combination of both, may have on pork meat quality. The data reported here is preliminary information based on samples from previous trials.

Experimental Procedures: We have conducted preliminary analysis of the calpain activity on a limited subset of longissimus muscle samples from previous trials, where either energy intake was restricted (McEwen) or protein intake was restricted (de Lange) during the grower phase, using zymography techniques established in our laboratory (Purslow et al, 2006).

Results to date: Both dietary regimes increased average daily gain in finisher pigs (ADGf), and increased proteolytic activity accompanies this. In samples from the total feed intake restriction trial, a correlation of Calpain-2 activity to ADGf was seen (+0.446; $P = 0.029$). In the protein intake restriction trial, a correlation of Calpain-1 to ADGf was seen (-0.442; $P = 0.058$). These findings suggest that increased ADG in finishing pigs following restricted feeding may increase the activity of the calpain system in post-mortem muscle, which could have a positive impact on pork meat quality. These are however preliminary findings that are now explored further in a side-by-side comparison of the two dietary regimes in one trial and with a large number of pigs.

Take home message: Inducing compensatory growth in finishing pigs may improve both feed efficiency and pork meat quality. These preliminary findings are being explored in a large scale study.

Acknowledgments: The authors would like to thank Ontario Pork and OMAFRA for their financial and technical support.

Meta-analysis of phosphorus balance data from growing pigs

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Background

Swine diets have been formulated traditionally to maximize growth without consideration given to the amount of nutrient excreted. However, there are economic and environmental reasons to reduce nutrient excretion. NRC (1998) suggested that phosphorus (P) rather than N will limit land application of manure in intensive swine producing areas and the success of management strategies for reducing P excretion is dependent on an accurate estimate of P requirements for a given level of performance. Therefore, in recent years research has focused on improving efficiency of conversion of dietary P into animal products and on accurate estimation of P requirement by the animal.

Objective

To collate data from P balance studies with growing pigs, and evaluate alternative mathematical functions to estimate biological determinants of P utilization with attention to endogenous P excretion, maintenance requirement and efficiency of dietary P conversion into animal products. The null hypothesis was that the relationship between retained P and dietary P is linear.

Methods

A database containing observations on 350 pigs was assembled from various studies. Four functions for analyzing P balance data were considered: straight line, monomolecular, Gompertz, and Richards. The nonlinear functions were specifically re-parameterized to assign biological meaning to parameters. Meta-analysis was conducted to estimate endogenous P, maintenance requirement and efficiency of utilization.

Results

There was evidence of nonlinearity and the monomolecular fitted the data best. Richards equation appears over-parameterized. Endogenous P excretion was estimated to be 17 mg/(kg BW^{0.75}·d) based on total P analysis using the monomolecular, which was within the range reported in the literature. A maintenance requirement value of 37 mg total P/(kg BW^{0.75}·d) was obtained. Average efficiencies of conversion of dietary P to retained P were 65 and 36% for available and total P, respectively.

Take home message

Non-linear models can provide useful estimates of endogenous P, maintenance requirement and efficiency of conversion of dietary P into animal products.

This project was supported by the NSERC–CRC program and the OMAF–University of Guelph Animal Research Program.

Determining Sow Performance and Mineral Requirements with Phytase Supplementation of the Lactating Sow Ration – Preliminary Report

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Introduction

Supplemental phytase offers interesting opportunities for farmers to reduce feed costs and lessen environmental pollution of minerals. In addition to binding up phosphorous, making it poorly available, phytate also renders calcium, iron, zinc, manganese and copper poorly available (Vohra et al. 1965). Much research has shown the effectiveness of adding phytase to hog rations to improve phosphorous availability (Ketaren et al. 1993; Young et al. 1993; Harper et al. 1997; Johnston et al. 2004; Omogbenigun et al. 2004). Recently, Shelton et al. (2004) sought to capitalize on the use of phytase to improve availability of calcium and the trace minerals as well. Shelton et al. (2004) observed no difference in growth performance and no negative response on carcass traits and pork quality when calcium and phosphorous were each reduced by 0.10% and the supplemental trace minerals were removed entirely.

Little has been done with respect to phytase with sows. Kemme et al. (1997b) observed that supplementation of phytase improved calcium, phosphorus and magnesium digestibility. They also observed that sows in different parities did not react differently to phytase supplementation in terms of mineral digestibility (Kemme et al. 1997b). Kemme et al. (1997a) and Nyachoti et al. (2004) observed an increase in calcium and phosphorus digestibility with phytase supplementation in lactating but not dry sow rations.

In lactating sows, no work has been done concerning the response due to phytase supplementation with respect to: 1) improved digestibility of trace minerals, 2) response of milk production and quality, and 3) piglet performance. Before farmers can safely incorporate such a product into their rations, these questions must be answered. The objectives of this trial are to address these three issues.

Experimental Procedures

After farrowing, sows were randomly assigned to one of four mineral-phytase treatments: A) calcium and phosphorus balanced at NRC levels and a trace mineral premix included with no phytase (control treatment), B) treatment A except with phytase (500 units/kg), C) treatment A with calcium content reduced by 0.12 percentage units and phosphorus content reduced by 0.10 percentage units of NRC requirements (differential reductions set to maintain calcium to phosphorus ratio of diets across treatments) and no supplemental trace minerals with no phytase, and D) treatment C except with phytase (500 units/kg).

Before entering the farrowing crate sow weight was recorded. All farrowing data (numbers of piglets born alive, mummified piglets and still born piglets; live born piglet weight and sex) was recorded. Piglets born within 12 h were cross-fostered to establish equal litter sizes on day 0. Pre-weaned piglet data (mortalities and weight gain) were recorded. Sow feed and water intake (individual water meters) was recorded daily. On days 14 and 28 of lactation the following samples were taken: 1) Feed and water samples were taken and frozen until further analysis. 2) During a milk let-down cycle, a milk sample was taken equally from 3 nipples (front-middle-hind). The sample was sent fresh for analysis. 3) A venous blood sample was

taken from sows, centrifuged and frozen until analysis later. 4) A fecal grab sample was taken and frozen for later analysis.

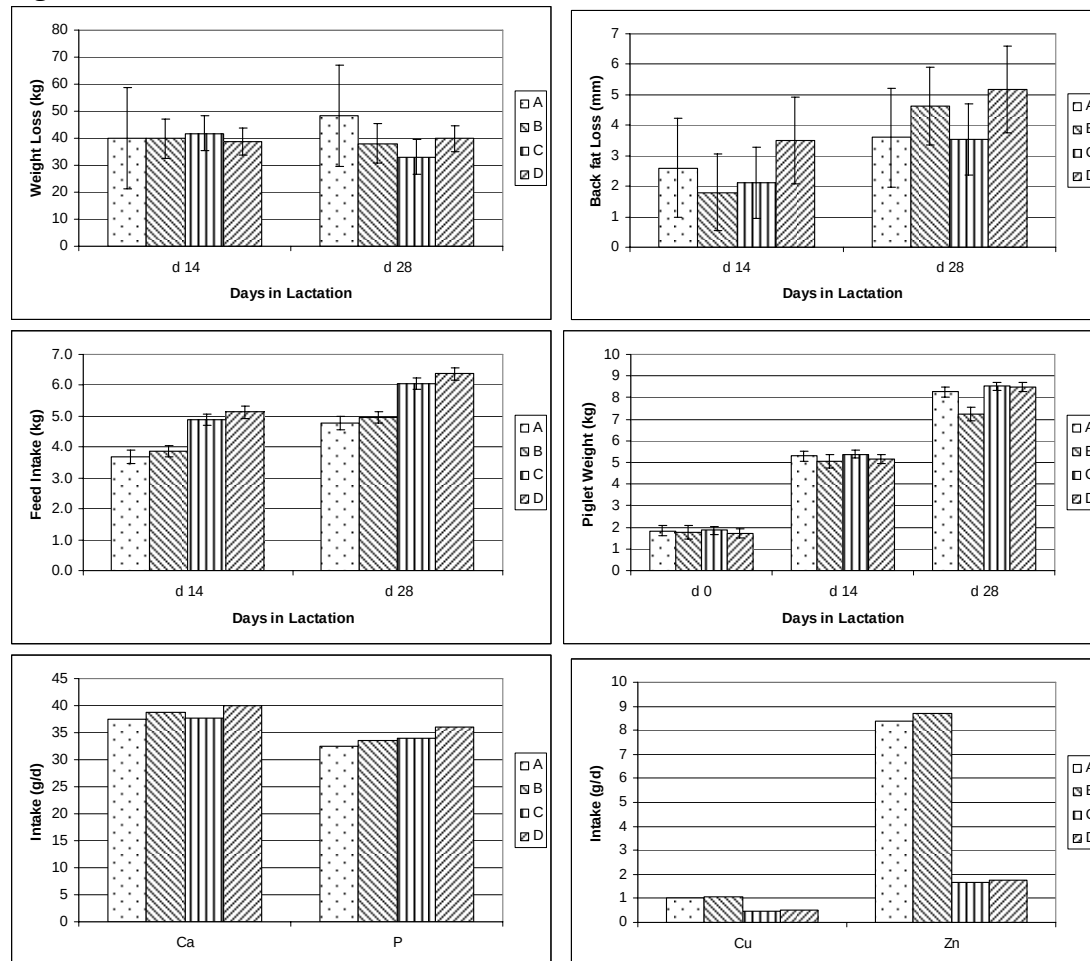
Feed, water, feces, milk and blood samples will be sent for analysis to reputable laboratories in Ontario for analysis of appropriate nutrients (including minerals). In addition, feed and feces samples will be analyzed for chromic oxide. Apparent digestibility of dry matter, crude protein, ME and minerals will be determined.

Preliminary data will be discussed for sow and piglet performance for 5 replicates of the experiment as the trial is incomplete and feed, water and fecal samples have not been analyzed.

Results to Date

Data presented in Figure 1 are raw means with standard errors. Copper (Cu) and zinc (Zn) are presented as examples of trace minerals. As the trial is incomplete and complete statistical analysis has not been done, results should be interpreted with some caution.

Figure 1. Results of trial to date.*



* Top left is sow weight loss at days 14 and 28 for the various treatments (see text). Top right is sow back fat loss at last rib at 14 and 28 for the various treatments. Middle left is average sow daily feed intake to days 14 and 28 for the various treatments. Middle right is the average piglet weights at birth, 14 days and 28 days for the various treatments. Bottom left is average sow intake of calcium (Ca) and phosphorus (P) based on actual feed intakes and table values of

mineral concentrations in the component feeds for the various treatments. Bottom right is average sow intake of copper (Cu) and zinc (Zn) based on actual feed intakes and table values of mineral concentrations in the component feeds for the various treatments.

Discussion

So far, it appears even the sows on the treatment with restricted calcium, phosphorus and trace minerals and no phytase (C) perform (in terms of piglet weaning weight) as well as the sows on the control (A) treatment. Interestingly, sows consuming the two treatments receiving lower mineral supplementation (C & D) appear to have consumed more feed than those sows consuming full mineral supplementation (A & B). This increase in intake led to those sows consuming equal amounts of calcium (Ca) and phosphorus (P) (assuming book values for mineral concentrations in feed). The sows receiving trace mineral restriction treatments (C & D) did consume less trace minerals such as copper (Cu) and zinc (Zn) shown above – again assuming book values for concentration of minerals in the feed. Caution must be used in interpreting these data but, if these trends translate into statistical significance, it would suggest that trace mineral supplementation for sows is not required. As this trial only followed the sows for one parity, any effect possible depletion of trace minerals would have on subsequent parities and longevity has not been investigated. More substantial conclusions will be possible as total tract disappearance of the minerals is determined.

Genetic and Environmental Regulators of Immune Response in Pigs

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Background: Immune response (IR) mediates resistance to infectious disease. Inappropriate IR mediates allergic diseases which are in epidemic proportions in humans. In pigs, the complex traits antibody (AMI or Type 2 IR) and cell-mediated (CMI or Type 1 IR) vary within and between litters with sufficient heritability to allow selective breeding of high or low immune responders. Immune response phenotype is also determined by environmental interactions and it is likely that early effects on the developing immune system influence the bias of AMI and CMI with lasting effects on expression of resistance/susceptibility to infectious and/or allergic disease. Ability to control IR variation and to regulate desirable balance in IR may be utilized to enhance health.

Objectives

- To enhance immunophenotyping methods to refine discrimination of expression of AMI and CMI by neonatal piglets
- To establish methods for inducing food allergy in neonatal piglets to peanut and ovomucoid (OVM)
- To determine immunomodulatory effects of Type 1 (Interferon- γ) or Type 2 (IL-13) cytokines and of the probiotic *Lactococcus lactis* on neonatal pig immune response

Results: The test immunogens hen eggwhite lysozyme (HEL) and killed *Candida albicans* (CA) given simultaneously by intramuscular injection to 14 day old piglets induce typical Type 2 and Type 1 IR as indicated by immediate and intermediate (HEL) and delayed-type (DTH) reactions (CA) at intradermal injection sites. Responses vary by individual and litter and between outbred and inbred litters. Ongoing analysis is testing possible correlations between individual expression of these traits and association of serum antibody with the putative Type 2 and 1 IgG isotypes, IgG₁ and IgG₂. Pigs were sensitized to peanut and OVM expressing typical food allergic signs upon being fed these allergens. Porcine IFN- γ has been cloned into a genetically modified, safe live vehicle *L.lactis* and into *E.coli*, the former to be given orally and the latter by im injection to neonates to test effects on immune response phenotype and allergy.

Take Home Message: Remarkable variation exists in IR of individual pigs within litters and between litters including expression of allergic diseases. It may be possible to modify IR phenotype by delivering regulatory cytokines to newborn pigs using oral probiotics to favourably alter IR to enhance resistance to infectious disease and to minimize allergic signs.

This research is supported by grants from the Natural Sciences and Engineering Research Council, Ontario Pork and the Ontario Ministry of Agriculture and Food

Prevalence and Impact of Coccidia in Suckling Piglets in Southwest Ontario

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Background

Coccidiosis caused by *Isospora suis* is recognized as a cause of diarrhea and poor growth rate in suckling piglets. No information regarding the current prevalence of coccidia in Ontario herds is available, but recent work in Europe suggests that over 75% of herds may be affected. In most countries Baycox® (toltrazuril) is used for control. In 2005 Canada banned the use of this product leaving pork producers without an effective alternative.

Objectives

To determine the herd prevalence of coccidia in southwestern Ontario.

To determine the association of coccidia with diarrhea and reduced growth rates in suckling piglets.

Results

Thirty-five of 50 farms tested (70%) were positive for coccidia. The likelihood of diarrhea being present in litters positive for coccidia was almost 4 times higher than in litters without coccidia ($P < 0.001$).

Pigs in positive litters were on average 400 g lighter than pigs in negative litters at weaning.

Take Home Message

Coccidiosis is widespread in the Ontario pig population and is associated with the prevalence of diarrhea and likely contributes to poor growth. This problem might be overlooked on many farms because mortality is low but the economic impact might be quite important. Developing an effective control program for coccidia should be an industry priority.

Financial Support was provided by Ontario Pork and OVC Dean's Office.

Clinical Trial Using Deccox® (Decoquinat) for Coccidiosis in Suckling Piglets

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Background

In a recent study, we found a prevalence of 70 % of farms in Ontario were positive for the presence of coccidia, and a relationship between the presence of coccidia and piglet diarrhea. We also found that piglets in positive litters tended to be lighter at weaning than piglets from negative litters. Research has shown that infected piglets may grow slower than non-infected piglets whether or not diarrhea occurs. The only drug with proven efficacy to treat coccidiosis in pigs is toltrazuril (Baycox®). However, this drug was banned in Canada in 2005. Alternative treatments are needed. There are a number of drugs used for coccidia in other species and these might prove effective.

Objectives

To determine the effectiveness of decoquinat (Deccox®) in controlling coccidiosis in suckling piglets

Preliminary Results

Pigs in 15 litters treated with decoquinat mixed with iron and provided ad-libitum in the creep area had an average daily weight gain (DWG) of 237 g versus an average DWG of 226 g for pigs from 15 litters provided with just oral iron. The ANOVA analysis did not show a statistical difference between these two groups. Diarrhea scores were similar in each group and coccidia was identified in both treatment and control litters.

Take Home Message

Decoquinat did not prove to be an effective control measure for piglet coccidiosis in this trial. It is possible that piglets did not consume adequate amounts of the drug.

Support was provided by Ontario Pork and Alpharma Animal Health.

Clinacox (diclazuril) Drug Trial for Coccidiosis in Suckling Piglets

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Background

A previous research study has shown that coccidia is widespread on farms in Southwestern Ontario, and the presence of these protozoa is associated with diarrhea and reduced growth in suckling piglets. A clinical trial testing a coccidiostat used in poultry and cattle, decoquinate (Deccox®), found that piglets in litters treated orally with iron and Deccox had similar growth rates and diarrhea scores to untreated controls.

Objectives

To determine the effectiveness of a single treatment of Clinacox (diclazuril) in controlling coccidia in suckling piglets

Preliminary Results

A clinical trial was performed on a farm with a coccidia problem. We found that piglets in 40 litters treated with Clinacox had average daily weight gains of 249 g and piglets in 40 control litters without Clinacox had average daily gains of 237 g. This difference was not statistically significant (p-value > 0.05). The level of coccidia recovered in fecal samples was similar.

Take Home Message

It did not appear that Clinacox as used in this trial was effective in the control of coccidiosis in pigs.

Financial Support was provided by Ontario Pork

Enhanced Resistance to Bacterial Infection in PG-1 Transgenic Mice

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Background

Respiratory infection is one of the major causes of morbidity and mortality leading to significant economic losses in the swine industry. There are increasing pressures to reduce the use of conventional antibiotics in food animals due to concerns of the impact of antimicrobial resistance on both human and animal health. Alternate approaches are therefore needed to enhance resistance to bacterial infection. Protegrin-1 (PG-1) is a small cationic cathelicidin antimicrobial peptide that possesses a broad spectrum of activity against various microorganisms including bacteria and some enveloped viruses in vitro.

Objectives

The long term goal of this research is to express PG-1 in the respiratory tract of transgenic pigs to potentially enhance their resistance to infection, and thus reduce the need for antibiotics in the pork industry. The short-term objective of the current study was to evaluate the effect of over-expressing PG-1 in transgenic mice on respiratory infection by microinjecting a PG-1 expression cassette into the pronuclei of C57/BL6 mice to generate PG-1 transgenic mice.

Results

Of the 126 mice that were intranasally challenged with *Actinobacillus suis*, 87% of the transgenic mice survived compared to a 31% survival rate for their non-transgenic littermates. The bacterial load in the lung of PG-1 transgenic mice was significantly lower compared with that in controls ($P < 0.001$). Histological examination PG-1 transgenic mice revealed reduced alveolar damage, interstitial edema, local hemorrhage, and infiltration of neutrophils in lung of compared to their transgenic littermates. Radial diffusion assays demonstrated that antimicrobial activity in neutrophil secretions of transgenic mice was significantly higher than that of their non-transgenic littermates. In addition, examination of differential cell types in bronchial alveolar lavage fluid revealed that the percentage of neutrophils in PG-1 transgenic mice was higher than that of their non-transgenic littermates ($P < 0.001$).

Take Home Message

Taken together, our data demonstrate that over-expression of PG-1 in mice confers enhanced respiratory resistance to experimental *A. suis* infection. These proof-of-principal experiments provide a basis for the development of PG-1 expressing pigs that potentially have superior resistance to a variety of microbial infections.

Financial support for this work was provided by Ontario Pork, the Natural Sciences and Engineering Council of Canada, and Ontario Ministry of Agriculture and Food and Rural Affairs.

Dental development in young swine

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Background

One consequence of early weaning is the frequent inability of piglets to successfully begin eating solid feed. Only two inexact studies have investigated the age at which tooth eruption occurs in commercial pigs, and these were undertaken prior to the swine industry's large advancements in genetic selection. Studies on dental development in miniature pigs show that molar eruption coincides with the initial eating of creep feed. No studies have investigated the relationship between tooth development and feed consumption during any period of the pig's lifecycle.

Objectives

To determine the variation in dental development from birth to 4 weeks of age. Determining the amount of individual variation, especially around the time of weaning, is necessary for designing future studies on how tooth eruption and occlusion affect the onset of feed intake and feeding efficiency both prior to and after weaning.

Methods

A total of 210 piglets (ages 0, 1, 2, 3 and 4 weeks) had their weight and sex recorded, along with the eruption progress of each tooth crown through the gingiva. Recording for dentition was done on a 3-point scale with 0 indicating the tooth was not through the gingiva, 0.5 indicating that part of the tooth crown was through the gingival, and 1.0 to indicate that the entire crown was through the gingiva. Each piglet had their scores added for each tooth type (incisors & molars) as well as for the overall number of teeth. Any abnormalities such as supernumery or missing teeth, discolouration, resorption, or infection were also recorded.

Results

- Discrepancies from previous studies include both significantly delayed molar eruption (i.e. the teeth used for chewing solid feed) ($p < 0.001$ for all molars) and earlier incisor eruption.
- Other interesting findings include (1) impaired development of tooth enamel, (2) development of cavities in newly erupted teeth, (3) discolouration of needle teeth, and (4) resorption of clipped needle teeth.

Take Home Message

Dental development is variable between litters and molar eruption is most variable between 3 and 4 weeks of age indicating that many piglets do not have the teeth required for chewing food at the time of weaning.

We gratefully acknowledge the funding support of NSERC and OMAFRA.

Increased resting behaviour associated with a shift in gastrointestinal microflora does not occur when weaned pigs are housed with healthy penmates.

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Background

Illness is known to lead to increases in slow wave sleep in an animal as part of the sickness behaviour response that aids in the combat of illness. Furthermore, lack of sleep is associated with increased mortality from disease and reduced immunity. As yet, little is known about how sickness alters rest in socially housed animals. Antibiotic associated diarrhea causes increased rest by singly housed weaned pigs. Pen design and behaviour of healthy penmates may impact sickness behaviour of pigs in commercial environments.

Objective

The objective of this study was to determine if a gastrointestinal microflora change in an individual leads to alterations in rest behaviour by the individual and its penmates.

Methods

Weaned pigs were housed in 21 groups of three pigs, over three replicates. In 11 Treated groups, one pig received three doses of 250 mg/kg ampicillin orally and penmates received placebo doses. In 10 Control pens, all pigs received placebo doses. Pens were video-recorded and interval scan-sampled every 10 minutes for 24 hrs/day on Days -1, +1 and +3 relative to dosing. Proportion of total rest, resting in isolation and heat pad use were statistically analysed as a repeated measures mixed model. Fecal samples were collected directly for microbial analysis.

Results

- Treatment was not associated with clinical signs of diarrhea. However, microbiological analysis revealed a significant microflora change on Day +3 for Treated pigs ($p=0.006$).
- For Treated pigs, proportion of time resting was not affected by treatment [treatment x day: $F(10,169) = 0.33$, $p=0.973$]. Furthermore, there was no evidence that Treated pigs spent more time resting in isolation after dose [treatment x day: $F(10,152) = 0.59$, $p=0.819$].
- Although there was no significant treatment x day interaction for heat pad use [$F(10,152) = 0.95$, $p=0.4894$], contrasts show that all pigs in treated pens rested on heat pads less on Day +3 than on Day -1 (RR: 0.555; 95% CI: 0.408, 0.756; $p=0.0002$).

Take Home Message

Changes in resting behaviour that occur when ill weaners are housed singly, appear to be thwarted when ill pigs are housed with healthy penmates. Ill pigs may benefit from separation into infirmaries or hospital pens.

We appreciate the financial support from NSERC and the OMAF-Swine Research Program at the University of Guelph

An Alteration of the Gastrointestinal Microflora in Weaner Pigs Leads to an Increase in Aggression Towards Penmates

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Background

Sickness is known to cause behavioural changes in an animal as a means to aid in the combat of illness, but little is known about how sickness alters social dynamics in animal populations. An antibiotic associated model developed in our laboratory is known to cause a shift in gastrointestinal microflora and behavioural changes in individually housed weaned pigs.

Objective

Our objective was to investigate the effects of gastrointestinal microflora change on the behaviour of weaned pigs when housed in mixed groups of ill and healthy individuals.

Methods

Weaned pigs were housed in 21 groups of three pigs, over three replicates. In 11 Treated groups, one pig received three doses of 250 mg/kg ampicillin orally and penmates received placebo doses. In 10 Control pens, all pigs received placebo doses. Pens were video-recorded and analysed for three 10-minute periods per day on Days -1, +1 and +3 relative to dosing. Frequencies and durations of social (aggression, play and oral-nasal contact), abnormal (belly-nosing, tail-biting) and non-social (feeding, drinking) behaviour were statistically analysed as a repeated measures mixed model. Frequency data was analysed as a Poisson distribution with a log link. Fecal samples were collected directly for microbial analysis.

Results

- Treatment was not associated with clinical signs of diarrhea. However, microbiological analysis revealed a significant microflora change on Day +3 for Treated pigs ($p=0.006$).
- Oral-nasal social contact, abnormal and non-social behaviour did not differ
- Overall aggression levels were low in all groups (Mean frequency per 10min $\pm$ [95% CI]: $0.7249 \pm [0.5718, 0.9189]$), but on Day +3, Treated pigs ($1.8644 \pm [1.086, 3.202]$) performed significantly a higher frequency of aggressive behaviour than pigs in the Control pens ($0.668 \pm [0.423, 1.05]$; $p=0.006$) and tended to be greater than Untreated Penmates ($0.918 \pm [0.583, 1.446]$; $p=0.055$).

Take Home Message

Gastrointestinal microflora caused weaned pigs to behave more aggressively towards their healthy penmates, with implications for pathogen transmission.

We appreciate the financial support from NSERC and the OMAF-Swine Research Program at the University of Guelph

Effects of a non-infectious gastrointestinal microflora shift on resting and social motivation of singly housed weaned pigs

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Background

Sickness is known to cause behavioural changes in an animal as a means to aid in the combat of illness. However, there has been little investigation to understand how illness may affect the behavioural needs of commercial swine.

Objective

Our objectives were to explore the effects of a non-infectious gastrointestinal microflora shift on behavioural needs of weaned pigs.

Methods

Nine pigs received three oral doses of 250 mg/kg ampicillin over 36 hours, a model previously developed in our laboratory and known to cause mild to moderate diarrhea for 24-48 hours. Pigs were housed individually in an 8ft x 4ft pen with resources for feeding, drinking, rooting, and warmth. A separate social area of the pen provided visual and nose-to-nose contact with two familiar healthy penmates. Behaviour was scored from time-lapse video recordings using 5-minute scans over eight one-hour periods on days -1, 0, +1 and +2 relative to dosing. Diarrhea was assessed on a 4-point scale, whereby 1=normal and 4=severe. Data were analyzed using a generalized mixed model examining repeated measures effects over time, with trial, room and pig as random effects. Tukey adjusted P-values are reported.

Results

- Pigs spent 82.9% of their time in the social area. Probability of spending time in the social area significantly differed by day ($P < 0.0001$), with odds of spending time in the social area being 1.8 times greater on day 0. There was also a significant effect of diarrhea score on probability of spending time in the social area ($P = 0.048$).
- Pigs rested 86.9% of the time. There was a trend for a day effect on time spent resting ($P = 0.0529$), with odds of resting being 1.4 times greater on day 0 compared to the average of days -1, +1 and +2.
- There was a significant effect of diarrhea score on probability of resting ($P = 0.0042$), with the probability of resting being 91.7% when fecal score was >1 versus 85.6% when fecal score was 1 or normal.

Take Home Message

Rest is an important behavioural component of the sickness response in the weaner pig. Furthermore, weaner-age pigs appear to be motivated to remain in social contact even during illness. Hence, hospital pen areas should allow for ill weaners to see and/or hear other pigs.

We appreciate the financial support from the Ontario Pork, NSERC and the OMAF-Animal Research Program at the University of Guelph

Boar Sperm, Their Enzymes and Fertility

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Background

Sperm have many enzymes that affect the way they function, and also affect their ability to go through the final changes required for them to fertilise an egg. In sperm from dairy bulls, an enzyme called NaK-ATPase is concentrated in the membrane surrounding the sperm's head. There it acts to move ions back and forth across the membrane, and controls the large influx of ions into the sperm that is necessary for the sperm to undergo 'capacitation', which is when the sperm becomes capable to actually penetrate and fertilise an egg. Our lab has recently identified an additional, important role for this NaK-ATPase enzyme in capacitating bull sperm: we found that, in addition to moving ions, the NaK-ATPase directly signals the sperm to add phosphate to proteins (a process known as tyrosine phosphorylation), which is another very important task sperm must complete in order to fertilize. No one has looked at NaK-ATPase in boar sperm, so this study set out to determine if it were present, where it might be in boar sperm, and what its component parts might be.

Approach and Results

To determine the existence and location of NaK-ATPase, we isolated the membrane over the head of the sperm and separated it from the rest of the sperm body membranes. To see if what we were calling head plasma membrane was indeed from the head, we tested it for the presence of molecules known to be markers for sperm head membranes. The markers confirmed that we had purified membranes mostly from the sperm heads, with only very minor contamination from the rest of the sperm structures.

NaK-ATPase is made of two parts, known as A and B. There are four known variants of the A (cleverly known as A1, A2, A3 and A4) and three variants of B (equally cleverly called B1, B2, and B3). We used a technique known as Western blotting to detect which of these forms were in intact sperm, and to see if any were particularly concentrated in the HPM. Interestingly, intact sperm had lots of A1, A3 and B1, but the head membranes had little of these forms. A2 and B3 were prominent in both intact sperm and the head membranes.

We then used immunofluorescence to make the A and B units fluoresce, so we could see exactly where these proteins were on the sperm. Fresh sperm from 4 ejaculates of different boars were viewed at either 37°C, 5°C or room temperature using a fluorescence microscope. The A3 subunit could be seen on the bottom of the sperm head regardless of temperature. All other forms also could be seen, but only at room temperature, suggesting that these other forms are very sensitive to temperature. The B forms were present over the inner face of the top of the sperm heads, while the A1 form was visible on the outer face of the top of the sperm heads.

Take Home Message

These results indicate that the enzyme NaK-ATPase exists in specific regions of boar sperm and are quite temperature-sensitive. The roles in the fertility of fresh and frozen-thawed boar sperm of each of these forms are currently being investigated.

Funding from NSERC, OMAFRA, Bioniche and Semex Canada is gratefully acknowledged.

Development of sperm-specific aptamers to boar sperm

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Background: In swine, and other livestock species, the sex of an animal is arguably the most important genetic trait with considerable financial implications. The ability of a producer to pre-determine the sex of an animal allows for maximal production efficiency, planned matings, and the faster genetic progress of a herd. Sex pre-selection is achieved by separating X-chromosome sperm from Y-chromosome sperm and using this sorted sperm for artificial insemination. Current methods for sperm sorting use a flow-cytometer to sort sperm based on slight differences in DNA content between X- and Y-sperm. Use of this technology in swine is hindered by excessive damage to sperm, poor sorting accuracy, and ultimately unrealistic costs. In order for the swine industry to reap the full benefits of sexed sperm, identification of sex-specific markers are required that could be used to develop new sorting methods. Aptamers are short single-stranded DNA molecules that adopt sequence-dependant secondary structures that in turn bind to specific ligands. Aptamers, are emerging as a superior tool for bio-marker discovery, often out-performing antibodies in affinity and specificity of binding.

Objectives

- 1) Assess the applicability of aptamers as a tool for molecular detection in sperm.
- 2) Select sex-specific aptamers to boar sperm and apply aptamers to novel sorting methods.

Methods and Procedures: Twelve rounds of a modified systematic evolution of ligands by exponential enrichment (SELEX) procedure were used here to select aptamers with the desired binding characteristics from a large randomized pool. Aptamers were co-selected to boar sperm and flow-sorted bull sperm to develop aptamers with both strong affinity for sperm, and furthermore, specific selectivity between X- and Y-sperm.

Results: The selected aptamer library exhibited a 1.52x greater affinity for sperm compared to the unselected random library. Fluorescent microscopy with FITC-labeled aptamers found that 66% and 30% of boar sperm bound X- and Y-aptamers respectively. X-aptamers were found to localize in concentrated regions of the plasma membrane potentially through binding to lipid rafts or specific membrane proteins. Y-aptamers were found to have even distribution over the entire sperm head with no clear concentrated regions.

Take Home Message: Aptamers are shown here to be suitable for use as DNA based antibodies in sperm research and were developed with respectively lower costs compared to alternative methods. Different binding patterns and ratios are observed when selected X- or Y-aptamers are bound to boar sperm. Ongoing research will investigate if aptamer binding is sex-specific, identify the binding proteins and will explore how these aptamers could be used for novel sperm sorting strategies.

Financial support from Ontario Pork and OMAF is greatly appreciated.

Glial cell line-derived neurotrophic factor enhances oocyte development competence *in vitro*

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Background: The success of early embryonic development depends on oocyte nuclear and cytoplasmic maturation. We investigated whether glial cell line-derived neurotrophic factor (GDNF) affects the *in vitro* maturation (IVM) of porcine oocytes and their subsequent ability to sustain preimplantation embryo development.

Approach and Results: GDNF and both its co-receptors, GDNF family receptor α -1 (GFR α -1) and the rearranged during transformation (RET) receptor were expressed in oocytes and their surrounding cumulus cells from small and large follicles.

When included in IVM medium, cumulus cell expansion was enhanced, and the percentage of small follicle-derived oocytes maturing to the metaphase II (MII) stage was significantly increased by GDNF, although the nuclear maturation of large oocytes was not significantly affected.

Examination of cyclin B1 protein expression as a measure of cytoplasmic maturation revealed that in the presence of GDNF, cyclin B1 levels were significantly increased in large follicle-derived oocytes. Its expression was also elevated in small follicle-derived oocytes to levels comparable to untreated large oocytes.

After activation, a significantly higher percentage of oocytes that were matured in the presence of GDNF developed to the blastocyst stage. A significant increase in the blastocyst rate was observed for small and large follicle-derived oocytes treated with GDNF compared to controls. Indeed, GDNF enhanced the blastocyst rate of small follicle-derived oocytes to levels comparable to those obtained for large oocytes matured without GDNF.

Take home message: Our study provides the first functional evidence that GDNF enhances oocyte maturation and preimplantation embryo developmental competence in a follicular stage-dependent manner.

This finding may provide insights for improving the formulation of IVM culture systems, especially for small follicle-derived oocytes.

We appreciate the financial support of Canadian Institutes of Health Research (CIHR), Natural Sciences and Engineering Research Council (NSERC), Ontario Pork, and Ontario Ministry of Agriculture and Food and Rural Affairs.

Comparison of proliferation, differentiation potential and gene expression pattern of skin- and brain-derived porcine fetal stem cells

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Background:

Stem cells from pigs offer an excellent model for studying porcine development and may provide an efficient means for the production of transgenic swine. We have previously reported the isolation, and neural differentiation of porcine skin-derived stem cells.

Background: Using the same isolation procedure, cells with similar growth characteristics were also isolated from the brain. Here we compare the proliferation, differentiation, and gene expression profiles of the two populations.

Approach and Results: Morphologically, the stem cell populations are similar, growing as suspended spherical aggregates of cells. Both skin- and brain-derived sphere cell populations expressed the neural progenitor marker nestin, with $41 \pm 11\%$ of cells in the brain-derived population and $52 \pm 10\%$ of skin-derived population staining positive for the protein. Immunocytochemistry revealed that a small subpopulation, $6 \pm 1\%$ and $5 \pm 2\%$, from brain- and skin-derived cells expressed Oct 4, respectively. Although both cell populations were capable of self-renewal *in vitro*, the brain originating cells appear to be more active in proliferation with a population doubling time of 79 ± 5 hours, as compared to that of skin originating cells, 119 ± 6 hours. Upon growth factor withdrawal, both populations generated cells expressing β -III tubulin that morphologically resembled neurons ($44 \pm 10\%$ for skin-derived and $21 \pm 7\%$ for brain-derived cells). The populations also formed cells that expressed GFAP with an astrocyte-like morphology ($31 \pm 5\%$ for skin- and $44 \pm 18\%$ for brain-derived cells). In addition, a subpopulation, $8 \pm 1\%$, and $3 \pm 0.2\%$, from brain- and skin-derived cells respectively differentiated into adipocyte-like cells when cultured in 10% fetal bovine serum, as determined by positive staining for oil red-O. Adipocytes are known to secrete leptin. Using Real Time RT-PCR, the transcript of leptin was detected in the brain and skin derived stem cells after but not before induced differentiation. To compare the global gene expression patterns of the brain and skin isolated stem cell populations, microarray analysis was performed using a 19k array. The correlation coefficient of the gene expression for the skin- and brain-derived stem cells was 0.994, suggesting a very similar gene expression pattern between the two cell types. Of the 19K genes analyzed, six were identified as differentially expressed in the two stem cell populations by microarray and subsequent Real Time RT-PCR analysis.

Take Home Message: Our data suggests that despite being derived from two distinct tissues, these two stem cell populations are remarkably similar in terms of their gene expression pattern, neural, and adipocyte differentiation potential. The mechanisms governing their differing self-renewal performance, and the possible involvement of the six identified differentially expressed genes in the process, is to be investigated.

We appreciate the financial support of Ontario Pork, Natural Sciences and Engineering Research Council (NSERC), and Canadian Institutes of Health Research (CIHR)

A growth-maturation system that enhances the meiotic and developmental competence of porcine oocytes isolated from small follicles

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Background: In livestock, most of the follicles on the ovarian surface are small follicles. A procedure that supports the *in vitro* growth and maturation of these small follicle-derived oocytes may offer a new source of useable oocytes for both biotechnological and fundamental research purposes.

Objective: The objective of the current study was to test the hypothesis that allowing oocytes isolated from small follicles to grow *in vitro* before induction of maturation may improve their competence of meiosis and embryo development upon activation.

Approach and Results: In our growth-maturation system (SGM group), cumulus-oocyte complexes (COCs) from small follicles (1-3 mm) were first cultured in oocyte growth medium for 24h, then in oocyte maturation medium for 20h. As controls, COCs from small (SM group) and large follicles (LM group) were cultured using conventional *in vitro* maturation (IVM) approach, in which they were directly cultured in oocyte maturation medium. At 24h of culture, the percentage of small follicle-derived oocytes that underwent germinal vesicle breakdown (GVBD) in the SGM group was comparable to that of large follicle-derived oocyte (LM group), while significantly higher than that of the SM group ($p < 0.05$). At 44h of culture, compared to 36% in the SM group, 55% of the SGM group oocytes reached metaphase II (MII; $P < 0.05$). In addition, although still lower than that of the LM group, elevated level of cyclin B1 was evident in oocytes of the SGM as compared to that of the SM group ($p < 0.05$). When activated, 7.3 times more parthenogenetic embryos developed to blastocyst stage in SGM than the SM group ($P < 0.05$). RT-PCR indicated that the expression level of three developmental important genes, DNMT1, Oct4, and FGFR2 in embryos of the SGM group was comparable to that from the LM group, while was significantly lower in those of the SM group ($P < 0.05$).

Take Home Message: Our data suggests that the oocyte growth-maturation system facilitates the final stage of oocyte growth and thus resulted in better oocyte nuclear, cytoplasmic maturation, and developmental competency compared to the conventional direct oocyte maturation system.

We appreciate the financial support of Ontario Pork, Natural Sciences and Engineering Research Council (NSERC), and Canadian Institutes of Health Research (CIHR), Ontario Ministry of Agriculture and Food and Rural Affairs.

Creation of a Molecular Catalogue for the Swine Liver using Omics Techniques

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Background: Genomic and proteomic profiling of tissues and cell types is becoming a powerful tool to characterize and identify the role of definite genes and proteins in the tissue and cell metabolism. In connection with this creation of molecular catalogue for different tissues and cells using Omics technologies is in the focus of many researches worldwide. The liver is the main chemical and energy factory for the body and is involved in production of plasma protein, synthesis of fatty acids and vitamin A, and furthermore is involved in metabolism of xenobiotics and drugs. Liver diseases such as viral hepatitis, liver cancer, alcohol and drug related injury are also affecting large portion of human population. Not surprisingly Human Liver Proteome Project (HLPP) was one of the first initiatives of the Human Proteome Organisation (HUPO) aimed at the establishment of a biological atlas of the liver. Our project is designed to create the first molecular catalogue of transcripts and proteins present in porcine liver to complement the extensive Human Liver Proteome project and to provide across species comparisons.

Objectives:

- 1) Identification of genes and proteins expressed in the swine liver.
- 2) Attempt to identify the role of genes and proteins in biochemical pathways and biological processes.

Methods and procedures: Transcriptome profiling has been performed using Affymetrix Porcine GeneChips (6 control vs. 6 transgenic). Normalization of microarray data was done using GCRMA, DChip, MAS5 and QFARM software, and further statistical analysis - using SAM software. Proteomic profiling has been performed using Isobaric Tagging for Relative and Absolute Quantification (iTRAQ) with further proteins identification using ProteinPilot software.

Results: Transcriptome profiling of 24123 transcripts identified 11205 as present in the normal liver. Data obtained were compared to swine muscle and parotid data to identify liver specific genes. The genes have been then classified into Gene Ontology (GO) categories (cellular component, biological process, and molecular function) using Ermine J and GOMiner software tools. Analysis of liver proteome identified 1181 liver proteins. We are currently working on creating confident liver protein list and identification of their biochemical and biological characteristics (sub-cellular localization, participation in GO pathways, Mw, pI, Gravy index). In the future, the porcine liver proteome will be compared with human and mouse liver proteomes.

Take Home Message: To our knowledge, this work represents the most comprehensive analysis of the porcine liver transcriptome and proteome today.

Our work is supported by the Advanced Foods and Materials Network.

Evaluation of sperm genomic DNA damage in SMGT by Alkaline Single Cell Gel Electrophoresis (SCGE)

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Background: Sperm mediated gene transfer (SMGT) is a vary promising technique to produce transgenic animals although it is highly controversial due to its low reproducibility. Binding and internalization of foreign DNA into sperm cells has been reported to lead to activation of endogenous nucleases and degradation of sperm endogenous chromosomal DNA. Such genomic DNA damage and eventual death of sperm *in vivo* could be one of the possible reasons for variability in SMGT. The SCGE (Single Cell Gel Electrophoresis) or “Comet assay” is one of the most sensitive techniques which can be used to detect DNA damage in a single sperm cell. Alkaline SCGE (pH > 13) enable the detection of the broadest spectrum of DNA damage and quantification of both single and double strand DNA breaks.

Objectives: The objectives of this study are to evaluate sperm genomic DNA damage induced in SMGT procedure using modified SCGE assay.

Methods and procedures: Modified Alkaline Comet assay was developed to evaluate sperm genomic DNA damage induced during preparation of sperm for SMGT. Sperm was collected from 3 boars and three different treatments for sperm by SMGT procedure were designed: (1) negative: without any treatment, (2) washed in SFM extender and (3) DNA: washed and DNA treatment (0.4 µg linearized pGFP-N1 plasmid /10⁶ sperm cells). Dose response curve was produced using hydrogen peroxide (DNA break inducing agent).

Results

- Modified Comet assay produced reliable and reproducible comets from boar sperm cells in this study showing linear correlation with increased level of DNA damage ($r^2=0.9$, $p<0.05$).
- Sperm genomic DNA damage was increased by 35% by sperm washing procedure ($p<0.05$). No additional effect from DNA incubation was detected

Take Home Messages: Sperm genomic DNA damage level was significantly increased by washing, which is essential procedure for SMGT. Therefore, further study to reduce DNA damage by washing might help to improve reproducibility of SMGT.

Financial support from Ontario Pork, OMAF and NSERC-CRD is appreciated.

Benchmarking the Ontario Pig Industry

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Summary

This study was undertaken to benchmark Ontario's pig production industry and study changes that have taken place since a similar study was undertaken in 1998/1999. A total of 2,199 people participated in the survey out of 2,539 contacted. This is a response rate of 86.6 percent and 82.2 percent of the respondents indicated that they had pigs at the time of the survey. Inventory numbers provided by survey respondents represented just over 2.9 million pigs or 80% of the Statistics Canada July 1 inventory estimate.

Results

The Ontario pig industry is continuing to change. There are fewer farms and they are becoming larger and more specialized over time. Farrow to finish is the most common production system in Ontario and more than one-third of all respondents were farmers older than 50 years of age. Sole proprietorships were the most common business structure (i.e. 43.4% of respondents) but family corporations have become more common with 23 percent of farms reporting this business structure, up from 15% of participants in the survey conducted in 1999. An indication that farm size is increasing is very large farms with more than \$1 million in total sales represented 12.7 percent of respondents and 63 percent of the pig inventory in 2006 compared to 4.8 percent of respondents and 37 percent of inventory in 1999. Nearly 13 percent of respondents reported having more than \$3 million in total farm assets in 2006.

Almost one-quarter of respondents indicated that they have off-farm employment and 43 percent of those that have off-farm employment income reported that their pay is greater than \$35,000 per year before tax and other deductions.

Objectives

- 1) Develop a database of every producer that owns one or more pigs in the province of Ontario. Key information to be captured would include producer demographics such as age, level of education, and business structure. Other data to be gathered would encompass production type, pig inventory, age of facilities, future expansion or contraction plans, and etc..
- 2) Sort and analyse producer information to benchmark changes in production type, farm size, marketing expertise and etc.. Identifying and monitoring these changes is important from a policy setting and issues management perspective.
- 3) Quantify present and future rates of change occurring in producer numbers by farm size, geographic location, and business type.

Summary

The trend to fewer but larger farms is evident in Ontario's pig industry. The proportion of small farms has decreased from 1996 to 2006 while the proportion of large farms has increased during this time frame. Large farms control a growing percentage of Ontario's pig inventory. In the future these large farms will continue to invest in their businesses while small farms will leave the industry.

Comparative evaluation of mathematical functions to describe growth in growing pigs

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Background

Traditionally, growth functions have been used to describe increase in body weight (BW) over time. One of the purposes of generating growth curves is to have the ability to predict accurately time at which pigs will be ready for market. Mathematical modeling has been used to describe many important aspects of inputs and outputs of pork production. Growth functions can be used to determine efficiency of nutrient utilization, which is the derivative of the relationship between BW and cumulative nutrient intake.

Objective

To evaluate 4 candidate mathematical functions for best fit in describing specific datasets on pig growth.

Methods

Two datasets with a total of 1120 observations from 48 pigs were used to conduct growth analysis. All datasets were constructed from independent trials that measured BW, age and intake. Four growth functions representing diminishing returns behavior (monomolecular), sigmoidal with fixed point of inflection (Gompertz) and sigmoidal with variable point of inflection (Richards and von Bertalanffy) were used. Meta-analysis of data was conducted to identify the most appropriate functions for growth and P utilization.

Results

Comparison of Bayesian information criterion values for the growth analysis revealed that Richards equation, perhaps due to the broad limits on its additional parameter, was superior to the other equations. The additional parameter of Richards equation was necessary because the data required a lower point of inflection (138 d) than the Gompertz (189 d) could accommodate, being fixed at $1/e$ times the final weight and found to be a limitation to accurate prediction.

Take home message

Non-linear mixed analysis can give reliable parameter estimates and is a useful tool when analyzing data from multiple studies. Although the Gompertz equation has been used extensively, the Richards equation was superior in describing growth over time and it is suggested for use in data analysis in monogastric animals.

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The effects of compensatory growth on carcass merit and pork quality.

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Background:

Most on-farm feeding systems try to maximize feed intake during the growing and finishing phase. However, Therkildsen et al. (2002) observed improved feed efficiency, protein synthesis, meat quality and tenderness when pigs were limit fed during the growing period.

Objectives:

The project is evaluating the effects of feeding strategy (full versus limit feeding) and gender (gilt versus barrow) on growth performance, feed intake, carcass and meat quality and economic returns.

Experimental Procedures:

One hundred and eight feeder pigs (32.9 ± 3.3 kg) were randomly assigned to eighteen pens with six pigs per pen. A specific gender (gilt or barrow) and feeding strategy was assigned to each pen to provide three replications (pens) of each treatment combination. Control pens were fed a grower diet *ad libitum* until the pigs were marketed at 110 kilograms BW. A second group of pigs (R₈₅) were limited to 85% of control feed intake until 60 kg followed by *ad libitum* feeding until market while the third group (R₇₀) was limited to 70% of control intake during the growing phase.

Results to date:

1. Compensatory gain ($P < 0.0001$) was observed during the finishing period (> 60 kg) when limit feeding was practiced during the growing phase for R₇₀ pigs (versus control) resulting in an improved F/G (2.6 vs. 2.4; SE=0.03; $P = 0.0001$).
2. Control fed pigs (FF) had an increased yield index ($P < 0.03$) while muscle depth was increased for FF versus R₇₀ (63.0 vs. 59.9 mm; SE= 1.0; $P = 0.04$).
3. Loin colour, pH, and loin eye areas were similar ($P > 0.05$) for each dietary treatment with increased loin tenderness for pigs limit fed in the growing period [4.7 (FF), 4.2 (R₈₅) and 4.2 (R₇₀); SE=0.17; $P < 0.05$].

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Dried distillers grains with solubles for finishing pigs

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Background:

An increased output of Dried Distillers Grains with Solubles (DDGS) is expected for North American livestock production. However, very little research has been completed in Ontario using product manufactured by GreenField Ethanol from their Chatham plant.

Objective

The project evaluated the effects of feeding Chatham DDGS (10 and 20 percent of diet) on pig growth rate, feed intake, economic returns and carcass quality.

Experimental Procedures:

After a three week adjustment period, ninety-six pigs (48.8 ± 5.2 kg) began the trial on February 14th, 2005. Each pen (3 barrows and 3 gilts) was randomly assigned to one of the four grower diets until they were 70 kilograms body weight (BW). They were then fed an assigned finisher diet until they were marketed (≥ 110 kg BW) by pen. The following dietary treatments were formulated and fed:

1. Grain corn, SBM (control diets) and premix. A grower diet [17% CP (0.8% lysine)] was fed until the pigs were 70 kg followed by a finisher diet [14% CP (0.6% lysine)] until they were marketed.
2. Similar diets and feeding strategy to control group. However a 10 percent inclusion of DDGS + crystalline lysine was added to produce diets with similar lysine content.
3. Similar diets and feeding strategy to control group. However a 20 percent inclusion of DDGS + lysine was added to produce diets with similar lysine content.
4. Similar crude protein levels to control diets. However a 10% inclusion rate of DDGS was added with no additional lysine supplementation to produce diets with reduced lysine content [0.7% (grower diet) & 0.5% (finisher diet)].

Results and take home message:

- Similar growth rate, feed intake and efficiency and gain costs were observed for each dietary treatment (0, 10 and 20 percent DDGS).
- Since feed efficiencies were similar, costs of gain were strongly related to ingredient costs.

Acknowledgments:

The authors would like to thank the Innovation and Risk Management Branch (OMAFRA), GreenField Ethanol, and OMAFRA for their financial and technical assistance. Support and technical input from each research team member was also greatly appreciated.

Effect of phytase supplementation on growth rate and bone characteristics in newly-weaned pigs that are liquid fed high-moisture corn based diets

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Background: Largely because of environmental concerns strategies to improve phosphorus utilization by pigs should be explored. It is thought that the use of enzymes to release phytate-bound phosphorus in corn is more effective in liquid feeding than in dry feeding systems. A starter pig performance study was conducted to explore the application of phytase in liquid feeding of high-moisture corn based diets to pigs.

Experimental procedure: A total of 384 Yorkshire pigs were weaned at 21 days of age and 5.8 kg, and pens of 16 pigs were assigned to one of four different three phase feeding programs. The high-moisture corn based feeding programs were formulated to vary in total phosphorus content (low, medium and high phosphorus), while phytase was added to the low phosphorus diet only (low +enz). Phase II diets were prepared by blending the phase I and III diets 50/50, and pigs were fed using the Big Dutchman Hydrojet™ liquid feeding system. Pig growth performance was monitored over a 6 week period. At the end of the experiment a sub-sample of pigs was sacrificed to evaluate breaking strength and ash content of the metatarsal bones.

Results: Effects of dietary phosphorus level on growth performance and bone characteristics of newly weaned piglets fed high-moisture corn based diets.

	Treatment (dietary phosphorus level)				SEM (n=6)	Probability		
	High	Medium	Low	Low +enz		Linear	Low vs Low+enz	High vs Low
Analyzed diet phosphorus content (% in diet based on 88% dry matter, Phase I/III diet)								
	0.70/ 0.64	0.69/ 0.62	0.65/ 0.54	0.68/ 0.55				
Gain, g/pig/d								
Day 0 to 7	41	32	38	49	14.0	0.91	0.61	0.91
Day 7 to 21	264	242	244	294	18.7	0.48	0.07	0.48
Day 0 to 42	364	352	351	377	14.1	0.55	0.22	0.55
Gain: Feed dry matter, g/g								
Day 0 to 42	0.63	0.65	0.66	0.68	0.02	0.47	0.55	0.47
Bone breaking								
strength, kg	36.57	37.21	33.31	40.27	1.21	0.08	<0.01	0.08
Ash content, g	2.03	2.02	1.92	2.09	0.04	0.06	<0.01	0.06

Take home message: Good starter pig performance was achieved when starter pigs were liquid-fed high-moisture corn based diets that contained as low as 0.68 and 0.55 % phosphorus in the phase I and III diets (typical 88% dry matter basis). The addition of phytase to the low phosphorus diet did not improve growth performance but improved bone characteristics.

Acknowledgement: Financial support was provided by a large number of organizations (www.slfa.ca).

Liquid feeding of newly-weaned piglets and use of whey permeate

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Background: Liquid feeding represents a means to reduce post-weaning growth lag, reduce the reliance on in-feed antibiotics and to use inexpensive co-products from the food or bio-fuel industry. In practice liquid feeding of newly weaned pigs is a challenge, balancing maximizing feed intake with maintaining freshness and homogeneity of the liquid diet.

Experimental procedure: In a starter pig study and based on a three phase feeding program, we compared (1) a conventional dry feeding program, (2) liquid feeding the conventional dry feeds, and (3) liquid feeding where all whey was removed from the dry feed and replaced with liquid whey permeate. Liquid whey permeate contained 35% dry matter and 4.8% protein within dry matter. Whey protein was substituted with a combination of herring meal and plasma protein in the phase I diet. In phase II and III diets, the use of whey permeate was gradually reduced or maintained at 20% of feed dry matter. Eight pens with 14 to 16 newly-weaned piglets were assigned to each treatment. The Big Dutchman Hydrojet systemTM was used for liquid feeding.

Results: Growth performance of newly-weaned piglets*.

	Dietary Treatment				SEM	P
	Control (dry)	Liquid	Whey permeate			
			20/10/0 %	20 %		
Initial body weight (kg)	5.76	5.76	5.87	5.67		
Gain (g/d/pig)						
Day 0 to 7	100	94		88	6.3	0.476
Day 7 to 14	201 ^A	146 ^B	189 ^{AB}	155 ^{AB}	13.4	0.075
Day 14 to 21	323	281	267	310	15.7	0.286
Day 21 to 28	537 ^A	403 ^B	319 ^B	537 ^A	19.0	0.001
Day 28 to 42	623	531	550	613	33.7	0.308
Day 0 to 42	406 ^A	334 ^B	351 ^{AB}	378 ^{AB}	15.7	0.047
Gain : Feed dry matter usage (g/g)						
Day 0 to 42	0.722	0.663	0.674	0.713	0.035	0.680

*Diets did not contain any growth promoting agents such as antibiotics, high copper and zinc or acids; Values followed by different superscripts differ (P<0.05).

Take home message: Largely because of feeding intake restriction, liquid fed newly-weaned piglets did not perform as well when compared to conventional dry feeding. Liquid whey permeate can replace expensive dry whey and enhances starter pig performance during phase II and III.

Acknowledgement: Technical support was provided by Arkell swine staff. Financial support was provided by a large number of organizations (www.slfa.ca).

Generating lactic acid by fermenting a mix of high-moisture corn and water

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Background: Blends of organic acid and inorganic acids are routinely added to starter pig diets to reduce reliance on in-feed antibiotics and to improve gut health of pigs. Lactic acid is one of the key acids to which gut health and performance benefits can be attributed. High costs generally limit the extensive use lactic acid in pig diets. However, lactic acid may be generated via controlled fermentation of liquid diets or feed ingredients. Laboratory based fermentation studies were conducted to explore the inoculation of high-moisture corn with commercially available lactic acid generating bacteria.

Experimental procedure: A simple feed fermentation system was developed previously to evaluate the impact of different fermentation conditions on changes in nutrient profiles and micro-biology (pro-biotics and pathogens). In this study 200 g samples of stored high-moisture corn (75% dry matter) were mixed with water in a 2 to 1 ratio and placed in square bottles. Individual samples were inoculated at a rate of 10^7 cfu/g of high-moisture-corn with either *Pediococcus acidilactici* (Bactocell; Lallemond, UK) or *Lactobacillus acidophilus* (Chris Hanssen Laboratories, USA), a non-inoculated sample served as a control, placed in the micro-fermentation unit at 25 °C, and agitated continuously. There were three replications per treatment.

Results: Appearance of lactic acid in samples of high-moisture corn that were not inoculated (control) or inoculated with either *Lactobacillus acidophilus* or *Pediococcus acidilactici*.

Take home message: Stored high-moisture corn, when mixed with water in a 2 to 1 ratio initially contains approximately 15 mM lactic acid, which is below the apparent threshold level to control feed pathogens and benefit pigs (75 mM). Simply steeping high-moisture corn mixed with water for about 36 h at 25 °C will increased the lactic acid content to this threshold level, but a faster increase is achieved when inoculated with certain strains of lactic acid producing bacteria.

Acknowledgement: Financial support was provided by a large number of organizations (www.slfa.ca).

Use of corn steep water for liquid feeding of growing-finishing pigs

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Background: Given the increased demand for corn for bio-fuel the cost of feed energy will increase. Corn steep water is a liquid co-product from the starch and syrup industry, has a pH of 4.3 and contains 45% dry matter. On a dry matter basis the product typically contains 50% crude protein, 2% lysine, 20% lactic acid, 18.0% ash, 4.8% potassium and 3.3% phosphorus. Approximately 80% of phosphorus is tied up in phytate. The use of corn steep water for liquid-fed finishing pigs was explored.

Experimental procedure: A batch of corn steep water was treated with a microbial phytase at source (CASCO, London, Ontario) to release phytate bound phosphorus. Based on analyses of total and soluble phosphorus content it was confirmed that most of the phytate had been degraded. This batch had also been allowed to ferment, to reduce the soluble sugar content, prior to feeding. In a finishing pig study, four dietary inclusion levels of corn steep water were evaluated. The Big Dutchman Hydrojet systemTM was used for liquid feeding. At the final body weight and in a sub-sample of pigs, carcass and meat quality was evaluated in detail.

Results: Growth performance of finishing pigs, carcass and meat quality traits*.

	Treatment (level of corn steep water in diet)				SEM*	Linear ¹	Quadratic ¹
	0%	7.5%	15%	22.5%			
Gain, kg/day	1,191 ^a	1,080 ^a	1,063 ^a	899 ^b	29.30	0.0002	0.4495
Feed intake, kg/day	2,759 ^a	2,491 ^{ab}	2,584 ^{ab}	2,293 ^b	75.37	0.0081	0.8681
Feed:gain	2.33 ^a	2.30 ^a	2.42 ^{ab}	2.55 ^b	0.05	0.0020	0.1466
Dressing %	80.44	81.17	80.90	81.63	0.41	0.10	1.00
Estimated carcass lean yield, %	60.3	60.3	60.5	60.1	0.47	0.90	0.63
Loin pH, 24 h	5.56	5.57	5.52	5.52	0.03	0.19	0.82
Loin drip loss, %	11.60 ^a	10.35 ^{ab}	9.04 ^b	9.61 ^{ab}	0.64	0.02	0.18

* Initial and final body weights were 70 and 108 kg, respectively; 4 pens of eight pigs per treatment.

¹ Probability of linear and quadratic effect of dietary inclusion levels of CSW; typically, a P value of less than 0.05 is considered significant.

^{a,b} Values followed by different superscripts differ (P<.05).

Take home message: Phytase treated corn steep water can be used effectively in finishing pig diets, provided that ingredient costs off-set the slight changes in feed efficiency and body weight gain, especially when the product is included at levels that exceed 15% of diet dry matter content. Feeding corn steep water to finishing reduces drip losses from loin cuts.

Acknowledgement: Technical support was provided by staff at Arkell and in the meats laboratory. Financial support was provided by a large number of organizations (www.slfa.ca).

Effect of immune system stimulation and dietary methionine plus cysteine intake on protein deposition and digestibility in growing pigs

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Background: Immune system stimulation (ISS) can result in substantial reductions in animal productivity. Previous reports have suggested additional requirements for the sulfur containing amino acids (SAA), methionine or cysteine, during ISS for synthesis of metabolites that have important roles in the animal's immune response, such as glutathione. Our objectives were to determine the impact of ISS on body protein gain, protein and amino acid digestibility, and to explore whether additional dietary SAA supply can reduce the negative impact of ISS on protein gain in growing pigs.

Experimental procedure: Twenty four Yorkshire barrows (23 kg body weight) were fed restricted (850 g/d), and exposed to either low (3.6 g/d) or medium (4.7 g/d) dietary intakes of SAA. Diets were formulated to be first limiting in SAA and fed for nine days prior to N-balance measurements. Following a first 5-day N-balance period (**pre ISS**), half of the pigs at each dietary SAA levels were injected intramuscularly with either saline or increasing amounts of *Escherichia coli* lipopolysaccharide (LPS, serotype 55:B5) every 48 h and over at least a 5 day period. A second 3-day N-balance (**during ISS**) was conducted after the start of LPS or saline injections. At the end of the second N-balance period, pigs were weighed and euthanized for sampling of liver tissue and measurement of ileal protein and amino acid digestibility.

Results: Impact of immune system stimulation (ISS) and intake of methionine plus cysteine (SAA) on apparent digestibility of crude protein (CP) and body protein deposition (PD).

SAA intake	Low (3.6 g/d)		Medium (4.7 g/d)		SEM	P values		
ISS	-	+	-	+		ISS	SAA	ISS × SAA
Liver weight, % of BW								
During ISS ¹	2.3	2.7	2.4	2.7	0.05	0.01	0.67	0.82
Fecal crude protein digestibility, %								
Pre ISS ¹	88.0		87.5		0.43	NA ²	0.3	NA
During ISS ¹	88.6	87.8	88.8	88.7	0.72	0.5	0.5	0.62
Ileal crude protein digestibility, %								
During ISS	78.7	78.0	74.0	69.4	3.5	0.44	0.02	0.60
Whole body protein deposition, g/d (N retention x 6.26)								
Pre ISS	83.2		95.9		1.75	NA	0.003	NA
During ISS	89.4	73.0	95.2	85.1	1.37	0.001	0.27	0.50

¹ Before (Pre ISS) or during immune system stimulation (during ISS) with a repeated and increasing dose of injected LPS. ² Not applicable.

Take home message: Immune system stimulation *per se* does not affect apparent ileal and fecal digestibility of crude protein in growing pigs. This study provides evidence that additional dietary intake of methionine plus cysteine can reduce the adverse effects of immune system stimulation on whole body protein deposition in growing pigs, and probably accelerates the recovery.

Acknowledgement: Financial support was provided Ontario Pork, OMAFRA, and Degussa AG.

Intake of fermentable fiber and body protein deposition in pigs fed methionine or tryptophan limiting diets

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Background: Due to increased feed energy costs the use of fibrous co-products from the food and bio-fuel industry will increase. In previous studies we have shown the feeding additional fermentable fiber increases the dietary threonine requirements of pigs, but not the dietary lysine requirements. In this study we explored the impact of feeding fermentable fiber on utilization of methionine and tryptophan; these essential amino acids are the generally second to fourth limiting amino acids in corn and soybean meal based pig grower diets.

Experimental procedure: Two nitrogen-balance experiments were conducted to determine the impact of dietary pectin (a source of purified fermentable fiber) level and dietary cellulose (a source of non-fermentable fiber) on whole body protein deposition in pigs fed cornstarch and soybean meal-based diets that were first limiting in either methionine (exp. 1) or tryptophan (exp. 2). At least 7 observations were made per treatment. The efficiency of utilizing standardized ileal digestible intake of these amino acids for whole body protein deposition was calculated based on procedures that have been outlined previously (Zhu et al., 2005).

Results: Efficiency of using ileal digestible methionine or tryptophan intake for body protein deposition in growing pigs fed soybean meal and cornstarch-based diets that are limiting in either methionine or tryptophan with added pectin or cellulose.

Item	Dietary treatments					SEM	Probability ¹		
	Added dietary pectin				Cellulose		Cello-lose	L	Q
	0%	4%	8%	12%					
					8%				
Methionine intake ² , g/d	1.95	1.94	1.95	1.88	1.88	0.02	<0.01	0.02	0.17
Protin gain ³ , g/d	95.7	90.5	89.2	84.0	89.0	2.63	0.09	0.01	0.99
K _{methionine} ⁴ , %	93.6	87.1	85.7	84.2	91.2	3.02	0.58	0.04	0.46
Tryptophan intake ² , g/d	1.55	1.56	1.50	1.40	1.51	0.01	0.06	<0.01	<0.01
Protein gain ³ , g/d	89.9	89.3	94.0	88.8	82.9	2.85	0.14	0.92	0.47
K _{tryptophan} ⁴ , %	65.0	63.6	72.7	70.9	62.3	2.96	0.57	0.08	0.95

¹8% cellulose versus 0% pectin diet (Cellulose), linear (L) and quadratic (Q) effects of dietary pectin level.

²Standardized ileal digestible intake.

³Whole body protein deposition (N retention x 6.25).

⁴Efficiency of using standardized ileal digestible AA intake above maintenance requirements for PD.

Take home message: Feeding additional fermentable fiber to pigs increases the dietary requirements for methionine, or methionine plus cysteine, and appears to reduce the dietary requirements of tryptophan. The latter may be attributed to the net supply of tryptophan by enteric microbes. The impact of enteric fermentation on amino acid utilization in pigs should be explored further.

Acknowledgement: Financial support was provided OMAFRA, NSERC and Degussa AG.

Intake of fermentable fiber stimulates mucin and mucosal protein synthesis in the pig colon

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Background: In a previous study, a reduced efficiency of using ileal digestible threonine intake for protein deposition was observed in growing pigs fed additional fermentable fiber. This reduced efficiency was not attributed to fiber-induced increase in endogenous protein loss in the upper gut. It was hypothesized that the synthesis of mucosal proteins, especially the threonine-rich mucins, in the hindgut of pigs is increased with dietary inclusion of fermentable fiber. An isotope tracer study was conducted to determine the impact of feeding additional fermentable fiber on mucin and mucosal protein synthesis in the upper and lower gut of growing pigs.

Experimental procedure: Twelve Yorkshire barrows (21.0 kg) were surgically fitted with catheters in jugular veins, and were given either a cornstarch and soybean meal-based diet (**Control**) or the control diet with 12% additional pectin (**Pectin**). Diets were fed for 10 days prior to administration of a flooding dose of valine (40% mol %; 1.5 nmol/kg BW) to measure fractional synthesis rates (**FSR**; %/d) of mucin and mucosal proteins in the jejunum and colon. Pure mucosal samples were obtained by gently scraping the surface of previously washed jejunum and colon tissues using a microscope slide. Mucins were purified from mucosal samples. Total mucosal mass and protein content were estimated from mucosal scrapings and used to calculate the absolute synthesis rates (**ASR**; g/d) of mucosal proteins.

Results: Fractional (FSR) and absolute synthesis rates (ASR) of mucin and mucosal proteins in the jejunum (upper gut) and colon (hindgut) of growing pigs fed diets without (Control) or with additional fermentable fiber (Pectin)¹.

	Control		Pectin		<i>P</i> value
	mean	SE	mean	SE	
<u>Mucin Protein</u>					
Jejunum (FSR, %/d)	135.3	8.8	143.1	29.0	0.807
Colon (FSR, %/d)	108.5	4.8	127.7	8.1	0.069
<u>Mucosal protein</u>					
Jejunum (FSR, %/d)	79.6	3.7	85.2	15.9	0.745
(ASR, g/d)	1.13	0.15	1.43	0.17	0.239
Colon (FSR, %/d)	65.8	4.7	83.5	4.6	0.025
(ASR, g/d)	0.16	0.02	0.21	0.01	0.051

¹ Enrichment of tissue free valine was used to estimate enrichment at the site of protein synthesis.

Take home message: Feeding additional fermentable fiber (12% pectin) to pigs increases the fractional synthesis rate of mucin and mucosal proteins in the hindgut, but not in the upper gut. The absolute mucosal protein synthesis rate in the hindgut was also increased with pectin feeding. The observed increase in mucin and mucosal protein synthesis contributes to the increased dietary threonine requirements of growing pigs when feeding additional fermentable fiber.

Acknowledgement: Financial support was provided NSERC, OMAFRA, and Degussa AG.

Sources of nitrogen for pig gut microbes: effect of feeding fermentable fiber

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Background: Pigs are capable of absorbing amino acids synthesized by microbes in the upper gut. Whether microbes make a net contribution to the amino acid supply of the pig depends on what sources of nitrogen (dietary protein, endogenous gut protein, ammonia) are used to synthesize microbial protein, and the metabolic costs associated with carriage of gut microbes. In addition, sources of nitrogen (dietary protein, endogenous gut protein, endogenous urea) for production of ammonia (NH₃) that appears in the gut through fermentation should be considered. An isotope tracer study was conducted to estimate the relative contribution of different nitrogen sources to microbial protein synthesis and NH₃ production in the upper gut of growing pigs.

Experimental procedure: Eight barrows were fitted with T-cannulas at the distal ileum and catheters in the jugular veins, and were assigned to either a cornstarch and soybean meal-based diet (**Control**) or the control diet with 12% pectin (**Pectin**). Pigs were adapted to diets prior to a 4-d continuous intravenous infusion of a saline solution containing L-1-¹³C valine and ¹⁵N₂ urea. Microbes were isolated from ileal digesta. Relative contributions of urea, NH₃, and endogenous valine to microbial valine at the ileum were estimated by relating enrichment of microbial valine (¹³C or ¹⁵N) to enrichment of plasma urea, digesta NH₃ or plasma valine, respectively. The relative contribution of dietary valine to microbial valine was estimated as the difference between unity and the sum of the relative contributions of NH₃ and endogenous valine. The proportion of digesta NH₃ produced by microbial fermentation of protein was estimated as the difference between unity and the relative contribution of urea to digesta NH₃, based on ¹⁵N enrichment.

Results: Relative contributions (%) of various sources of nitrogen to microbial valine at the distal ileum of pigs fed the control diet (Control) or control with added Pectin.

	Control (n=3)	Pectin (n=4)	SD	P value
Ammonia	3.2	7.2	1.4	< 0.05
Urea	0.8	1.4	0.3	< 0.10
Dietary + endogenous	2.4	5.9	1.3	< 0.05
Pre-formed valine	96.8	92.8	1.4	< 0.05
Endogenous	27.8	32.7	3.1	0.10
Dietary	69.0	60.0	3.9	< 0.05

Take home message: Microbial protein in the upper gut of pigs is synthesized mainly from amino acids that are derived directly from dietary and endogenous protein. A large proportion of NH₃ in ileal digesta is produced via microbial fermentation of protein. These amino acid losses should be quantified and considered when estimating the available amino supply for pigs. These findings have implications for estimates of amino acid requirements of humans as well.

Acknowledgment: Financial support was provided NSERC, OMAFRA, and Degussa AG.

Evaluation of partly hydrolyzed soy protein for newly weaned piglets

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Background: With recent concerns about the use of animal products in animal feeds, alternative protein sources should be explored. This applies in particular to newly weaned piglets that have limited digestive capacity, poorly developed immune systems, and are sensitive to dietary anti-nutritional factors (anti-trypsin, some types of lectins, allergenic proteins). A promising product is partly hydrolyzed and purified soy protein (**HPS**). This product was evaluated in a starter pig performance study.

Experimental procedure: Pigs were weaned at 16 to 19 days of age (mean body weight 6.52 kg) and exposed to one of 4 treatments: (1) 4% HPS, (2) 2% HPS, (3) 6% soy protein concentrate (64% crude protein), (3) 4% blood plasma (AP920, 78% crude protein). Diets were free of medication and acidifiers. Pigs were fed these diets during the first 2 weeks post-weaning (Phase I) and then fed a common pig starter diet for another 3 weeks (Phase II) to evaluate carry-over effects. Diets were formulated to be similar in estimated available lysine content and to exceed established requirements for essential nutrients (NRC, 1998). There were six pens of six piglets per treatment.

Results: Growth performance of piglets during the first 5 weeks post-weaning.

	Dietary treatment				SE	P value
	4% HPS	2% HPS	Plasma	Soy Conc.		
Gain, g/pig/day						
Weeks 1+2	169.8 ^b	162.5 ^b	205.5 ^a	176.4 ^{ab}	9.60	0.01
Weeks 3+4+5	485.5	482.0	476.3	482.3	16.5	0.98
Overall	359.4	354.2	373.1	361.7	11.9	0.73
Feed intake, kg/pig/day						
Weeks 1+2	0.226	0.218	0.235	0.217	0.01	0.72
Weeks 3+4+5	0.775	0.761	0.773	0.761	0.02	0.93
Overall	0.560	0.543	0.558	0.543	0.013	0.82
Gain:Feed						
Overall	0.65	0.65	0.65	0.67	0.014	0.79

^{a,b} Values followed by different superscripts differ (P<0.05).

Take home message: Replacing blood plasma with either soy protein concentrate or partly hydrolyzed and purified soy proteins slightly reduced growth rate during the first two weeks after weaning in early weaned piglets. However, growth rate thereafter was not influenced by dietary treatment.

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