THE 12TH MIKE WILSON SWINE RESEARCH DAY

JUNE 3, 2015

9:30 AM – 3:30 PM

Arboretum Center, University of Guelph

UNIVERSITY of GUELPH

ONTARIO PORK

Ontario

The 12th Annual Mike Wilson Swine Research Day

June 3, 2015
9:30 AM – 3:30 PM
Arboretum Centre, University of Guelph

Morning session (Chaired by Bob Friendship)

10:00 Tim Nelson - Keynote: Perspective on future swine research and LRICs role in determining priorities

10:45 Juliana Ferreira - Swine influenza

11:00 Lee-Anne Huber - Effect of dietary amino acid imbalance on lysine utilization in lactating sows

11:15 Emma Allen-Vercoe - Management of the gut microbiota to promote swine health

11:30 Amanda Kubik - Anemia in pigs after weaning

11:45 Peter Park - Non-nutritive additives in grower-finisher diets to control boar taint

Lunch and poster session

Afternoon Session (Chaired by Kees deLange)

1:15 Dan Hurnik - Keynote: Pig movement and traceability

1:45 Kristen Alves - Lifetime genetic evaluation of piglet growth - birth to market weight

2:00 Josep Gasa - The relevance of the Iberian pig in Spanish pig production

2:15 Longfeng Weng - An economic evaluation of elimination strategies for Porcine Epidemic Diarrhea

2:30 Krysia Walczak - Swine dysentery pattern based on drug use data

2:45 Ron Johnson - Analgesics mixed with iron to make compliance with code of practice easier

3:00 Tamas Revay - Copy number variations in high and low fertility breeding boars

Wrap-up, prizes for top posters

TABLE OF CONTENTS

Oral Presentations

Abstracts of Posters for competition

Additional Abstracts

Perspective on future swine research and LRICs role in determining priorities

Tim Nelson
CEO Livestock Research & Innovation Corporation (LRIC)

The issue for future swine research, actually all livestock research, is how to keep ahead of the demands of society, industry and scientific rigour when the pace of change has increased so dramatically and will continue to increase even more dramatically probably exponentially, over the next 20-30 years? This was not always the case. Livestock research used to be aimed at increasing productivity by keeping animals healthy, feeding them as closely as possible to meet their nutritional needs at different stages of growth in order to maximize performance without waste and making sure that, in the case of swine, sows were pumping out healthy piglets as often as possible.

The fact that genetics has placed us on the cusp of being able to absolutely predict the performance of an individual animal has sped up breeding programs to a point that was unimaginable just10 years ago.
Who could have foreseen the enduring productivity damage corona viruses such as Porcine Respiratory Corona Virus Infection (PRCV) and Transmissible Gastro Enteritis, (TGE) could do and in the 80's when a new virus Porcine Reproductive and Respiratory Syndrome virus (PRRSv) first appeared, who would have thought that in 2015 it would still remain somewhat of a mystery. And who could have foreseen speed and the devastation that Porcine Epidemic Diarrhea virus (PEDv) would wreak and is still wreaking across N. America and African Swine Fever (ASF) across Europe.

Just 10 years ago who would have predicted the speed at which the marketplace can force changes to production systems that we have previously scientifically validated as having triple bottom line outcomes; good for the environment, good for productivity (including animal welfare) and good for society as a whole.
The answer is nobody can predict these things. So the future of swine research lies in forecasting, to the best of our ability, using our experience and knowledge of what's been developed and what is being developed to combat, what the 'experts' in their various fields and disciplines can subjectively argue, will challenge the industry.

All living systems rely on 3 seemingly simple objectives; stay healthy, get adequate nutrition and reproduce. Swine research is therefore very focused on these. For each of these objectives there are many real world current and future challenges that will direct our research efforts. And, there are a burgeoning number of new technologies, techniques and management systems that will help refine and more accurately target faster more flexible research efforts and facilitate bringing research into practice more quickly in an attempt to keep up with the pace of change.
If we are to have insight into the future of swine research we need to ask ourselves two fundamental questions;

- Who are we doing the research for? and,
- Why are we doing it?

If we can honestly answer these questions we have half a chance of predicting what research will look like in the next 20 years. The LRIC is engaged in trying to answer this question in a number of ways which will be discussed during the presentation.

LRIC is a not for profit organization supported by; Ontario Pork, Dairy Farmers of Ontario, Beef Farmers of Ontario and the Poultry Industry Council. LRIC also receives funding through a Growing Forward Transfer Payment from OMAFRA.

Dynamics of influenza virus transmission in a swine herd and analysis of risk factors for recurrent infections

Ferreira JB[a], Grgić H[a], Friendship R[a], Wideman G[b], Nagy È[c], Poljak Z[a].

[a]Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada; [b]South-West Veterinary Services, Stratford, Ontario; [c]Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada. Email: ferreirj@uogueph.ca

Background: Swine influenza outbreaks are usually recognized by the sudden appearance of respiratory signs and also by quick recovery of sick animals. Results from different studies show that this classical pattern has no longer been observed; suggesting that circulation of influenza virus could be more complex in some populations. The complexity of influenza circulation in large multi-site and multi-source herds has not been well described. For that reason, the objectives of this study are to describe the dynamics of influenza virus circulation in multi-source nursery herds and identify risk factors for recurrent infection.

Methodology: The nursery barn included in the study was a ~2200-head operated on an all-in/all-out basis. Pigs from 5 different sow herds, each with a different health status, were mixed in 4 rooms (each with 24 pens). In the first 2 hours of arrival at the nursery barn, 400 pigs were selected for the initial virological testing. Additionally, 81 and 75 pigs were included in the longitudinal study for ongoing weekly testing for influenza virus, respectively for study 1 and 2 in two different periods. Virus isolation and propagation were done in Madin-Darby canine kidney (MDCK) cells. Serology was performed by hemagglutination inhibition (HI) using 6 different influenza viruses. Risk factor analysis for virological positivity and likelihood of recurrent infection was conducted using logistic regression.

Results: No pig tested positive for influenza virus at the first sampling on trial 1. At ~30 days post weaning pigs were positive and shedding viruses, with 53% being positive more than once. A different pattern was observed on trial 2 with 48% of pigs being positive and only 16% of pigs being positive more than once. There was a significant difference in positivity of pigs among the sow sources on both trials ($p<0.05$). Also, on trial 1 likelihood of recurrent infection was higher in pigs with higher titers against heterologous viruses ($p<0.05$). Hierarchical cluster analysis conducted on HI titers against 3 H3N2 viruses grouped pigs into 2 distinct clusters. Pigs in cluster 2 were more likely to have recurrent infection, but not statistically significant ($p>0.05$).

Conclusions: Results from these studies indicate that influenza virus can circulate during the nursery phase in a cyclical pattern, against the rule that disease would follow a regular outbreak pattern. Possible explanations would be the circulation of more than one strain, or reinfection with the same virus strain in a different period, due to waning of maternal immunity, or a combination of factors. Furthermore, the likelihood of recurrent infection was higher for pigs with higher level of heterologous (within-subtype) maternal immunity, which could also explain ongoing issues in the nursery phase of production. Also, the non-isolation of any influenza virus, on the first sampling, does not let us conclude where the virus came from. Those findings will be useful in developing control strategies.

Acknowledgements: Agriculture and Agri-food Canada, Ontario Pork, OMAFRA, Swine Innovation Porc, Ontario Veterinary College

The effect of dietary amino acid (AA) imbalance on lysine utilization in lactating sows

L Huber*[1], CFM de Lange[1], U Krogh[2], D Chamberlin,[3] and NL Trottier[3]

[1]Dep. Animal and Poultry Science, University of Guelph, Guelph, ON, N1G 2W1; [2] Dep. Animal Science, Aarhus University, Foulum, Denmark; [3] Dep. Animal Science, Michigan State University, East Lansing, MI, 48824

Background: The use of crystalline AA (**CAA**) provides the opportunity to meet the AA requirements and adjust AA profiles in swine diets while lowering dietary crude protein (**CP**) concentration; this will reduce catabolism of AA that are supplied in excess of dietary requirements as well as excretion of nitrogen (**N**) products into the environment. There is evidence that AA transporters in the mammary gland may be more sensitive to AA imbalance than those in the gastrointestinal tract of growing pigs. The objective of this study was to determine N and Lysine (**Lys**) utilization for milk production in sows fed diets containing varying concentrations of CP and different levels of CAA to meet requirements for limiting AA.

Methodology: Forty lactating multiparous Yorkshire sows were assigned to 1 of 4 diets: [1] 16.0% CP (as-fed; analyzed contents; **HCP**); [2] 15.7% CP (**MHCP**); [3] 14.3% CP (**MLCP**); [4] 13.2% CP (**LCP**); diet HCP was formulated using soybean meal and corn as the only Lys sources. The reduced CP diets contained CAA to meet requirements of the limiting AA. Sow and piglet BW were measured on d 1, 3, 7, 14, 18 and 21 of lactation and N retention was measured on sows between d 14 and 18 (peak) of lactation. Milk true protein output was calculated from estimated milk yield and analyzed true protein concentration. N and Lys utilization was expressed several ways, including the efficiency of using retained N for true milk protein.

Results: N intake decreased as dietary CP decreased (Linear (**L**): $P < 0.05$), from 169.5 for HCP to 145.1 g/d for LCP. Litter growth rate over the 21-d lactation period tended to increase with decreasing dietary CP (L: $P = 0.084$). N retention (intake – feces and urine) decreased with decreasing diet CP (L: $P < 0.05$): 122.5, 123.8, 121.2, and 109.0 ± 4.88 g/d for HCP, MHCP, MLCP, and LCP, respectively. The estimated efficiency of using retained N for milk N output increased with lowering diet CP (L: $P < 0.05$): 44.5, 51.0, 54.9, and 62.9 ± 5.9 % for HCP, MHCP, MLCP, and LCP, respectively. Lys utilization efficiency was greater in sows fed MHCP than sows fed HCP diets ($P < 0.05$), with no additional improvement with further reductions in CP ($P < 0.05$; 59.8, 68.4, 65.4, 67.6 ± 2.9 % for HCP, MHCP, MLCP, and LCP, respectively).

Benefits to the swine industry: The current findings indicate that the efficiency of using retained N for milk protein production, estimated mammary milk protein production, and litter growth rate increase when dietary CP is lowered. Therefore, feeding diets with reduced CP and improved AA balance is a feasible means to reduce N excretion from lactating sows into the environment and improve both N and Lys utilization efficiency for milk production.

Acknowledgements: The researchers acknowledge financial support form: National Pork Board, Ontario Pork, Royal De Heus, Heartland Lys Inc./Ajinomoto, and OMAFRA and technical support from the Michigan State University Swine Teaching and Research Center.

Management of the gut microbiota to promote health; is there a role in swine?

Emma Allen-Vercoe
eav@uoguelph.ca

Background: Currently, using antimicrobials for growth promotion in farm animals is coming under strong scrutiny in Canada and US, for the most part because of the concurrent increase in antimicrobial resistance. A second, less appreciated issue related to overuse of antimicrobials, however, is the collateral damage that is done to the host animal's microbiota (the collection of microbes living on and in the animal's body). In humans, we now understand that such collateral damage may contribute to a range of acute infections and chronic diseases. This is because, as we are now starting to recognize, the microbiota, particularly that of the gut, contains a microbial ecosystem that plays very important roles in host immunity, resistance to infection, and metabolism. The innovation we plan to bring forward, and which I will speak about, is the production of an ecosystem probiotic tailored to the swine GI tract.

Methodology: Since it is now clear that the gut microbiota of mammals plays a central role in several animal health metrics of concern to farmers, for example weight gain, response to antibiotics and resistance against pathogens, we hypothesize that a cultured microbial ecosystem product from a pig selected for its optimal health and rate of weight gain will impart these same desirable qualities onto piglets when administered to farrowing sows, even when the piglets are raised in an intensively reared farm environment. Such a product leverages our capability to develop and deliver a therapeutic microbial product that contains multiple strains of bacteria in a functioning ecosystem; we have already successfully used this concept in human medicine to treat recurrent *Clostridium difficile* infection. A key benefit of the proposed innovation is that, unlike a probiotic, the cultured ecosystem product will need to be administered only transiently, since unlike a probiotic it will be able to colonize and proliferate inside the gut. We expect that, through incorporation of microbes that promote immune system development, treatment with our product should increase the effectiveness of vaccination in the animals. By incorporating into animal feed selected prebiotic substrates that stimulate ecosystem microbes to produce beneficial metabolites such as butyrate, we also expect that our product will promote animal health. Since weight gain in humans has now been unequivocally linked to gut microbiota diversity and structure, and since human and porcine gut microbiota compositions are similar, we also hope to be able to influence animal weight gain through administration of our product, negating the need for antimicrobial growth promoting strategies.

Benefits to the swine industry: If our porcine microbial ecosystem product is successful the Agri-Food industry, and in particular, farmers, will benefit by being able to shift away from antibiotic use on the production farm, decrease the risk of antimicrobial resistance and improve the health/production value of the animals. This, in turn, will raise the value of the farm and improve the public image of the farming industry.

Acknowledgements: We are grateful to funding from OMAFRA through the Gryphon's LAAIR competition, awarded May 2015, that will allow us to explore a microbial ecosystem-based approach to animal health and production value.

An investigation of iron deficiency and anemia in piglets

A Kubik[1], T O'Sullivan[1], J Harding[2], R Friendship[1], akubik@uoguelph.ca
[1]*Department of Population Medicine, University of Guelph, Guelph, Ontario, Canada,*
[2]*Department of Large Animal Clinical Sciences, University of Saskatchewan, Saskatoon,*

Background: Iron supplementation is a necessary farm management practice carried out in order to prevent piglets from iron deficiency and anemia. There are four main reasons why piglets require iron supplementation: 1) born with limited iron stores, 2) low content of iron in sow milk/colostrum, 3) limited to no access to soil and 4) high iron demand due to rapid growth rate (1). A 200 mg dose of iron administered intramuscularly within the first week of life has been the accepted standard protocol for many years. The objectives of this study were to investigate whether current iron supplementation protocols are adequate to meet the needs of today's piglets by determining the prevalence of anemia or iron deficiency in piglets at the time of weaning and to determine whether iron status at the time of weaning affects post-weaning performance.

Methodology: Twenty commercial swine farms were visited across Ontario. All farms used injectable iron (iron dextran or gleptoferron) and administered in the first week of life. Three piglets (small, medium and large) per litter were chosen for the study and approximately 60 pigs per farm were sampled. Pigs (n=1095) were sampled 1-2 days prior to weaning. Each piglet was individually weighed and had blood samples taken upon enrollment. Blood samples were submitted to the Animal Health Laboratory (AHL), University of Guelph for complete blood count (CBC) analysis. Three weeks later the same pigs were re-weighed and had a second blood sample taken which was analyzed for hemoglobin concentration. The hemoglobin concentration from each piglet was defined as follows: normal (>110g/L), iron deficient (>90g/L but < 110g/L), and anemic (≤90g/L) (2). Statistical analysis was designed to evaluate the association and to assess nursery performance between hemoglobin status at weaning and 3-wk post-weaning weight.

Results: At weaning, the between herd prevalence of iron deficiency and anemia were 28% and 6%, respectively. Anemic pigs at weaning had a 0.81 kg reduction in their 3-wk post-weaning body weight compared to piglets with normal hemoglobin values at weaning. Also, anemic pigs at weaning had a 0.68 kg reduction in their 3-wk post-weaning body weight when compared to iron deficient pigs at weaning. The largest piglets at weaning had lower hemoglobin values compared to small pigs. The fastest growing suckling pigs have the largest blood volume, therefore their hemoglobin is diluted, but in addition, these animals have the highest requirements for all nutrients. The results from this study confirm that 200 mg of injectable iron in the first week of life was often not sufficient to prevent anemia or iron deficiency for the larger, faster growing pigs. Anemia at weaning was associated with reduced growth in the first 3 weeks post weaning. Surprisingly piglets generally remained anemic or iron deficient during the 3 weeks post-weaning although starter rations were well fortified with iron.

Benefits to the swine industry: Understanding the consequences of iron deficiency and anemia is important for the swine industry and producers in order to prevent economic losses. This project has demonstrated that large fast growing pigs are often iron deficient and possibly anemic at weaning and this is having an impact on post-weaning performance. However, more work is needed in order to determine if additional supplementation or different protocols are beneficial. Pork producers need to re-evaluate their iron supplementation program.

Acknowledgments: This work was supported by Ontario Pork and the University of Guelph-OMAFRA Research Partnership. We are grateful for the participation of pork producers and the assistance of AHL in analyzing blood samples.

References: 1. Svoboda, M., and Drabek, J. (2005). Iron deficiency in suckling piglets: etiology, clinical aspects and diagnosis. *Folia Vet*, 49, 104-111. **2**. Nielson, JP. *et al*. (2013). Herd diagnosis of iron deficiency in piglets. Proceedings European Symposium Porcine Health Management. p168.

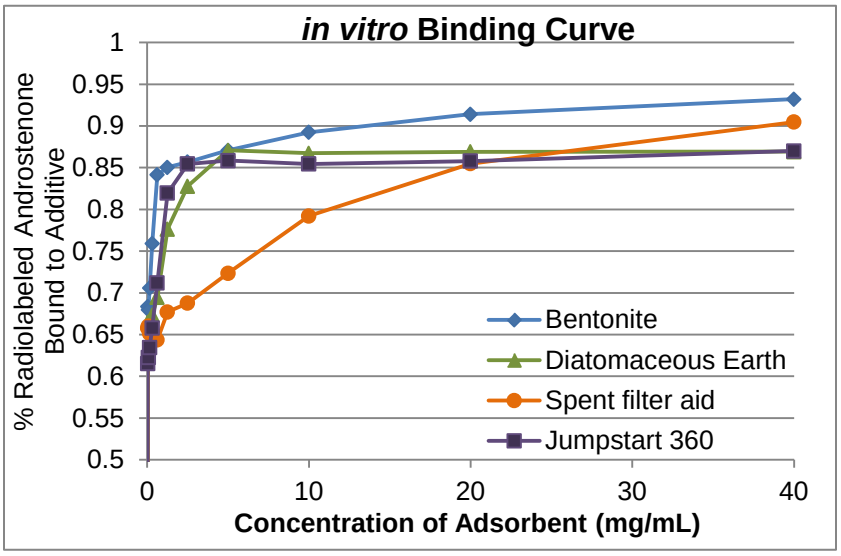
The use of non-nutritive adsorbents to control boar taint

S. Park, I.B. Mandell, C.F.M. de Lange, and E.J. Squires
Department of Animal & Poultry Science, University of Guelph; jsquires@uoguelph.ca

Background: The practice of surgical castration to prevent boar taint and reduce aggression is commonplace in North American swine production and is often performed without local analgesia. Mounting public pressure against this practice has caused the European Union to set 2018 as the target year to ban surgical castration, marking a search for alternative methods to control boar taint. Current alternatives include early slaughter, genetic selection for low boar taint, and immunocastration; however, these procedures are still underdeveloped, labour-intensive, and/or not very economically feasible. The aim of this study is to examine the effectiveness of low-cost feed additives with adsorbing capacities previously used as successful mycotoxin binders against the boar taint compounds skatole and androstenone. This will be investigated both *in vitro* and in an animal model.

Methodology: Candidate additives (bentonite, **BNT**; diatomaceous earth, **DE**; spent filter aid, **SFA**; sodium-calcium aluminosilicate, **JUMP/"Jumpstart 360"**) have diverse origins but have all demonstrated effective binding of the mycotoxins aflatoxin B1 and zearalenone in the gut of pigs and chickens. They were serially diluted in phosphate buffer saline solution (pH 7.4). Radiolabeled androstenone (AND) was used to estimate hormone binding; this was quantified as a ratio of AND bound to adsorbent compared with total radioactivity in the stock androstenone sample. Each additive was mixed with an equal amount of hormone and incubated in a shaking water bath at physiological temperatures. Tubes were then centrifuged, and the supernatant was transferred to liquid scintillation tubes to be counted for radioactivity. The data produced from the above procedures was used to extrapolate inclusion levels of each additive into a corn-soybean meal finisher diet. The currently ongoing feeding trial consists of 90 purebred Duroc intact male pigs (housed at Ponsonby General Animal Facility) equally divided into 5 groups (4 treatment + 1 control), with 6 pens per group and 3 pigs to a pen. The treatment groups are fed their respective diets for 28 days, with a recovery period of 21 days, in which they are fed a commercial diet for the remainder of the trial. All pigs are sampled for their blood and backfat as well as weighed for performance measurements. Androstenone concentrations in plasma and adipose will be analyzed and compared between groups.

Results: All adsorbents bound androstenone above 80% of total radioactivity of hormone sample in high concentrations. An ideal adsorbent ought to be cheap and selectively bind boar taint compounds without any compromise in a pig's performance. Due to the complexity of the gastrointestinal environment and the unclear physical mechanisms of these additives, *in vitro* results may not always translate readily to similar results in an animal model. We are still awaiting results for the feeding trial that is currently underway.



Benefits to the Swine Industry: This nutritional method to control boar taint may be a cost-effective and less labour-intensive option to control boar taint in a commercial operation than other existing alternatives. If successful, it could be paired with current research in genetic selection for low-taint lines of intact males to ensure that boar taint can be controlled without surgical castration.

Acknowledgements: Thanks to the de Lange & Friendship laboratories for the technical support in the animal trial. Financial support was provided by Swine Innovation Porc, Natural Sciences and Engineering Research Council, and Ontario Ministry of Agriculture and Food.

Pig movement and traceability in Canada

Daniel Hurnik
University of Prince Edward Island

This abstract will attempt to demonstrate the current status and direction of traceability systems in the pork production industry in Canada, with particular emphasis on what it will mean for Canadian pork producers. Traceability by definition is the ability to trace pork through the production chain. Research into options for traceability in Canadian production systems has indicated the following options:

Ear tags:
Identification of individual animals, while employed in the bovine and ruminant industries, was found to be too costly for commercial pig production. The cost of ear tags, plus administration costs, in addition to problems with plastic and metal tags at slaughter, the Canadian industry found the cost an ear tag in all pigs to be in excess of the benefits it would bring. Animals that are at higher risk of spreading disease to other farms, notably breeding stock and animals that move through sales auctions or shows, do need to be traced as individuals in the event of an outbreak. Through a traceability pilot, Canadian Pork Council has recommended that breeding stock and animals moving to unknown destinations be given an ear tag. Standardized ear tags have been introduced to the industry, and the commercial movement of pigs in Canada be recorded in a movement database.

Movement recording:
The majority of commercial pigs in Canada move in large groups and the pilot studies indicated electronic recording of animal movements could be done feasibly. The 2004 pilot study tracked 3,000 animal movements capturing over 250,000 pigs and an audit comparing farm records to database records indicate that movement records can accurately capture movement data[1]

The same movement database can be used to model the spread disease and can be effective in modeling size of disease outbreaks and can lead to a greater understanding of animal and vehicle movements among pig farms in Canada [2,3]

Molecular Traceback:
Identification of animals is lost once animals are processed into primal cuts. Traceability from meat samples thus cannot go to farm of origin unless molecular techniques are used to match animals at farm to meat at retail. Pilot studies indicate such traceback is possible[4] and can be used commercially when validating sources and origins of meat at retail.

Traceability through parentage is also possible where DNA sampling of sires can detect farm of origin where that sire is used and can also detect performance differences between sires and this may be used for genetic selection and for health improvements strategies [5]

[1]Hurnik et al. Proc of the 19th IPVS Congress, Copenhagen, Denmark, 2006 · Volume 1 p 307
[2] Thakur et al .Prev Vet Med DOI:10.1016/j.prevetmed2015.01.06
[3] Thakur et al. Transboundary and Emerging Diseases, DOI 10.111/tbed 12225
[4] MacDonald AASV proceedings 2004, p 85
[5] Yamazaki proc. AASV 2014 p 315

Lifetime genetic evaluation of piglet growth - birth to market weight

Kristen Alves, Andy Robinson, Flavio Schenkel

An area of swine genetics that has not been well explored is the analysis and selection of piglets on the basis of individual performance in early life stages; birth and weaning weights. No genetic parameters for individual birth and weaning weight were found in the literature for Canadian swine breeding herds. Hence, commercial production systems typically overlook this information, but it is information that can be valuable in predicting future weight gain, piglet survival and suckling behaviour. CCSI's annual report from 2011 identified this lack of means to select on early growth performance as a Canadian problem that should be addressed. The purpose of this research was to estimate genetic parameters for individual birth weight, weaning weight and probe weight of purebred Yorkshire and Landrace swine in Canada. Data were collected from two large and related breeding herds from Quebec and Manitoba from 2003-2015. Heritabilities and genetic correlations were estimated using bivariate models in ASReml. Direct heritability for traits were low to moderate from 0.13 for birth weight, 0.03 for weaning weight and 0.27 for probe weight for the Yorkshire breed and 0.05 for birth weight, 0.01 for weaning weight and 0.25 for probe weight in the Landrace breed . Maternal heritability estimates were 0.16 for birth weight, 0.11 for weaning weight and 0.03 for probe weight in the Yorkshire breed and 0.24 for birth weight, 0.11 for weaning weight and 0.06 for probe weight in the Landrace breed. As expected, the direct heritability increased with age as a result of the maternal influence on that animal decreasing. Strong direct genetic correlations and maternal genetic correlations were found between birth weight and weaning weight in both breeds. Based on the estimates of genetic parameters, recording and selecting on individual birth weight would improve the early growth performance of piglets. Individual early growth performance should be evaluated and considered in genetic evaluations and breed selection programs.

Iberian pigs in Spanish pig production: relevance and unique characteristics

J. Morales, J.F. Perez and J. Gasa
Departament de Ciència Animal i dels Aliments, Universitat Autònoma de Barcelona, 08193 Bellaterra, Spain;
Josep.Gasa@uab.cat

Background: The "Iberian" (IB) is an autochthonous pig breed, black or brown, produced in the southwest of the Iberian Peninsula (Portugal and Spain). Compared to the more typical "white" commercial pigs the IB pig grows slowly and is more rustic and fatter. IB pig products are highly appreciated locally and worldwide, specially the cured ham. Hams are cured more than one year in a dry and low light atmosphere ("bodega"). The final product has a high intramuscular fat content ("beteado o marmoleo") with high proportions of oleic acid (C18:1) which confer a special flavor and taste to the final product.
IB pig inventory is slightly over two million animals (2012), which represent about 9% of the Spanish total pig inventory. Furthermore, less than 10% of the commercialized IB pigs are "pure" IB; most IB pigs are crosses with different proportions of Duroc. The traditional production system takes around 15-16 months to raise a pig to about 160 kg live weight. During the last month's fattening pigs are located in "the Dehesa" and are fed a diet of grass and acorns from several species of oak trees. During this finishing period (called "montanera"), daily gain would approach 1 kg/pig and pigs eat up to 8-10 kg/d of dehulled acorns and grass.
The high intramuscular fat content and fat quality are determined by the breed and the animals' high level of physical activity. However nutrition is also involved, since diet fatty acid profiles are closely related to body fat quality.

Experiments were conducted to better understand diet effects on fat content and quality in IB products. The initial hypothesis was that IB digested better the fiber than commercial "white" pigs and volatile fatty acid produced in the hind gut would affect intramuscular fat deposition.

Methodology: In a 2x2 factorial design, 24 pigs (12 IB and 12 landrace (LD)) were fed "ad libitum" a corn-soybean diet (C) or a cereal, acorn (40%)-soybean diet (A) from about 105 to 135 kg body weight. Feed intake (FI), average daily growth (ADG) and feed to gain (FCR) were measured. Organic matter (OM), starch (St) and fiber (NSP) digestibility coefficients (d) were measured using chromium oxide as marker. At slaughter backfat thickness (mm), intramuscular fat (g/100g fresh muscle), the amount of feed present in different gut segments and mean retention time of feed in the hind gut (MRT) were also measured.

Results: Backfat thickness and intramuscular fat were not significantly affected by the diet (see table 1). As expected, IB had a higher backfat thickness and intramuscular fat ($p<0.001$) than LD, although the difference in intramuscular fat was from about double to four times depending on the muscle (see table 1).
IB had a 50% higher ($p<0,001$) FI and a 33% poorer FCR ($p=0.062$) than LD. As expected, diet C had higher fecal digestibility coefficients than diet A ($p<0.001$). IB had lower fecal digestibility coefficients than LD ($p<0,01$), specially for NSP (21% less, $p<0.001$). In any case, IB pigs ate about 44% more digestible organic matter per day than LD ($p<0.001$).

Table 1. Effect of the breed (IB vs LD) and the diet (Corn vs Acorn) on feed intake, digestibility, fat deposition and gut contents.

Breed	Landrace		Iberian		*Significance*	
Diet	Corn	Acorn	Corn	Acorn	*breed*	*diet*
Feed Intake (kg/d)	2,57	2,30	3,74	3,41	*<0,001*	*<0,10*
Total OMd (%)	86,4g	81,8	85,5	79,8	*<0,01*	*<0,001*
Total NSPd (%)	61,1	73,4	50,0	56,4	*<0.001*	*<0,01*
Backfat thickness (mm)	35,4	28,3	72,5	70,8	*<0,001*	*<0.10*
Gluteus medium (g/100g)	2,98	3,07	9,43	8,21	*<0.001*	*NS*
Longissimus dorsi	2,42	2,23	6,26	5,80	*<0,001*	*NS*
Masseter (g/100g)	2,32	2,34	4,07	4,31	*<0,001*	*NS*
Stomach content (kg)	0,88	1,34	1,76	2,16	*<0,01*	*<0,15*
Hind gut content (kg)	2,30	3,23	2,04	2,06	*<0,001*	*<0,01*
Hind gut MRT (h)	24,7	22,6	8,6	6,6	*<0,01*	*NS*

The stomach and hindgut digesta contents were higher for diet A ($p<0.001$), specially for LD pigs. Compared to LD, IB had a higher stomach content ($p<0.01$) but a lower hindgut content ($p<0.01$). The diet did not affect the hind gut MRT but IB pigs has a lower MRT than LD (23.7 vs 7.6 hs, $p<0.01$).

Conclusions and implications: As expected, IB had more backfat and intramuscular fat than LD. However, the diet did not affect fat retention or distribution. IB pig had higher FI than LD but had lower digestibility coefficients of both OM and NSP, mainly due to a much lower MRT of the digesta in the hind gut. The IB pig is more ravenous than LD; it has biologically been adapted to the surrounding conditions, were feed intake capacity has higher priority than digestive efficiency.

Acknowledgements: This study was supported by the Spanish Government throughout the CICYT funded project AGF98-0506. Dr. Gasa is a visiting scientist in the Department of Animal and Poultry Science.

An Economic Evaluation of Control Strategies for Porcine Epidemic Diarrhea Virus

Longfeng Weng[1], Alfons Weersink[1]*, Zvonimir Poljak[2], Kees De Lange[3], Mike von Massow[4]
[1]Department of Food, Agricultural and Resource Economics (FARE), [2]Department of Population Medicine; [3]Department of Animal of Poultry Science; [4]Department of Hospitality, Food and Tourism Management; University of Guelph, Guelph, ON Canada, N1G 2W1; aweersin@uoguelph.ca;

The recent outbreak of PED in North America, including Ontario, highlighted the severe threat posed by this disease for the swine industry. In completely susceptible herds, there is no immunological protection in piglets to the PED virus so the mortality rate is initially very high for young pigs (almost 100%) as is the morbidity rate. However, the economic costs of a PED outbreak, including production losses and expenditures on PED-control strategies, remain poorly documented. Veterinary practitioners have recommended several PED-control strategies with the aim to completely eliminate PED infection from herds but the cost-effectiveness of these practices is unknown. The purpose of this study is to calculate the costs of a PED outbreak on an individual farrow-to-finish farm in Ontario and to estimate the reduction in these costs as compared to the expense associated with implementing alternative control actions. The analysis considers a combination of four practices: (1) the breeding herd closure; (2) feedback exposure in all mature herds for a certain time period; (3) the implementation of farm biosecurity protocols involving applications of different sanitation protocols; and (4) the use of vaccines. The presentation today describes the model used to estimate the costs of PED and its treatment. It estimates the weekly number of pigs in each population cohort on the basis of production parameters such as farrowing rate and mortality rates. Combining costs of feed and other production expenses with hog prices, the net returns with and without PED are calculated. Future work will stochastically simulate the production impact of a PED outbreak and quantify the economic impact of various preventive actions on the PED outbreak.

Swine dysentery epidemiology: challenges and what we learned

Krysia Walczak, Zvonimir Poljak, Robert Friendship, Amy Greer, Alfons Weersink
kwalczak@uoguelph.ca

Background: Swine dysentery (SD) is a disease caused by *Brachyspira hyodysenteriae*, which recently re-emerged in the North American swine industry. *B. hampsonii* is the causative agent of the re-emergence and other forms of SD-like diseases. Due to the rapid implementation of treatment and incorporation of feed treatments, swine dysentery epidemiology is difficult to study. Most knowledge about SD epidemiology is gained from empirical data obtained from experimental challenges. There are certain challenges with studying this disease as certain parameters important for transmission are not clearly defined. This research project hopes to answer the questions related to the epidemiology of SD, and to provide a clear understanding of the disease and determine the most cost-effective treatment protocols related to this disease.

Methodology: Using production data, we determined factors associated with clinical morbidity. From these results, and given what we know from the literature about swine dysentery, we determined important parameters for mortality due to swine dysentery through uncertainty analysis of deterministic modelling. Furthermore, we built a stochastic model to understand the epidemiology of SD and reproduce what is observed in the field.

Results: From the production data, we assumed treatment rates were indicative of clinical morbidity due to SD. We found that SD had a seasonality component in that the use of lincomycin had more use in the winter, thereby indicating that SD was a problem during the winter months. Treatment with tiamulin showed a 17 day pattern indicating that SD clinical cases recurs in a little over two weeks, although there were multiple modes for this treatment which shows variability of treatments between different batches. The deterministic models indicated that, no matter the description of the history of the disease, the duration of infectiousness is an important parameter that influences mortality (Figure 1). According to these results, one must change the duration of infectiousness to influence mortality. Stochastic modelling replicated what was seen in the production data (i.e., prevalence of infection, treatment rates) if there were a small proportion of clinical animals. Mortality from historical reports was replicated if 25% of infectious animals became clinical and if there was no effective intervention in the simulation. Using these stochastic models, we will incorporate a cost-benefit analysis to this model.

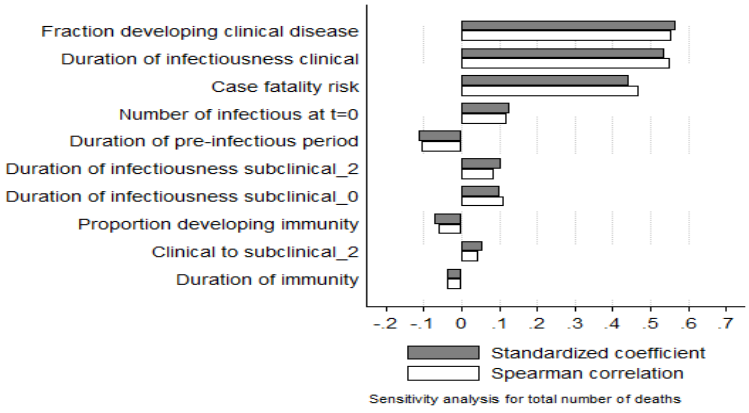


Figure 1 - Uncertainty analysis to determine parameters important for mortality. Duration of infectiousness has a strong influence on mortality.

Benefits to the swine industry: This project will give insight on the epidemiology of swine dysentery. Attempts to shorten the duration of infection will reduce mortality due to clinical SD. Furthermore, the research hopes to determine the most cost-effective treatment to increase production of a herd affected by swine dysentery.

Acknowledgements: Funding was provided by the Ontario Ministry of Agriculture, Food and Rural Affairs. We would like to acknowledge the swine producers and veterinarians for their contribution and participation for this project.

Compounding Iron Dextran with NSAIDs for Use in Piglets at Time of Processing

T. O'Sullivan[1], R. Friendship[1], S. Ramkissoon[1], S. Enouri[2], R. Johnson[2]
[1.]*Department of Population Medicine,* [2.]*Department of Biomedical Sciences, University of Guelph, Guelph, Ontario*

When NSAIDs (anti-inflammatory/analgesic agents) such as meloxicam or flunixin meglumine are administered to piglets at the time of processing, it is tempting to mix (compound) the NSAID with iron dextran to be delivered in a single injection, thereby reducing the number of injections to the piglet. This practice constitutes extra label drug use. Extra label drug use is acceptable provided it is approached in a rational manner. Therefore, if the practice of compounding iron dextran with NSAIDs is to be justified, it is prudent to evaluate possible drug interactions that could affect the availability and efficacy of the NSAID, or the iron dextran. The study was conducted with three separate experiments carried out at the University of Guelph, with the following objectives i) evaluate the bioavailability of meloxicam (Metacam® 20 mg/mL Solution for Injection, Boehringer Ingelheim Canada LTD) and flunixin meglumine (Banamine®, Merck Animal Health) when compounded with iron dextran (Dexafer-200®, Vetoquinol) and administered to newborn piglets of approximately 5 days of age, ii) evaluate the effect of compounding these agents on iron dextrans ability to increase piglet hemoglobin concentrations, and iii) evaluate the effects of compounding these agents on measured concentrations of the NSAIDs *in vitro*.

Measurement of recoverable flunixin meglumine and meloxicam when compounded in iron dextran *in vitro* at levels similar to those employed by private practitioners was accomplished using high performance liquid chromatography. Our results showed that recoverable levels of either NSAID were reduced, beginning as early as 2 hours post-mixing, and with over 30% reduction in recoverable flunixin meglumine concentrations and over 10% reduction in meloxicam concentrations by 24 hours post-mixing. These findings suggested a probable drug interaction that could result in reduced NSAID being available for systemic absorption when administered to piglets. In the first of our two live animal experiments, we found no significant effects of compounding either NSAID with iron dextran on measured blood hemoglobin levels (hemoglobin determined at pre-dose at about 3 days of age and 21 days post-dosing) when administered in piglets. The results of our bioavailability study comparing blood NSAID levels for flunixin meglumine and meloxicam when administered to piglets alone versus compounded in iron dextran did show notable findings. Piglets receiving flunixin meglumine were dosed intramuscular at 2.2 mg/kg either as the NSAID alone or when compounded with iron dextran. Piglets receiving meloxicam were also dosed intramuscular at 0.4 mg/kg as the NSAID alone or when compounded with iron dextran. Blood samples collected shortly after dosing to 72 hours post-dosing were analyzed for meloxicam or flunixin meglumine using validated mass spectroscopy methods. Results showed significantly reduced concentrations (reduced Cmax and AUC) of both NSAIDs when compounded with iron dextran compared to levels noted when NSAID was given alone.

The results of our study show that the mixing of meloxicam or flunixin meglumine with iron dextran produces a likely drug interaction, which does not appear to affect iron dextrans ability to maintain adequate hemoglobin concentrations, but does reduce the availability of the NSAID for absorption into the systemic circulation. The clinical ramifications of the reduced blood NSAID levels when compounding with iron dextran require additional efficacy studies to evaluate whether adequate analgesia is being provided at the current NSAID concentrations in the compounded formulation. Importantly, practitioners compounding flunixin meglumine or meloxicam with iron dextran for administration to piglets at the time of castration and processing are strongly recommended to dose piglets with freshly mixed active ingredients in order to minimize reduced bioavailability of the drug over time.

This project was funded by Ontario Pork and the Ontario Farm Innovation Program

Copy number variations in high and low fertility breeding boars

Tamas Revay[1], Anh Quach[1], Laurence Maignel[2], Brian Sullivan[2] and W. Allan King[1]
trevay@uoguelph.ca, *waking@uoguelph.ca*
1 *University of Guelph, OVC Biomedical Sciences, N1G2W1 – Guelph – Canada;*
2 *Canadian Centre for Swine Improvement Inc., K1A0C6 – Ottawa - Canada*

Variability in genomes (including single nucleotide polymorphisms (SNP), copy number variations (CNV) and chromosomal rearrangements (CA) is responsible for a significant proportion of the diverse phenotypes associated with many important traits including fertility. CAs have proven their potential detrimental effects through the identification of numerous infertile or subfertile animals. Smaller scale structural alterations represent the territory of CNVs that are estimated to occur more frequently than SNPs, thus can be considered as a prominent source of individual genetic variation and candidate markers for diseases or economically important traits.

In this study we applied the extreme groups / selective genotyping approach for identifying copy number variations in high and low fertility breeding boars. The fertility indicator was the calculated Direct Boar Effect on litter size (DBE) that was obtained as a by-product of the national genetic evaluation for litter size (BLUP). The two groups of animals had DBE values at the upper (high fertility) and lower (low fertility) end of the distribution from a population of more than 38,000 boars. Animals from these two diverse phenotypes were genotyped with the Porcine SNP60K chip to screen for CNVs and to identify putative markers of fertility.

Among the identified 35 CNVs, 14 were specific to the high fertility group, while 19 CNVs were specific to the low fertility group. The CNVs encompassed 50 genes, overlapped with 137 QTLs of various reproductive traits. A functional analysis of several databases revealed that the genes found in CNVs from the low fertility group have been significantly enriched in members of the innate immune system, Toll-like receptor and RIG-I-like receptor signaling and fatty acid oxidation pathways.

Research support was obtained from NSERC, Agriculture and Agri-Food Canada, and the Canada Research Chairs program.

Using genetics to keep your food safer

Ainslie MH.[1*], Farzan AV.[1,2], Friendship RM.[2], de Lange CFM[3], Lillie BN.[1]
[1]Department of Pathobiology, [2]Department of Population Medicine, [3]Department of Animal and Poultry Science, University of Guelph, Guelph, Ontario, Canada
**Corresponding author: mainslie@uoguelph.ca*

Background

Salmonella infects over 2500 people in Ontario per year. Some cases arise from pork products or produce fertilized by pig manure. Since 2000, Canada has seen reductions in other foodborne illnesses, but rates of salmonellosis remain high.

Objective

This project is investigating single nucleotide polymorphisms (SNPs) in porcine innate immune response genes and their association with *Salmonella* shedding and colonization.

Materials and Methods

1296 pigs on 12 commercial Ontario farms will be sampled five times from birth to market. *Salmonella* will be detected in fecal and tissue samples. Serum will be analyzed for cytokines and antibodies. DNA will be extracted from tail dockings for SNP analysis.

Results

To date, 172 pigs over 3 trials on two farms have been sampled, including 618 blood and fecal samples, and 70 tissue samples collected at slaughter. 23 samples cultured positive for *Salmonella* at weaning (17) and end of nursery (6); to date, no samples have been positive at later time points.

Conclusion

This research aims to identify genotypes that may be used in swine improvement programs to breed robust pigs that shed less *Salmonella*. Reduced salmonellosis associated with pork production will benefit society, while the pork industry should experience improved herd health, animal welfare and economic productivity.

Characterizing *Streptococcus suis* from clinical cases and healthy-carrier pigs

Emily Arndt[1], Vahab Farzan[1], Glenn Soltes[2], Janet MacInnes[2], Robert Friendship[1*]
*[1]Department of Population Medicine, [2]Department of Pathobiology, University of Guelph; *rfriends@uoguelph.ca*

Background: Infection with *Streptococcus suis*, which is prevalent on Ontario swine farms, can cause decreased performance and mortality resulting in significant economic impacts on swine production. *S. suis* can reside as a commensal in the upper respiratory tract of clinical healthy pigs, and can be shed from sows through bodily fluids such as vaginal secretions. On most pig farms several different *S. suis* serotypes are present within the herd, and some serotypes are more likely to cause disease than others. Many healthy pigs carry pathogenic *S. suis*, but in general disease outbreaks seem to require triggering factors such as stress.

Objectives: The objectives of this study are to investigate the distribution of *S. suis* serotypes, virulence factors, and antimicrobial resistance profiles from clinical cases and healthy-carrier pigs; to determine the ability of a new multiplex PCR to identify *S. suis* serotypes; and to investigate risk factors and treatment measures used on Ontario farms.

Methodology: A total of 50 Ontario farrow-to-finish swine farms will be studied: 25 farms undergoing outbreaks of *S. suis* disease, and 25 farms with no recent history of *S. suis* infection. Nasal and tonsillar swabs will be collected from pigs with clinical signs of infection; a tissue sample from tonsils and/or lymph nodes will be taken if the pig is dead or euthanized. Also, for each farm visited nasal and vaginal swabs will be taken from 5 sows, and tonsillar swabs taken from 5 suckling, nursery, and grower-finisher pigs. Samples will be cultured for *S. suis* quantitatively. Multiple isolates from each positive sample will be selected and serotyped using coagglutination and PCR tests. Selected isolates will also be tested for antimicrobial susceptibility. In addition, bacterial community DNA will be extracted directly from samples and tested for the presence of *S. suis* DNA by PCR. A survey will be administered to participating pig producers to collect information regarding disease history, vaccination, and farm management practices.

Results: To date, 7 farms have been visited. Three farms had no pigs with signs of *S. suis* disease when visited, and the other 4 farms had pigs with clinical signs or outbreaks of *S. suis* disease when visited. In total, 120 samples were collected from 110 pigs (85 healthy pigs and 25 sick pigs). *S. suis* could be isolated from 73% of suckling and 88% of nursery pig samples, and was detected in samples from 47% and 50% of sows and grow-finisher pigs, respectively. To date, 126 *S. suis* isolates have been identified in 81 samples of which 65 isolates have been serotyped. *S. suis* isolates recovered from pigs in healthy herds have been untypable with the exception of one isolates which was serotype 9. However, isolates from herds with pigs showing clinical signs of disease were serotype 2, 4, 8, 9, 22, 23, 25, 34, and untypable. Isolates from healthy pigs, including those from infected herds, were serotype 9, 22, 34, and untypable; whereas, isolates from pigs with clinical signs were serotype 2, 4, 8, 23, 25, 34, and untypable. The most common serotypes found from pigs on farms with outbreaks of *S. suis* disease have been serotype 8 and 34. However, since this study is still ongoing, more farms and pigs need to be tested to determine the differences in prevalence and *S. suis* serotypes from healthy and diseased pigs.

Benefits to the Swine Industry: This research will provide valuable information on existing *S. suis* serotypes and current antimicrobial resistance in *S. suis* isolated from healthy carrier pigs as well as from sick pigs on Ontario swine farms. The knowledge gained will help to identify the most effective antibiotics, ensure that the correct strains are chosen for autogenous vaccines, and design appropriate management changes to reduce the prevalence of *S. suis* disease outbreaks.

Acknowledgements: OMAFRA-University of Guelph Research Partnership, Gallant Custom Laboratories, Animal Health Laboratory, Dr. Kalie Pettit from South West Ontario Veterinary Services, and participating pig producers.

Investigation of the spread of PRRS virus between swine herds participating in an ARC&E project in Ontario using molecular and network data

Arruda, A. G.[1]; Poljak, Z.[1]; Friendship, R.[1]; Carpenter, J.[2], Hand, K.[3]
[1]Department of Population Medicine, University of Guelph; [2]Ontario Swine Health Advisory Board; [3]Strategic Solutions Group

Background: A porcine reproductive and respiratory syndrome area regional control and elimination (PRRS ARC&E) program began in the Watford region of Ontario in 2012. In 2014, concerns with regard to spread of a specific PRRS virus (PRRSV) genotype within the region (so-called "RFLP 1-3-2") were identified. The objectives of this study were to investigate spatial location and network membership as risk factors for infection with specific PRRSV genotypes.

Methodology: Swine sites were enrolled in the Watford ARC&E project during 2012-2014. Site coordinates, truck network, and PRRS diagnostics data were entered into the online PRRS control database, which served as the primary source of data. Nucleotide sequences of the ORF5 gene for cases in the region were obtained from the Animal Health Laboratory (University of Guelph). Alignment of the ORF5 gene sequence was done using the MUSCLE algorithm. A phylogenetic tree was constructed on R 2.15.0 using Tamura and Nei's distance and genotypes were identified based on the tree's clades. Three kilometer buffers were constructed in ArcMap 10.1 for each of the sites. Network analysis of trucking data was conducted using UCINET.
Logistic regression models using generalized estimating equation approach were constructed to investigate location and transportation as risk factors for being positive with a specific PRRSV genotype of interest.

Results: A total of 89 swine sites were enrolled in the project. The phylogenetic tree included 34 cases from 32 sites, and the so-called "RFLP 1-3-2" was found to be located in two distinct clades. Those two "clusters" were used separately as outcomes in the models. Twenty- seven truck companies were responsible for transporting pigs from 75 sites; one company transported animals for over 40% of the sites. Presence of at least one neighbouring herd with a specific genotype was not positively associated with positivity for this specific genotype. Truck membership was positively associated with being positive for both clusters, but not statistically significant ($P > 0.16$).

Conclusions: Ontario PRRS database contains data that could be used for the purposes of regional disease investigations. In this example, proximity to another herd with the same genotype was not identified as a risk factor, whereas preliminary results suggest transportation could play a role.

Acknowledgements: Ontario Ministry of Agriculture and Food and Ontario Ministry of Rural Affairs, Ontario Swine Health Board Advisory, Canadian Swine Health Board, Ontario Pork, Natural Sciences and Engineering Research Council, Agricultural Adaptation Council, Animal Health Laboratory (University of Guelph).

The prevalence of umbilical and scrotal hernias in a large production system

Melissa Atkinson[1]*, Tina Widowski[1], Robert Friendship[2], Radu Zorzolan[3]
[1] *Department of Animal and Poultry Science,* [2] *Department of Population Medicine, University of Guelph,* [3]*Agribrands Purina*

Introduction: A hernia is an abnormal protrusion of an organ through a defect or natural opening of the skin or muscle. The most common hernias in swine are umbilical and inguinal/scrotal hernias. Hernias are a concern because they can be a source of monetary loss for producers and may be a cause of compromised animal welfare. Producers are advised to euthanize pigs with large hernias or to ship such pigs at an early age before the hernia becomes too large. The "barbecue pig" market, which accepts small pigs, is a lower value market and represents a significant loss of potential income. If herniated pigs are shipped later, when the hernia is larger, packers are more likely to reject the pig due to the added risk of hernia rupture and carcass contamination. In addition, if the hernia is allowed to grow, the animal may be banned from transport because of Ontario legislation (the Safety and Quality Act). Thus, hernias cause monetary loss due to culling, early slaughter or condemnation. Furthermore, larger hernias are more likely to impede motility, become ulcerated, infected and painful, and are a very visual animal welfare issue. The objective of this study was to determine the prevalence of umbilical and inguinal hernias in pigs in a large Ontario production system.

Methods: The records from 10 years of nursery and grower barn fills were used to estimate the prevalence of the number of pigs identified as having a “belly rupture “or a “scrotal rupture”. Samples of pigs with these conditions from the same production system are being submitted for post mortem examination to verify the presence of a hernia and to determine if the condition is associated with inflammation, necrosis or adhesions.

Preliminary results: Records from 509,346 animals were examined in the preliminary observations. These data included196,710 grower pigs, representing 152 barn fills. In this group, there were 132 inguinal hernias (scrotal ruptures), or 0.07% affected animals, and 309 pigs with umbilical hernias (belly ruptures), or 0.16% affected animals. Also included were 312,636 pigs entering the nursery, representing 424 barn fills. In this group, 873 pigs or 0.28%, were identified with inguinal hernias (scrotal ruptures), and 348 pigs or 0.11%, were identified with umbilical hernias (belly ruptures). In the entire system under observation, the total prevalence of both varieties of ruptures was 0.33%, accounting for a total of 1,662 affected animals. A prospective study using post mortem examinations is being conducted to verify that animals identified as having hernias do have hernias and not other conditions that might be mistaken for a hernia.

Acknowledgments: This project is funded by a grant from the Ontario Farm Innovation Program and Ontario Pork. We wish to thank the pork producers who have participated.

Polymicrobial interactions between *Streptococcus suis* and *Haemophilus parasuis*

Allison M.E. Barre and Janet I. MacInnes*
*macinnes@ovc.uoguelph.ca

Background: There is growing evidence that cohabiting organisms are able to form synergistic and/or antagonistic relationships through metabolic interactions, chemical signals, and physical associations. *Haemophilus parasuis* and *Streptococcus suis* are often found together as commensal residents of tonsils in healthy pigs but can also cause severe disease. However, nothing is known of the relationship between these two important swine pathogens.

Methodology: *S. suis* serovar 2 (SS2) reference strain and *H. parasuis* serovars 3 and 5 (HP3 and HP5) reference strains were chosen to study the interactions between these two species. Experiments included co-culture in planktonic and biofilm environments to investigate changes in growth rates and biofilm formation. Antibiotic susceptibility of mono-cultures and co-cultures of SS2 and HP3/5 was also compared.

Results: Planktonic growth curves indicated that SS2 reached a 58% greater final concentration when grown with HP3. In the same experiment, it was found that the presence of SS2 in co-culture inhibited the growth of HP3, with an 84.4% reduction in the final concentration. HP3 growth in a biofilm with SS2 decreased 3307-fold ($p<0.0005$) compared to HP3 mono-culture biofilms. When SS2 was grown in a biofilm with HP5, a significant increase of 113-fold ($p<0.0001$) in SS2 cell numbers was also seen. Both *S. suis* and *H. parasuis* were protected from the effects of ampicillin in co-culture. The MIC of HP3 and HP5 increased from 200 μg/ml to >1000 μg/ml when grown in co-culture biofilms with SS2. As well, the MIC of SS2 increased from 200 μg/ml to >1000 μg/ml when grown with both HP3 and HP5. *S. suis* was also protected from the effects of bacitracin in co-culture with HP3 and HP5, with its MIC increasing from 100 μg/ml to >500 μg/ml with both strains (Fig. 1).

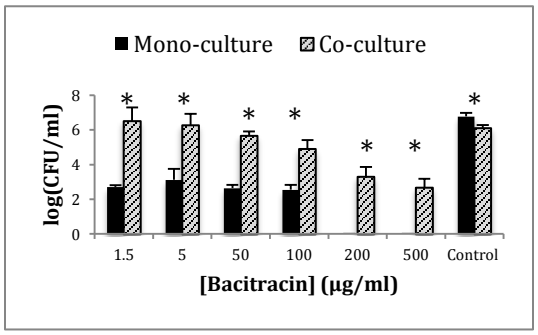


Fig. 1: Biofilms of SS2 alone and in co-culture with HP5 exposed to a range of bacitracin concentrations. There were significantly more ($p<0.005$) SS2 cells in co-culture biofilms compared to mono-culture biofilms at all concentrations tested. * = $P<0.05$

Conclusions: The results here suggest *H. parasuis* may aid the inhabitation of *S. suis* in swine, by enhancing its growth in both the planktonic and biofilm state. This may allow *S. suis* to better establish itself in the host by creating a biofilm for protection and increasing the chance of survival. As well, biofilms of both species provide significant protection against the effects of two antibiotics used in the swine industry, which suggests that co-culture of these species might be important for the development of persistent infections and carriers. Further understanding the interplay between *S. suis* and *H. parasuis* could lead to the development of new approaches to reduce swine respiratory disease.

Acknowledgements: Funding provided by NSERC and the OVC

Enhancing production of porcine epidermal growth factor in *Pichia pastoris* yeast

Michael Ben-Israel, Evanna Huynh, & Dr. Julang Li*
*jli@uoguelph.ca

Background: Piglets deprived of milk-derived growth factors during early weaning experience slower growth rates, reduced digestive function, and higher susceptibility to infection. We have previously shown that supplementing piglet feed with epidermal growth factor (EGF), one of the vital factors found in sow milk, enhances intestine development and growth during early weaning. In order to scale EGF application to industry levels, we are seeking to enhance the production efficiency of an EGF-secreting strain of *Pichia pastoris* yeast. Rapid EGF expression is likely stressing the protein-folding machinery in *P. pastoris*, causing it to be overloaded with unstable and misfolded proteins, thereby reducing the yield of secreted EGF. The goal of the current study was to stabilize and enhance EGF production by co-expressing an archeae-derived chaperone called small heat shock protein (sHSP) with EGF in *P. pastoris*. Chaperone proteins bind to and stabilize newly synthesized unfolded proteins to prevent misfolding. We hypothesize that co-expression of sHSP with EGF will reduce EGF degradation and enhance overall EGF secretion.

Methodology & Results: The gene for sHSP was cloned into an expression vector using a methanol-inducible pAOX1 promoter for expression. This vector was introduced into the EGF-expressing yeast strain, generating a series of isogenic clones, which were then screened for enhanced EGF secretion. After fermentation in the presence of methanol, EGF quantity in culture media was measured by Western blotting. Preliminary results have identified 2 colonies with significantly higher EGF secretion than the control parent strain (Figure 1). Next steps include determining sHSP gene copy number in clones demonstrating enhanced EGF secretion over the parent strain, and verifying their improved secretion in a large-scale fermentation.

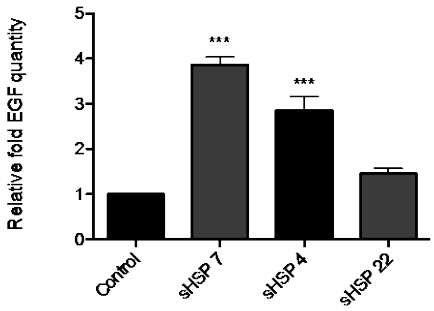


Figure 2: Co-expression of sHSP increases EGF secretion in P. pastoris. Western blots were performed to detect secreted EGF after small-scale fermentation. Data shown are densitometry quantification of Western blot results showing relative level of EGF from different sHSP transformed clones. Data represents the mean ± SE of two Western blot analyses. Asterisk (*) denotes significant difference compared to Control parent EGF expressing strain $P < 0.05$.

Benefits to the swine industry: Feed supplementation with EGF during weaning increases piglet health, growth rate, and feed conversion efficiency, thereby reducing industry costs. Enhancing EGF synthesis will decrease production costs and amplify industry savings.

Acknowledgements: The authors would like to thank Ontario Pork and NSERC CRD for the funding support of the study.

Electronic sow feeder development: towards precision feeding of gestating sows

R. Q. Buis, D. Wey, and C. F. M. de Lange
Dept. of Animal and Poultry Science, University of Guelph; cdelange@uoguelph.ca

Background: Nutrient requirements of sows change during gestation and across parity, reflecting dynamic changes in protein deposition in conceptus and the maternal body (NRC, 2012). The current approach of feeding one common diet to all sows within a herd is inappropriate to meet the changing needs of individual sows. The transition from gestation stalls towards group housing presents a unique opportunity to implement electronic sow feeders (ESF) as a valuable management tool. Commercially available ESF can be modified and a precision feeder can be created to meet the nutrient requirements of each individually identified sow, which is likely to improve sow productivity and/or nutrient utilization efficiency.

Methodology: In collaboration with a local company, we designed and built precision ESF. These ESF are installed at the Arkell Swine Research Station. Unique features of this system are:

- Computer controlled stepper motors capable of delivering accurately small amounts of up to four different (basal) feeds; these feeds are blended to meet the unique energy and nutrient requirements of each sow, at each day of gestation.
- The NRC (2012) gestating sow nutrient requirement model was adjusted to store daily calculated energy and nutrient requirements for multiple sows and to calculate the optimum ratio between the basal diets for each sow and each day of gestation. These data files are easily uploaded into the computer controlling ESF.

An experiment is being conducted to test the benefits of precision feeding gilts, in comparison to a conventional one-phase feeding program. The precision feeding regime is based on blending two iso-caloric diets, one high protein and one low protein (0.8 and 0.2 g/kg lysine respectively), to match estimated protein (i.e. lysine) and energy requirements of each gilt and on each day of gestation. Gilts were mixed into static groups 3-7 days after breeding. We are evaluating the effects of precision feeding on gilt reproduction and welfare, feed cost, and nutrient utilization.

Preliminary results: The accuracy of feed delivery was improved, based on the amount dispensed from a single 180° rotation of the stepper motor and controlling the number rotations, rather than the duration of feed delivery. Large variability in average daily gain was observed after weekly weighing of gilts, likely due to variation in gut fill. More frequent weighing or calculating daily gain over longer time periods (e.g. 4 weeks) is required to support precision feeding. Various aspects of the original ESF required alterations to make it operational. The entrance gates needed re-enforcement, and the mid-way gate placed immediately after the feed bowl needed re-designing to reduce congestion in the ESF. We continue to monitor performance.

Benefits to the industry: With the move towards group housing systems for gestating sows, this research aims to extend the use of ESF to meet the changing nutrient requirements of individual sows housed in groups, improving sow productivity and nutrient utilization.

Acknowledgements: This project is supported by OMAFRA, OMAFRA HQP, Farms.com (PigChamp), Canarm Ag (Sow Choice Systems), lab mates and technical staff.

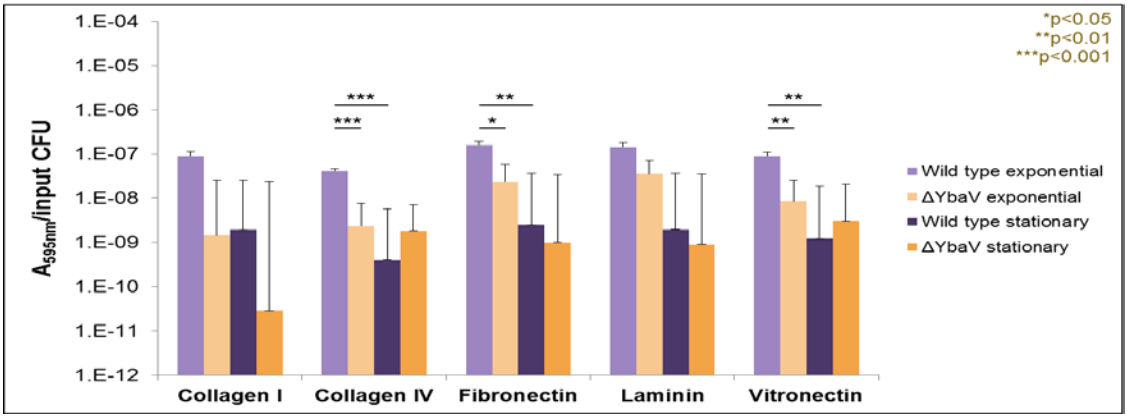
Extracellular matrix components and *Pasteurellaceae*: elucidating host-pathogen interactions in swine tonsils

Adina R. Bujold, Kearin L. Devlin, Janet I. MacInnes*
*macinnes@uoguelph.ca

Background: The tonsils of the soft palate of swine provide a first line of defense against antigens entering the upper respiratory tract. Paradoxically, they are also important sites of colonization for many microbes, and in some cases, may provide a route of entry into the bloodstream for pathogens. Despite their importance, little is known about how bacteria colonize these sites, and the host cell types and receptors involved in these interactions. Therefore, the objective of this study was to characterize the extracellular matrix (ECM) components and host cell receptors present in the tonsils of the soft palate of swine, and to characterize how *Actinobacillus suis*, an opportunistic pathogen of swine, attaches.

Methodology: To identify ECM proteins and cell receptors, tonsils were homogenized by various methods including chemical treatment and fractionation, and subjected to trypsinization and LC-MS/MS followed by comparative bioinformatics. For ECM attachment assays, *A. suis* wild type and a knockout mutant (ΔYbaV) for a putative fibronectin-binding gene were grown to exponential or stationary phase in BHI, and enumerated by plate counting. Culture was added to wells pre-coated with purified human ECM proteins and incubated at 37ºC + 5% CO_2 for 0, 15, 30, 45, 60, or 120 minutes post-attachment. Wells were stained with crystal violet and A_{595nm} was measured and standardized to input colony forming units (CFU).

Results: MS results identified putative adhesin receptors type VI collagen, vitronectin, fibrinogen, integrin β1, and mucin. Surprisingly, fibronectin was not identified in preliminary searches. There was increased attachment of wild type *A. suis* to ECM components during exponential growth phase relative to stationary, consistent with previous expression studies of *ybaV*. Furthermore, attachment of ΔYbaV to collagen IV, fibronectin, and vitronectin was reduced in exponential cultures relative to wild type.



Benefits to the swine industry: These studies should provide insight into how *A. suis* and other pathogens cause disease in the upper respiratory tract of swine.

Acknowledgements: JIM – NSERC, OMAFRA; ARB – OVC, OGS scholarships

Investigation of the potential relationship between swine influenza virus and *Streptococcus suis* infections in weanling pigs

Danielle Hopkins, Zvonimir Poljak, Vahab Farzan, Helena Grgić, Robert Friendship
Department of Population Medicine, University of Guelph

Background: Respiratory viral infections have been shown to increase bacterial colonization (Hament et al., 1999) and consequently, lead to an increase in severity and incidence of disease. A recent cell culture study demonstrated a potential synergistic relationship between the adherence and virulence of *Streptococcus suis* in swine epithelial cells that had been pre-infected with swine influenza virus (Wang et al., 2015). Both pathogens are commonly present on swine farms and sporadic outbreaks of streptococcal infection are an important cause of post-weaning mortality. In addition, both pathogens have zoonotic potential. It is unknown what triggers outbreaks of streptococcal disease.

The objective of this project is to determine if swine influenza viral infection predisposes piglets to *S. suis* infection resulting in clinical disease.

Methodology: The main goal is to identify if a piglet showing clinical signs associated with *S. suis* has been recently infected with swine influenza virus. This will be determined by performing a case-series study where piglets will be selected and identified as "case positives" if they are demonstrating the clinical signs associated with S. *suis* infection. The case positives will then be humanely euthanized, post mortems conducted and swabs of the tonsils, meninges, serosal cavity and joints will be cultured and PCR analysis performed in order to confirm a *S. suis* infection and the cause of death. Influenza infection will be determined by taking nasal swabs from the case positive piglets, as well as blood samples to identify the antibody titers, which will provide information on the timing of the influenza infection. Due to the multiple *S. suis* serotypes and influenza virus strains, in addition to confirming the presence of each pathogen the *S. suis* isolates will be serotyped and the influenza virus sequenced to provide insight into the possible interaction between these two pathogens and potential virulent strains. Finally, an active healthy piglet will be randomly selected from the same pen as the case-positive to serve as a "control", where we will gather information on the pathogens present within that pen as well as potential genetic markers that may explain why some piglets remain subclinical while others become clinical.

Results: The project has just started and there are no results to present.

Benefits to the swine industry: These are two very important post weaning pathogens that are commonly present on many Ontario pig farms. Understanding and potentially identifying a relationship between these pathogens can lead to a more focused vaccination/ prevention protocol, decreased potential economic loss and improvement of overall herd health.

Acknowledgments: This work is funded by Swine Improvement Porc, and the University of Guelph/OMAFRA Research Partnership. The participation of pork producers is appreciated.

References:

Hament, J.M., Kimpen, J.L.L., Fleer, A., and Wolfs, T.F.W. (1999). Respiratory viral infection predisposing for bacterial disease: a concise review. *Immunology and Medical Microbiology*, 26:189-195.

Wang, Y., Gagnon, C.A., Savard, C., Music, N., Srednik, M., Segura, M., Lachance, C., Bellehumeur, C., and Gottschalk, M. (2015). Capsular salic acid of *Streptococcus suis* serotype 2 binds to swine influenza virus and enhances bacterial interactions with virus infected tracheal epithelial cells. *Infection and Immunity*, 81:4498-4508

Production of porcine antimicrobial peptide, protegrin-1, in *Pichia pastoris* for potential use as an alternative to conventional antibiotics

E. Huynh, J. Li*
*Department of Animal & Poultry Science, University of Guelph, Canada; *jli@uoguelph.ca*

Background: The increase prevalence of bacterial resistance to conventional antibiotics is a growing public health concern. To overcome antibiotic resistance and retain consumer confidence in food safety, searching for effective antibiotic alternatives is a current challenge. Protegrin-1 (PG-1) is a porcine cathelicidin antimicrobial peptide (AMP) that can exert its activity against a broad range of microorganisms including bacteria, fungi and enveloped viruses, allowing it to be an attractive candidate for therapeutic use as an alternative to antibiotics. However, chemically synthesized AMPs are too costly to be feasible for routine use in the food-animal industry.

Methodology & Results: Recombinant expression of PG-1 using a safe and nonpathogenic microbe such as yeast is a potentially inexpensive alternative approach to chemical peptide synthesis for larger-scale food and animal application. Here, we report a codon-optimized protein corresponding to proform PG-1 that is highly expressed in *Pichia pastoris* yeast. For potential oral application of recombinant proform PG-1, an intestinal enterokinase (EK) cleavage site was included for EK-mediated activation of the cathelicidin. A *P. pastoris* transformant harboring multiple copies of the expression cassette was selected for downstream expression studies. Secreted proform PG-1 reached 1.2 g/L at 52 h during high cell density bioreactor cultivation. The unpurified proform PG-1 exhibited antimicrobial activity against *S.aureus* and *E.coli* after *in vitro* EK cleavage (Figure 1).

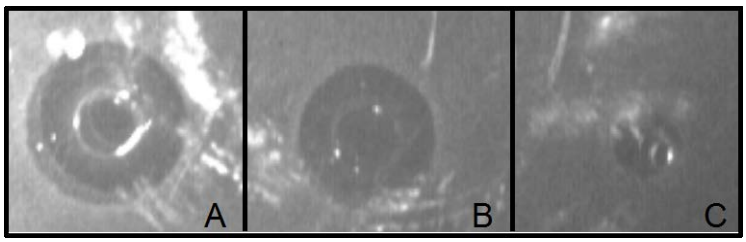


Figure 1. After cleavage of proform PG1 with EK, the resulting mature peptide exhibits antimicrobial activity against E.coli. Radial two-stage diffusion assay was used to detect antimicrobial activity. **(A)** Chemically synthesized PG-1 control. **(B)** Cleaved pro-form PG-1after EK digestion **(C)** and uncleaved proform PG-1 against *E.coli*.

Benefits to the swine industry: Resulting data establishes the potential feasibility of using microbes, in particular the yeast *P. pastoris*, as bioreactors to express and secrete biologically active swine-derived antimicrobial peptides for potential application as alternative to antibiotics.

Acknowledgements: The authors would like to thank Ontario Pork and NSERC for the funding support of the study.

Protective effects of protegrin against ulcerative colitis

E. Huynh, J. Li*
*Department of Animal & Poultry Science, University of Guelph, Canada; *jli@uoguelph.ca*

Background: The pig-derived cathelicidin, protegrin, is known to exert antimicrobial activity. As the peptide is an integral part of the innate immune system, protegrins may have other functions such as immuno-stimulating or –modulating effect, similar to its human cathelicidin counterpart. Little is known regarding the involvement of porcine cathelicidin in this regard. Early-weaning stress in piglets can result in negative effects such as impaired intestinal epithelial barrier and immune function, leading to inflammation and decreased growth performance.

Methodology & Results: The objective of this study was to examine the potential modulatory and protective effects of recombinant protegrin in its cathelin, pro- and mature-form) in a *dextran sulfate sodium (DSS)*-induced ulcerative colitis mice model. Body weight, clinical symptoms, histology and gene expression of colonic tissues were assessed. Relative expression of inflammatory cytokines (*COX2* and *TNF*α) was significantly reduced in protegrin treatment groups ($P < 0.05$). Protegrin treatment prevented significant body weight loss and improved disease activity index (DIA) scoring ($P < 0.05$) compared to the untreated DSS-control mice (Figure 1). Histological analyses indicate reduced mucosal erosion and sub-mucosa inflammation in protegrin-treated (pro- and mature-) groups. Overall, oral administration of protegrin was demonstrated to be protective against colitis induction in mice. Histological and gene expression results are reflective of the phenotype observed in protegrin *dextran sulfate sodium*-treated mice and the controls.

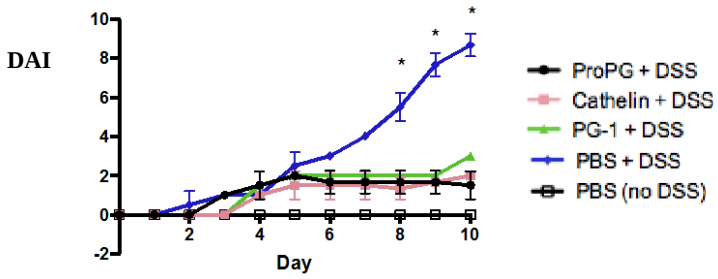


Figure 1. Protegrin treatments improve disease activity index (DAI). By day 8, DSS- colitis mice treated with protegrin (ProPG, Cathelin and PG-1) have a significantly (*; $P < 0.05$) improved total DAI scoring compared to the PBS untreated mice. Clinical symptoms were evaluated on a point scale. A higher score indicates more severe disease symptoms.

Benefits to the swine industry: Our data demonstrated protegrin-1 is active in enhancing intestine recovery from colitis *in vivo*. It may be an alternative means for treatment/prevention of colitis resulting from early weaning stress or infection in the pork industry.

Acknowledgements: The authors would like to thank Ontario Pork and NSERC CRD for the funding support of the study.

Evaluation of algae meal as an omega-3 PUFA supplement in nursery pigs

A.V. Lee, R.E. Fisher-Heffernan, J. Zhu, D. Wey, C.F.M. de Lange, N.A. Karrow
Department of Animal and Poultry Science, University of Guelph; nkarrow@uoguelph.ca

Background: Omega-3 polyunsaturated fatty acids (n-3 PUFA) are well-known for their anti-inflammatory properties. These n-3 PUFAs are essential nutrients, as longer chain fatty acids such as docosahexanoic acid (DHA) cannot be readily synthesized in mammals. Until recently, fish have been considered a major source of the long chain fatty acids. This has put a great strain on the fishing industry and therefore algae meal has been suggested as an alternative. Algae meal is equally rich in DHA and may provide a more sustainable source of omega-3 enrichment for growing animal diets. The aim of this study was to compare algae meal (AM) and fish oil (FO), matched for DHA content and the effects on piglet performance and immune response.

Methodology: Ninety-six cross-bred piglets were selected, weaned and placed on a low quality protein diet supplemented with either 2.5% FO or 1.25% AM for three weeks followed by a common diet for three weeks. Performance was measured over the duration of the study (42 days). Serum samples were collected from 24 pigs for PUFA analysis on days 7 and 21. In addition, half of the pigs in each treatment were sensitized to two novel antigens, OVA (ovalbumin) and CAA (*Candida albicans*) on day 7, and subsequently received boosters on day 21 to assess the effects of AM and FO on immune response. The cutaneous hypersensitivity response was assessed using 41 pigs (FO n=18, AM n=23) at 6, 24 and 48 hours post-antigen challenge.

Results: Results from this study show no differences in plasma DHA concentration between the two dietary treatments. No differences in piglet production parameters as measured by ADG and feed efficiency were detected over the study period. Lastly, no differences were observed between the FO and AM treatments to either antigen following the dermal hypersensitivity test.

Benefits to the swine industry: Results from this study suggest that AM is a dietary supplement comparable to FO, promoting piglet health and growth. AM may also be a more sustainable supplement than FO and as further research is conducted in this area, AM may become a more economical choice.

Acknowledgements: Alltech Inc., NSERC, OMAFRA, Arkell Swine.

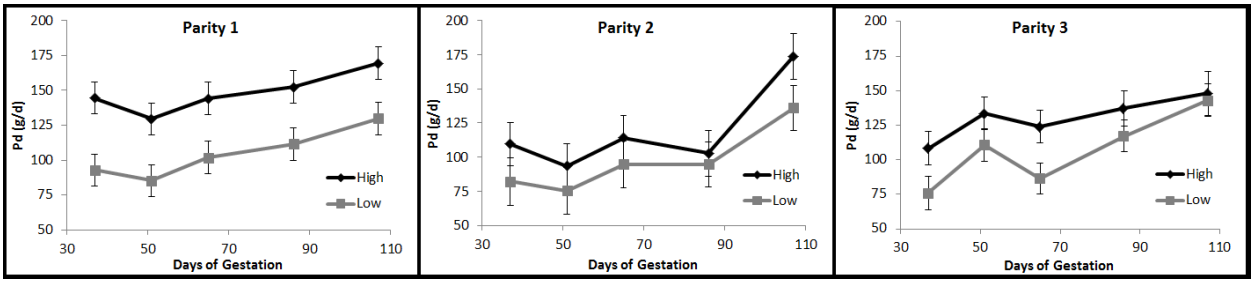
The dynamics of whole body nitrogen retention in gestating sows across three parities

E.G. Miller[1], D.C. Wey[1], C.L. Levesque[2], and C.F.M. de Lange[1]*.
[1]*Department of Animal & Poultry Science, University of Guelph;* [2]*Department of Animal Science, South Dakota State University;*
**cdelange@uoguelph.ca*

Background: Whole body protein deposition (**Pd;** Nitrogen (N) retention x 6.25) is a main determinant of amino acid and energy requirements of gestating sows. Empirical data on the dynamics of Pd in gestating sows remains limited (NRC, 2012). Further research is needed to characterize patterns of Pd, especially as it relates to the gradual transition of maternal Pd in early gestation to fetal (pregnancy-associated) Pd in late gestation, as well as parity effects.

Methodology: 52 gestating Yorkshire gilts (initial body weight [**BW**] and P2 back fat [**BF**] at 25d of gestation 168.9±2.2 kg and 16.9±0.8 mm, respectively) from the Arkell Swine Research Station were used for repeated N-balance observations over 3 successive parities, with 30 sows completing the entire trial. During each gestation cycle, sows were randomly assigned to one of two feeding levels (high and low, ±15% estimated energy requirements, respectively) based on average BW and BF at breeding and the NRC (2012) gestating sow nutrient requirement model. A common corn and soybean meal diet was used for both feeding levels (3.30 Mcal ME/kg, 17.8% CP, 0.82% SID Lys) and fed from d 30 to 110 of gestation. During each gestation, 5 N-balance periods (4d in length) started at d 35, 49, 63, 84, and 105 of gestation. BW and BF was measured bi-weekly. Pregnancy-associated Pd (fetus, mammary gland, uterus, and placenta and fluids) was calculated using litter size, average piglet birth weight, and NRC (2012). Maternal Pd was calculated as the difference between whole body Pd and pregnancy-associated Pd.

Results: For all three parities, initial BW and BF (d 25 of gestation) did not differ between feeding levels ($P>0.15$), with the exception of parity 3 BF ($P<0.01$). At d 109 of gestation, BW ($P<0.01$) and BF ($P<0.02$) were greater at the high feeding level. For each parity, whole body Pd was greater at the high feeding level and increased with day of gestation for both feeding levels ($P<0.05$), but there was no interaction ($P>0.54$). For all 3 parities, maternal Pd was greater for the high feeding level ($P<0.05$) and was affected by day of gestation (parity 1 and 2, $P<0.01$; parity 3, $P=0.17$), but there was no interaction ($P>0.53$). Carry over effects of the previous gestation feeding level were not observed for BW, BF, or Pd.



Benefits to the Swine Industry: Across parities, increasing feed intake during gestation leads to an increase in whole body and maternal Pd, which is constant throughout gestation and consistent with NRC (2012). However, the effect of feeding level on maternal Pd is parity specific, with greater impact during parity 1 and 2, when maternal Pd is higher. Parity specific differences in Pd have important implications for the factorial estimation of amino acid requirements of gestating sows and thus, warrant consideration when formulating diets.

Acknowledgements: Thanks to lab mates and technical staff. Financial support provided by Ontario Pork, Ontario Ministry of Agriculture and Food, de Heus, and Ajinomoto.

A cytogenetic study of young breeding boars in Canada

Quach TA, Revay T, Macedo M, King WA
Department of Biomedical Sciences, University of Guelph, Guelph ON

The fact that chromosome rearrangements are major etiologic factors behind subfertility has been shown in many studies, which have revealed three major types of abnormalities; reciprocal translocations, centric fusions and inversions. It is also observed that, although not fully explained, "*de novo*" chromosome rearrangements occur more frequently in pig than in other species. In our previous pilot study (TA Quach et al. 2009) we showed that chromosome abnormalities in the Canadian swine population are very high (2.5%). Therefore, the aim of this study is to detect the potential carriers of chromosomal anomalies in a much larger sample size. In total, 300 young boars from 4 different breeds (Duroc, Landrace, Pietrain and Yorkshire) were karyotyped by G-band techniques. Four previously unreported reciprocal translocation including rcp(1;5), rcp(3;4), rcp(8;13) and rcp(7;15) and one Robertsonian translocation rob(13;17) were found, thus the frequency of chromosome abnormalities in this study is 1.67%. We are able to determine that rcp(3;4) and rob(13;17) were inherited from their dams and rcp(8;13) was a "*de novo*" event. Prolificacy of rcp(3;4) and rcp(7;15) translocation carriers was noted to be reduced (24% and 38%, respectively) while it was slightly reduced 9% in carriers of rob(13;17). More studies need to be carried out to further investigate the effect of these translocations.

Funding for this project has been provided by the Canada Research Chairs program and Agriculture and Agri-Food Canada through the Canadian Agricultural Adaptation Program (CAAP). In Ontario, this program is delivered by the Agricultural Adaptation Council

Evaluation of porcine reproductive and respiratory syndrome control methods using agent-based modelling

Arruda, A. G.[1]; Poljak, Z.[1]; Greer[1], A.; Friendship, R.[1]; Carpenter, J.[2]
[1]*Department of Population Medicine, University of Guelph;* [2]*Ontario Swine Health Advisory Board*

Background: Porcine reproductive and respiratory syndrome (**PRRS**) is an important endemic swine disease in North America, and even though elimination of the virus from swine sites is feasible, virus re-introduction and recurrent outbreaks are common. Gilt acclimation is a procedure commonly used to minimize the likelihood of new virus introductions and re-emergence of previously existing viruses occurring in the breeding herd. Acclimation can be achieved using vaccination with a commercial modified live vaccine, or immunization based on exposure to the PRRS virus resident to the herd (field virus). Information on the comparative efficacy of the above-mentioned strategies for preventing future outbreaks is currently unavailable for two main reasons: traditional studies would be unethical to carry in field settings, and reaching a counterfactual state is problematic due to the variability of management and characteristics amongst swine farms.
The objective of this study was use disease modelling to investigate which of the control measures above-mentioned would best minimize the likelihood of an outbreak in a typical Ontario farrow-to-wean swine site compared to a baseline of no control measures implemented.

Methodology: A stochastic, agent-based model was developed in order to capture different animal characteristics such as disease status and location in the farm for female pigs and produced offspring, as well as heterogeneity of contacts within a herd. The model was created using Anylogic®7.1.2, and the outcome of interest was the maximum number of infected animals resulting from re-introduction of the virus into herds of different compositions. One hundred model iterations were generated for each scenario and sensitivity analysis was conducted to examine the impact of variation in the expected outcome when duration of infection and initial conditions related to virus introductions were modified.

Results: Model results demonstrated that both PRRS control strategies produced a higher frequency of simulations resulting in the absence of outbreak after the introduction of the virus, compared to the baseline scenario. A decrease in the duration of infectiousness resulted in an overall reduction on the maximum number of pigs infected. Finally, the frequency of no outbreaks occurring decreased as the number of infected animals introduced into the herd increased.

Conclusions: In conclusion, our findings suggest that homologous virus exposure would decrease the likelihood of occurrence of large PRRS outbreaks the most; and attempts to reduce the introduction of infected animals/ viral loads are valuable in decreasing the likelihood of major outbreaks.

Acknowledgements: Ontario Ministry of Agriculture and Food and Ontario Ministry of Rural Affairs, Ontario Swine Health Board Advisory, Canadian Swine Health Board, Ontario Pork, Natural Sciences and Engineering Research Council, Agricultural Adaptation Council, Animal Health Laboratory (University of Guelph).

Neonatal piglets are vulnerable to intestinal infection and inflammation due to their expressing very low intestinal alkaline phosphatase affinity

Nicole Burello, Tania Archbold and Ming Z. Fan*
Department of Animal and Poultry Science, University of Guelph, Guelph, ON N1G 2W1
**Correspondence author: (519) 824-4120, ext. 53656; E-mail: mfan@uoguelph.ca*

Background: Intestinal alkaline phosphatase (IAP) is located on the small intestinal apical membrane and is in the interface between host tissue, ingested food and digestive microorganisms (Lallès, 2010, *Nutrition Reviews*, 68, 323-332). The major role of IAP is to convert toxic lipopolysaccharides (LPS) into their non-toxic monophophoryl forms (Lallès, 2010). The IAP kinetics especially its activity affinity (K_m) represents its activity efficiency and its measurement is affected by assay medium pH. The IAP K_m values are typically measured by using a synthetic substrate *p*-nitrophenyl phosphate and are often measured at the enzyme optimal pH (10.5-11) (Lackeyram et al., 2010, *Journal of Nutrition*, 140, 461-468). Thus, determination of IAP K_m at a relevant physiological pH of 7.4 in suckling neonatal pigs will be more relevant to project how efficiently IAP is mitigating inflammation caused by LPS.

Objectives: The objectives of this experiment were to determine IAP kinetics by using jejunal tissues derived from several 10-day-old suckling piglets at physiological pH of 7.4 by using *p*-nitrophenyl phosphate.

Methods and procedures: The IAP K_m values were measured by using *p*-nitrophenyl phosphate according to our established protocol (Lackeyram et al., 2010) with media pH at 7.4.

Results

- Overall, the IAP jejunal K_m value for the suckling piglets was determined to be 0.437 ± 0.027 mM ($P < 0.05$, n = 48) at the pH = 7.4 by using *p*-nitrophenyl phosphate, which is considerably lower than the K_m values (6.00-6.99 mM) reported in previous experiments performed at a pH 10.5 with the same substrate and the same source of Yorkshire piglets by Lackeyram et al. (2010).

- Furthermore, the IAP jejunal K_m of 0.437 at a pH 7.4 from this study in the suckling neonatal pigs was drastically higher than the value of 0.024 uM performed in adult humans under the same conditions by Kiffer-Moreira et al. 2014 (*PLoS ONE* 9(2): e89374. doi:10.1371).

Take Home Messages: The jejunal IAP K_m value in the neonatal suckling pig is about 19 folds higher than the reported adult human gut K_m value. This comparison suggests that suckling piglets have considerably lower IAP affinity are susceptible to infection and LPS inflammation in the small intestine.

Acknowledgements: Financial support from the OMAFRA-University of Guelph Animal Research Program and NSERC is appreciated.