

2018 Dr. Kees de Lange Memorial Lecture

Dietary starch and fiber properties affect digestive physiology in pigs

Ruurd T. Zijlstra

Professor and Chair

Department of Agricultural, Food and Nutritional Science

University of Alberta, Edmonton, AB T6G 2P5, Canada

ruurd.zijlstra@ualberta.ca

Dr. Kees de Lange

The scientific accomplishments of Dr. Kees de Lange were outstanding. In the Journal of Animal Science, Dr. Patience and Fan published recently a biography that describes highlights of Kees' life and career (Patience and Fan, 2018). The reading of this paper is encouraged to grasp the impact that Kees had on his colleagues and discipline. I was fortunate to interact with Kees, especially during the last decade when funds became available that sparked research collaborations across Canada.

Abstract

Dietary antibiotics will be used less as growth promotant; thus, alternatives are investigated. Some efforts are focused on using feed additives as alternatives, but macronutrients in feedstuffs may also be part of a toolkit to manage gut health in pigs. Dietary carbohydrates include starch, fiber (non-starch polysaccharides) and oligosaccharides. Antibiotics are hypothesized to control gut health via manipulations of intestinal microbial profiles or reduced intestinal inflammation. Starch is mostly digested and absorbed as glucose; however, resistant starch is not digested but fermented. Resistant starch acts as fiber but is unique, because it 1) specifically increases digesta bifidobacteria that have been associated with improved gut health and 2) is completely fermented within the gut. Sources of fiber differ in 2 key characteristics: viscosity and fermentability. Increased kinetics of fiber fermentation is associated with changes in microbial profiles and increased metabolite production. Oligosaccharides may be rapidly fermented and thereby influence intestinal microbial profiles and metabolite production. Raw materials and prebiotic feed additives both influence kinetics of fermentation and have prebiotic activity. In conclusion, dietary carbohydrates via their prebiotics activity are part of the solution to remove antibiotics as growth promotant from swine diets.

Introduction

The gastrointestinal tract in pigs is colonized with a diverse population of bacteria that supports physiological development and immunologic functions (Willing and Van Kessel, 2010). However, pigs can have an unstable gut microbiome at various life stages, allowing opportunity for pathogenic bacteria to colonize and cause disease (Pieper et al., 2008, 2009). A combination of digesta passage rate, digestibility, fermentability, and viscosity contributes to nutrient availability and commensal bacteria colonization in the lower gastrointestinal tract (Metzler-Zebeli et al., 2010; Regmi et al., 2011). Starch and fiber may serve as energy source for the intestinal microbiota and thereby modulate its composition. Dietary starch and fiber are important nutrients for pigs but are underappreciated in their complexity.

Starch

Starch ranging from low to high amylose changes from rapidly enzymatically-digestible in the upper gut to fermentable in the lower gut including distal small intestine, respectively, due to changes in physico-chemical characteristics such as viscosity, fermentability, and water-holding capacity (Regmi et al., 2011). Starch can thus be a source of glucose or volatile fatty acids (also known as short-chain fatty acids) and for the latter is thus similar to fiber. If starch is fermented instead of digested, whole body energy utilization might be affected (Fouhse et al., 2018). In swine nutrition, the paradigm is that non-digestible carbohydrates are a negative dietary factor due to their fermentation and adverse effects on whole body nutrient utilization (Drew et al., 2012). In human nutrition, with health and not growth as main objective, fermentable or resistant starch is gaining popularity due to suppression of rate of nutrient absorption and stimulation of intestinal health (Bird et al., 2008).

Switching from dietary digestible to resistant starch provides readily-available substrates for microbes in the large intestine. Dietary fiber is also used by colonic microbiota as fermentative substrate (Topping and Clifton, 2001).

Diets high in amylose or resistant starch favor production of commensal bacteria such as *Bifidobacterium* and *Lactobacillus* groups in pigs (Brown et al., 1997; Bird et al., 2007). Decreasing in vitro starch digestion rate by increasing amylose content increased available nutrients (starch and protein) in the colon, thereby increasing commensal *Bifidobacterium* spp. in feces (Regmi et al., 2011). Moreover, dietary inclusion of highly viscous carboxymethyl cellulose increased prevalence of *E. coli* virulence factors, indicating the importance of post-ileal nutrient flow on substrate availability for commensal microbial colonization (Metzler-Zebeli et al., 2010). Although certain fiber sources share physico-chemical properties such as viscosity and fermentability, they do not consistently affect small intestinal digestion, large intestinal substrate availability or microbial responses; hence, fiber sources work according to individual fractions rather than shared functional properties (Metzler-Zebeli et al., 2010). Feeding high amylose starch creates an increasing flow of starch into the large intestine and thereby has a bifidogenic effect (Fouhse et al., 2015).

Fiber

Similarly, dietary fiber has a contradictory status in nutritional sciences. In swine nutrition, fibers such as β -glucans and arabinoxylans are regarded as negative dietary factors due to their negative effects on nutrient digestibility and feed intake (de Lange, 2000). In contrast, fiber gains popularity in human nutrition due to their adverse effects on rate of nutrient digestion and, therefore, glycemic index (Jenkins et al., 2002) and stimulatory effects on intestinal health (Kudo, 2004), and is increasingly regarded as a functional food component. Previously, we reviewed fiber digestion, absorption of its metabolites, and the impact of digestive physiology in the pig (Zijlstra et al., 2012). Among labs, our lab also has used in vitro fermentation methods to mimic in vivo digestion of fiber (Jha and Leterme, 2012; Jha and Zijlstra, 2018). Fiber can be important for energy metabolism of the pig. Fiber varies greatly in characteristics such as fermentability and viscosity that are important for its ability to affect physiological functions (Dikeman and Fahey, 2006). In the gut, fiber via its metabolites may directly stimulate physiological functions via local endocrine responses (Hooda et al., 2010). Obviously, because fiber cannot be digested by the pig itself, it is fermented by the gut microbiota. A combination of digesta passage rate, fermentability, and viscosity that are all influenced by fiber contributes to nutrient availability and commensal bacteria colonization in the lower gastrointestinal tract (Metzler-Zebeli et al., 2010).

Some oligosaccharides and polysaccharides are known prebiotics for human and animal nutrition (Topping et al., 2003; Bach Knudsen et al., 2012). Non-enzymatically digestible oligosaccharides (NDO) are highly fermentable, decrease gastrointestinal pH producing an unfavorable milieu for pH-sensitive microbes (Macfarlane et al., 2006). The NDO provide prececal prebiotic effects in weaner pigs (Houdijk et al., 2002). As pigs age, their microbiome becomes more stable and inclusion of prebiotic feedstuffs, such as resistant starch, NDO, or high amylose starch grain cultivars, have seemingly fewer effects. Supplementing fructan, a NDO, caused minor changes in digestibility without changes in microbiota (Hedemann and Bach Knudsen, 2010). Interestingly, when resistant starch and NDO were fed together to pigs, effects on colon and fecal bifidobacteria numbers were additive (Bird et al., 2009).

Combining soluble and insoluble NSP may cause similar additive effects on ileal bifidobacteria and enterobacteria populations (Owusu-Asiedu et al., 2006). Multiple studies in humans and other animals indicate that dietary resistant starch and NDO have a prebiotic effect across species (Brown et al., 1998; Tuohy et al., 2001). Oat β -glucan, either concentrated or within the cereal matrix, also has a prebiotic effect in pigs (Metzler-Zebeli et al., 2010); dietary β -glucan selectively increases colonic lactobacilli and bifidobacteria (Metzler-Zebeli et al., 2011) promoting butyrate-producing bacteria (Pieper et al., 2008).

Conclusion

Combined, convincing evidence exists that various starch and fiber fractions have a prebiotic effect in pigs. The carbohydrate fractions can be added to diets as purified sources; however, application via the use of unique cereal grain or pulse grain cultivars may create similar benefits (Fouhse et al., 2017a, 2017b). However, the singular or additive effects that carbohydrate fractions have on microbial diversity and colonization remain to be elucidated.

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2018 Mike Wilson Keynote Presentation

A Critical View of the Opportunities and Challenges in Swine Health Management

Cesar A Corzo

Associate Professor

Allen D. Leman Chair in Swine Health and Productivity

College of Veterinary Medicine

University of Minnesota

The North American swine industry has consistently evolved, not only because pig farms continue to reach production levels that, at some point, most thought were unachievable. It is also because of the level of sophistication with the adoption of new technologies, and the optimization of processes and production. This evolution occurred in part due to the team approach between the producer and the herd veterinarian seeking better ways of producing pigs with less resources. During this process, questions such as: “how we can do better” or “what if we try this or try that” kept being asked until a solution was found. Otherwise they would go back to the drawing board.

Swine production medicine has closely accompanied this evolution through the adoption of new technologies (i.e. PCR and serology assays, vaccines, antimicrobials, air filtration, electronic sow feeding) that was paired with a better understanding of disease epidemiology with a better, more informed decision-making process. For instance, some decades ago, pig production was based on the classical 100 to 300 sow one-site farrow-to-finish farm. As time went by, areas of expertise in veterinary medicine such as epidemiology of infectious diseases together with better diagnostic tools allowed veterinarians to understand that such a production model was not the best option from an infectious disease control standpoint, thus, the idea of segregating the breeding and growing pig herd was adopted (i.e. multi-site production). This mindset shift, generated a big change in the swine industry in that the number of one-site production systems decreased over time as they were replaced by larger multi-site production systems. This shift brought interesting challenges to the veterinary community in that the concept of herd health and population medicine became even more important since populations were larger and thus the impact would be considerably higher. Furthermore, what at some point we thought it would solve many health issues contributed to the generation of another challenge since regions that were perhaps low dense in the past became rapidly populated with growing pig barns creating the most challenging environment for pig production, high dense regions.

The veterinarian’s role throughout this industry developmental phase has changed in that in the early stages the focus was on performing individualized tasks as farms were much smaller whereas today the focus is more population based with prevention and control strategies being part of the day-to-day tasks. This adaptation brought in new areas for the swine veterinarian to work on, for instance, boar stud management, nucleus, multiplier and commercial herd biosecurity, gilt development and introduction protocols, system wide pig flow and viral or bacterial elimination from sow herds. Even with all these new developments and access to technology, veterinarians continue to face challenges.

I asked a group of seven veterinarians who manage the health of approximately one million sows to list the three main challenges the swine industry has today. Their responses are summarized below (Table 1).

Table 1. Three most important challenges in the swine industry

Veterinarian 1	Veterinarian 2	Veterinarian 3	Veterinarian 4	Veterinarian 5	Veterinarian 6
People – High turnover	Foreign animal diseases	PRRSv	Excessive amount of pork stored	Foreign animal diseases	Foreign animal diseases
PRRSv	People – High turnover	Wean-to-market mortality	Foreign animal diseases	People – High turnover	Consumer and social pressure
People – Training procedures	Regulations	Sow mortality	People – High turnover	Consumer and social pressure	Reliance on exports

By no means is the above table an accurate representation of the swine veterinary community; however, from their responses and as expected it is easy to deduce that health is high on their priority list. However, other type of

challenges such as people (turnover and training), industry regulations and consumer demands were raised. Together with these challenges, there are more challenges in our industry that did not make it to the top 3, for instance, veterinarian to pig ratio, optimum secondary pathogen (i.e. *Streptococcus suis*, *Haemophilus parasuis*) control; antimicrobial resistance, transport biosecurity, disease control in high dense regions among others.

For the purpose of this paper I will briefly focus on two challenges which are may be related, people and PRRS. Even though there is scarce data on the relationship of PRRS occurrence and people poor biosecurity protocol execution, there is enough data on how biosecurity procedures (conducted by people) can decrease the odds of occurrence.

People

Animal production relies heavily on people to perform different tasks that can range from very simple (i.e. feeding) to more complex (i.e. semen dilution and evaluation). For every task there are basic requirements but most importantly, there is a need for consistency in order to have predictable outcomes.

There are examples such as two sow farms with basically the same health status, same feed source, same genetic level, same technology, same building type and the only difference besides their physical location is the people who manage the farm. Interestingly these two farms end up performing differently. These scenarios may seem rare to some but we would be surprised with how common they may be around the world. A typical example is when a new farm manager or breeding crew leader joins the team and suddenly performance improves which leads us to think that people play an important role. Such improvement may be due to a better degree of execution together with discipline. Without aligning these two characteristics, sow farms would have not been able to reach unthinkable levels of productivity such as 35+ pigs/sow/year.

There are different examples in human medicine that relate to the sow farm example. For instance, patients undergoing Tuberculosis treatment are required to take one antibiotic caplet per day but research has demonstrated that patients do not follow the protocol if they are sent home and asked to do it, therefore, they are asked to allow a health professional to come to their houses and provide the antibiotic. Another example is patients with heart conditions that do not follow their cardiologist recommendations such as modifying their diets, exercising and, in some cases, taking lipid-lowering agents. Adherence to treatment is currently an area of research with since discipline can be questionable. Therefore, if human patients are not disciplined with tasks directly related to their own health, we must wonder if we should expect to see lack of discipline on our farms when it comes to following biosecurity practices or vaccination protocols?. This phenomenon generates several questions and probable associations between lack of discipline and disease outbreaks due to poor biosecurity protocols compliance or poor reproductive performance for instance. The challenge continues to be aggravated if we take into consideration that people turn over in pig farms is also an issue.

We then wonder what other industries have done to deliver consistently throughout time and perhaps we are already seeing such a trend in our industry. The swine industry has gradually been incorporating technology (i.e. automatic feeding systems, automated boar collection and sow heat detection technologies) aiming at consistency as well as lowering costs. Therefore, there may be less workforce required on the farms; however, it will be difficult to run a farm without people performing tasks such as detecting sick pigs for timely injections, breeding, cleaning and disinfection, pig movement and farrowing assistance. It is on our hands now to figure out the best procedure to hire the correct individual, appropriately train our staff together with maintaining our workforce motivated.

PRRS

It is no mystery for anyone that PRRS continues to be a devastating disease in North America. The North American veterinary community has been able to learn how to stabilize and eliminate the virus from breeding herds and entire systems in a consistent manner. However, we continue to struggle to maintain the virus out from these, which warrants further investigation into the epidemiology of this disease.

Through programs like the “Morrison Swine Health Monitoring Project”, the US industry has been able to better understand the epidemiology of this virus. One take-home message from monitoring approximately half of the US

breeding herd is that year after year the virus continues to disseminate at higher or lower rate infecting at least 20% of the breeding herds including filtered farms and those located in remote isolated areas. In the last few years, Dr. Bob Morrison was constantly challenging the industry by asking “Why are we not making any progress?” despite all the technology (i.e. Thermo-assisted drying and decontamination truck system, sow farm filtration, shower-in, UV-light chambers, disinfectants, vaccines, downtime requirements, intensive biosecurity protocols). Dr. Morrison’s question brings up many possibilities, poor biosecurity compliance (internal and external), airborne transmission, unknown routes of transmission.

One of the possibilities is adherence to protocols meaning that with the size of production systems today, it is important to consider that the larger the system, the larger the number of people working in the system therefore the larger the chances of making mistakes. This is where a great deal of time may be invested in auditing processes to make sure that all the tasks we believe are being performed are actually being done. This is especially important when dealing with a large fleet of trucks or PRRS elimination projects in that specific task may be overlooked and put the project at risk.

Another challenge is a shortage of food animal veterinarians, which unfortunately is a limitation when it comes to overseeing systems in an appropriate manner. The industry continues to grow at a steady pace but the number of swine veterinarians may not be keeping its pace therefore one individual may be responsible for a large number of herds which increases the probability of missing important details when building a health program, especially a biosecurity program which is key to preventing new introductions for PRRS.

In closing, swine health management challenges will continue to exist as the industry evolve and grow. In some cases, we should wonder then if we require more tools to keep up with these challenges or if we need to revisit our basics and make sure that we are meeting the expectation with the basic principles of animal health.

How network analysis can help us understand the 2014 Canadian porcine epidemic diarrhea outbreak

Amanda M Perri MSc¹; Zvonimir Poljak DVM, MSc, PhD¹; Cate Dewey DVM, MSc, PhD¹; John CS Harding DVM, MSc, Dipl. ABVP²; Terri L O'Sullivan DVM, PhD¹.

Department of Population Medicine, University of Guelph¹, Large Animal Clinical Sciences, University of Saskatchewan²

Introduction: Network analysis is an important methodological approach in veterinary epidemiology. It can be used to describe livestock contact movement patterns and to visualize and estimate the potential for disease transmission among animals through these contacts.¹ The objectives of this study were to describe the contact structure of porcine epidemic diarrhea (PED) positive (case) herds and matched PED negative (control) herds with feed suppliers; and to evaluate possible mechanisms of PED spread during the early phase of the 2014 Canadian outbreak using computer generated networks.

Methods: A questionnaire was used to gather information on herd contact patterns with feed suppliers between Dec 2013-Feb 2014. A total of 23 Canadian swine herds (n=9 case herds; n=14 control herds) were included in the study. A case was defined as any swine herd with confirmed positive results for PED virus based on RT-PCR and with typical clinical signs at the herd level within the study period. Control herds were randomly selected and matched to cases based on herd size, herd type, and time of PED onset in case herds. A full network of all herds and separate case and control networks were generated to represent herd contact patterns with feed suppliers.

A series of randomized computer-generated networks (point source hypothesis testing) were used to compare the proportion of case herds linked to a feed supplier with maximum number of connections in the observed and simulated networks.

Results: Viral transmission of PED during the early months of the 2014 outbreak was most likely associated with a point source outbreak through connections with feed suppliers. This finding was based on an unusually high observed proportion of cases in the largest network of a single feed company compared to randomly generated networks. Using network descriptive measures, the outgoing contact chain (OCC) was evaluated to determine the number of direct and indirect connections in a path during a specific time sequence. The largest OCC for the case network (n=9) was longer than the OCC of the control network (n=4). The origin of the largest OCC in the case network was a unique feed supplier (FS1), and the origin of the largest OCC in control network was different. The case herd network also had a higher mean out-degree (the number of direct contacts) (1.83; range: 1-8), compared to the control herd network (1.43; range: 1-3). The facility with the largest out-degree in the case network was FS1.

Conclusions: The results from this study suggest that the early phase of the 2014 PED Canadian outbreak was most likely due to a common source (i.e. point source transmission) through connections with feed suppliers after comparing the randomized generated networks and the observed network. The network descriptive measures indicate that that FS1 the most important point source for PEDV transmission during the early outbreak.

Industry Implications: Network analysis and the interpretation of the point source hypothesis used in this study has facilitated further understanding of the contribution of feed suppliers and subsequent network connectivity during the early months of the 2014 PED Canadian outbreak.

Acknowledgments: Funding provided by OMAFRA, Ontario Pork, and NSERC- CRD

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Prevalence of porcine chromosomal rearrangements in Canadian swine herds

Brendan Donaldson BSc¹, Daniel A.F. Villagomez DVM, PhD^{1,2}, Tamas Revay MSc, PhD¹, Samira Rezaei BSc¹,
W. Allan King MSc, PhD¹

Department of Biomedical Sciences, University of Guelph¹, Departamento de Producción Animal, Universidad de Guadalajara²

Introduction: Chromosome rearrangements are one of the major factors behind reproductive dysfunction in pigs, often leading to early embryonic mortality. Chromosome rearrangements, such as translocations, result from mismatched DNA strand repair during meiosis, creating derivative chromosomes consisting of genetic material from two or more chromosomes. Although carriers may appear normal, predictable reproductive dysfunction occurs as derivative chromosomes may misalign during meiosis creating unviable gametes, leading to embryonic loss. Carriers of chromosome rearrangements on average experience a 50% decline in fertility, while passing on their rearrangement to 50% of successful offspring, allowing the rearrangement to propagate throughout the population. The negative impact of chromosome rearrangements on swine reproduction has led to the establishment of cytogenetic screening programs in many countries.

Methods: The King Lab at the University of Guelph has initiated the largest swine cytogenetic screening operation in North America, screening over 3700 boars since January 2015. Peripheral blood is obtained weekly, cultured for 72 hours, and harvested using standard chromosome preparation techniques and GTG-banding (1). Metaphase chromosomes are imaged under a camera mounted microscope, and the resulting images are karyotyped via SmartType software, allowing for the detection of chromosome rearrangements.

Results: Since the initiation of this screening program, 21 unique chromosome rearrangements have been found amongst 34 carriers. Considering only unique rearrangements we report a prevalence of 0.56% in our population, while considering all rearrangement carriers we report a prevalence of 0.91%. Carriers are reported for all major breeds in our program. Screening over successive generations shows a noticeable drop off in the number of rearrangements seen by the fourth generation, whilst an increase in mosaic (single cell) chromosome rearrangements has been found in the population.

Conclusion: Chromosome rearrangements are quite prevalent in the Canadian swine population, and we report a similar de-novo rate of formation as another program, 0.47% (2). Chromosome rearrangements form at similar rates amongst different populations, and different breeds, indicating the susceptibility of the swine population. Continued screening efforts show a noticeable decline in the number of chromosome rearrangements in the population. Our lab will begin to observe the genetic landscape of rearrangement carriers in order to study rearrangements closely, and identify the genomic factors behind their formation.

Industry Implications: Chromosome rearrangements occur in approximately every 1 in 200 pigs, regardless of origin. Carriers of rearrangements often go undetected, and experience predictable declines in fertility. Screening programs are currently the only method of detecting and removing carriers from swine populations.

Acknowledgements: Funding provided by: The University of Guelph, the Ontario Veterinary College, and OMAFRA.

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Stress and resilience among agricultural producers in Canada: a mixed methods approach.

Briana Hagen, MSc, PhD(Candidate)¹, Terri O'Sullivan, DVM, PhD¹, Sherilee Harper, PhD¹, & Andria Jones-Bitton, DVM, PhD¹

Department of Population Medicine, University of Guelph¹

Purpose/Objectives: Farming is a stressful occupation and farmers face disproportionately high rates of mental health issues and suicide compared to other occupations. There is a serious gap in knowledge regarding Canadian farmer mental health. This research comprehensively explores mental health in Canadian agriculture to inform strategies that will help achieve a healthier and more productive agricultural community. The objectives are to: (i) identify factors associated with mental health outcomes (stress, resilience, anxiety, depression and burnout); and (ii) characterize the lived experience of mental wellness among Canadian farmers, its impacts, and how this influences use of mental health services.

Methods: This project uses a mixed-methods sequential explanatory design. **Quantitative methods:** Jones-Bitton conducted an online cross-sectional survey in 2015-2016 to collect national data from Canadian farmers (n=1,134), using validated psychometric scales (including perceived stress, resilience, anxiety, depression, burnout, and resilience). These data were used to construct multivariable linear and logistic regression models to explore relationships between demographic variables, lifestyle, self-rated health and mental health variables, and mental health outcomes. **Qualitative methods:** To characterize the lived experience of mental health and wellness among farmers, 65 semi-structured, in-depth qualitative interviews were conducted across all factions of agriculture, including all major farming commodities in Canada, industry, veterinarians, and governmental representatives. A thematic analysis of the data is underway.

Results: In the multivariable linear regression model examining factors associated with **stress**, pig farming was the only commodity significantly associated with higher levels of perceived stress among Canadian producers. Other variables significantly associated with higher perceived stress included female gender, financial stress, and perceived lack of support from family and industry. As resilience increased, perceived stress significantly decreased. Additionally, there was a significant moderator effect of depression and anxiety, meaning the association between depression score and stress depended significantly on the anxiety score. In the multivariable logistic regression model examining **resilience**, increasing age, self-rated health, perceived support from friends, and lower depression scores were significantly associated with increased resilience scores. Thematic analysis of the qualitative data is currently underway. Themes associated with stress and resilience will be discussed.

Implications: These essential baseline data provide the first-ever comprehensive understanding of mental health in Canadian farmers. Further, these data are informing the development of culturally appropriate and evidence-based resources to support farmers, and in turn, Canadian agriculture and economy. More specifically, data from the qualitative interviews provide context to the factors identified in the quantitative analysis, and will be used in conjunction with a series of stakeholder working group meetings with members of agricultural groups, to inform the co-development of an agriculture-specific mental health and wellness intervention.

Acknowledgements: Funding provided by the Ontario Ministry of Agriculture Food and Rural Affairs – University of Guelph Partnership (Emergency Management program), Ontario Sheep Federation, Ontario Pork, Egg Farmers of Ontario, Ontario Federation of Agriculture, and the Canadian Animal Health Coalition.

The relationship between hemoglobin levels and growth performance and antibody response in nursery pigs

Victoria CJ Seip, BSc; Robert M Friendship DVM, MSc; Vahab Farzan DVM, MSc, PhD
Department of Population Medicine, University of Guelph

Introduction: Administration of iron (200 mg Fe as iron dextran per piglet) on day 2 or 3 after birth to prevent anemia is a common practice in modern pig husbandry. However, it has been shown that despite supplementation, iron deficiency is common among fast-growing pigs at weaning when pigs are faced with stress and disease-challenge. The objective of this study was to determine whether iron status (based on hemoglobin levels) has an effect on antibody response to *Mycoplasma hyopneumoniae* vaccine and on growth rate in nursery pigs.

Materials and Methods: All piglets (n=254) from 22 litters were included in two trials conducted at the Arkell Research Station. At 3 days of age, one-third of each litter were given 100 mg of iron dextran (Uniferon®200, Pharmacosmos Inc.) by intramuscular injection, and the remaining two-thirds of the litter were given 200 mg of iron dextran. One-third of the pigs that received 200 mg of iron on Day 3 were injected with a second dose of 200 mg of iron on Day 14. At weaning a subset of piglets (n=145) were moved to the nursery and followed for 6 weeks. All of these pigs were vaccinated against *Mycoplasma hyopneumoniae* and revaccinated 3 weeks later. Pigs were weighed, and blood samples were taken at weaning, 6 weeks of age (prior to receiving the *M. hyopneumoniae* vaccine) and 9 weeks of age. Blood samples were submitted to the Animal Health Laboratory (AHL) for a non-differential analysis and to determine hemoglobin levels. Serum samples were tested for presence of antibody to *M. hyopneumoniae* using an IDEXX antibody ELISA.

Results: At weaning, 145 piglets were categorized based on their hemoglobin (hgb) levels into three groups including anemic (n=33) hgb <90g hgb/L, iron deficient (n=36) 90-110g hgb/L, and normal (n=76) >110g hgb/L. Among the anemic and low iron groups, hgb levels increased during the nursery phase and prior to exit from the nursery, the majority of pigs were classified as having normal hgb levels (n=134) and the remaining pigs were classified as being iron deficient (n=11). Pigs that were iron deficient at exit experienced slower growth throughout the nursery than other pigs with normal hgb levels ($P<0.05$). The iron status at weaning did not affect the pig's response to vaccination with *M. hyopneumoniae* vaccine ($P>0.05$). Further analysis identifying the significance of antibody response based on iron status just prior to exiting the nursery is currently incomplete.

Conclusions: These findings indicate that anemic (<90g/L hgb) or iron deficient (90-110g/L hgb) pigs at weaning might have the ability to replenish their iron stores throughout the 6-week nursery period. Pigs that don't overcome low iron status during the nursery phase tend to grow slower than those pigs which do reach adequate iron levels.

Industry Implications: Iron deficiency at weaning doesn't appear to interfere with antibody production with respect to response to vaccination but in this trial iron status tended to improve quickly in the nursery. In other trials anemia has persisted in the nursery and this needs to be further investigated with respect to immunity.

Acknowledgements: We would like to thank Pharmacosmos, OMAFRA HQP, OMAFRA U of G Research Partnership for financial support, and thank Rocio Amezcua and Arkell staff for their assistance.

Association between tonsilar viral profile and clinical *Streptococcus suis* infections in nursery pigs

Kaushalya (Kash) Kuruppu BSc, DVM; Emily Arndt BSc, MSc; Zvonimir Poljak DVM, PhD; Vahab Farzan DVM, MSc, PhD; Robert Friendship DVM, MSc, Dip ABVP; Davor Ojkic, DVM, MSc, PhD
Department of Population Medicine, Ontario Veterinary College, University of Guelph,
Guelph, ON

Introduction: *Streptococcus suis* can be found in almost all swine herds. Piglets acquire *S. suis* through vertical transmission from the sow and environmental contamination at birth, but only some piglets are colonized, and only a few develop bacteremia and meningitis (1). Colonized pigs have been found to carry *S. suis* in their tonsils and/or genital tracts and infections are common in all types of production systems (1). Outbreaks of *S. suis* in nursery piglets may be suggestive of an underlying viral pathogen such as porcine reproductive and respiratory syndrome virus (PRRSV) or circovirus (1). Nursery pigs coinfecting with PRRSV and *S. suis* experience severe CNS disease, bacteremia and higher mortality than those infected with *S. suis* alone (1). Some of these interactions could be tracked using high-throughput technology, such as next generation sequencing (NGS). The primary objective of this study is to compare the respiratory virome of nursery pigs clinically affected with *S. suis* with healthy pigs from the same group using NGS technology in order to explore whether viral-bacterial interaction is associated with *S. suis* clinical disease.

Methods: This study involves collecting nasal, tonsillar, rectal, meningeal swabs and whole blood from cases and matched controls from farms with outbreaks of *S. suis* in the nursery pigs. Cases are selected based on clinical signs including ataxia, incoordination, convulsions, paralysis, nystagmus and controls based on health, appropriate body condition and exhibition of normal behavior. Tonsilar swabs of cases and controls are screened for common nursery pig viruses using PCR for PRRSV, influenza A virus, porcine circovirus 2 (PCV-2) and next generation sequencing.

Results: To date, tonsilar swabs of 30 cases and 30 controls were found positive for at least one virus using PCR. Preliminary results showed that 17% of the *S. suis* cases and 13% of healthy controls were positive for PRRSV, while only 3% of *S. suis* cases were positive and none of the healthy animals were positive for PCV-2 and influenza A virus. Further, 53% of *S. suis* cases and 59% healthy controls were positive for porcine cytomegalovirus (CMV).

Conclusion: Interestingly, healthy piglets were found to have infectious levels of PRRSV, influenza A virus, PCV-2 and CMV in their tonsils with PCR (Ct <36.99), which encourages in depth investigation of viral communities of healthy animals using next generation sequencing. This also illustrates the need for on-farm surveillance of viruses and investigation of complex disease dynamics in the nursery.

Industry Implications: Studying the interaction between viruses and *S. suis* infection may help prevent *S. suis* related outbreaks more effectively. Creating a profile of the nursery pig respiratory virome may provide the swine industry with baseline information for evaluating emerging viruses.

Acknowledgments: Funding provided by Canada First Research Excellence Fund.

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The influence of azaperone treatment at weaning on reproductive function in sows: ovarian activity and endocrine profiles during the weaning-to-ovulation interval

B. Baker BSc¹; T. Schwarz PhD²; A. Ziecik PhD⁴; M. Murawski PhD³, DSc; J. Nowicki PhD²; R. Tuz PhD²; P. M. Bartlewski DVM, MSc, PhD¹

Department of Biomedical Sciences, Ontario Veterinary College, University of Guelph¹, Department of Swine and Small Animal Breeding², Department of Animal Biotechnology³, Agricultural University of Cracow, Poland; Department of Hormonal Action Mechanisms, Institute of Animal Reproduction and Food Research, Polish Academy of Sciences⁴

Introduction: Azaperone is a neuroleptic sedative of the butyrophenone class of drugs that is commonly used in commercial settings to limit stress experienced by the sow during the weaning-to-ovulation interval. The reproductive consequences of azaperone administration during this sensitive time period have not been thoroughly scrutinized. The objectives of the present study were to assess ovarian follicular development, endocrine profiles and reproductive performance of sows given azaperone at the time of weaning.

Methods: Twenty-four (24) parity II sows (Polish Landrace x Polish Large White) were randomly allocated into azaperone treatment (n=12) or a saline control (n=12) groups. An i.m. azaperone (40 mg/ml) injection (1 ml/20 kg b.w.) was given on day 28 of lactation, immediately before weaning. Blood samples in both groups were collected via indwelling jugular catheter every 10 minutes for the first hour after azaperone injection, then every hour until the 6th hour, and every 4 hours until ovulation. Serum samples were analyzed for concentrations of cortisol, estradiol 17 β (E₂-17 β) and luteinizing hormone (LH). Sows were artificially inseminated (AI) at the onset of behavioral estrus using PIC 337- or PIC 408-line boar semen (3x10⁹ spermatozoa per 100 ml of inseminate). Antral follicular growth rates were monitored and corpora lutea were detected using daily transrectal ovarian ultrasonography (Aloka PS2 scanner equipped with a 7.5-MHz linear-array transducer) performed from 2 days before weaning until the end of estrus, and again at 15-16 days post-AI.

Results: All sows ovulated and became pregnant following AI; however, only 11 animals in each group carried piglets to full term. Azaperone treatment prolonged the intervals from weaning to the onset of estrus (99.3 hr. vs. 85.7 hr.), first service (116 hr. vs. 104 hr.), second insemination (138 hr. vs. 128 hr.) and ovulation (141.6 hr. vs. 129.6 hr.; azaperone-treated vs. control sows, respectively). Azaperone-treated sows had greater ovulation rate compared with control animals (13.7 vs. 12.6; p<0.05), but no significant differences were seen in mean litter size or numbers of live-born and stillborn piglets. The mean growth rate of ultrasonographically identified ovarian antral follicles was lower (p<0.05) in azaperone-treated (1.08 $\pm$ 0.17 mm/day) than control sows (1.23 $\pm$ 0.18 mm/day). A transient suppression (p<0.05) of cortisol release was observed in the treatment group (at 10 and 30 min after azaperone injections) but circulating cortisol concentrations were variable in both groups of sows for the remainder of the study. Azaperone treatment significantly delayed the peak in LH (118 hr. vs. 102 hr.) and E₂-17 β concentrations (69.6 hr. vs. 57.7 hr.; time 0 min=azaperone injection), and prolonged the duration of the preovulatory LH surge (42.7 hr. vs. 32 hr.; p<0.001).

Conclusions: The administration of azaperone at weaning significantly enhanced antral follicular growth and ovulation rates in second parity sows. Changes in ovarian kinetics could be attributed to variations in periovulatory patterns of reproductive hormone secretion. More studies are needed on causative relationships between endocrine variables and ovarian activity during the weaning-to-ovulation interval in sows.

Industry Implications: In addition to its sedating properties (e.g., control of stress during the relocation/re-grouping of sows), azaperone administration can be used to synchronize the onset of behavioral estrus and boost fertility in commercial pig herds.

Acknowledgements: Supported by a grant from the Polish Ministry of Science and Higher Education (MNiSW; no. N N311 370837) and Statutory Funds of the Department of Swine and Small Animal Breeding, Agricultural University of Cracow, Poland (DS 3265/ZHTChiDI).

Can tryptophan modify behaviour and growth in growing pigs?

Maggie L Henry, BSc¹; Robert M Friendship DVM, MSc, Dip ABVP¹; Anna K Shoveller, PhD²;

Anita L Tucker, PhD¹

Department of Population Medicine, University of Guelph¹, Department of Animal Biosciences, University of Guelph²

Introduction: In growing pigs, aggression and aberrant behaviour such as tail- and ear-biting can result in decreased growth, diminished health and welfare, increased morbidity and mortality and increased labour on the part of the producer. Tryptophan (TRP), an essential amino acid in the pig's diet, has been shown to produce calming effects in both rats and humans (1) through its role in the serotonergic system. The objective of this study is to determine the effect of varying inclusion rates of dietary TRP on aggression, aberrant behaviour and growth in grower pigs.

Methods: This study examined the effects of 3 feed treatments on a total of 90 grower pigs (over 2 trials) divided equally across the three diet treatments in a completely randomized block design. Sex, weight and litter origin were balanced across pens in each trial. There were 5 pigs/pen and 3 pens/treatment. This feeding trial lasted a total of 29 days, with feed and water being fed *ad libitum*. A single diet was formulated based on providing all nutrients at or above their estimated NRC requirements. Amino acid mixtures were then added to the base diet to provide: 1) Control diet (TRP at 100% of its standard ileal digestible (SID) requirement), 2) TRP at 175% of its SID requirement, and 3) TRP at 250% of its SID requirement. All feed was weighed and feed intake was measured for the duration of the trials. All pigs were weighed weekly. All pens had continuous behaviour recordings done for 12 hours (06:00-18:00) 3 days/week. An ethogram was used to examine 13 mutually exclusive behaviours and to evaluate the severity and duration of aggressive interactions taking place; the number of bites and head-knocks, as well as the duration of time spent fighting; ear- and tail-biting were also recorded at this time using 10 minute scan sampling. Plasma and serum samples were taken from 3 pigs/pen (N=27/trial) at four different time points (day 8, 15, 22 and 29) with TRP and serotonin levels being measured respectively, using ELISA.

Results: Preliminary results indicate that the increased levels of tryptophan did not appear to have an effect on growth rate or the prevalence of abnormal and aberrant behaviour.

Conclusions: Data continues to be analyzed as it is gathered.

Industry Implications: The use of therapeutic TRP in pig diets could positively impact the entire pork industry if the producers could benefit from reduced labour costs in treating injured and ill animals, higher growth rates and better carcass quality; the industry could benefit from an improved public perception of how pigs are raised commercially; and the growing pigs could have increased health and welfare due to decreased levels of aggression.

Acknowledgements: Funding provided by University of Guelph-OMAFRA Research partnership, Grand Valley Fortifiers and OVC Departmental Graduate Growth Support.

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Effect of flavophospholipol on the gut microbiota of nursery pigs challenged with *Salmonella*

Saranya Nair MSc¹; Vahab Farzan DVM, MSc, PhD¹; Zvonimir Poljak DVM, MSc, PhD¹; Scott Weese DVM, DVSc, Dipl ACVIM²; Robert Friendship DVM, MSc, Dip ABVP¹

¹Department of Population Medicine, ²Department of Pathobiology,
University of Guelph, Guelph Ontario, Canada

Introduction: The presence of multi-drug resistant *Salmonella* Typhimurium DT104 on swine farms is a food safety concern. Research suggests that flavophospholipol, an antibiotic with nontransferable resistance, can alter the intestinal microflora in favor of beneficial bacteria inhibiting the colonization of *Salmonella*¹. The objective of this study was to evaluate the intestinal microbiome of weaned pigs that received in-feed flavophospholipol and were challenged with *Salmonella* Typhimurium DT104.

Methods: Thirty-two 4-week-old pigs were housed in a level 2 biosafety isolation facility over the duration of the trial (36 days). Pigs were fed either a diet containing 4-ppm in-feed flavophospholipol (Flavomycin[®], Huvepharma) or a non-medicated feed (Day 1). On Day 7 and 8 of the trial, piglets were orally challenged with a 2-mL dose of 10⁸ colony forming units (CFU)/mL of *Salmonella* Typhimurium DT104. Fecal samples were collected multiple times and cultured for *Salmonella*. Bacterial community DNA was extracted from fecal samples collected at three sampling points: Day 0 (before treatment, challenge), Day 6 (after treatment, before challenge) and Day 36 (after treatment, challenge) and assessed for microbiome by 16S rRNA gene sequencing. Sequencing data were analyzed using mothur, while the statistical analysis was conducted on StataSE.

Results: On Day 0 and Day 6, all pigs tested *Salmonella* negative with the exception of 1 pig from the treatment group on Day 0. Post-challenge, on Day 36, all pigs tested *Salmonella* positive. No significant difference in *Salmonella* CFU/g in feces was found between the treatment and control group post-challenge. Preliminary results revealed the dominance of phyla Firmicutes followed by Spirochaetes, Bacteroidetes, Proteobacteria and Verrucomicrobia on Day 0. After treatment, on Day 6, a decline in Firmicutes was noted in both groups while Proteobacteria and Verrucomicrobia were found to increase in both groups. The three most frequently identified genera on Day 0 and Day 6 were *Clostridiales*, *Ruminococcaceae*, and *Lactobacillus*. At Day 6, a more even distribution in genera was noted in both groups compared to Day 0. A larger number of *Lactobacillus*, a genus associated with beneficial health effects in swine, was found in the treatment group (8.1%) compared to the control group (4.6%). *Proteobacteria*, a genus associated with *Salmonella*, was found in higher numbers in the control group (6.7%) in comparison to the treatment group (2.9%). When assessing the distribution of phylum one day before challenge (Day 6) with that on Day 36, Firmicutes, Spirochaetes, Bacteroidetes, Proteobacteria and Actinobacteria were prominent. At Day 36, both groups had an increase in Firmicutes, with Firmicutes being more dominant in the control group (81%) than the treatment group (70%). Previous research has reported the dominance of Firmicutes in the pig gut microbiome. The distribution of Proteobacteria was smaller in number when Firmicutes were dominant. The three most frequently identified genera from pigs at Day 6 and Day 36 were similar to the genera identified at prior to challenge. As the pigs aged, a more even distribution in genera was seen. A large increase in *Streptococcus*, a genus associated with potential pathogens, was noted at Day 36, being more prevalent in the control group.

Conclusion: Further analysis will provide researchers with an understanding of the impact of flavophospholipol on the porcine fecal microbiome in *Salmonella* infected pigs.

Industry Implications: This study will allow producers and industry partners to assess whether flavophospholipol is beneficial in reducing *Salmonella* in swine while improving food safety.

Acknowledgements: OMAFRA-FSRP, OMAFRA-UofG Research Partnership and Huvepharma

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Antibody responses to porcine reproductive and respiratory syndrome and swine influenza viruses from weaning up to marketing in Ontario commercial swine herds

Elana Raaphorst BSc¹; Vahab Farzan DVM, MSc, PhD^{1,2}; Pauldeep S. Virk BSc¹; Robert M. Friendship DVM, MSc, Dip ABVP²; Brandon N. Lillie DVM, PhD, Dip AVCP¹

Department of Pathobiology¹, Department of Population Medicine², University of Guelph

Introduction: Infectious diseases are a prevailing problem on commercial swine farms across Ontario. Porcine reproductive and respiratory syndrome (PRRS) is a highly contagious viral disease that causes reproductive problems such as late-term abortions, weak piglets, failure to farrow, and sow death, and respiratory disease such as pneumonia, resulting in poor performance and death¹. Swine influenza (SI) is an infectious respiratory disease caused by type A influenza viruses. This disease is characterized by coughing, dyspnea, fever, and prostration². Both of these viral pathogens may contribute to decreased herd health resulting in impaired animal health, decreased producer profits, and poorer quality meat products. As such, understanding the trends in seropositivity of these pathogens from weaning to the end of the finisher stage may help in developing improved control strategies to minimize the presence and impact of disease on commercial swine farms. The present study will investigate the antibody response against PRRS and SI viruses in pigs at different stages of production.

Methods: Fourteen groups of 54-60 pigs (totaling 809 pigs) were selected from eight farrowing farms in Ontario and followed from birth until slaughter. A summer and a winter cohort were tested on each farm, except on two farms where the animals were shipped to the abattoir prior to sample collection. As part of a larger project, half of the piglets from each litter were assigned to either a high complexity (HC) or low complexity (LC) nursery diet treatment at weaning, balanced for sex and weight where possible. Fecal and blood samples were collected at weaning and at the end of nursery, grower, and finisher stages³. Sera from a subset of pigs (n=629) were analyzed by ELISA for the presence of PRRSV and SIV antibodies for use in the present study.

Results: Overall, 38.5% and 5.7% of serum samples tested positive for SIV and PRRSV, respectively. In the winter cohort, 57.3% and 28.4% of pigs tested positive for SIV and PRRSV, respectively, while 10.0% and 6.0% of pigs tested positive for SIV and PRRSV in the summer cohort. 58.3% and 7.8% of pigs at weaning, 19.5% and 1.3%, of pigs at the end of the nursery stage, 30.9% and 6.3% of pigs at the end of the grower stage, and 47.2% and 8.6% of pigs at the end of the finisher stage tested positive for SIV and PRRSV, respectively.

Conclusions: The level of PRRS antibodies present in the pigs sampled was low and may not be representative of Ontario commercial swine herds. The current study investigated universal SIV antibodies, and therefore further studies are needed to investigate the specific SIV subtypes that are most prevalent on farms. SIV seropositivity indicates a high level of maternal antibodies present in pigs at weaning and a decline towards the end of the nursery stage. The increase of antibodies towards the end of the finisher stage indicates exposure to the virus during production.

Industry Implications: These findings provide baseline information regarding seropositivity for two major pathogens in swine from weaning up to marketing, which can be used to improve control strategies for the associated diseases. SIV monitoring using ELISA antibody test kits are a practical and less expensive method for screening swine farms for SIV, and further testing for specific SIV subtypes can then be used in order to improve vaccination strategies.

Acknowledgements: We would like to thank NSERC, Ontario Pork, OMAFRA, and Swine Innovation Porc for financial support.

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Nutritive value of corn distiller's dried grains with solubles steeped with or without exogenous feed enzymes for 24 h and fed to growing pigs

Youngji Rho, MSc, Elijah Kiarie, MSc, PhD, C.F.M. de Lange¹, MSc, PhD.
Department of Animal Biosciences, University of Guelph

Introduction: Corn distiller's dried grains with solubles (DDGS) is a good source of nutrients. However, utility in swine feed programs is limited due to its high fiber concentration. Fiber reduces nutrient digestibility and utilization (Urriola and Stein, 2010). We previously demonstrated that steeping corn DDGS with exogenous fiber degrading enzymes (FDE) and adding it in a complete corn soybean meal diet improved FCR in growing pigs (Rho et al., 2017). However, it is unknown whether improved efficiency was due to improved nutrient absorption in the small intestine or hindgut fermentation. Therefore, the focus of the present study was to evaluate apparent ileal digestibility (AID), standardized ileal digestibility (SID) and apparent total tract digestibility (ATTD) of components and digestible energy content in DDGS steeped with or without two commercial FDE (A and B).

Methods: Three semi-purified corn starch-based diets were formulated with steeped DDGS as the sole source of crude protein. The basal mixture contained 0.2 % TiO₂ as indigestible marker. Steeping was done in a sterile plastic container. Mixture of 350 g of DDGS with or without FDE and 1.5 L of water was incubated at 40°C for 24 h with 15 min agitation every 40 min. Targeted enzyme activity for FDE-A was 5,500 U of xylanase and 1,050 U of β -glucanase while FDE-B (multi-enzyme complex) was 1,200 U of xylanase, 150 U of β -glucanase, 500 U of cellulase and 5,000 U of protease per kg of DDGS. Samples of steeped DDGS were taken at 0, 4, 8 and 24 h for organic acids and pH measurements. Six ileal cannulated pigs were assigned to diets in a 3 x 3 Latin Square design (n=6). Each period lasted for 11 d: 7 d of adaptation, with 2 d of grab fecal samples and 2 d for continuous 8 h ileal digesta collection.

Results: There was no ($P > 0.05$) treatment and sampling time interaction or treatment effects on pH and lactic concentration. Lactic and acetic acids increased, and pH decreased ($P < 0.05$) overtime. The AID of CP, NDF and crude fat and SID of CP were not different ($P > 0.05$) among treatments. Steeping DDGS with FDE-A had lower ($P = 0.01$) ATTD of NDF than control but higher ($P = 0.001$) ATTD of crude fat compared with control and FDE-B. The digestible energy content in three steeped DDGS were not different ($P > 0.05$) and amounted to 4,095, 4,039 and 3,974 kcal/kg DM for the control, FDE-A and FDE-B, respectively.

Conclusions: In this study steeping corn DDGS at 40°C for 24 h with these fiber degrading enzymes did not improve fiber and energy digestibility.

Industry Implications: Co-products have a generally complex fiber-protein structure compared to their parental grain. Therefore, in order to maximize fiber degrading enzyme effects, studies to understand the structure of fiber is needed.

Acknowledgments: Financial support was provided from Danisco Animal Nutrition-DuPont Industrial Biosciences and Canadian Bio-Systems.

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¹In memory of Dr. Kees de Lange

The impact of nursery diet complexity on *Salmonella* and biomarkers related to immunity and growth performance in swine on commercial farms

Corinne H. Schut BSc¹; Vahab Farzan DVM, MSc, PhD^{1,2}; Margaret H. Ainslie-Garcia MSc¹;
Robert M. Friendship DVM, MSc, Dip ABVP²; Brandon N. Lillie DVM, PhD, Dip AVCP¹
Department of Pathobiology¹, Department of Population Medicine², University of Guelph

Introduction: Feed is one of the greatest expenses on commercial swine farms, more so during the nursery stage in which expensive ingredients are needed to help transition weaned pigs onto solid food. Recently, a lower cost, low complexity nursery diet which replaced the majority of animal-based proteins with plant-based proteins was tested on a research farm. The diet did not affect subsequent growth or marketability of grower-finisher pigs (1, 2) and was calculated to save producers approximately \$2.80 per pig (2). However, the impact of the low complexity diet on pig health and disease susceptibility on commercial farms remains unknown. This study aimed to assess the impact of a low complexity nursery diet on health and disease susceptibility in pigs on commercial farms by examining *Salmonella* shedding and antibody responses on-farm, internal colonization of *Salmonella* at slaughter, and biomarkers related to growth and immunity.

Methods: Fourteen groups of 54-60 pigs (totalling 809 pigs) were selected from eight farrowing sources in Ontario and followed from birth until slaughter. At weaning, half of the piglets from each litter were assigned to either a high complexity (HC) or low complexity (LC) nursery dietary treatment, balanced for sex and weight when possible. Fecal and blood samples were collected at weaning, and at the end of the nursery, grower, and finisher stages. From each farm, a subset of pigs which had reached market weight were shipped to the abattoir where palatine tonsils and submandibular lymph nodes were harvested. Fecal and tissue samples were cultured for *Salmonella* (3) and sera from all pigs were analyzed by ELISA for the presence of *Salmonella* antibodies, while sera from a subset of 116 pigs were tested for immune and growth biomarkers (HP, T3, IGF-1, IgG1, IFN- γ , and TNF- α) by ELISA. Multilevel mixed-effects regression methods were used to analyze the data.

Results: In total, *Salmonella* was recovered from 11.7% (195/1670) and 13.5% (226/1669) of fecal samples collected from pigs in HC and LC diet group, respectively. *Salmonella* shedding detected in pigs fed HC and LC diets, respectively, was 10.2% and 10.7% at weaning, 10.6% and 14.5% at the end of nursery, 12.2% and 12.5% at the end of grower, and 18.5% and 21.9% at the end of finisher. Over the entire production period, 20.2% (277/1370) and 21.2% (285/1347) of serum samples collected from pigs fed the HC and LC diet, respectively, tested positive for *Salmonella* antibodies. Data analysis indicated that nursery diet complexity had no impact on *Salmonella* antibody response or isolation of *Salmonella* from tissues at slaughter ($p>0.2$). However, pigs fed the LC nursery diet had an increased tendency to shed *Salmonella* on-farm ($p=0.065$) and had lower serum concentrations of IGF-1 than HC pigs ($p=0.050$). The remaining biomarkers were not affected by nursery diet complexity ($p>0.2$).

Conclusions: These findings suggest that the use of a LC nursery diet may be beneficial on commercial farms with limited disease pressures, as it did not adversely affect health. However, additional research is necessary to assess the impact of this diet on susceptibility to other endemic and emerging swine pathogens in Canada.

Industry Implications: If the LC diet's impact on disease susceptibility is further tested and confirmed to be negligible, its use on commercial farms will have major potential cost-saving benefits for producers.

Acknowledgements: Funding and support was provided by NSERC, Ontario Pork, OMAFRA, Swine Innovation Porc, the Canadian Center for Swine Improvement, and Alliance Genetics Canada.

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Measurements of circulating progesterone (P₄) and estrone sulfate (E₁S) concentrations as a diagnostic and prognostic tool in porcine pregnancy revisited

C. Sharma BSc¹; X. Liu MD, PhD²; A.M.P. Granados MSc¹; T. Schwarz PhD³; M. Murawski, PhD, DSc⁴; C. Tayade PhD⁵; R.T. Kridli PhD⁶; P. M. Bartlewski DVM, MSc, PhD²

Department of Biomedical Sciences, Ontario Veterinary College, University of Guelph¹, 204 Shenyang Hospital, China², Department of Swine and Small Animal Breeding³, Department of Animal Biotechnology⁴, Agricultural University of Cracow, Poland; Department of Biomedical and Molecular Sciences, Queen's University⁵; Department of Animal Production, Faculty of Agriculture, Jordan University of Science and Technology⁶

Introduction: Optimizing reproductive efficiency is essential to increase productivity of commercial pig operations. Two periods of embryonic/fetal mortality in swine peak around gestational days 20 and 50 (gd20 and gd50). Several hormones are necessary to maintain the pregnancy that will culminate in the birth of healthy offspring. Deviations from the normal profile of hormone synthesis and bioavailability may lead to impairment of embryonic and fetal development (i.e., developmental arrest and/or demise). Progesterone (P₄) is a key hormone during the establishment of pregnancy in mammalian species. Progesterone receptors (PRs) are expressed in pig oocytes and early embryos up to the 4-cell stage, but not during the morula or blastocyst stages, suggesting that (P₄) effects on embryonic development are both direct and indirect (the latter potentially exerted via PR-regulated factors produced in the uterine endometrium). Determination of E₁S concentrations in blood or urine samples has been used as an early pregnancy test in pigs but the concentrations are too variable to accurately predict the number of developing conceptuses. In ruminants, serum E₁S levels are positively correlated with the weight of placenta as well as calf birth weight and post-natal viability. The main goal of this study was to examine the utility of measuring systemic concentrations of P₄ and E₁S for monitoring the progression of porcine pregnancy and predicting sow fertility.

Methods: There were three subsets of artificially inseminated sows used in the present experiments: 1) animals sacrificed on gd20 (n=16) or 2) gd50 (n=16; Experiment 1), and 3) animals maintained throughout gestation (3.8 months, n=24; Experiment 2). Blood samples (10 ml) were drawn from the orbital sinus on gd20 and gd50 (Experiment 1) or gd0, gd1, gd2, gd11, gd20 and gd50 (Experiment 2). The endocrine data recorded at different time points (i.e., around artificial insemination (gd0-2) and maternal recognition of pregnancy (gd11) as well as on gd20 and gd50) were examined for correlations with the numbers of healthy, arrested and absorbing embryos or with the numbers of live, stillborn and mummified piglets.

Results: No correlations were observed between circulating concentrations of both steroids and the numbers of healthy, arresting or reabsorbing conceptuses on gd20 or gd50 (Experiment 1). In Experiment 2, circulating P₄ concentrations on gd11 related directly to the number of live-born piglets (r=0.46, p<0.04). Systemic E₁S concentrations on gd0, gd1, gd2 and gd50 were correlated with the number of mummified fetuses recorded at farrowing (r=0.50, p=0.03; r=0.59, p<0.01; r=0.48, p=0.04; and r=0.56, p=0.01, respectively) and blood concentrations of E₁S on gd20 related directly to the number of stillborn piglets (r=0.60, p=0.02). Moreover, serum E₁S concentrations gd0, gd1 and gd2 were greater (p<0.05) in sows with than in those without mummified fetuses at farrowing, and on gd20 they were greater (p<0.05) in sows that had stillborn piglets compared with all other sows.

Conclusions: Measurements of P₄ and E₁S at the time of AI and in the early and middle pregnancy of sows showed limited diagnostic value, but have the makings of the method to predict gestational outcomes.

Industry Implications: Measurements of P₄ and E₁S at the time of mating and relatively early in gestation may become a simple and inexpensive method to predict piglet productivity. Depending on the accuracy and consistency of these hormone assays, they may be employed as a primary method or, in conjunction with measurements of vagina-cervix length (VCL), as an additional predictor of fertility in sows.

Acknowledgements: Funding in the form of an operating research grant to CT was provided by the Ontario Pork.

Genomic determinants of alkaline phosphatase catalytic affinity along the intestinal longitudinal axis of weanling pigs

Xindi Yin, MSc; Weijun Wang, PhD; Tania Archbold, BSc; Nicole Burello, MSc; Michael Scolaro; Kevin Zhou, BSc; Ming Z. Fan, MSc, PhD

Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada N1G 2W1

Introduction: Intestinal alkaline phosphatases (AP), one group of the most abundant apical membrane-bound enzymes in the gut, play a pivotal role in dephosphorylation of endotoxin lipopolysaccharides (LPS) lipid moiety and other emblematic members of pathogen-associated-molecular patterns (PAMPs) such as ATP, therefore preventing gut dysbiosis and enteric diseases (1). Catalytic affinity (K_m) of IAP, which can be affected by nutritional and physiological factors, is the limiting factor for the detoxification of LPS and other PAMPs compounds in the gut (2). This study was conducted to elucidate the genomic determinants of alkaline phosphatase catalytic affinity along the intestinal longitudinal axis of weanling pigs.

Methods: Herein, jejunal, ileal, cecal and colonic segmental samples were collected from 8 crossbred (Duroc $\times$ Yorkshire $\times$ Landrace) weanling barrows fed a corn and soybean meal-based diet, with an average final BW of 10.95 (SE = 0.68) kg. These gut tissues were homogenized for AP kinetics characterization using *p*-nitrophenyl phosphate as a substrate at pH 7.4 and 37 °C for 30 min. Data were analyzed by the pooled *t* test, and were presented as means $\pm$ SE. The computational mining of the intestinal AP isomer genes was based on sequences from the porcine genome database (*Sus scrofa* Ver. 11.1). The 3-dimensional models of 5 porcine intestinal AP isomer proteins were generated by the SWISS-MODEL online server using the crystal structure of a homologous human placenta AP (RCSB-PDB#:1EW2) as a template.

Results: Enzyme kinetic results were showed as parameter estimates $\pm$ SE, $P < 0.05$, $R^2 = 0.33 - 0.69$, $n = 40$. The AP affinity (K_m , μM) in the jejunum (27.40 ± 9.66) and the colon (30.01 ± 12.42) was lower ($P < 0.05$) than that measured in the ileum (22.87 ± 5.01) and the cecum (21.69 ± 9.96). The maximal specific activity (V_{max} , $\text{nmol} \cdot \text{mg protein}^{-1} \cdot \text{min}^{-1}$) displayed a decreasing gradient ($P < 0.05$) from the jejunum (27.46 ± 1.96), to the ileum (20.89 ± 0.86), to the colon (9.88 ± 0.85); and to the cecum (3.03 ± 0.26). The computational mining results further identified 4 AP isomer genes, including 3 intestinal-like AP isomer genes located in the chromosome 15, and 1 tissue-non-specific AP isomer gene in the chromosome 6 with multiple transcripts of two protein coding sequences, resulting in 5 AP isozymes that are all likely expressed in the intestine along the entire small and the large intestinal longitudinal axis. The predicted 3-D protein structure models for the 5 AP isomers have revealed that although the catalytic site architectures, including the heavy metal-binding sites, are highly conserved, the mapped N-glycosylation sites are very variable among the 5 AP isomers.

Conclusion: Overall, differences in these AP isomers distributions and the different N-glycosylation sites are likely the major genomic determinants affecting the alkaline phosphatase catalytic affinity along the intestinal longitudinal axis and gut health status of weanling pigs.

Industry Implications: This study results suggest that variation of AP isomers distributions in the porcine gut and the different N-glycosylation sites among isomers would greatly influence their enzyme affinity towards detoxifying pathogenic bacterial LPS and other emblematic PAMPs members in the gut lumen for protecting gut health particularly young pigs in commercial swine production.

Acknowledgements: Funding provided by the NSERC Discovery Program; the University of Guelph-OMAFRA partnership program; and the Food From Thought research program at the University of Guelph with funding from the Canada First Research Excellence Fund. Xindi Yin is also supported by a Ph.D. scholarship from the China Scholarship Council (CSC).

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Communication of antimicrobial use measurements in the swine industry: assessing stakeholder understanding and preferences

Angelina L. Bosman, DVM MPH^{1,2}; Anne Deckert DVM MSc PhD^{1,2}; Richard J. Reid-Smith DVM DVSc^{1,2}; Carolee A. Carson DVM PhD²; Zvonimir Poljak, DVM MSc PhD¹; Scott A. McEwen, DVM DVSc Dip ACVP¹.

¹Department of Population Medicine, University of Guelph; ²Centre for Food-borne, Environmental and Zoonotic Infectious Diseases, Public Health Agency of Canada

Introduction: Antimicrobial use (AMU) in the food animal industry is an issue of increasing public concern. Surveillance programs that gather data on AMU in livestock are in place or are in development globally(1). Useful information can be extracted from AMU data by applying various measures (or metrics). Several AMU measures are available; each one captures different pieces of information about the use of antimicrobials(2).

Users of AMU information, including animal producers and veterinarians, may require different types of information from AMU data, and may prefer different measures. With a better understanding of how different users of AMU information interpret the various AMU measures and which measures they find most useful, communication of AMU information from surveillance data to stakeholders could be improved.

The objectives of this study are: 1) to assess the understanding of various AMU measures among producers and veterinarians in the swine industry, and 2) determine which AMU measures they prefer and find most useful.

Methods: An online questionnaire will be developed in Qualtrics® (Qualtrics, Provo, UT) that will be distributed via email and/or made available at various meetings during the latter half of 2018. Swine veterinarians and producers who work in Ontario will be invited to participate. The survey will have four main sections: 1) Introduction (including informed consent) 2) Demographics, 3) Understanding of AMU measures and 4) Preferences for AMU measures. Understanding of AMU measures will include a brief introduction to the various AMU measures available.

Associations between various demographic factors, such as years spent in the industry, and understanding of AMU measures will be examined. Comparisons will be made between the various measures in terms of understanding and preferences. Measures that will be examined include percent rations medicated, milligrams of antimicrobial per population correction unit, and number of defined daily doses per 1000 animal-days.

Results: The questionnaire is under development, data collection will begin after ethics approval.

Conclusions: It is anticipated that simple measures will be better understood than those that are more complex. Understanding of AMU measures may be affected by prior education in this area, and years of experience.

Industry Implications: From this study, we hope to produce information useful for improving communication of AMU findings to stakeholders and to identify areas where further education around AMU measures is needed.

Acknowledgements: This project is supported by the Ontario Veterinary College PhD Fellowship program, the Ontario Ministry of Agriculture, Food and Rural Affairs New Directions Research Program, and the Public Health Agency of Canada.

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The fate of disadvantaged piglets at weaning: an intervention study

Jordan Buchan; Robert Friendship DVM, MSc¹; Rocio Amezcua DVM, PhD, MSc¹

Department of Population Medicine, University of Guelph¹

Introduction: A common challenge faced in the pre-weaning stage of swine production is the presence of pigs that do not grow as large as others in their litter, commonly termed disadvantaged piglets or runts¹. This decreased growth can be due to intrauterine growth retardation or factors post-farrowing including poor nutrition or disease². This decreased weight gain becomes an issue downstream in production, as it can compromise production throughput and disrupt overall herd health¹. Thus, the objectives of this study are; to quantify the decreased weight gain in these underweight pigs, and to implement an intervention method that will minimize these losses.

Methods: The farm chosen for the study weaned pigs at around 3 weeks of age and adhered to an antibiotic free program. To obtain post-weaning growth performance data, one batch of pigs was observed from weaning until shipment to the grower/finisher barn. Weights were obtained individually for the pigs at weaning and 7 weeks later at exit. Pigs were classified as underweight if they were <4.5 kg at weaning. The intervention method was implemented with a different batch of pigs in the same production system, involving 2 trials of 30 underweight pigs each. Pigs were selected at weaning and, rather than being moved to the nursery with the rest of their batch, were put in special care pens. Here, they received a diet of milk supplement and solid nursery feed 3 times per day for 2 weeks before being reintegrated with their same batch from weaning. This intervention method was designed to create a more gradual transition to the nursery to encourage maximal weight gain in pigs underweight at weaning. Weights were obtained at weaning, 2 weeks post-weaning, and at exit from the nursery to compare to the pigs in the observational group that did not receive any type of special care post-weaning.

Results: The mean weaning weight and standard deviation for underweight pigs (n=41 of a total of 240) in the initial batch with no intervention was 3.5 ± 0.6 kg. The mean nursery exit weight for these underweight pigs was 19.1 ± 3.7 kg, compared to the non-underweight pigs which weighed 23.5 ± 4.0 kg at exit. This group had a mortality rate of 6%, none of which were pigs that classified as underweight at weaning. For the group receiving the intervention method, the mean weaning weight was 3.4 ± 0.6 kg and the exit weight was 20.0 ± 4.0 kg. This mean exit weight is numerically greater than that of the underweight pigs that did not receive the intervention; however, the difference between the 2 groups was found to be non-significant (P -value=0.28). Furthermore, the intervention group had a mortality rate of 8%, compared to 0% mortality observed in the underweight pigs of the benchmark group.

Conclusions: The implementation of this intervention method to encourage greater weight gain in underweight pigs at weaning did not yield a significant increase in weight at nursery exit 7 weeks post-weaning. The intervention required extra labour and added expense for milk replacer but did not appear to provide a cost-benefit to the producer.

Industry Implications: This trial demonstrated that, contrary to popular opinion regarding providing special care for under-weight pigs at weaning, the results of this trial suggest that there is no obvious advantage in doing so.

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Growth performance in antibiotic-free and conventional nursery herds in Ontario

Karen M. De Bruyn¹, Vahab Farzan¹, Terri L. O'Sullivan¹, Paisley Canning², Robert M. Friendship¹

Department of Population Medicine, University of Guelph¹, Southwest Ontario Veterinary Services²

Introduction: The nursery period presents a unique set of stressors for pigs. In the nursery barn, piglets that are just weaned off their dams and are thus losing passive immunity are mixed together in an environment where common endemic diseases seem to linger. This stressful transition may result in reduced growth rate and increase susceptibility to disease. Being able to control disease and optimize growth in the nursery stage can improve the productivity of an entire herd. Feeding low levels of antibiotics in feed is a common practice that has been shown to improve nursery pig growth rates (Cromwell, 2002). However, due to public concern of antibiotic usage, pigs being raised without antibiotics is a growing niche market in Ontario. The objective of this study is to compare growth rates of antibiotic-free nursery pigs to those of conventionally raised nursery pigs. It is hypothesized that antibiotic-free pigs will have reduced growth rates compared to conventional pigs.

Methods: Samples are collected from antibiotic-free nursery barns. Each barn is visited twice, shortly after pigs enter the nursery and again shortly before they leave. At the initial barn visit, producers fill out a survey describing their type of production system and basic management practices. Twenty pigs at each farm are randomly selected and tagged. The selected pigs are weighed at both visits. Weight gain and average daily gain (ADG) will be calculated for each animal and used to determine the average production parameters for each farm.

Results: Preliminary results comparing 6 antibiotic-free nurseries to pre-existing data from 21 conventional nurseries shows that the mean growth rate of antibiotic-free farms is lower, at 380.5 g/day with a minimum value of 285 g and a maximum value of 494 g, than that of conventional farms at 469.2 g/day with a minimum value of 296 g and a maximum value of 494 g (Table).

Farm System	Mean ADG (g)	Lowest ADG (g)	Highest ADG (g)
Conventional (n=21)	469.2	296.0	597.0
Antibiotic-free (n=6)	380.5	285.0	494.0

Conclusions: Antibiotic-free nursery pigs may have lower weight gains and growth rates than conventionally raised nursery pigs. However, the variation that may exist between management practices of the two production types need to be investigated.

Industry Implications: This research can provide relevant information about how pigs in antibiotic-free programs grow compared to conventionally raised pigs and whether certain management practices can be used to optimize production. The results of this study can also provide benchmarking data about nursery pig production for Ontario hog producers.

Acknowledgements: We would like to thank OMAFRA New Directions Research Program, OMAFRA U o G Research Partnership, and Ontario Pork for their financial support.

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Investigation into the molecular characteristics of *Streptococcus suis* isolates in Ontario nursery pigs

Leann C. Denich BSc¹; Emily Arndt MSc¹; Zvonimir Poljak DVM, MSc, PhD¹; Vahab Farzan DVM, MSc, PhD¹; Robert M Friendship DVM, MSc, Dip ABVP¹; Marcello Gottschalk DMV, PhD².

¹Department of Population Medicine, University of Guelph, Ontario Veterinary College, ²Université de Montréal

Introduction: *Streptococcus suis* (*S. suis*) is a bacterium that naturally inhabits the nasal cavity and tonsils of many pigs. Some strains under certain conditions, can cause systemic infection leading to a wide range of disease conditions. A major concern is meningitis, with piglets 4-8 weeks of age being particularly vulnerable. The exact pathogenesis involved in clinical disease is not completely known, but it is likely that factors related to host, farm management, and bacteria play a role. There are 35 known serotypes of *S. suis*, with certain strains presenting as more virulent and transmissible. The objective of this study is to determine the serotypes and molecular characteristics of *S. suis* isolates in nursery pigs with clinical signs of disease, and healthy controls.

Methods: A case control study involving 4-8-week-old nursery pigs from Ontario farms is being conducted. Cases showing clinical signs of *S. suis* infection are selected and matched with an equal number of healthy controls based on herd, time of visit and pen. Nasal, tonsil and rectal swabs, as well as blood samples are collected from each case and control. In addition, cases are euthanized to collect meningeal swabs and tissue samples from spleen and ileum. Samples are cultured on phenylethyl alcohol blood agar and incubated for 24 to 48 hours at 35°C with 5% CO₂. *S. suis* isolates are then identified by testing for presence of glutamate dehydrogenase (*gdh*) and recombination protein N (*recN*) genes using a PCR method as well as using 16S rRNA. A two step-multiplex PCR is used to serotype the isolates, and a subset of isolates are subjected to whole genome sequencing to determine their molecular characteristics.

Results: To date, 11 farms have been visited and 337 samples from 67 cases and 272 samples from 67 controls have been sampled. *S. suis* was recovered from at least one sample in 27 cases and 24 controls. Thus far, 550 isolates from 56 pigs on 5 farms have been serotyped. The serotypes found in cases included serotypes 9,15,21,29,31 from the tonsil, serotypes 11,15,16,21,30 from the nasal cavity, serotypes 9,30,31 from the rectum, serotypes 7,8,9,29 from the meninges, serotypes 3 and 9 in the blood and serotype 9 from the ileum. In controls, serotypes 16,29,30,31 were found in the tonsil and serotypes 7,16,17,29 were found in the nasal cavity. Untypable isolates were also identified in all samples in cases and controls. Thus far, 8 isolates recovered from meningeal swabs, 3 isolates from blood, 4 isolates from rectal swabs and 1 isolate from a tonsillar swab were examined by 16S rRNA and subjected to whole genome sequencing. All 12 typeable isolates (similarity >99%) and 2 untypable isolates from meningeal swabs (similarity >98% but <99%) were confirmed as *S. suis*, while the untypable isolates from the rectal swabs were identified as *S. pasteurianus* (similarity 100%). It is noteworthy to mention, that multi-locus sequence typing indicated that one strain of serotype 9 appeared to be circulating through one farm over time.

Conclusions: Multiple serotypes are identified in each pig; the serotypes in the meninges and blood differ from those found in the tonsil or rectum. The isolates identified as untypable are either very similar to *S. suis* or are a different streptococcus species.

Industry Implications: The results obtained from this study will give a better understanding of the serotypes and associated virulence genes involved in outbreaks in Ontario nurseries. This knowledge can be used to ensure the right strains are chosen for autogenous vaccines, to limit drug use, to help reduce mortality and to improve the welfare of the pigs in the nurseries.

Acknowledgements: Funding provided by Food from Thought

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Determining benchmark values for growth rate of nursery pigs in Ontario.

Emily K Hanna; Zvonimir Poljak DVM, MSc, PhD; Terri L O'Sullivan DVM, PhD; Robert M Friendship DVM, MSc.

Department of Population Medicine, University of Guelph

Introduction: The nursery phase of swine production presents many challenges to pigs, often resulting in sub-optimal growth performance. A common practice among producers is to compare current performance of their herds against some standard measures, a process commonly known as benchmarking. The objective of this study was to examine nursery pig growth performance on different farms and gain an understanding of the variation between farms and possibly identify factors that influence growth during the nursery phase.

Methods: Fifty Ontario nurseries were selected for the study and data collection was completed on forty-nine farms. At the initial farm visit a questionnaire was administered and a subset of 20 average newly weaned pigs were individually identified and weighed. At a second visit approximately 6 weeks later these pigs were re-weighed and information related to the entire batch was collected. If available, historical close-out data was collected as well as the information related to the study batch. On one farm, each pig in the batch was weighed individually at entry and exit, with an additional four subsets of pigs weighed. Descriptive statistics have been examined to compare performance and variation within and across farms.

Results: The average weights of 20 pigs from the 49 nurseries upon entry into and exit from the nursery were 7.3 kg and 24.8 kg, respectively. The mean average daily gain (ADG) was 451 g/day. There are many factors that need to be considered to accurately compare results from these farms. For example, there was variation in weaning age (average: 23 days, range: 18 to 39 days). However, when weaning age was controlled for, mean ADG and variation around the ADG for farms weaning at 3-weeks of age were unchanged (mean: 450 g/day, sd: 0.07 g/day). Batch performance records were routinely kept on 24 farms with 22 farms providing records for the study. When comparing the entire batch performance to the subset of 20 pigs from each farm, ADG was not significantly different (batch: 430 g/day; subsets 450 g/day; $P=0.09$). On the farm that weighed all pigs individually ($n=236$) as well as four additional subsets ($n=56$) the means and standard deviation for ADG, weight at entry and exit were comparable with the 20 average pigs in the study group.

Conclusions: Sampling a subset of 20 pigs is a practical means for producers to gain an understanding of overall nursery pig growth rate and gain some information about variability in growth. There were considerable farm to farm differences in growth rate suggesting that for farms with slow growth, there is an opportunity for improvement.

Industry Implications: The data from this study will allow pork producers to set realistic growth targets for their nursery barns.

Acknowledgments: This project is funded (or partially funded) by the OMAFRA-University of Guelph Strategic Partnership, under the Disease Surveillance Plan, which is a joint federal-provincial Growing Forward 2 project. Other funding sources included the OMAFRA New Directions program and Ontario Pork.

Presence of porcine reproductive and respiratory syndrome virus in nursery pigs.

Emily K Hanna; Zvonimir Poljak DVM, MSc, PhD; Terri L O'Sullivan DVM, PhD; Robert M Friendship DVM, MSc

Department of Population Medicine, University of Guelph

Introduction: Porcine reproductive and respiratory syndrome (PRRS) is regarded as the most economically important disease in swine production and outbreaks are associated with reproduction failure including abortion and high mortality in young pigs due to respiratory disease (1). Common clinical signs in weaned pigs include fever, anorexia, impaired growth, labored breathing, and coughing (2). The nursery can become a reservoir for the pathogen with the virus spreading from older pigs to newly weaned pigs, often with minimal clinical signs being apparent. The objective of this study was to investigate the impact of PRRS status on performance in Ontario swine nurseries.

Methods: This study collected data from 30 Ontario swine nurseries. A management and biosecurity questionnaire was administered to producers. A subset of twenty average pigs were weighed on entry and exit from each nursery enrolled. Additionally, individual blood samples were collected from these pigs on thirty of the farms and tested for PRRS using PCR (Animal Health Laboratory, University of Guelph).. Descriptive statistics were generated for growth performance. Multi-level regression analysis will be used to determine the impact of PRRS positivity on growth performance on a herd-basis.

Results: None of the 30 farms reported PRRS as a clinical problem but 10 farms tested positive for PRRS virus. Descriptive analysis of the 30 farms sampled showed that the mean ADG was 453 g/day (95% CI: 426.8, 479.5). The top 10 farms based on ADG were all PRRS negative at entry into and exit from the nursery with a mean ADG of 527 g/day (95% CI: 506.7, 546.5). Based on univariable analysis of effect of PRRS +/- on coefficient of variation: Farms positive for PRRS had 4.3% more variation in ADG than negative farms ($P<0.05$).

Conclusions: Based on preliminary results from this study, presence of PRRS virus in nursery pigs reduces growth and increases variation in growth performance, however further analysis needs to be done to further elucidate this relationship.

Industry Implications: The presence of subclinical disease on farms results in increased variation and sub-optimal growth performance. This study demonstrates the value of disease monitoring in herds whether or not clinical disease is observed.

Acknowledgments: This project is funded (or partially funded) by the OMAFRA-University of Guelph Strategic Partnership, under the Disease Surveillance Plan, which is a joint federal-provincial Growing Forward 2 project. Other funding is the from OMAFRA New Directions program, Merck Animal Health and Ontario Pork.

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Investigating the association between the tonsil microbiota and clinical *Streptococcus suis* infection

Sarah V. Hill BScH¹; Vahab Fazan DVM, MSc, PhD^{1,2}; Janet I. MacInnes PhD¹

Department of Pathobiology, University of Guelph¹, Department of Population Medicine, University of Guelph²

Introduction: The gram-positive bacterium *Streptococcus suis* is part of the normal commensal microflora (microbiota) of the upper respiratory tract (URT) of pigs of all ages¹. However, in response to unknown factors, *S. suis* can cause disease leading major economic losses in the swine industry^{2,3}. The tonsils of the soft palate are an important site of bacterial colonization in the URT. Although these tonsils are secondary lymphoid organs that survey, detect and initiate the immune system⁴ they have a large number of small indentions (crypts) may be the portal of entry for *S. suis* and other pathogens^{4,5}. Currently, it is not known why some pigs remain healthy while others develop clinical *S. suis* disease. We hypothesize that the composition of the tonsil microbiota plays a role in the development of *S. suis* disease. Thus, the aim of the current research is to compare the microbiota of healthy and *S. suis* affected piglets, in the hopes of being able to identify bacterial species that might promote or inhibit *S. suis* disease.

Methods: The tonsils of the soft palate were removed from “healthy” culled (e.g., lame) animals and from weanling pigs with signs of *S. suis* disease. Bacterial DNA was extracted using a Qiagen DNeasy blood and tissue kit following the gram positive protocol including a bead beating step. Illumina MiSeq sequencing of the 16S V3-V4 hypervariable region was done to assess the composition of the microbiota. Phylogenetic classification of the bacteria making up the microbiota was assigned using the 16S Metagenomics app available as part of the Illumina BaseSpace Sequencing hub.

Results: For optimization of the DNA extraction method, the microbiota of 3 thirds of a tonsil from a “healthy” animal was evaluated. There were marked differences amongst the samples; however, *S. suis* was detected in all thirds. In total, 8 phyla were identified in each sample; the core phyla were Firmicutes, Bacteroidetes, Fusobacteria, Proteobacteria, Actinobacteria. Accordingly, the whole tonsil was used for DNA extractions. As part of a larger Food from Thought project, we plan to evaluate the microbiota of tonsils from 50 healthy and 50 *S. suis*-infected animals. To date, tonsil samples have been collected and DNA prepared from 21 *S. suis*-infected animals and 10 matched case-controls and sequencing is currently underway.

Conclusions: Based on preliminary data, it appears that there are spatial differences in the microbiota of the tonsil of the soft palate of swine, but Firmicutes, Bacteroidetes, Fusobacteria, Proteobacteria and Actinobacteria are likely to be present. The further analysis of the various phyla and their interactions with *S. suis* is needed.

Industry Implications: It is hoped that by identifying bacterial species that might promote or inhibit *S. suis* disease, antibiotic alternatives (eg., probiotics) to control this important disease could be developed.

Acknowledgments: We thank the Canadian First Research Excellence Fund for financial support and Joyce Rousseau, Emily Arndt and Jeff Gross for expert technical assistance. We also thank the Ontario pork producers who very generously granted us access to their facilities and for their patient assistance during the sampling processes.

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Utilizing swine carcass lesions as indicators of welfare during post-mortem inspection

Kristen N Jakub MSc; Anita Tucker MSc, PhD

Department of Animal Biosciences, University of Guelph, Department of Population Medicine, University of Guelph

Introduction: Meat inspection at the abattoir has long been utilized as a tool for animal health control and public health assurance (1). Abattoir data is now being investigated for its use in monitoring and detecting animal welfare issues in many animal production industries, including pigs, due to the advantages it possesses over traditional on-farm assessments (2,3). Meat inspection data is cost-effective and efficient, and avoids biosecurity issues associated with entering a farm (3,4,5). A wide variety of welfare-related lesions can be observed at the abattoir during meat inspection, which could serve as valuable information for producers to improve the welfare of their animals (2,5). The occurrence of lesions on pig carcasses not only negatively affects the welfare of the pigs, but affected carcasses are commonly associated with lower carcass weights, and partial or full carcass condemnation, all of which negatively impact producer profit (6,7). The objectives of this study will be to investigate the origin of welfare-related lesions on slaughtered market pigs, to determine if there is variation in the prevalence of these lesions between years and different seasons, and to determine the prevalence of lesions currently observed on carcasses diverted to the hold rail.

Methods: This study will be conducted at Conestoga Meat, an abattoir located in Breslau, Ontario, Canada. Swine carcasses diverted to the hold rail and/or in the cooler, will be visually examined and scored on various welfare-associated lesions, such as tail and ear damage resulting from tail and ear biting, scratch scores on the body, joint swelling (e.g. bursitis), bruising and toe lesions. The scoring will be performed by the same individual during normal slaughter operations. Condemnation data will also be analyzed from previous years to determine if there is variation in the prevalence of welfare-associated lesions between years or seasons, and to determine the origin of the lesions (farm versus during transport or in the plant).

Results: To be completed

Conclusions: To be completed

Industry Implications: The goal of this research is to provide producers with useful information to better inform them of welfare issues that may be evident on their farm and during transport, in order to prevent welfare-associated lesions observed at slaughter. Not only could this information improve the welfare of commercial production pigs in the future, but it could also have economic benefits to the producers, who would be more aware of the carcass condemnation reasons and associated loss of profit. Consumers could also benefit from this research, as it demonstrates the continued effort to monitor welfare issues in pigs, so they can be confident in the products they purchase.

Acknowledgements: We would like to thank the staff at Conestoga Meat for their accommodation and assistance with this research project.

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Assessing haplotype-based genomic predictions in Canadian swine breeds

Z. Karimi^{1,2}, M. Jafarikia^{1,2}, M. Sargolzaei^{1,3}, J.A.B. Robinson¹, and F. S. Schenkel¹

¹Centre for Genetic Improvement of Livestock, Department of Animal Biosciences, University of Guelph, Guelph, Ontario, Canada N1G 2W1

²Canadian Centre for Swine Improvement, Ottawa, Ontario, Canada K1A 0C6

³Semex Alliance, Guelph, Ontario, Canada N1H 6J2

Introduction: Individual single nucleotide polymorphism (SNP) genotypes are currently used to build the genomic relationship matrix (G) for genomic best linear unbiased prediction (GBLUP) in Canada. (1) While SNPs are bi-allelic, haplotypes are usually “multi-allelic” and, thus, they may better capture multi-allelic quantitative trait loci (QTL) compared to individual SNPs, which are “bi-allelic”. The aims of this study were to compare the performance of haplotype-based GBLUP ($G_{HAP}BLUP$) to individual SNP-based GBLUP ($G_{SNP}BLUP$) with respect to prediction reliability, and prediction bias in three major Canadian swine breeds, i.e., Duroc, Landrace and Yorkshire.

Methods: Genomic relationship matrices based on individual SNP genotypes or haplotype blocks of different sizes (i.e., 5, 10, 15, 20 and 30 SNPs) were built using imputed 70K SNP genotypes and, then, they used to predict genomic estimated breeding values (GEBVs) for backfat thickness, total number of born, and age adjusted to 100kg of live weight and loin depth adjusted to 100kg of live weight. In addition, Spearman rank correlation between $G_{SNP}BLUP$ and $G_{HAP}BLUP$ GEBVs was calculated for the individual traits, as well as for an index of the traits obtained using the same weights as in the Canadian national selection indexes for terminal and maternal lines provided by Canadian Centre for Swine Improvement to evaluate how strongly the use of haplotypes instead of individual SNPs can influence the ranking of selection candidates.

Results: Except for backfat thickness in Duroc, $G_{HAP}BLUP$ increased the reliability of predicting future EBVs of selection candidates and reduced prediction biases from 0.3 to 8.2% points and from 2.6 to 11.2 points, respectively, across breeds and the traits studied. Furthermore, the optimum haplotype block length was not consistent across traits and across breeds; however, longer haplotype blocks (i.e., 15, 20 and 30) resulted in higher improvements in prediction reliabilities and less prediction biases compared to the short ones (i.e., 5 and 10).

Conclusions: $G_{HAP}BLUP$ outperformed $G_{SNP}BLUP$ in terms of predictive ability and may be an alternative to individual SNP genotypes for genomic evaluation of swine. Moreover, the results from Spearman rank correlation indicated that $G_{HAP}BLUP$ would change selection decisions in swine breeding programs.

Industry Implications: The results from Spearman rank correlation of the calculated indexes, using trait weights in the Canadian national selection indexes, were rather low, especially for Yorkshire. This suggests that the use of $G_{HAP}BLUP$ would change selection towards more reliable decisions in swine breeding programs. This is due to the better performance of $G_{HAP}BLUP$ compared to $G_{SNP}BLUP$ in terms of prediction reliabilities and prediction for the sample of important traits analyzed in this study.

Acknowledgments: Funding for this study was partly provided by Genome Canada and Genome Quebec. Financial support was also provided by the Canadian Centre for Swine Improvement (CCSI) and participating Canadian breeders who shared their data.

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Identification of genetic markers for stress in pigs

Shayla R Larson BHSc¹; Krysta LH Morrissey PhD²; Tess Faulkner BA²; Rebecca J Parra BSc²; Renée Bergeron PhD²; Mohsen Jafarikia PhD^{2,3}; Ray Lu PhD¹

Dept. of Molecular & Cellular Biology, University of Guelph¹, Dept. of Animal Biosciences, University of Guelph², Canadian Centre for Swine Improvement Inc.³

Introduction: Stress negatively impacts swine immunity and health, affecting animal welfare and meat quality. Behavioral and neuroendocrine responses to stress are highly variable and can be attributed significantly to differences in genetic background and prior experiences (1). Currently, the underlying genetic component for stress-responsiveness is unclear. Two stress regulatory genes, namely Luman and Luman recruitment factor (LRF), are of particular interest, having been shown to function as important regulators of the hypothalamic-pituitary-adrenal (HPA) axis and stress hormone signaling in mouse models (2). Recently, we have found that Luman- and LRF-deficient mice are less susceptible to environmental stress. Based on these findings, investigation of these two stress sensitivity regulatory genes represents a promising avenue for exploring potential applications in farm animals, including pigs. We propose that there are naturally occurring variations in the Luman and LRF genes in pigs that can be used as markers for stress-responsiveness for animal breeding.

Methods: In our ongoing study of 200 pure Yorkshire pigs, stress-responsiveness scores are determined for each pig. Behavioural responses in four standardized stress tests (backtest, open-field test, novel object test, human approach test) are measured, along with physiological responses to a restraint test by measuring stress hormone levels present in blood collected before and after the event. DNA from each pig is extracted from blood samples, and the Luman and LRF loci are sequenced and analyzed for the presence of naturally occurring genetic variations. Carcass traits will be measured at slaughter in a sub-sample of animals. Genetic polymorphisms identified in the Luman and LRF loci will be analyzed for their correlation with stress-responsiveness scores in piglets and meat quality measurements, to identify potential genetic markers for stress-responsiveness and meat quality in pigs.

Results: Preliminary results of 46 pigs show large variations in stress response, with cortisol levels varying greatly both within and between litters. In our current analysis of the Luman gene in 100 pigs, we have identified 8 naturally occurring polymorphisms that exist throughout the sample population, including 5 single nucleotide polymorphisms (SNPs) in the non-coding regions, 1 synonymous SNP, and 2 missense SNPs, one of which has the potential to alter the structure and function of the Luman protein.

Conclusions: Our preliminary analysis suggests that there is large variation in physiological stress response between pigs. Our current data also shows that genetic variation exists naturally within the Luman locus in swine breeding herds. It is thus possible that the genetic variation identified in the Luman locus can account for the variable stress response that is observed between pigs. Through correlation analysis, this study may identify potential genetic markers for stress-responsiveness and meat quality in pigs.

Industry Implications: Identified genetic markers can be added to an existing commercial genetic marker panel to enable the selection of low-stress pigs in breeding programs. Improving the adaptability of animals to their environment will improve animal well-being and general health, thereby reducing antibiotic use and management costs, while improving the quality of pork products and animal welfare. With increasing societal pressures and consumer awareness, improving animal welfare will also aid in the marketability of the pork product and overall sustainability of the pork industry.

Acknowledgements: Participating organizations and funding sources for this project include AGC (Alliance Genetics Canada), OMAFRA, NSERC, CFREF, and Swine Innovation Porc.

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Effect of dietary supplementation with fish oil or microalgae on nursery pig growth and acute-phase response

Alison V. Lee B.Sc.¹, Lan You B.Sc.¹, Se-Young Oh Ph.D.¹, Ziwei Li, M.Sc.¹, Michael Alcorn, B.Sc.¹, Julia Zhu B.Sc.¹, Rebecca E. Fisher-Heffernan Ph.D.¹, Tim Regnault², Ph.D., Lee-Anne Huber, Ph.D.¹, Cornelius F.M. de Lange Ph.D.¹, Niel A. Karrow Ph.D.¹.

Department of Animal Biosciences, University of Guelph¹; Department of Obstetrics and Gynecology and Physiology and Pharmacology, Western University²

Introduction: Piglet performance can be adversely affected by stress at weaning. Dietary supplementation with omega-3 polyunsaturated fatty acids (n-3 PUFA) reduces inflammatory stress, and may promote piglet health and growth. Fish oil (FO) is considered a major source of n-3 PUFA; however, microalgae (AL) may be a more sustainable alternative. The aim of this study was to assess the health benefits of supplementing nursery pigs with AL (All-G-Rich, Aurantiochytrium limacinum biomass (AURA; CCAP 4087/2; Alltech Inc., KY, USA) containing 70% crude fat and 17% DHA) or FO.

Methods: Seventy-two cross-bred piglets were placed on a low-quality protein diet supplemented with either 1.25% FO or 3.12% AL (equal in n-3 PUFA), or 5% corn oil as a control (CON) for three weeks (feeding phases 1 and 2), followed by a common diet for three weeks (feeding phase 3). At the end of phase 2 feeding, 8 pigs per treatment underwent an *i.m.* LPS immune stress challenge, and the acute-phase response was assessed. Eight pigs per treatment were also vaccinated with two novel antigens throughout the feeding trial, and the antigen-specific acquired immune response was assessed.

Results: No significant differences in piglet average daily gain were observed, but the FO piglets had a decreased feed intake when placed on the common diet. While both AL and FO supplementation attenuated the LPS-induced fever response, only AL pigs had an attenuated cortisol response and exacerbated the pro-inflammatory cytokine responses (TNF- α , IL-1 β , and IL-6); the IL-10 response in the AL treatment was also augmented compared to the FO treatment. Chromogranin A levels were also greater in AL pigs compared to FO and CON pigs at 15 min following LPS challenge. The acquired immune response was unaffected by the dietary treatments.

Conclusions: Results suggest that AL or FO supplementation in nursery diets differentially modulated the acute-phase response, possibly due to differences in n-3 PUFA profile.

Industry Implications: Results from this study suggest that AL and FO supplementation of nursery diets may promote the use of cheaper, lower-quality nursery diets without compromising piglet health. AL may also be a more environmentally sustainable supplement than FO, and as further research is conducted in this area, AL may also become a more economical choice.

Acknowledgements: Funding provided by NSERC, OMAFRA, Swine Innovation Porc and Alltech Inc. AL was provided by Alltech Inc. FO was provided by Valley Feeds. Assistance with animal trials was provided by the Arkell Swine Research Station staff.

Fermentation of soybean meal using a novel *Bacillus subtilis* isolate to improve nutritive value in growing pigs

Yang Lu PhD^{1,2}; Nadeem Akhtar PhD¹; Cuilan Zhu MSc¹; Elijah Kiarie PhD²; Julang Li PhD^{1,*}

¹Institute of Animal Husbandry and Veterinary Sciences, Shanghai Academy of Agricultural Sciences, Shanghai 201 106, China; ²Department of Animal Biosciences, University of Guelph, Guelph, Ontario N1G 2W1, Canada

Introduction: Soybean meal (SBM) is a common plant-based protein source in the swine industry. The crude protein of the SBM is 44-50%. However, the presence of anti-nutritional factors (ANFs), allergens and other high molecular weight, difficult to digest proteins restrict its use in pigs especially those at younger age. The objective of the current study was to optimize a solid-state fermentation using a novel *Bacillus subtilis* CP-9, which produces battery of cellulose, xylanase, and proteinases to improve the nutritive value of SBM, and to examine the digestibility of the fermented SBM in growing pigs.

Methods: A commercial SBM was subjected to solid state fermentation (SBM: water, 1:1; inoculum, 1%; temperature, 22-25°C) using a novel *Bacillus subtilis* CP-9 expressing high level of cellulase, xylanase and protease activities. Protein profile of the SBM after 48 h fermentation showed degradation of high molecular weight proteins including antigenic proteins into small-size peptides on sodium dodecyl sulfate polyacrylamide gel electrophoresis. To examine if fermentation altered the nutritive value of SBM, eight barrows (40 ± 2 kg BW) fitted with terminal ileal T-cannula were used. Two semi-purified corn starch-based diets were formulated with unfermented (UF) and fermented (F) SBM as the sole source of AA (min 18% CP, as-fed basis). Pigs were allocated in a two-period cross over design (n = 8) and were fed at 2.8 × maintenance energy requirement. Each period was 9 d; 5 d for adaptation, d 6 and 7 for grab fecal collection and d 8 and 9 for 8 h continuous ileal digesta collection. The diet was considered fixed effect whereas pig and period were considered random effects in statistical analysis.

Results: Pigs fed F-SBM had higher ($P < 0.05$) apparent ileal digestibility (AID) of CP (83.5 vs. 78.6%), NDF (42.0 vs. 34.8%), ADF (35.6 vs. 22.6%), DM (76 vs. 71.7%), and ash (50.5 vs. 40.0%) compared with pigs fed UF-SBM. There was no treatment effects ($P > 0.10$) on ATTD of CP, NDF, ADF, DM, ash, and GE.

Conclusions: Fermentation of SBM by a novel *Bacillus subtilis* CP-9 increased ileal utilization of crude protein and minerals suggesting improved nutritive value in pigs. The bacterial solid-state fermentation strategy may also be tested on other similar plant-based feed materials which show antigenic properties for animal feed use.

Industry Implications: The study has showed potential to deliver an improved SBM fermentation system to the Pork industries. It is anticipated that the optimized fermentation system could be done on-farm with minimal use of equipment at low cost.

Acknowledgements: Funding supported by Swine Innovation Pork.

Investigating the potency, stability and yeast viability of antimicrobial peptide GNU7-derivatives as alternatives for bacterial therapy

Anna Maystrenko, Erin Mieke, Jenna Penny PhD, Julang Li PhD

Department of Animal Biosciences, University of Guelph, Guelph Ontario N1G 2W1, Canada

Introduction: Concerns over antimicrobial resistance has spawned research in antimicrobial peptides (AMP). AMP are an integral part of the mammalian innate immune system. Due to AMP's ability to target bacterial membranes, bacterial resistance to AMP is less likely. Previous work has showed that GNU7, a synthetic AMP, and its derivative peptides have antimicrobial activity towards *Escherichia coli* and *Salmonella typhimurium*⁽¹⁾. However, it is unknown whether there is activity against antibiotic resistant bacteria such as methicillin -resistant *Staphylococcus aureus* (MRSA), and their susceptibility to serum enzyme degradation is to be verified.

Objectives: The objectives were as follows: i) to examine the minimal bactericidal concentration (MBC) for GNU7-derivative peptides to MRSA and verify the results to *E. Coli*, ii) to verify their stability in physiological conditions, iii) to determine their influence on yeast viability.

Materials and Methods: Antimicrobial Assay: Peptide was tested against gram-negative (*E. coli*) and gram-positive bacteria (MRSA) at concentrations ranging from 0.1ug/mL to 4ug/mL

Stability assay: Antimicrobial activity against gram-negative bacteria was assessed after specified incubation time with 25% pig serum.

Yeast viability: Peptides were then incubated with culture of *Pichia pastoris* for different time points to determine Live Cell % using Bio Rad TC20 Automated Cell Counter.

Results: MBC results against the gram-negative bacteria ranged between 2ug/mL and 4ug/mL for all GNU7-derivative peptides tested, while MBC results for the gram-positive bacteria tested ranged between 0.5ug/mL to 2ug/mL for all peptides tested. Of the 4 GNU7-derivative peptides tested, Syn-GNU7 and newly designed GNU7-repeat had the highest stability, remaining active for up to 7hrs of serum incubation. In addition, our results revealed that both Syn-GNU7 and GNU7-repeat were not cytotoxic to yeast cells at up to 48hrs of incubation. More replicate experiments are required to further confirm results.

Conclusion: Our data suggests that GNU7 derivatives and our newly designed GNU7-repeat has activity against MRSA. These two antimicrobial peptides are relatively stable have minimal cytotoxicity to yeast under the tested condition. Further experimental data is needed to confirm stability and yeast viability results.

Industry Implications: GNU7-derivative peptides may be potential candidates for recombinant production for application as alternatives to antibiotics in the pork industry.

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Synchronized ovulation and advanced semen catheter design to increase sow productivity and reduce breeding costs

Matthew D McBride BSc, Robert M Friendship DVM, MSc, Dip ABVP, Terri L O'Sullivan DVM, Maria D Rocio Amezcua PhD, Glen Cassar DVM

Department of Population Medicine, University of Guelph

Introduction: Optimal timing of semen delivery is one of the most influential elements affecting swine reproductive performance. Sows exhibit a great deal of variation in the duration of estrus, wean-to-estrus interval and estrus-to-ovulation interval¹. Hormones can be used to induce ovulation and allow a single fixed-time insemination protocol to be used¹. This, combined with using a superior semen catheter design may aid in decreasing the number of inseminations and the number of sperm per insemination². The objective of this study is to determine if the use of single fixed-time insemination and improved insemination catheter design will result in optimal reproductive performance while using substantially smaller dosages of semen.

Methods: The research is being conducted at Arkell Swine Research Centre, University of Guelph. Over the course of eleven months 432 mixed parity sows will be randomly assigned to one control and three treatment groups of 108 sows per group. **Group 1** (Control): estrus detection performed twice per day beginning on Day 3 with sows exhibiting estrus being bred by AI (3 billion sperm, conventional catheter) when first discovered in strong standing heat and rebred 24 hours later. **Group 2:** sows will be injected with eCG at weaning and 72 hours later with pLH to induce ovulation. Sows will be inseminated with a single dose of approximately 3 billion sperm 36 hours after pLH using 3 billion sperm and conventional catheter. **Group 3:** sows will be injected with eCG at weaning and 72 hours later with pLH to induce ovulation. Sows will be inseminated with a single dose of approximately 3 billion sperm using a Gedis® catheter. **Group 4:** sows will be injected with eCG at weaning and 72 hours later with pLH to induce ovulation. Sows will be inseminated with a single dose of approximately 1 billion sperm using a Gedis® catheter. Farrowing rate and litter size are being recorded.

Results: Our preliminary findings included a total of 296 sows assigned to a treatment group, of which 26 were removed from the trial due to culling and 7 sows were removed at initial pregnancy check. Conception rate for the treatment groups are: Group 1(84.4%), Group 2 (86.1 %), Group 3 (77.6%), and Group 4 (74.6%).

Conclusions: Initial findings show that the use of the Gedis® catheter appears to be associated with a lower conception rate than the conventional catheter but this is based on small numbers of breeding and farrowing data. Synchronizing ovulation and single AI using a conventional catheter resulted in a good conception rate, which was comparable to the control group. Although reproductive performance appears to be compromised in the Gedis® treatment groups, we expect that this may change with further data collection.

Industry Implications: The synergistic effect of single fixed-time insemination via the Gedis® catheter might possibly result in high reproductive efficiency but with economic benefits associated with reduced labour and lower semen costs.

Acknowledgments: Funding and in-kind contribution provided by UofG–OMAFRA Research Partnership, Eastgen, Gene Diffusion, Ontario Swine Improvement and Ontario Pork. The assistance of the staff at Arkell Swine Research Centre is greatly appreciated.

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Monitoring antimicrobial usage on Ontario swine nurseries

Chris McLaren-Almond BSc¹, Robert M Friendship DVM, MSc, Dip ABVP¹; Zvonimir Poljak DVM, MSc, PhD¹; Terri O'Sullivan DVM, PhD¹, Maria Amezcua DVM¹, MSc; Emily Hanna BSc¹
Department of Population Medicine, University of Guelph¹

Introduction: The nursery phase of swine production is the most challenging phase of pork production from a health standpoint. Pigs face changes in environment, feed, and social grouping at a time when they are losing passive immunity and becoming exposed to new disease challenges. There is pressure on the swine industry to reduce antibiotic use but it may be difficult for pork producers to significantly reduce antibiotic use in the nursery because of the disease challenges during this phase. The objective of this study was to investigate the level of antibiotic use in Ontario swine nurseries.

Methods: Information regarding antibiotic usage was collected from 33 Ontario swine nurseries from May 2016 to July 2017. Data collected included what antibiotics were used and route of administration. During a farm visit, a survey was completed by the producer and included questions about diseases present, treatments and preventive steps such as sanitation and vaccination. One batch of pigs was followed through the nursery with intentions of recording treatments.

Results: Treatment records revealed individual treatments by injection: beta lactams (42%), cephalosporins (24%), fluoroquinolones (18%), macrolides (18%), and trimethoprim-sulfa (12%). Use of tetracyclines, chloramphenicols, and lincosamides were occasionally used at 6%, 3%, and 3%, respectively. Beta lactams appeared to also be the preferred method of mass medication by means of water at a rate of 36%. Less commonly found were potentiated sulfas, aminoglycosides, and tetracyclines at 6%, 6%, and 3%, respectively. Medicated nursery diets used chlortetracycline (86%), oxytetracycline (38%), neomycin (38%), sulfamethazine (29%), penicillin (29%), and tiamulin (29%). Tilmicosin, tylosin, and lincomycin were less commonly used at 14%, 5%, 5%, and 5%, respectively. Producers reported that the most common bacterial disease challenges were *Streptococcus suis* meningitis (55%), Glässers disease (18%), and *E. coli* diarrhea (18%). Antibiotic treatment varied from herds that used over one pig treatment per day for every pig each day they were in the nursery to herds that used no antibiotics. Production levels and management didn't appear to be associated with antibiotic use.

Conclusions: The extreme variation in antibiotic use suggests that there are obvious opportunities to reduce use on certain farms. The largest quantity of antibiotics are delivered by medicating feed but the antibiotics of greatest concern for human medical use (cephalosporins and fluoroquinolones) are injectable products, and these appear to be used in a limited fashion on only a few farms.

Industry Implications: As concerns about antimicrobial usage and antimicrobial resistance continue to grow, it is important to better understand how antimicrobials are used and whether reducing antibiotic use can be accomplished without decreasing animal welfare. Antimicrobial monitoring programs at present are only mandatory for grower-finisher pigs but these should be extended to the nursery phase because of the disease challenges faced by this age group.

Acknowledgments: This project is funded by the OMAFRA-University of Guelph Strategic Partnership, under the Disease Surveillance Plan, which is a joint federal provincial Growing Forward 2 project. Other funding is from the OMAFRA New Directions program and Ontario Pork.

Investigation of transportation practices in an Ontario swine system using descriptive network analysis

Dylan Melmer BSc, MSc¹; Terri L O'Sullivan DVM, PhD¹; Zvonimir Poljak DVM, PhD¹.

Department of Population Medicine, University of Guelph¹

Introduction: The transportation of livestock, and in particular, the use of transportation vehicles to move them can play an important role in disease spread between locations. Therefore, knowledge regarding livestock movement patterns is essential for understanding the potential for disease spread and control (1,2).

Methods: A dataset containing animal movements among 224 swine production facilities was obtained from an Ontario swine management company. The data contained 5,398 unique movements that occurred between January and December of 2015. These data were then used to construct networks of contacts between production facilities that occurred over a weekly period, after considering connections through transportation vehicles. From each of these series of contacts, features of networks that could be critical for understanding the potential for disease spread were extracted and examined over time. For example, the maximum weekly weak component (MWCw), which refers to the number of facilities that are directly or indirectly connected during a specific week. Additionally, “betweenness”, which was utilized to identify demographics of herds that were frequent transfer points in a specific week, and whether the number of transfer points changed over time.

Results: After adding transportation vehicles as a facility type, the number of facilities in the networks totaled 335. The maximum MWCw ranged from 3 to 123 facilities, and significantly increased during the year ($p < 0.01$). The composition of MWCw was stable over time, with trucks accounting for an average of 24% of the MWCw, but only 11% of the trucks in the source population were present in the MWCw. Number of facilities with high betweenness and high in-out degree value (i.e. transfer points in animal movement) was higher during warmer period of the year ($p < 0.05$). The number of trucks utilized per week was increasing as the year progressed ($p < 0.01$), together with the number of trucks that had a high betweenness ($p < 0.01$).

Conclusion: The network analysis presented here makes it possible to conceptualize how disease could spread within a network. Component size could be used as a potential estimator of the upper bound of an epidemic (3). Additionally, a peak time of connectivity was found during the summer months, which increases the potential for disease spread.

Industry Implications: The use of network measures to investigate swine movements allows for an in-depth investigation into patterns over time to aid in biosecurity efforts within the industry. From these results we have found that up to 33% of study population could be involved in disease outbreak that effectively spreads through animal movement and transportation practices.

Acknowledgments: Funding provided by, Ontario Ministry of Agriculture Food and Rural Affairs

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The effect of dietary energy allowance for gestating sows on energy status and growth potential of offspring at birth.

Jessica Miller¹, Emily G. Miller PhD¹, Cornelis F. M. de Lange PhD¹, Lee-Anne Huber PhD¹
Department of Animal Biosciences, University of Guelph¹

Introduction: With the relatively recent industry initiatives in Australia and North America to move gestating sows from single stalls to group pens, the nutritional implications must be considered, particularly the challenges associated with and feeding strategies for groups of sows [1]. When housed in groups it can be difficult to meet individual feed requirements, especially in competitive environments. The objective of this study was to determine the effect of over- or under-supplying energy to gestating sows on energy status and growth potential of the offspring at birth.

Methods: In a previous study, pregnant sows were fed either 15% above (HIGH, n=25) or below (LOW, n=24) estimated metabolizable energy requirements over 3 consecutive parities [2]; all sows received amino acids to meet or exceed estimated requirements. Two piglets were sacrificed from each sow at each parity, immediately after birth and before first suckle for tissue (blood, muscle, liver) collection and body composition analysis [3,4]; from these piglets, plasma samples were randomly selected (n=28) for glucose and IGF-1 analyses. Muscle (n=18 and n=12 for HIGH and LOW, respectively) and liver tissues (n=18 and n=14 for HIGH and LOW, respectively) were randomly selected for glycogen analysis. Statistical analyses were conducted using maternal feeding level, parity, and the interaction between feeding level and parity as fixed effects.

Results: Neither parity nor maternal feeding level influenced piglet body weight, body protein content, plasma glucose, or muscle or liver glycogen content at birth. Maternal feeding level did not influence piglet body fat content or plasma IGF-1 at birth. Piglet plasma IGF-1 increased with increasing parity number (linear, $P=0.09$; quadratic, $P<0.05$); plasma IGF-1 was greater for piglets born to parity 2 versus parity 1 sows (73 vs. 58 ± 4.5 ng/mL; $P<0.05$), but was not different between piglets born to parity 2 or 3 sows.

Conclusions: Providing gestating sows with metabolizable energy 15% above or below estimated energy requirements, while meeting or exceeding amino acid requirements did not influence energy storage in the piglet, nor the concentration of plasma IGF-1 at birth; however, piglet plasma IGF-1 increased as sows matured between parities 1 and 2.

Industry Implications: With the current shift in housing for gestating sows from stalls to group pens, sows could receive fluctuating amounts of feed, with some receiving under or over recommended amounts of nutrients; altering energy intake by 15% (above or below estimated requirements) does not have negative implications for piglet energy storage or plasma growth factors. Where sow feed intake can be controlled (i.e. precision feeding), feed costs can be reduced by reducing the provision of energy by up to 15%, without influencing energy storage in the offspring.

Acknowledgements: Financial support was provided by Ontario Pork, Royal De Heus, Heartland Lys Inc. / Ajinomoto, the Ontario Ministry of Agriculture Food and Rural Affairs, and the Natural Sciences and Engineering Research Council of Canada. Thank you to Cuilan Zhu for all of your help in the lab, and everyone else that volunteered their time to help this research conclude on time.

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Identification of genomic regions and markers with transmission ratio distortion affecting reproduction in pigs

S. Nayeri¹, M. Jafarikia^{1,2}, J. Casellas³, P.A.S. Fonseca¹, A. Suarez-Vega¹, A. Robinson¹, and A. Cánovas¹.

¹Centre for Genetic Improvement of Livestock, University of Guelph, Guelph, ON; ²Canadian Centre for Swine Improvement Inc. Ottawa, ON; ³Department of Animal and Food Science, Autonomous University of Barcelona, Spain

Introduction: In swine industry, the efficiency of pig production is to a large extent evaluated by the number of piglets born alive and litter size at weaning (Bergfelder-Drüing et al. 2015). Among these traits, litter size is the major driver of the profitability associated with farming sows. Selection for litter size in the pig industry was successful, however, it was accompanied by an unfavorable increase in piglet mortality (Zak et al. 2017). Postnatal mortality represents a significant economic loss in the piglet industry which might be associated with physiological effect (Panzardi et al. 2013) or the association of lethal genes that decrease the survival of the newborn animal (Moore, 2006). Genetic elements that affect embryo or fetal survival, postnatal viability and others can exhibit deviation of the Mendelian allelic segregation (also known as Transmission Ratio Distortion (TRD)). This phenomenon is basically the deviation from the expected Mendelian inheritance of alleles from the heterozygous parents (Pardo-Manuel De Villena et al. 2000). Several biological mechanisms are associated with TRD, including the preferential transmission of one of the two alleles carried by a heterozygote parent to the zygote at the time of fertilization, embryo or fetal failure and differential viability during early neonatal life. Recently, our research group developed a Bayesian methodology to identify TRD across the genome (Casellas et al. 2014). Moreover, mapping embryo lethal factors showed that alleles can be tightly linked to lethal factors exhibit TRD (Crow 1991). Therefore, the objective of this study is mainly to identify genomic regions with altered deviations in Mendelian segregation that could affect fertility, viability in early developmental stages and postnatal survival in pigs.

Methods: A total number of 30,000 individuals from three breeds (Duroc (n=10,000), Landrace (n=10,000) and Yorkshire (n=10,000)), genotyped with high-density (50K, 60K and 70K) SNP panels will be used to assess identifying genome regions with TRD. For the analyses, a Bayesian approach will be used to estimate the TRD parameters. The models developed by Casellas et al. (2014) accommodate a wide range of population structures and present a flexible parametrization allowing to differentiate for specific- and unspecific-parent TRD. The statistical relevance of TRD can be tested by a Bayes factor (BF), a ratio of probabilities between the models with and without TRD effects.

Results: Based on previous results obtained in dairy cattle we anticipate to obtain significant SNPs with TRD in pigs. For example, SNPs displaying TRD in dairy cattle show functional consequences identifying lethal haplotypes related to significant biological processes associated to embryonic stages, such as regulation of mitotic cell cycle, stem cell population maintenance, or forebrain development.

Conclusions: Detection of markers in the regions associated to TRD may help us to identify regions associated with piglet survival. The identified regions may lead to an early selection of animals that do not carry these lethal alleles and help producers to improve reliability of breeding programs in the pig production industry.

Industry Implications: This project will increase the competitiveness of the Canadian swine industry through identifying genomic regions with TRD that contain genes and markers with expected effect on survival in pigs and to improve productivity and sustainability in the swine industry.

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Mosaic reciprocal chromosome translocations in pigs

Samira Rezaei BSc¹; Daniel A.F. Villagomez DVM, PhD²; Nicolas Mary MSc³; Tamas Revay MSc, PhD¹;

Brendan Donaldson BSc¹; W. Allan King MSc, PhD^{1,4}.

Department of Biomedical Sciences, University of Guelph, Guelph, ON, Canada¹; Departamento de Producción Animal, Universidad de Guadalajara, Zapopan, Mexico²; GenPhySE, Université de Toulouse, INRA, INPT, ENVT, Toulouse, France³; Karyotekk Inc, University of Guelph, Guelph, ON, Canada⁴

Introduction: Mosaic chromosome rearrangements result from post-zygotic events due to mistakes during mitotic division. Depending on the distribution of mosaicism in the animal, mosaic chromosome rearrangements may be found in one or more cell types. Traditional cytogenetic screening practices, developed for identifying constitutional aberrations, may allow for detection of mosaic chromosome rearrangements such as translocations in peripheral blood. Constitutional chromosome translocations lead to reduced fertility in pigs thus routine cytogenetic screening is performed on breeding boars in many countries (1). However, mosaic translocations are often missed in screened populations. Identifying low-grade mosaic chromosome rearrangements is difficult since traditional cytogenetic screening techniques detect chromosome rearrangements by analyzing only a few metaphases which is suffice for detection of constitutional chromosome aberrations. Nevertheless, cytogenetics is the conventional practice to characterize mosaic chromosome translocations in pigs.

Methods: Peripheral blood samples were obtained from young unproven boars. Blood samples were cultured for 72 hours. Cultures were harvested to arrest and fix the cells at the metaphase stage. Cells were spread onto glass slides to be stained, after a week of ageing, with standard GTG-banding (2). Metaphase chromosomes were captured using a camera mounted microscope. Through a karyotyping software (SmartType), 2-3 metaphases were analyzed for each animal in order to identify chromosome rearrangements. With identification of a mosaic carrier, more cells were imaged and 25 metaphases analyzed to confirm the degree of mosaicism. Additionally, ear biopsies and blood samples from carriers and available family members were obtained. Skin fibroblast cultures were established and chromosomes of 25 metaphases were analyzed according to the standard pig karyotype.

Results: Through routine karyotype analysis of over 3700 young boars, the King lab at the University of Guelph has found 17 carriers of mosaic reciprocal chromosome translocations. All the 17 carriers were detected with low-level chromosomal mosaicism since less than 9% of cells carry a reciprocal translocation. Moreover, 2 animals (11% of the mosaic carriers) were identified with two different mosaic abnormalities. Furthermore, analysis of fibroblast cells for 2 carriers revealed no mosaic chromosome rearrangements. Additionally, we identified that the dam of a mosaic mos t(7;9) carrier carried a different translocation, mos t(9;13), from its offspring.

Conclusion: There are no reports of mosaic chromosome translocations in pigs. Thus, detection of 17 mosaic translocations within the screened Canadian population is an unexplained phenomenon. The biological effects and the underlying genetic mechanisms leading to this type of chromosome abnormality are yet to be elucidated in pigs. Investigating the family members such as dams, brothers, and sisters of the carriers allows for the identification of familial trends and for elucidating the possibility of a genetic predisposition in developing mosaic translocations.

Industry Implications: Heritable chromosome abnormalities are major contributors of low fertility, however mosaic chromosome rearrangements are not previously documented or studied in pigs. Thus, the biological and economical impacts of mosaic chromosome rearrangements in pigs are unknown.

Acknowledgments: Funding provided by the Canada Research Program, the OVC, and OMAFRA.

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Can feeding plant-based *E. coli* FaeG prevent post-weaning diarrhea?

Victoria, CJ Seip¹, BSc; Robert M Friendship¹ DVM, MSc; Rima Menassa² PhD; Vahab Farzan¹ DVM, MSc, PhD

¹Department of Population Medicine, University of Guelph; 2AAFC London research and Development Centre

Introduction: Post-weaning diarrhea (PWD) caused by enterotoxigenic *E. coli* (ETEC) is a major economic concern on Ontario swine farms.. Fimbrial appendages allow pathogenic *E. coli* to attach to receptors in the mucosal layer of the gastrointestinal tract. The fimbria of the most common ETEC variant found on commercial swine operations is F4 which is composed of the major sub-unit FaeG. A recombinant variant of the FaeG protein, rFaeGntd/dsc has been produced in plant chloroplasts, and accumulation levels of 2.0 g rFaeGntd/dsc per 1 kg fresh leaf tissue have been obtained (1). It is possible that lyophilized plant leaves containing FaeG administered orally to pigs following weaning might reduce disease when piglets are challenged with ETEC, because the plant FaeG protein might compete for receptors and therefore block ETEC from colonizing in the GIT of the pig. The objective of this study was to determine if the feeding of tobacco leaves containing recombinant FaeG can protect pigs from developing diarrhea when experimentally challenged with ETEC..

Methods: Three trials were conducted. For each trial, 24 piglets previously tested to confirm genetic susceptibility to F4+ETEC attachment using RFLP PCR were transported to the OVC Isolation Facility and housed in 4 rooms (Day 0). All pigs in each room (n=6) were assigned to one of four treatments including 2.5g of a wildtype of tobacco (Treatment 1), 2.5g of a wild type of tobacco(Treatment 2), 2.5g of FaeG product (Treatment 3), or 1.25g of FaeG product (Treatment 4). In each treatment, pigs received in total 5 feedings of the allotted treatment dose prior to challenge. Over the course of the trial, piglets were provided with a non-medicated starter feed ad-libitum. On Day 4, all pigs except Treatment 1 were challenged by oral gavage with 2mL of 10⁹ CFU of *E. coli* O149:K91:F4 (JG280) . Prior to and post-challenge the clinical observations (diarrhea score, depression, dehydration, temperature and appetite) were recorded and fecal swabs were taken and cultured for ETEC. Pigs were euthanized 2 days after challenge and samples from jejunum, ileum and colon were taken and examined histologically for lesions and bacterial colonization. Colon samples were also collected and cultured for ETEC.

Results: Control pigs (Treatment 1) did not develop diarrhea. Diarrhea scores were lower in pigs receiving the higher concentration of the plant product containing FaeG (Treatment 3) compared to pigs receiving the wild-type tobacco (Treatment 2) ($P<.05$). However, no significant differences were seen in bacterial colonization, histological lesions and bacterial shedding among the pigs in 3 different groups challenged with *E. coli*.

Conclusions: Feeding 5g/day of a dried leaf powder containing recombinant variant of the FaeG protein reduced the incidence of diarrhea in newly weaned pigs when experimentally challenged with F4+ETEC.

Industry Implications: If increased restrictions regarding the use of antibiotics and heavy metals forces the swine industry to seek alternative solutions to the problem of post-weaning diarrhea, then the use of plant-based products might be a consideration but further research is required to investigate the application of this product under commercial condition.

Acknowledgements: Technical help from Dr. Rocio Amezcua and Dr. Josepha DeLay, and OVC Isolation staff. Funding provided by OMAFRA HQP, OMAFRA-U of G Research Partnership, and Swine Innovation Porc.

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Effects of pre-weaning iron supplementation on post-weaning diarrhea in pigs challenged with enterotoxigenic *E. coli* (ETEC)

Victoria CJ Seip, BSc; Robert M Friendship DVM, MSc; Vahab Farzan DVM, MSc, PhD
Department of Population Medicine, University of Guelph

Introduction: Administration of iron (200 mg Fe as iron dextran per piglet) on day 2 or 3 after birth to prevent anemia is a common practice in modern pig husbandry. However, it has been shown that despite supplementation, iron deficiency is common among modern fast-growing pigs at 3 weeks of age when pigs are under stress and facing disease-challenge. The objective of this study was to determine if pigs with iron deficiency at weaning are more susceptible to develop post-weaning diarrhea after challenging with ETEC than pigs with adequate iron stores.

Materials and Methods: Two trials were conducted. For each trial all piglets from 11 litters at the Arkell Research Station were ear tagged at 2 days of age. At 3 days of age, one-third of the litter were given 100 mg of iron dextran (Uniferon®200, Pharmacosmos Inc.) by intramuscular injection, and the remaining two-thirds of the litter were given 200 mg of iron dextran. One-third of the pigs that received 200 mg of iron on Day 3 were injected with a second dose of 200 mg of iron on Day 14. At 9 days of age, pig DNA was extracted from blood samples collected from a subset of pigs and subjected to RFLP-PCR to determine the pig susceptibility to F4 ETEC. At weaning, 12 susceptible pigs from each treatment (total of 36 pigs) were weighed and a whole blood sample was taken from each pig and submitted to AHL for a complete blood count using a non-differential evaluation. Piglets were then transported to the OVC Isolation Facility and housed in 6 rooms (2 pigs from each iron treatment in each room). One day after arrival, pigs in 5 rooms were challenged by oral gavage with 2 mL of 10^9 CFU of *E. coli* O149:K91:F4 (JG280). Prior to and post-challenge the clinical observations (diarrhea score, depression, dehydration, temperature, and appetite) were recorded and fecal swabs were taken and cultured for ETEC. Pigs were euthanized two days after challenge and tissue samples were taken from the jejunum, ileum and colon for histological examination; colon samples were also taken and cultured for ETEC.

Results: At weaning 72 piglets in two trials were categorized based on their hemoglobin levels as anemic ($n=17$) (hgb <90 g/L), iron deficient ($n=18$) (hgb between 90 to 110g/L), and adequate iron levels ($n=37$) hgb >110 g/L). Over the course of three collection periods post-challenge 53% of anemic pigs, 57% of iron deficient pigs and 55% of the pigs with adequate iron levels had diarrhea. No significant difference in response to ETEC challenge was observed among pigs with three different pre-weaning iron supplementation doses or with different levels of hgb determined at weaning.

Conclusions: Pigs that are challenged with ETEC and are classified as anemic, iron deficient or have adequate hemoglobin levels show no difference in clinical signs, bacterial colonization/shedding, and histological lesions ($P>0.05$).

Industry Implications: Although piglets receiving the standard dose of one injection of 200 mg of iron dextran were mostly classified as iron deficient at the time of weaning, this does not appear to have an influence on ETEC infection. However, this study was conducted under controlled conditions, and it is possible that under field conditions with a natural challenge the anemic pigs be more susceptible to enteric diseases.

Acknowledgements: Technical help from Dr. Rocio Amezcua and Dr. Josepha DeLay, as well as OVC isolation staff. Funding provided by Pharmacosmos, OMAFRA HQP, and OMAFRA U of G Research Partnership

The effect of reduced dietary glycine and supplemental threonine on growth performance and collagen content in skin of pigs fed low crude protein diets

Kayla E. Silva BSc¹, Wilfredo D. Mansilla PhD¹, Anna K. Shoveller PhD¹, John K. Htoo PhD², John P. Cant PhD¹, Lee-Anne Huber PhD¹, and Cornelis F. M de Lange PhD¹

¹Department of Animal Biosciences, University of Guelph. ²Evonik Nutrition & Care GmbH, Germany.

Introduction: Essential amino acid (EAA) requirements are reasonably well defined for growing pigs (1), whereas estimates for nitrogen (N) and non-essential amino acids (NEAA) requirements are limited. The latter is in part because typical ingredients, such as corn and soybean meal, contain relatively high concentrations of N and NEAA. Conversely, the inclusion of crystalline amino acids (AA) allows for formulation of low-crude protein (CP) diets that maintain EAA but decrease NEAA supply. When feeding growing pigs low-CP diets, endogenous synthesis of specific NEAA (or N) may limit maximum growth, particularly if the dietary supply of Gly is low (2). In this scenario, Thr catabolism may be upregulated to produce additional Gly, via the enzyme Thr-dehydrogenase, which reduces the utilization efficiency of expensive EAA for body protein retention (3). The objective of the current study was to determine the effect of supplementing dietary Thr above estimated requirements on pig growth and skin collagen abundance when fed low-CP low-Gly diets during the grower phase.

Methodology: A total of 42 barrows (BW=15.1±2.72 kg) from the Arkell Research Station were used and housed individually at the University of Guelph. Initial body composition was determined (n=7) and the remaining pigs (n=35) were randomly assigned to 1 of 5 iso-nitrogenous diets: 1) Control, semi-purified diet that met EAA requirements (CON; 12.1% CP). The remaining diets were formulated by reducing Gly and Ser content to 60 and 20%, respectively, of CON and supplementing with either Glu or Thr at 2 levels each, to maintain similar CP levels. For diets 2 and 3, Thr was included at 1.59% (LT) or 2.34% (HT), at the expense of the NEAA mix. For diets 4 and 5, Glu was included at 3.47% (LG) or 4.64% (HG), at the expense of the NEAA mix. All treatments were supplemented with synthetic NEAA in the same proportion as found in whole-body protein of pigs to increase the EAA:N ratio to 0.48 (2). Pigs were restriction-fed at 2.8×estimated ME requirements for maintenance (191 kcal/kg BW^{0.60}; 3) in 3 equal meals per day over a 21-day experimental period. Pigs were weighed once per week for the determination of average daily gain (ADG). At slaughter, final body composition was determined and skin samples were collected for collagen analysis.

Results: All statistical analyses were conducted using Proc GLIMMIX (SAS 9.4). There were no differences in initial or final BW. Overall, ADG for pigs fed diets supplemented with Glu (378 g/d) was greater than for those fed diets supplemented with Thr (359 ± 9.45 g/d; $P=0.041$). Feed efficiency for pigs fed diets supplemented with Glu (0.431) tended to be greater than for those fed diets supplemented with Thr (0.411 ± 0.01; $P=0.074$). Pigs fed LG, HG and HT diets had reduced skin collagen content compared to CON ($P < 0.05$); skin collagen content was not different between pigs fed LT versus CON diets.

Conclusions: Diets supplemented with Thr decreased body weight gain in growing pigs. Skin collagen was not different between pigs fed a low-CP diet with 1.59% Thr, compared to the CON diet.

Industry Implications: Better estimates of NEAA requirements for growing pigs are warranted in order to maximize the efficiency of utilizing dietary amino acids for both growth and underlying metabolic processes. Feeding low-CP diets reduces N excretion into the environment therefore reducing the impact of pork production.

Acknowledgements: Financial support was provided by Evonik Industries, Ontario Pork, OMAFRA and Swine Innovation Porc.

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A novel monomodular and multifunctional processive β -1,4-endoglucanase from porcine gut microbiome

Weijun Wang, PhD¹; Tania Archbold, BSc¹; Joseph S Lam, MSc, PhD²; Matthew S Kimber, MSc, PhD²; Ming Z Fan, MSc, PhD¹

Departments of Animal Biosciences¹, and Molecular and Cellular Biology², University of Guelph, Guelph, Ontario, Canada N1G 2W1

Introduction: Microbial anaerobic fermentation of dietary fibre in the gastrointestinal tract (GIT) is indispensable for sustaining animal and human nutrition and health (1). Cellulose-degrading enzymes catalyze some of the initial reactions in dietary fibre digestion *in vivo* in swine. These enzymes also play key roles in multiple industrial bioprocessing applications.

Methods: A plasmid metagenomic expression library was constructed for mining cellulose-degrading enzymes from the pig hindgut microbiota that was modulated by feeding a purified crystalline cellulose supplemented diet (1). One of the cellulase genes, referred to as *p4818Cel5_2A* and mined from this metagenomic expression library, was analyzed in sequence and over-expressed in *E. coli* BL21(λ DE3). The resulting cellulase was further purified and biochemically characterized.

Results: Within the sequence preceding the *p4818Cel5_2A*, -10 and -35 promoter elements were identified along with three transcription-factor binding sites. The enzyme possesses a catalytic domain belonging to the glycoside hydrolase family 5 subfamily 2 (GH5_2), thus it was named as p4818Cel5_2A. The protein was over-expressed, purified, and characterized; and it displayed optimal enzymatic activity at pH 6.0 and 50 °C. The enzyme also exhibited resilience to trypsin digestion, where >70 % activity was retained after 6.0 h incubation with trypsin at 37 °C. This p4818Cel5_2A cellulase exhibited a broad substrate profile with the highest specific activity towards β -glucan, carboxymethyl cellulose (CMC), followed by hydroxyethyl-cellulose and regenerated amorphous cellulose (RAC). The enzyme was also active on other substrates including crystalline cellulose substrates such as Avicel and Solkaflocc, as well as the hemicelluloses of glucomannan and xyloglucan. Furthermore, with viscosity and hydrolysis end product analyses, the enzyme behaved as a typical endo- β -1, 4-glucanase, and displayed hydrolytic processivity towards RAC.

Conclusion: The novel cellulase of p4818Cel5_2A mined in this study is a novel mono-modular and multifunctional processive β -1,4-Endoglucanase. Dietary modulation of porcine gut microflora together with functional metagenomic mining is a powerful tool to discover novel and active fibre-degradation enzymes; and to better understand the molecular mechanism of fiber digestion *in vivo* in the porcine gut.

Industry Implications: The newly discovered processive cellulase of p4818Cel5_2A from the porcine gut microbiota has exhibited great potential for industrial applications, particularly as a novel exogenous feed enzyme to improve fiber nutrition in animal production.

Acknowledgements: Funding provided by the Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA) New Directions & Alternative Renewable Fuels Research Program; and the University of Guelph Gryphon's LAAIR (Leading to Accelerated Adoption of Innovative Research) program (to M.Z.F.).

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Increased intestinal alkaline phosphatase maximal activities mediate improvements in growth and gut health status in weanling pigs fed the antibiotic-supplemented diet

Xindi Yin, MSc¹; Tania Archbold, BSc¹; Nicole Burello, MSc¹; Michael Scolaro¹; Mengyun Li, MSc, PhD²; Weijun Wang, PhD¹; Kevin Zhou, BSc¹; Ming Z. Fan, MSc, PhD¹

Department of Animal Biosciences, University of Guelph¹, Guelph, ON, Canada, Henan University of Animal Husbandry and Economy², Zhengzhou, China

Introduction: Improved understanding of the biological mechanisms of antibiotic actions on increasing growth rate and gut health aids to develop alternative strategies in weanling pig nutrition. As one group of the most abundant apical membrane-bound enzymes in the gut, intestinal alkaline phosphatases (AP) are important defense proteins preventing gut dysbiosis and enteric diseases through detoxifying bacterial endotoxin lipopolysaccharides (LPS) (1). Therefore, we hypothesized that dietary antibiotic could improve growth performance and gut health by enhancing the intestinal endogenous alkaline phosphatase detoxification capacity in weanling pigs.

Methods: A total of 104 crossbred (Duroc × Yorkshire × Landrace) barrows were weaned on day 19, with an average initial body weight (BW) of 6.81; SE = 0.09 kg BW, from 62 litters; and were randomly assigned to two groups according to a randomized complete block design. Both groups of pigs were fed a corn and soybean meal-based diet for 3 weeks; and the antibiotic-treatment diet was supplemented with 550 mg aureomycin per kg diet. Pigs were weighted weekly and fecal score was assessed twice a day. At the end of the trial, jejunal, ileal, cecal and colonic segments were collected from 8 barrows of each dietary treatment group, and were homogenized for AP kinetics characterization using p-nitrophenyl phosphate as substrate ranging 0 – 0.8 mM in incubation media in 4 replicates at pH 7.4 and 37°C for 30 minutes. Growth performance and fecal score data were analyzed for the analysis of variance and the F-test with the software package R. The kinetic comparisons were analyzed by the pooled *t* test and were presented as means ± SE, and P-values < 0.05 were considered significant.

Results: The dietary antibiotic supplementation increased ($P < 0.05$; $n = 26$ pens) the 3-week average daily gain by 19%; and improved ($P < 0.05$; $n = 26$ pens) the 3-week average daily fecal score of the weanling pigs in comparison with the non-antibiotic control group. The kinetics data were shown as parameter estimates ± SE, $P < 0.05$, $R^2 = 0.33 - 0.83$, $n = 40$. For pigs fed the diet with the antibiotic supplementation, the V_{max} (nmol·mg protein⁻¹·min⁻¹) values in the jejunum (38.18 ± 1.22 vs. 27.46 ± 1.96), ileum (28.19 ± 1.61 vs. 20.89 ± 0.86), cecum (3.20 ± 0.24 vs. 3.03 ± 0.26), and colon (12.01 ± 1.18 vs. 9.88 ± 0.85) were increased ($P < 0.05$) by 39.04, 34.94, 5.64 and 21.56%, respectively, compared with the the non-antibiotic fed control group of pigs.

Conclusion: These results indicated that dietary antibiotic could mediate improvements in growth rate and gut health status in weanling pigs through increasing intestinal alkaline phosphatase maximal activities.

Industry Implications: Results of this study help us to better understand the action modes of feed supplemental antibiotics in improving weanling pig performances and gut health. Effective alternative strategies on increasing intestinal alkaline phosphatase maximal activities need to be further developed to replace the current use of feed antibiotics to address the concerns of antimicrobial resistance and the overuse of antibiotics in the pork production facing the global community.

Acknowledgements: Funding provided by the NSERC Discovery Program; the University of Guelph-OMAFRA partnership program; and the Food From Thought research program at the University of Guelph with funding from the Canada First Research Excellence Fund. Xindi Yin is also supported by a Ph.D. scholarship from the China Scholarship Council (CSC).

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Responses in gut permeability, total tract dry matter digestibility and growth performances in weanling pigs fed the diet supplemented with the antibiotic aureomycin

Xindi Yin, MSc; Tania Archbold, BSc; Wenyi Fan, MSc; Nicole Burello, MSc; Zeyu Yang, BSc; Hongzhi Wu, MSc; Michael Scolaro; Kevin Zhou, BSc; Weijun Wang, PhD; Ming Z. Fan, MSc, PhD
Department of Animal Biosciences, University of Guelph, Guelph, ON, Canada N1G 2W1

Introduction: Aureomycin is widely used as a growth promoter in commercial weanling swine diets for prevention and treatment of porcine intestinal inflammation and enteritis caused by pathogenic bacteria such as *Escherichia coli* and *Salmonella*, even though it can lead to the disturbance of gut beneficial microbial community and development of antimicrobial resistance (1). Until now, its modes of actions are still largely unknown. The objectives of this study were to determine the effects of dietary antibiotic aureomycin on gut permeability, nutrients digestibility and growth performance in weanling pigs.

Methods: A total of 104 crossbred (Duroc × Yorkshire × Landrace) barrows were weaned on day 19, with an average initial body weight (BW) of 6.81 kg; and were randomly assigned to two groups according to a randomized complete block design. Both groups of pigs were fed a corn and soybean meal-based diet for 3 weeks; and the antibiotic-treatment diet was supplemented with 550 mg aureomycin per kg diet. Titanium dioxide was added at 0.30 % as a digestibility marker. Pigs had free access to water and feed. Pigs were weighted and received an oral bolus D-mannitol (0.3 g/kg BW) 4 h prior to collect the plasma samples every week. Feed intake was recorded daily, and fecal samples were daily collected during last 7 days. Data were analyzed for the analysis of variance and the F-test with the software package R; and were presented as means ± SE, P-values < 0.05 were considered significant.

Results: The results showed that pigs fed with the dietary antibiotic increased (0.350 ± 0.016 vs. 0.295 ± 0.015 kg/d, $P < 0.05$) the average daily gain by 19% during d 0-22; and increased (0.17 ± 0.01 vs. 0.13 ± 0.01 kg/d, $P < 0.05$) the average daily feed intake by 31% during d 0-7 post-weanling growth, respectively, in comparison with the non-antibiotic pigs. However, the apparent total tract digestibility of dry matter in the pigs fed with antibiotic was decreased (77.84 ± 0.65 vs. 82.29 ± 0.80 %, $P < 0.05$) by 6% in comparison with the non-antibiotic pigs. Compared with the starting day-1 weaning baseline, *in vivo* gut permeability was higher ($P < 0.05$) during the weeks 1 and 2 after weaning; and then became lower ($P < 0.05$) at the end of the week-3 after weaning in the antibiotic-fed pigs compared with the non-antibiotic control.

Conclusion: Results of this study indicated that feed antibiotic use improved the growth performances with decreased *in vivo* gut permeability as an adaptive response; however, reduced total tract dry matter digestibility was not a contributing factor to the feed antibiotic-associated growth promotion in the weanling pig.

Industry Implications: This study helps us to better understand relevant biological mechanisms regarding how supplemental feed antibiotics can improve weanling pig performances and effectiveness in inhibiting negative pathogenic bacterial impacts on the intestinal microbiota and host weanling pigs, thus effective alternative strategies can be further developed to replace the current use of feed antibiotics to address the concerns of antimicrobial resistance and the overuse of feed antibiotics in the pork production facing the global community.

Acknowledgements: Funding provided by the NSERC Discovery Program; the University of Guelph-OMAFRA partnership program; and the Food From Thought research program at the University of Guelph with funding from the Canada First Research Excellence Fund. Both Xindi Yin and Hongzhi Wu are also supported by a Ph.D. scholarship from the China Scholarship Council (CSC).

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Nutritive value of soybean products fed to growing pigs without or with multi-enzyme supplement

C. Zhu¹, I. Parenteau¹, N. E. Ward², A. J. Cowieson³ and E. Kiarie¹

¹Department of Animal Biosciences, University of Guelph, Guelph, ON, N1G 2W1; ²DSM Nutritional Products Inc., Parsippany, NJ 07054; ³DSM Nutritional Products, Kaiseraugst, Switzerland

Introduction: Indigestible fiber-protein-phytate complexes reduce feeding value of soy products. The objective of the study was to investigate effects of multi-enzyme supplement (**MES**) on standardized ileal digestibility (**SID**) of AA and DE content in expeller soybean meal (**ESBM**) and roasted full fat soybean seed (**FFSB**) fed to growing pigs.

Methods: The ESBM was a commercial product and FFSB was roasted at 118-120°C for 75 min in a local farm. The CP was 42.8 and 33.4% DM in ESBM and FFSB, respectively and corresponding values for crude fat were 11.8 and 17.4% DM. Semi-purified diets with 50% of either ESBM or FFSB as sole source of AA were prepared without or with MES supplying phytase, protease, xylanase, β -glucanase at 1,500, 5,625, 270 and 70 U/kg of feed, respectively. Diets had TiO₂ indigestible marker and ratio of cornstarch to sucrose and corn oil was identical to our published N-free diet to calculate DE by difference method. Eight ileal-cannulated barrows (BW = 22.1 $\pm$ 0.61 kg) were fed 4 diets in a replicated 4 $\times$ 4 Latin square design (n=8). Period lasted for 9 d; 5-d for acclimation, 2-d for fecal and 2-d for ileal digesta samples collection. Fixed effects of soy product, MES and two-way interactions were evaluated.

Results: There was no interaction (P>0.05) or MES effect on AID and SID of CP and AA, except AID and SID of Phe (P<0.05). ESBM had higher (P<0.05) AID and SID of CP and AAs than FFSB. There was no interaction (P>0.05) or MES effect on apparent total tract digestibility (ATTD) of components and DE content (P<0.05). ESBM had higher (P<0.05) DE content than FFSB. Supplemental MES improved (P<0.05) ATTD of Ash and CP.

Conclusions: MES had no effect on SID of AA and DE content whereas ESBM had higher SID of AA and DE content compared to FFSB. Supplemental MES improved mineral (ash) utilization

Industry Implications: Expeller soybean meal had better nutritive value than roasted full fat soybean seed in growing pigs. This partly reflected the impact of processing on nutrient utilization. Multi-enzyme supplement reduced nitrogen and mineral excretion which may economic and environmental benefits in pork production.

Acknowledgements: Funding supported by NSERC discovery grant and DSM Nutritional Products Inc.