

ABSTRACTS of the 15th CRIPA SYMPOSIUM

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CONFERENCES – APRIL 1st, 2026



KEYNOTE SPEAKER

Prof. Dirk Werling,

DMV, PhD, MRCVS

Professor of Molecular Immunology

Department of Pathobiology and Population Sciences RVC Royal Veterinary College University of London, UK

Prof. Dirk Werling earned his Doctor of Veterinary Medicine degree from the University of Veterinary Medicine Hannover. Then he completed his doctoral studies at the ETH Zurich, in Switzerland, investigating how bovine leukaemia virus infection affects the capacity of bovine macrophages to respond to lipopolysaccharide (LPS). His early work was supported by competitive funding from the Swiss National Science Foundation and the German Research Foundation. Prof. Werling subsequently received a Marie Curie Research Fellowship from the European Union, which allowed him to join the research group of Chris Howard at the Institute for Animal Health. There, he focused on the development and characterisation of dendritic cells and their role in respiratory syncytial virus infection. He later returned to ETH Zurich as a Senior Scientist, expanding his research to include the development of the innate immune system in ruminants and pathogen escape mechanisms in innate immune cells. In 2001, he accepted an Assistant Professorship at the University of Bern within the Institute of Virology, working in the group of Thomas Jungi. In 2003, he joined the Royal Veterinary College as a Senior Lecturer and was promoted to a personal tenured Chair as Professor of Molecular Immunology in 2007. His research has attracted substantial external funding and has led to the submission of three patent applications. His current work is supported by the Biotechnology and Biological Sciences Research Council, the European Union (FP7 and EMIDA programmes), and the Bill & Melinda Gates Foundation. Prof. Werling's main research interests focus on the ontogeny of the innate immune system across species, the role of single-nucleotide polymorphisms in innate immune receptors and ligand binding, and the application of innate immunology to the design of new or improved vaccine strategies. His current work places particular emphasis on carbohydrate recognition and the development of carbohydrate-based vaccines.

Presentation of results New initiative of CRIPA

Study of the genomic diversity of *Staphylococcus hyicus* strains in Eastern Canada, a pathogen affecting piglets

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Staphylococcus hyicus is the etiological agent of porcine exudative epidermitis, a disease of major health and welfare concern in piglets. Despite its importance, relatively few genome sequences are available for this species. In this study, we analyzed 50 *S. hyicus* isolates from Eastern Canadian swine herds between 2021 and 2023, and sequenced the genome of 22 of them, to better document their genomic diversity and antimicrobial resistance profiles. Taxonomic identification based on molecular phylogeny revealed substantial genomic diversity among the isolates available. Overall, 74% of the isolates displayed phenotypic resistance to at least one of twelve tested antibiotics. Genomic screening showed that 26% of the isolates carried the *exhA* exfoliative toxin gene, 38% had a CRISPR-Cas9 system and 56% possessed tetracycline resistance genes. Two distinct tetracycline resistance determinants were identified: a chromosomal *tet(M)* gene located on a Tn916/Tn1545 transposon, and a *tet(L)* gene carried by various mobile genetic elements. To further characterize the vectors involved in *tet(L)* dissemination, 11 isolates carrying *tet(L)* as their sole tetracycline resistance gene were examined. Eight different *tet(L)*-bearing plasmids were identified, two isolates carried chromosomal *tet(L)*, and only one plasmid was shared among multiple isolates, highlighting marked plasmid diversity. CRISPR-Cas9 system presence did not have apparent association with plasmid carriage or antibiotic resistance. Altogether, these results underscore the considerable genomic diversity of *S. hyicus* in Eastern Canadian swine and the dynamic nature of tetracycline resistance gene circulation within this species.

Characterization of the wild red junglefowl microbiota to postulate members of the missing microbiota in domesticated poultry

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Humans living a Western lifestyle have gut microbiota with significantly reduced species richness compared to humans living traditional hunter-gatherer lifestyles, such as the Yanomami in South America. We asked whether a similar pattern could be observed in domesticated chickens compared to their wild ancestors. Wild red junglefowl (*Gallus gallus*), the likely undomesticated ancestors of modern domestic chickens, continue to inhabit several regions of Southeast Asia, including Singapore, and provide a unique opportunity to study the avian gut microbiome prior to domestication. In this study, fecal samples were collected from six wild red junglefowl in Singapore and analyzed using both culture-dependent and culture-independent approaches. These data will be analyzed in parallel with samples from six Canadian egg-laying hens to enable comparative genomic and microbiome-level analyses. Extensive culturing efforts have yielded 534 bacterial isolates from wild red junglefowl, reflecting the high microbial diversity present in the wild avian gut. Ongoing species identification and genomic characterization are being used to assess taxonomic diversity and functional traits that may be absent or underrepresented in domesticated poultry. Together, this work aims to improve our understanding of microbial diversity lost during chicken domestication and to highlight the ecological and functional diversity of the wild avian gut microbiome in Singapore.

Cross-Regulation of Type 1 and P-like Fimbriae in Extraintestinal Pathogenic *Escherichia coli* Drives Pathogenesis in Humans and Poultry

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Avian pathogenic *Escherichia coli* (APEC) harbor diverse virulence factors, permitting localized and systemic infections in poultry. APEC are genetically closely related to human-associated extraintestinal pathogenic *E. coli* (ExPEC), representing a potential foodborne zoonotic risk. Among the virulence mechanisms shared by ExPEC, fimbriae, filamentous adhesins, dictate host range and pathogenesis by mediating tissue adhesion and invasion. Most ExPEC strains express *fim* genes encoding type 1 fimbriae to establish an infection, whereas alternative fimbriae are preferentially expressed at later stages, promoting systemic dissemination. This temporal shift in fimbrial expression is influenced by environmental cues and regulatory crosstalk mechanisms, that are often poorly characterized. A recently identified genetic cluster, termed *plf*, encodes P-like fimbriae carried on conjugative colicin V (ColV)-like plasmids. This *plf* locus encodes two regulators, PlfX and PlfB, which may inversely regulate *fim* expression, similar to PapB and related fimbrial regulators. To investigate this regulatory interplay, high-copy plasmids containing the *plf* regulatory region, with or without these regulators, were introduced into *E. coli* K-12 MG1655 and selected ExPEC strains. Expression of PlfX reduced Fim activity by 1.5-fold ($P < 0.05$) in MG1655, as determined by yeast agglutination, with similar effects among ExPEC strains. Electrophoretic mobility shift assays demonstrated that PlfX binds the phase-variable *fimS* regulatory element. Deletion of the *fim* locus increased *plf* expression 4-fold ($P < 0.01$), as confirmed by luciferase reporter assays and qPCR. Together, these findings reveal reciprocal regulation between *fim* and *plf*, highlighting the importance of coordinated adhesin expression in ExPEC pathogenesis, providing a foundation for therapeutics targeting fimbrial regulation.

KEYNOTE SPEAKER



Prof. Margie D. Lee

DVM, MS, PhD

Associate Dean for Research and Graduate Studies

Virginia-Maryland College of Veterinary Medicine, Virginia Tech, USA

Professor Margie Lee is a renowned veterinary scientist and academic leader with a distinguished career spanning research, education, and institutional leadership. She serves as Associate Dean for Research and Graduate Studies and Director of the Biomedical and Veterinary Sciences Graduate Program at Virginia Tech's Virginia-Maryland College of Veterinary Medicine, where she is also a Professor in the Department of Biomedical Sciences and Pathobiology. Dr. Lee earned her Doctor of Veterinary Medicine from Virginia Tech and completed her Master's and PhD in Medical Microbiology at the University of Georgia. Her pioneering research has focused on the molecular epidemiology of food-safety pathogens, microbial virulence, antimicrobial resistance, and the ecology of the intestinal microbiome in poultry, resulting in two U.S. patents for diagnostic methods and enabling advancements in antibiotic-free poultry production. A prolific scholar with more than 90 peer-reviewed publications, Dr. Lee has received numerous honors throughout her career. She is the 2023 recipient of the Phibro Animal Health Excellence in Poultry Research Award for sustained excellence in poultry disease research over two decades. She has also been recognized with the J.C. Feeley Award for Environmental Microbiology, the Dave Tyler Award for innovations in teaching, the Margaret Green Award for Outstanding Service in Microbiology Education, and the P.P. Levine Award for best paper in Avian Diseases. Earlier in her career, she was named a Distinguished Alumnus of the Virginia-Maryland College of Veterinary Medicine. Dr. Lee's leadership has shaped research and training programs that bridge animal, human, and environmental health, and she continues to serve on national scientific advisory boards and editorial committees. Her career reflects a commitment to scientific excellence, education, and transformative impact in veterinary medicine.

Presentation of results Portfolio IRSST–CRIPA

Occupational risks of cooling strategies in pig and laying hen farms

Prof. Caroline Duchaine, Université Laval, Canada

Institut de recherche Robert-Sauvé en santé et en sécurité du travail (IRSST) – Presentation of R&D priorities

Dr. Alain Marchand, Directeur scientifique, Direction de la recherche, IRSST, Canada

Health and Economic Burden of Foodborne Salmonella in Canada: Evidence to Support Chicken Antimicrobial Stewardship

Yarina You and **Paul J. Thomassin**

McGill University

Antimicrobial-resistant (AMR) Salmonella linked to chicken production remains a key One Health concern because it connects antimicrobial use in animal production to human illness, health care use, and economic loss. We estimate the health and economic burden of chicken-attributed non-typhoidal Salmonella infections in Canada from 2015 to 2019 and report separate results for AMR and susceptible infections. We use a Markov model with annual and lifetime horizons to estimate cases, hospitalizations, deaths, and quality-adjusted life year (QALY) losses. Total Salmonella cases and total costs declined over the period, but AMR cases increased and generated higher costs per case and higher QALY losses than susceptible infections. Chicken-attributed Salmonella infections declined from 96,424 in 2015 to 67,097 in 2019, with total costs declining from \$122.7 million to \$93.6 million. These findings support continued antimicrobial stewardship and surveillance across the chicken production chain to limit AMR Salmonella and reduce human health and economic burden.

New CRIPA member - Research focus

A One Health approach to mitigate zoonotic diseases of poultry

Prof. Nitish Boodhoo, McGill University, Canada

Abstract: Zoonotic diseases originating from poultry pose a growing risk to livestock animals, for food security and public health. By adopting a One Health approach we aim to identify gut-based interventions that reduce colonization, shedding, and spread of zoonotic pathogens. Emphasis is placed on non-antibiotic strategies, including microbiome modulation and immune-targeted interventions, to enhance intestinal health in poultry. Such a strategy offers a sustainable pathway to protect animal welfare, limit zoonotic spillover and safeguard poultry and human health.

Comparative genomic analysis highlights diversity among *Enterococcus cecorum* isolates from broiler chickens in Quebec, Canada

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An increasing incidence of osteoarthritis, spondylitis, and polyserositis has been reported in broiler chickens and broiler breeders in Quebec, Canada. *Enterococcus cecorum* (EC), a Gram-positive facultative anaerobe and member of the normal intestinal microbiota, has been identified as the causative agent. Borst et al. (2015) described *cpsO*, a gene specific to pathogenic EC strains, proposed as a marker to distinguish pathogenic from commensal isolates. However, *cpsO*-negative strains are frequently recovered from clinical cases, suggesting that additional factors may contribute to EC pathogenicity. Phylogenetic relationships among *cpsO*-positive and *cpsO*-negative EC isolates from clinical cases were examined, along with comparisons of antimicrobial resistance genes (ARGs), virulence factors (VFs), and mobile genetic elements (MGEs). A total of 92 isolates (47 *cpsO*+ and 45 *cpsO*-) were whole-genome sequenced, assembled, and annotated using an in-house pipeline. Core genome phylogeny was inferred using Roary and RAxML-NG. ARGs, VFs, and MGEs were predicted using CARD, ResFinder, VFDB, MOB-suite, and ISEScan. Substantial genomic diversity was observed across isolates, with no clear clustering based on *cpsO* status or sample type. Isolates from different organs within the same clinical case often clustered together, although exceptions occurred. No significant differences were detected between *cpsO*+ and *cpsO*- groups in the number of ARGs, VFs, or MGEs per isolate. These findings support an opportunistic lifestyle for EC and suggest that infections are frequently systemic and involve multiple distinct isolates rather than a single dominant strain.

LLM-Based In-Context and Transfer Learning for Predicting Broiler Livability with Multispecies Farm Data

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Livability, defined as the percentage of chickens surviving to market age, is a critical performance indicator in commercial broiler production, directly reflecting animal welfare standards and economic sustainability. Although accurate forecasting of this metric is essential for proactive management, the development of robust predictive models is frequently hindered by the scarcity of high-quality, annotated datasets within the poultry sector. This study addresses this data deficiency by proposing a novel computational framework that leverages Transfer Learning (TL) and In-Context Learning (ICL) to transfer knowledge from a data-rich source domain (e.g., commercial aquaculture) to a data-constrained domain, like broiler production. The methodology involved aligning disparate production features through domain-agnostic engineering and comparing two distinct learning strategies: a Machine Learning-based TL approach and a Large Language Model (LLM)-based ICL approach. The models were evaluated on their ability to predict cumulative livability rates in broiler production and identify key risk factors. The results demonstrate that cross-species learning is feasible, with the In-Context Learning model (RMSE 1.51%) slightly outperforming the Transfer Learning model (RMSE 1.53%). Crucially, both models achieved error rates lower than the dataset's natural standard deviation (1.60%). Feature analysis identified stocking density, heat stress, and Feed Conversion Ratio (FCR) as the primary determinants of livability. Conversely, Antimicrobial Use (AMU), though critical for herd health monitoring, exhibited limited predictive influence compared to environmental stressors in this cross-species framework. These findings validate the hypothesis that fundamental production dynamics are transferable and demonstrate the potential of Foundation Models to overcome data scarcity.

Fédération des producteurs d'oeufs du Québec (FPOQ) – Presentation of R&D priorities

M. Jacques Cloutier, Producteur, Administrateur de la FPOQ, Canada

Presentation of results Portfolio FPOQ–CRIPA

Efficacy of cleaning and decontamination strategies against avian pathogens in enriched cage and aviary housing systems for laying hens

Prof. Marie-Lou Gaucher, Université de Montréal, Canada

CONFERENCES – APRIL 2nd, 2026

KEYNOTE SPEAKER



Prof. Hiep Vu

PhD

Associate Professor Department of Animal Science, University of Nebraska-Lincoln, USA

Prof. Hiep Vu, is an associate professor in the Department of Animal Science at the University of Nebraska–Lincoln, where he also holds an adjunct appointment in the School of Veterinary Medicine and Biomedical Sciences. He joined the department in 2017 and advanced to his current role in 2022.

Prof. Vu earned his BVSc degree (equivalent to DVM) from Nong Lam University in Vietnam in 2005 and completed both a Master of Science in Veterinary Sciences (2009) and a PhD in Integrative Biomedical Sciences (2013) at the University of Nebraska–Lincoln. Prof. Vu’s research focuses on viral diseases that impact animal production, health, and well-being, with an overarching goal of developing novel and effective intervention strategies to control these infections. His laboratory studies host immune responses to viral infections and vaccinations to identify correlates of protection and viral antigens that induce protective immunity. Current research efforts include the development of vaccine platforms that enhance immune responses using delivery systems such as lipid nanoparticles, and translational studies of major swine viruses including porcine reproductive and respiratory syndrome virus (PRRSV), swine influenza virus (SIV), and African swine fever virus (ASFV). His work aims to generate broadly protective and long-lasting vaccines to improve animal health and support sustainable animal production. Prof. Vu has published extensively in peer-reviewed journals and is recognised internationally for his contributions to swine virology and vaccine research.

From Birds to Humans: Antiviral Efficacy Against Clade 2.3.4.4b Zoonotic A/H5N1 Virus at the Animal-Human Interface

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Highly pathogenic avian influenza A/H5N1 viruses continue to spread and infect multiple mammalian species, including humans, raising concern about zoonotic risk and pandemic preparedness. Immunocompromised individuals are vulnerable to severe and prolonged disease, yet antiviral guidance remains limited. We evaluated the pathogenesis and antiviral efficacy of a human A/H5N1 virus recently isolated in British Columbia using a cyclophosphamide-immunosuppressed hamster model. Animals were intranasally infected with 10⁵ TCID₅₀/100µL of A/British_Columbia/2032/2024 (H5N1). Morbidity, weight loss, survival, viral shedding, and viral loads in lungs, nasal turbinates, and brain were assessed. Contact transmission was evaluated by cohousing naïve hamsters. Additional groups received oseltamivir (20 mg/kg BID), baloxavir (50 mg/kg subcutaneous, two doses), molnupiravir low-dose (50 mg/kg BID), molnupiravir high-dose (200 mg/kg BID), or an oseltamivir + molnupiravir low-dose combination, starting 24h post-infection for 5 days. Pulmonary cytokine expression was quantified by qPCR. H5N1 infection caused severe morbidity and mortality by day 10 post-infection, with viral replication in respiratory tissues and brain. No contact transmission was detected. Baloxavir markedly shortened viral shedding, suppressed lung replication and prevented neuroinvasion, conferring 100% survival, with a trend toward lower pro-inflammatory cytokine expression. Molnupiravir high-dose prevented mortality and achieved viral clearance. The oseltamivir + molnupiravir low-dose combination reduced lung and brain viral loads, whereas monotherapies provided limited protection. These findings demonstrate high pathogenicity of this human A/H5N1 strain in immunosuppressed hamsters and highlight baloxavir as a key therapeutic option, as well as the potential of molnupiravir to improve outcomes. Ongoing analyses will determine antiviral resistance emergence.

Porcine Reproductive and Respiratory Syndrome type 2 virus (Betaarterivirus americense) whole genome classification system combining ORF5, nsp3-4-5 and Indels

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Porcine Reproductive and Respiratory Syndrome disease was first observed in 1987 in the United States of America. This disease is responsible for the loss of billions of dollars worldwide in the pig industry and since its discovery its denomination and classification method has often changed. The current PRRS virus classification system is based on the ORF5 viral gene phylogeny which represent only 4% of the viral genome. However, veterinarian practitioners are confronted with cases of unexpected severity while viral isolates are classified as vaccinal strains. As this virus evolves at high speed by combining an error prone RNA polymerase and a high recombination rate, an improved classification system is hereby proposed to better discriminate vaccinal strains from viral recombinants while remaining simple to use. This system combines the current ORF5 classification with a phylogeny of the nsp3, nsp4 and nsp5 segments of ORF1a viral gene as well as groups based on insertions and deletions (indels) at the whole genome scale. For example, the reference strain ATCC VR-2332 would be classified as 5A-n67-IDVR-2332 in this proposed system. Lineages of ORF5 and nsp3-4-5 groups are shown to be more frequently associated than others, allowing the quick identification of unusual strains. For example, of 50 Canadian isolates sharing the same ORF5 lineage as the MLV vaccinal strain, 22 were identified as different using the full classification. Bioinformatic tools will be presented and made available for anyone who would like to analyze their own sequences in the form of a Nextrain community dataset and the IDindel suite of scripts.

Dispersion modeling of airborne antibiotic-resistance genes emitted from Canadian livestock buildings

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Introduction. Animal livestock buildings generate significant bioaerosol emissions through mechanical ventilation systems that expel indoor air via extraction fans. These bioaerosols often contain zoonotic agents and antibiotic-resistance genes (ARGs), which can disperse beyond farm boundaries and reach nearby communities and environments. **Objectives.** (1) Assess the dispersion of ARGs emitted from conventional pig finishing buildings (PFBs) and broiler chicken barns (BCBs) toward specific receptors (SR) such as houses or villages in Québec and Saskatchewan using AERMOD. (2) Determine how many hours ARG concentrations at SR exceed natural background levels measured at a rural control site. (3) Estimate relative respiratory exposure values for individuals located at SR. **Methods.** PFBs and BCBs were sampled during the warm season in Québec (peak emissions) and year-round in Saskatchewan. Indoor air and fan exhaust bioaerosols were collected using a SASS®3100 Dry Air Sampler. DNA was extracted and ARGs quantified by PCR. Ventilation rates (m³/h) at extraction fans were measured to calculate emission rates (ARG copies/h), which were then modeled in AERMOD using meteorological and topographic data. **Results.** Annual median modeled concentrations at SR were low. However, maximum concentrations reached 10⁴–10⁶ copies, even at SR located up to nine kilometers from farms. The number of hours above natural background varied by farm, distance, wind direction, and antibiotic class. Beta-lactam ARGs reached SR less frequently (0–50%) than tetracycline ARGs (2–100%). Over five years of modeled dispersion, estimated relative respiratory exposure could be substantial, with macrolide ARGs reaching up to 10⁶ copies.

The regulation of curli in *Salmonella enterica* serovar Typhi is riddled with polymorphisms

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Salmonella enterica can infect a broad range of hosts. While some serovars are generalists, others are host-restricted, like Typhi, a human-specific serovar. *S. Typhi* is endemic in many regions, and we are facing an antibiotic resistance crisis. Chronic carriers harbour *S. Typhi* biofilm in their gallbladder, contributing to transmission. Curli-type fimbriae are important for *Salmonella* biofilm formation, and anti-curli antibodies have been found in patients, suggesting their involvement during infection. Curli is encoded by the *csg* operons, in which there are numerous polymorphisms (SNPs) in *S. Typhi*. Thus, we hypothesize that curli is distinctly regulated in *S. Typhi*. The objective of this study is to identify the regulators involved in curli expression. Previously, we demonstrated that the main curli activator, CsgD, is unable to bind DNA due to a nonsense mutation. The curli-positive phenotype was not restored upon correction, suggesting the existence of an alternative regulatory pathway. To identify those regulators, we performed a promoter pulldown assay using curli promoter region and identified the EnvZ/OmpR two-component system. We demonstrated that EnvZ/OmpR exerts an inhibitory effect on curli expression, while it is an essential activator in other *Salmonella*. The SNPs identified in the curli promoter region correspond to predicted OmpR binding sites. Furthermore, EnvZ itself carries mutations that reduce its activity. These SNPs potentially contribute to the strain-specific variations in curli expression observed in *S. Typhi*. Thus, understanding the distinct regulatory mechanisms of *S. Typhi* compared to other *Salmonella* will pave the way for the development of new antimicrobial treatments.

Systematic characterization of four novel Twort-group bacteriophages infecting *Staphylococcus hyicus*

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5. Département de sciences cliniques, Faculté de médecine vétérinaire, Université de Montréal, Saint-Hyacinthe, Quebec, Canada.

In piglets, exudative epidermitis (EE), a skin disease primarily caused by *Staphylococcus hyicus*, remains a persistent concern for the swine industry in Quebec, especially given the increasing antimicrobial resistance.

In this study, four novel bacteriophages (BQE1, BQE4, BQE7 and BQL4) infecting *S. hyicus* were isolated from piglet drinking water and manure collected from one EE infected Quebec swine farm environments. All four phages produced clear lysis plaques (<1 mm) and reached high titers ($\geq 10^8$ – 10^{10} PFU/mL). Transmission electron microscopy revealed that they all displayed a myovirus morphology, characterized by isometric capsids and long contractile tails. Genomic analysis revealed genome sizes ranging from 115.4 and 134.5 kb, with close phylogenetic relationships to the Twort and other *S. hyicus* bacteriophages. Notably, no virulence factors, antimicrobial resistance genes, or CRISPR elements were detected. Host range analysis across 58 staphylococcal strains showed broad lytic activity, particularly against *S. hyicus*, where most strains were susceptible (77–80%), whereas the Twort phage displayed limited effectiveness with only 4 % of the *S. hyicus* strains. Adsorption assay and one-step growth curve experiments conducted with representative phages (BQE7 and BQL4) confirmed efficient host interaction, short latent periods of ~50 min, and moderate burst sizes of 10–13 PFU/cell. Both phages remained infectious for extended periods at 4 °C and room temperature (21–23 °C), and 31°C. Overall, these findings delineate the morphological, phenotypic, and genomic features of newly isolated Twort-group phages and highlight their potential as promising, locally adapted candidates for phage-based EE control in Quebec's swine industry.

Éleveurs de porcs du Québec (EPQ) – Presentation of R&D priorities

Raphael Bertinotti, M. Sc., Directeur – Santé, Qualité et Recherche et Développement des EPQ, Canada

Presentation of results Portfolio EPQ–CRIPA

A novel porcine beta-Defensin: Small peptide, big potential

Prof. Matheus Costa, University of Saskatchewan, Canada

Phytobiotics improve intestinal health in broilers challenged with *Eimeria* or inflammatory challenges

Sara Aouissi¹; Jacinthe Julien²; Vincent Demers-Caron²; Marie-Pierre Létourneau-Montminy; Bertrand Medina³; Carl Julien²

1 Université Laval, Canada; 2 CRSAD, Canada; 3 Probiotech International, Canada

Coccidiosis is still one of the most important digestive pathologies affecting broilers by impairing intestinal integrity. Phytogenics have been proposed as anticoccidial alternatives and to strengthen gut health. This study aimed to evaluate the effect of phytogenic-based feed or drinking water additives (PBA) on intestinal health and growth performances in broilers exposed to *Eimeria* (EI) or enteric inflammatory (IC) challenges. A 35-day trial was conducted on 1,152 Ross 308 males, divided into 12 replicates of 12 birds/cage and subjected to the 8 experimental treatments: naive controls (NI); EI; IC; EI+conventional anticoccidial control; EI+three PBA with various proportions of star anise, cinnamon, rosemary, garlic and thyme essential oils, Curcuma longa and Yucca schidigera extracts; and IC+Capsicum oleoresins. EI was induced using 160,000 *E. acervulina* and 40,000 *E. tenella* oocysts and IC was provoked by dextran sodium sulfate (DSS). Data were analyzed by a mixed model including treatment and barn section as fixed and random effects and by Kruskal-Wallis tests. PBA reduced fecal oocyst excretion ($-0.8 \log_{10}$ oocysts/g, $P < 0.05$) and qPCR data showed a trend to reduce *E. tenella* ($-0.7 \log_{10}$ copies/g, $P = 0.10$) 6 days post inoculation. However, they did not improve intestinal lesion scores nor growth performances ($P > 0.05$). The *Eimeria* (+117%, $P < 0.05$) and DSS (+125%, $P < 0.05$) challenges increased serum fluorescein isothiocyanate-dextran (FITC-d) levels. PBA (-25%, $P < 0.05$) and Capsicum oleoresins (-32%, $P < 0.05$) reduced FITC-d levels, compared to their challenge controls. Globally, PBA revealed beneficial results on intestinal permeability following *Eimeria* and inflammatory challenges, suggesting they could promote intestinal health in broilers.

Evaluating Species-Level Resolution in Microbiome Analysis Using Nanopore Sequencing

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Chaire de recherche en salubrité des viandes de l'Université de Montréal, Canada

High-throughput sequencing have transformed microbiology, particularly the study of bacterial microbiota. To date, the most accessible and widely used approach relies on partial sequencing of the variable regions of the 16S ribosomal RNA gene. A new alternative is now available to researchers: Nanopore sequencing technology, which enables sequencing of the full-length 16S gene (~1,500 bp), thereby offering the potential to achieve taxonomic resolution at the species level rather than the genus. Despite this promise, few validated bioinformatics tools are available to reliably analyze full-length 16S Nanopore reads. The objective of this study was therefore to perform a comparative analysis of Nanopore sequencing data covering the entire 16S gene using two bioinformatics approaches: Nanopore platform pipeline (Epi2Me/Minimap2) and a in-house workflow based on EMU. The comparison was conducted using commercial mock microbial communities (Zymo) that were sequenced on multiple occasions. The results indicate that the Nanopore-provided analysis pipeline failed to correctly identify all members of the mock community at the species level, regardless of the analysis parameters applied. In contrast, the EMU-based in-house workflow achieved accurate species-level identification for all eight members of the mock community. Moreover, EMU yielded the lowest proportion of unclassified sequences or sequences assigned to genera absent from the mock community and demonstrated strong stability across independent sequencing runs. Overall, this study highlights the critical importance of including mock communities as positive controls in microbiome analyses and suggests that full-length 16S Nanopore sequencing, while still imperfect, can provide adequate species-level resolution, although improvements in accuracy remain necessary.

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- B1 Valérie Létourneau.** Eastern Canadian hatching egg houses: seasonal variability of air pollutants and animal health and welfare.
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N1 Evaluating the Nutritional Value of Canola Meal in Broilers: Contributions from Meta-Analysis.

Abdou Salam LO; Marie-Pierre Létourneau-Montminy; Hector Salgado-Romero

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Meta-analysis is a rigorous statistical approach that allows for the quantitative synthesis of results from independent experimental studies while explicitly incorporating sources of inter-study variation. It relies on statistical models (fixed and random effects, regressions) aimed at accounting for both intra- and inter-study variability to obtain more robust and generalizable estimates (Sauvant et al., 2008). In animal nutrition, where experimental heterogeneity is high (differences in protocols, ages, inclusion levels), this approach enables a shift from a descriptive logic to a predictive approach. The application of the meta-analysis tool presented concerns the evaluation of the nutritional value of canola meal in chickens. A total of 44 articles (182 treatments) were structured and harmonized in Excel. Apparent ileal amino acid digestibilities were converted to standardized digestibilities, and metabolizable energy was adjusted to fixed levels of residual fat based on the relationship estimated in the database. An exploratory analysis (correlations, PCA) identified relationships between variables and guided predictor selection. Multiple and mixed regression models (with study random effect) were then developed to quantify the impact of chemical composition and zootechnical factors on the Y variables. For illustration, the models highlight a marked negative effect of fiber content (NDF) on metabolizable energy and the digestibility of lysine and methionine, while crude protein content exerts a significant positive effect. This work demonstrates how meta-analysis can become a formulation aid tool by improving the precision of nutritional values.

N2 Reducing dietary calcium is a key component to reduce phosphate in broilers while reducing footpad dermatitis without modifying growth

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Phosphorus (P) is critical issue in monogastric animals and optimizing its use requires careful calcium (Ca) management. This study evaluated the interactive effects of dietary Ca and P on broiler growth performance, tibia mineralization, footpad dermatitis, and litter characteristics from 10 to 28 days of age. A total of 3,200 one-day-old male Ross 308 were fed a common starter and finisher diet. In grower phase, nine experimental diets were offered following a 3 × 3 factorial design with three total Ca levels (0.51, 0.68, 0.85%) and three digestible P levels (0.23, 0.31, 0.39%) corresponding to 75, 100 and 125% of CVB recommendations. Digestible P levels were achieved by reducing monocalcium phosphate inclusion and adjusting limestone accordingly. Data were analysed as a randomized block design to test Ca, P and their interaction effect. Broilers consuming a low-P diet responded to increasing Ca with reduced feed intake (-12.5%) and weight gain (-11.6%), alongside a higher feed conversion ratio (+2.6%; Ca × P; P < 0.001). Tibia ash increased with higher Ca and P level combined, thus was maximized at 0.85% Ca and 0.39% P (+3.6 % vs. 0.51% Ca and 0.23% P; Ca × P ; P = 0.002). At 34 days, footpad dermatitis incidence increased from 3.71% to 23.0% with increasing Ca (0.51% vs. 0.85%; P = 0.02). Litter moisture showed a numerical increase (day 27: 34.6% vs. 36.9%; P = 0.11), which may partially explain this response. Overall, reducing Ca while maintaining a balanced Ca/P ratio preserved performance, reduce footpad dermatitis and decreased phosphate use, though slightly lowering bone mineralization.

N3 Bone mineral density by DEXA scan as a method for determining bone mineralization in growing pigs

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Bone assessments, such as ash and mineral content, mainly calcium and phosphorus (P), are commonly performed to determine bone mineralization. However, these invasive methods require animal slaughter and contribute to cumulative estimation errors. This study aimed to test the bone mineral density (BMD) using Dual-Energy X-ray Absorptiometry (DEXA) as a substitute for the traditional method of bone ash. Thirty-five animals (initial weight 19.93 ± 2.53 kg) were distributed in a randomized block design across seven treatments: 1) basal diet (BD; 0% supplemental P); 2) BD + dicalcium phosphate (BD+DCPLow; 0.14%) 3) BD+DCPHigh (0.28% P); 4) BD + tricalcium phosphate (BD+TCPLow; 0.14%), 5) BD+TCOPHigh (0.28% P); 6) BD + monosodium phosphate (BD+MSPLow; 0.14%) and 7) BD+MSPHigh (0.28% P). After a 30-day feeding period, animals were euthanized, and the left foot was removed for BMD determination via DEXA. Subsequently, the 3rd and 4th metacarpals were removed, cleaned, dried, weighted, and burned in a muffle furnace at 600°C to determine total bone ash (BAsh, g) and bone ash concentration (BAshC, %). Data was analyzed using Pearson correlation in Jamovi software and considered significant at $P < 0.05$. Total BAsh and BAshC were significantly correlated with BMD (0.876 and 0.664, respectively; $P < 0.001$). Furthermore, correlations between digestible P intake and BAsh (0.599; $P < 0.001$) were numerically similar to those with BMD (0.568; $P < 0.001$). These results demonstrate that DEXA scans can effectively replace traditional bone ash analysis.

N4 Effects of phytase and dietary calcium-to-STTD phosphorus ratio on net intestinal absorption of zinc and copper in growing pigs

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This study evaluated the effects of dietary calcium (Ca) to standardized total tract digestibility phosphorus (STTD P) ratios and phytase supplementation on net intestinal absorption of Zn and Cu in growing pigs. Six pigs (42.9 ± 2.2 kg) were surgically prepared and assigned to four dietary treatments in a 2×2 factorial arrangement with high or low Ca:STTD P (2.3 vs 1.3) and the inclusion or not of phytase (750 FTU/Kg). Treatments were administered following a crossover design. Blood samples were collected from portal vein and carotid artery 5 min before feeding, every 30 min during the first 2 h post-feeding, and hourly during the subsequent 8 h. Venous and arterial Zn concentrations exhibited a treatment \times time interaction ($P \leq 0.001$) with phytase inclusion increasing Zn concentrations ($P \leq 0.05$) between 120 and 420 min post-feeding in the vein and between 120 and 360 min in the artery. Treatments were administered following a crossover design. Blood samples were collected from portal vein and carotid artery 5 min before feeding, every 30 min during the first 2 h post-feeding, and hourly during the subsequent 8 h. High Ca: STTD P ratio increased ($P \leq 0.058$) venous and arterial Zn concentrations at 540 and 600 min. For Cu, no treatments effect were observed for any parameter ($P \geq 0.480$) but time effect was observed ($P \leq 0.001$) on venous and arterial Cu concentrations. In conclusion, phytase inclusion and Ca: STTD P impact post-prandial net Zn absorption but not Cu.

N5 Impact of xylanase supplementation on nitrogen efficiency and ammonia emissions in growing pigs

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Carbohydrases are feed enzymes that improve the digestibility of plant-based diets by breaking down non-starch polysaccharides, complex fiber components that pigs cannot fully utilize. By increasing the availability of energy and nutrients such as nitrogen (N), these enzymes may reduce nitrogen excretion into the environment and enhance sustainability. This study evaluated whether supplementing a reduced-protein diet with xylanase could improve nitrogen utilization and reduce gaseous emissions without impairing growth. Forty-eight growing pigs (39.9 ± 2.4 kg) were assigned to three diets for 30 days: following a completely randomized design: T1, positive control (16,3%, 2476 kcal/kg); T2, negative control (CP and NE reduced to 14.9% and 2426 kcal/kg without enzyme); and T3, negative control + xylanase (100 g/ton), an endo-1,4- β -xylanase of bacterial origin. Growth performance, nitrogen balance, slurry composition, and gaseous emissions were measured, and data were analyzed using a generalized linear model. Xylanase supplementation (T3) maintained growth performance while improving nitrogen efficiency. Compared with T1, total nitrogen excretion per kg of gain decreased from 28.0 to 22.9 g ($P = 0.013$). Fecal N decreased from 13.4 to 12.1 g ($P = 0.013$), urinary N from 14.6 to 10.8 g ($P = 0.013$), and ammonia-N emissions from 6.83 to 5.34 g ($P = 0.014$). The negative control (T2) showed intermediate values, not statistically different from T3. No effect was observed on CH₄ or CO₂ emissions. These results demonstrate that xylanase supplementation can reduce nitrogen losses while maintaining performance, representing a promising strategy to improve the environmental sustainability of pig production.

N6 Optimizing phosphorus use through precise estimation of needs in a precision feeding context

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Phosphorus (P) is non-renewable resource that plays a critical role in sustaining global food production, making its efficient utilization essential. Approximately 75% of the body P reserves are stored in bone tissue in the form of hydroxyapatite, a calcium-bound compound characterized by a fixed Ca:P ratio of 2.16 (Crenshaw, 2001; Quiniou et al., 2019). Consequently, optimizing P utilization requires that its dietary supply be considered in relation to calcium (Ca) requirements. Several predictive models have been developed to estimate the phosphorus and calcium needs of growing pigs. Among them, the mechanistic and deterministic model proposed by Lautrou et al. (2019) currently represents the most advanced and comprehensive approach in the field of phospho-calcium nutrition in growing pigs. This model is driven by the potential for calcium deposition in bone tissue. Furthermore, because bone and lean growth are not tightly correlated, the Ca:P ratio evolves throughout the growth period of finishing pigs. The value of such mathematical models lies in their ability to support precision feeding strategies, which aim to deliver the appropriate quantity of feed with optimal nutrient composition at the right time, either to groups of animals or to individual pigs within a group (Pomar, Remus, and van Milgen, 2019).

N7 Using artificial intelligence to predict and help reduce cellulitis rates in broiler chicken farms

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In 2024, 11 million broiler chicken carcasses were rejected at the slaughterhouse due to pathological defects in Canada. Over 70% of these condemnations are due to cellulitis, a bacterial infection, resulting in more than 22 million Canadian dollars in lost revenue. Cellulitis is caused by *Escherichia coli*, which enters the skin through wounds or scratches. Several risk factors, such as environment, production, and health can affect its development in chicken barns. However, detecting and correcting these various factors to minimize the rate of cellulitis is complex, and the very short production cycle (about 30 days) leaves little time for adjustments. We hypothesize that the pattern-recognition capacity of Artificial Intelligence (AI) can effectively analyze risk factors to predict cellulitis-related condemnations. Our main objective is to identify AI models to predict the cellulitis rate for each production cycle based on chicken rearing conditions. We will collect environmental data (i.e temperature, humidity and CO₂) using sensors installed in chicken barns and complementary data like mortality records and stocking density from the Éleveurs de volailles du Québec. Slaughterhouses will provide our target variable, the condemnation rate for cellulitis. We will clean and integrate multiple data sources into a single database and perform exploratory analysis to uncover structures and relationships for model development. Using this data, we will select, train, and evaluate AI models to predict cellulitis rates in chicken barns under specific conditions. Based on the model's output, we will provide recommendations for early interventions in poultry production, improving animal welfare and profitability.

N8 Impact of vitamin d supplementation on extending the cycle of laying hens up to 100 weeks of age

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This project aims to study the prolongation of production cycles up to 99 weeks of age and to evaluate the impact of supplementation in 25(OH)D₃ in varying doses. A total of 330 Lohmann White LSL hens were assigned to one of three experimental diets from 19 to 85 weeks and housed in cages of five birds (22 reps per treatment). At 85 weeks, the birds were moved to a late cycle phase up to 99 weeks, keeping the same treatments. The control diet (CON) was formulated based on the recommendations of the Lohmann, including 2500 IU of vitamin D₃. The VITD diet was the CON + 2,500 IU of 25(OH)D₃, while the VITD+ diet included 5,000 IU of 25(OH)D₃. The weekly measurements included body weight and eggs production and quality. To assess body composition, including bone mineral content (BMC) and bone mineral density (BMD), the dual X-ray absorptiometer (DXA) was used; at weeks 30, 42, 54, 66 and 78, five hens per treatment were euthanized to be scanned, while at weeks 87, 90, 94, 96 and 99 the hens were anesthetized and scanned. The inclusion of 25(OH)D₃ increased feed intake in VITD group (P < 0,001). Body weight was reduced in the VITD group, while VITD+ and CON had similar weights. VITD showed a higher laying rate, number and mass of eggs than CON. Eggshell weight, area and mineral content and density were slightly lower in the VITD. The body composition of hens has not been modified by dietary treatments.

T1 The effect of substances secreted by lactic acid bacteria on the swine pathogen *Staphylococcus hyicus*

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Exudative epidermitis, a swine disease present in Quebec, is caused by the pathogenic bacteria *Staphylococcus hyicus*. Without a commercial vaccine available, this disease is treated with antibiotics. However, the swine pathogen frequently presents resistance to the antibiotics used, which complexifies disease treatment. It is therefore necessary to study *S. hyicus* to find new ways to impair its growth or its virulence against swine. Namely, lactic acid bacteria represent a potential treatment alternative. These bacteria are largely used in the food industry for fermentation and conservation purposes. They produce antimicrobial compounds which can prevent or restrain the growth of various pathogenic bacteria. The goal of this project is to study the effect of substances secreted by lactic acid bacteria on the growth of *S. hyicus*. Namely, among the bacteria tested, Lactococcus strains produce a substance that effectively limits the growth of certain strains of *S. hyicus*. This substance is thermostable and proteinase K resistant, while its production is independent of oxygenation conditions. Results indicate the substance is not nisin, a bacteriocin often produced by Lactococcus strains. Identification and purification of the substance are ongoing. Once this process is completed, this substance could eventually provide a better way of treating exudative epidermitis in Quebec swine farms.

T2 Antimicrobial phenotypic resistance profiles of staphylococcus hyicus isolates involved in exudative epidermitis in suckling piglets

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Exudative epidermitis (EE), caused by *Staphylococcus hyicus*, usually requires antimicrobial treatment in affected pig farms. Antimicrobial resistance (AMR) could impair treatment efficacy. The objective was to describe AMR profiles of *S. hyicus* isolated from EE suckling piglets. Between 2023 and 2025, breeding sites in Quebec were invited to report outbreaks of EE defined as ≥ 4 litters with EE in the same farrowing batch. At each reporting site, 5 piglets from different litters (4 with EE, 1 without EE) were swabbed prior to any treatment and cultured to isolate *S. hyicus*. For up to 3 isolates per swab, minimum inhibitory concentrations were obtained for 19 antibiotics (10 classes) by broth microdilution (Sensititre) following the CLSI guidelines. Resistance breakpoints were established according to CLSI or literature. The proportion of resistant isolates was described for each antibiotic, class and profile at the isolate, piglet and site levels. Across the 9 sites, 42 of the 45 swabbed piglets tested positive to *S. hyicus*, yielding 120 isolates. Resistance to ≥ 1 antimicrobials was detected in 87/120 isolates, 34/42 piglets, 9/9 sites. Penicillin resistance was the most frequent at the isolate (68/120), piglet (27/42) and site (7/9) levels. The proportion of isolates resistant to ≥ 1 antimicrobial of each class was: beta-lactams-57%, amphenicol-45%, lincosamides-28%, aminocyclitols-21%, pleuromutilins-18%, macrolides-12%, tetracyclines-9%, sulfonamides 3%, aminoglycosides-quinolones-0%. Multiple AMR profiles were observed in 29/42 piglets. Multidrug resistance (≥ 3 classes) was observed 41/120 isolates, 17/42 piglets, 6/9 sites. AMR may account for some treatment failures. These results suggest a significant genetic heterogeneity among strains.

T3 Preclinical evaluation of a candidate vaccine against *Pseudomonas aeruginosa* in a porcine translational model

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Pseudomonas aeruginosa (Pa) is an opportunistic bacterium that can be associated with severe infections, particularly in cystic fibrosis patients and in hospital settings. Classified by the WHO among the ESKAPE multidrug-resistant pathogens, Pa represents a global public health concern and causes an estimated 559,000 deaths annually, driven by antimicrobial resistance. In this context, *P. aeruginosa* has become a symbol of this crisis due to the combination of multiple antimicrobial resistance mechanisms, high adaptive capacity, and efficient strategies for immune system evasion. Currently, there are no approved vaccines against *P. aeruginosa*. This gap results from intrinsic limitations of the pathogen, such as high antigenic diversity, the ability to form biofilms, and rapid modulation of surface antigens. This project aims to evaluate pre-clinically a candidate vaccine combining a glycoantigen (type A polysaccharide conjugated to CRM197 protein) and an adjuvant (SLA) in a porcine model. The polysaccharide is conserved across strains and promising target. Weaned piglets (8/group) will receive three intramuscular doses over 28 days, followed by bronchiolar challenge with a reference strain (PaO1). Four groups will be compared: full vaccine, adjuvant alone, PBS control, and uninfected/non-immunized controls. Efficacy, innocuity and immunogenicity will be assessed through clinical signs, weight gain, bacterial load, C-reactive protein levels, cytokine production, and antibody responses (IgA, IgM, IgG). Functional assays will evaluate opsonization and bacterial neutralization. Expected results include reduced bacterial load, no elevation of inflammatory markers, increased specific antibodies (IgG/IgA), and enhanced neutralization, supporting progression to clinical trials and vaccine development with global public health impact.

T4 Characterization of the Interaction Between *Pseudomonas aeruginosa* and Porcine Respiratory Epithelium and Evaluation of Cell-Mediated Immune Responses During a Vaccine Trial

Romarc Bonhomme; Hugo Chanfreau-Paris; Fanny Renois; François Meurens

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Antibiotic resistance is a major and growing problem, particularly for *Pseudomonas aeruginosa* (Pa), a multi-resistant, opportunistic bacterium responsible for nosocomial infections. Ubiquitous in nature, Pa is particularly pathogenic in patients with cystic fibrosis and intubated immunocompromised individuals, increasing morbidity and mortality. No vaccine is currently available to prevent these infections. A novel target antigen in the A-band polysaccharide of Pa, developed by Glycovax Pharma and the CNRC with CQDM support, is conserved in over 79% of strains. This glycoantigen, conjugated to the protein CRM197 and combined with SLA adjuvant, demonstrated a specific and protective immune response against Pa infection in a murine model. The global objective of this project is twofold: conduct an in vitro study to characterize the interaction between Pa and porcine respiratory epithelium, and to perform a preclinical in vivo trial in a translational porcine model to assess the safety, immunogenicity and efficacy of the candidate vaccine. To achieve these objectives, we will engineer a bioluminescent Pa strain (nanoLuc) derived from the ATCC PAO1 strain to monitor infection progression and characterise interactions in Newborn Pig Trachea (NPTTr) cells. Subsequently, we will analyze key immune response transcripts (TLRs, effectors, cytokines...). For the vaccine, assessments of immunity (lymphocyte proliferation, phenotypic and functional analysis of T cells, cytokine quantification, and histopathology) will be conducted. These findings will provide critical insights into the dynamics of Pa infection and evaluate whether the elements of this candidate vaccine could offer a promising solution to protect pigs initially and then at-risk patients.

T5 Phytogetic strategies as anticoccidial alternatives in broilers

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Coccidiosis remains one of the major diseases in the broiler industry, leading to reduced growth performance, impaired feed efficiency. Anticoccidial drugs are widely used; however, long-term use has led to the development of resistance. Although vaccines are available, their success is variable and requires stricter on-farm management. Phytogetic products are emerging as potential anticoccidial alternatives, either through direct effects on *Eimeria* or by enhancing the bird's intestinal health, immune response and gut integrity. This study evaluated the effects of 3 phytogetic formulations (PHY1-3) in broilers either vaccinated against coccidiosis or challenged with *Eimeria* during 35-day trial. A total of 3,384 male broilers were allocated to 8 replicates of 47 birds/pen and assigned to 9 treatment groups, including a standard (1X) and a high (30X) dose of Coccivac B52 vaccine. The 1X vaccine and the *Eimeria* challenge were administered via feed on days 1 and 14, respectively. In 30X challenged birds, PHY2 improved the following parameters compared to 30X controls: d20-d34 feed conversion ratio (FCR) (-3.1%, $P < 0.05$), the d20-d34 European Broiler Index (EBI) (+6.7%, $P < 0.05$), fecal oocyst excretion (-42%, $P < 0.05$) and the Anticoccidial Index (ACI) (+56%, $P < 0.05$). PHY2 also tended to improve overall (d0-d34) FCR (-1.7%, $P = 0.09$) and overall EBI (+5.5%, $P = 0.09$), compared to 30X controls. These improvements are expected to be associated with lower intestinal inflammation (calprotectin and lipocalin 2) and permeability (decreased serum fluorescein isothiocyanate-dextran), indicating potential beneficial effects on intestinal health. Overall, phytogetic supplementation represents a promising strategy to mitigate coccidiosis-related performance losses in broilers.

T6 Interactions of *Streptococcus suis* with the porcine intestinal mucosa

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Streptococcus suis (*S. suis*) is a major pathogen in pigs and a zoonotic agent that can cause meningitis, septicemia, and arthritis in humans. While the respiratory tract is considered the main route of entry, recent studies suggest that the digestive tract may also be involved in its spread. Our hypothesis is that *S. suis* uses the intestinal route as an alternative route, crossing the intestinal epithelial barrier to colonize the host. To investigate this mechanism, we will use porcine intestinal epithelial cells (IPEC-1) which are differentiated on Transwell, mimicking the intestinal barrier. Cells will be infected with wild-type and virulence factor deficient mutants of *S. suis* serotype 2 the predominant North America serotype. We will assess many factors to study the impact of *S. suis* on intestinal epithelial cells such as: barrier integrity (trans-epithelial resistance), bacterial adhesion and invasion, cytotoxicity on cells (LDH release), disruption of tight junction (quantity of key protein involve) and local immune response by measuring the expression of genes involved in the intestinal mucosal response (like IL-8, TNF- α , PBD-1 etc.). To monitor *S. suis* dissemination in real time in next experiments, a virulent strain will be transformed with a lux-CDABE expressing plasmid, which produces autonomously bioluminescence. Expected results will contribute to clarify the role of gastrointestinal tract in *S. suis* pathogenesis and provide a better understanding of *S. suis* mechanisms of infection. Future work will focus on in vitro model with porcine intestinal organoids and an in vivo ligated intestinal loop pigs to better reflect physiological conditions.

T7 Bacteriocins as Sustainable Alternatives: Preserving Intestinal Metabolic Homeostasis in Post-Weaning Piglets

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Given the global concern over antibiotic resistance, there is an urgent need for sustainable alternatives in livestock production. Bacteriocins, such as Microcin J25 (MJ25) and Nisin (NIS), offer promising solutions due to their potent antimicrobial activity and high specificity without disrupting host physiological balance. In this study, 288 weaned male piglets (21 d old; 5.9 ± 0.83 kg) were blocked by weight and assigned to 48 pens ($n=6/\text{pen}$). Four dietary treatments were applied from d 1 to 21 post-weaning: 1) No antibiotics; 2) Antibiotics (AB; 660 ppm chlortetracycline); 3) Microcin J25; and 4) Nisin z. Fecal samples were collected on d 0, 14, 22, and 38. Untargeted metabolomic analysis was performed using the ANOVA-Simultaneous Component Analysis (ASCA) model to partition total variance and isolate metabolic changes associated with natural growth (time factor) from those induced by antibacterial treatments. Results indicated that while growth significantly altered the fecal metabolome, bacteriocins did not significantly impact global metabolic activity compared to the AB group. Unlike the antibiotic treatment, which caused broader perturbations, MJ25 and NIS showed limited influence on the fecal profile. This suggests a more targeted action that preserves intestinal metabolic homeostasis in post-weaning piglets, confirming the potential of bacteriocins as effective alternatives to conventional growth-promoting antibiotics.

T8 Development and Validation of a Reproducible Experimental Challenge Model for Assessing Colibacillosis Interventions in Laying Hens

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Avian colibacillosis, caused by avian pathogenic *Escherichia coli* (APEC), represents a challenge for the egg industry due to increased mortality, reduced hen health, and lower egg production. APEC serogroups O1, O2, and O78 are most frequently associated to disease, with virulence driven by adhesins, iron uptake systems, and protective surface structures. A reliable experimental model that reproduces APEC infection in laying hens at peak production remains lacking, despite being essential for evaluating prevention and control strategies. This study sought to establish inoculation conditions that reproduce clinical and pathological features of field colibacillosis in Canada. Sixty 28-week-old Lohmann hens were assigned to three control and three infected groups and exposed to 0, 6, or 12 hours of light stress (100 lux) before inoculation. Challenged groups received an intraperitoneal (IP) inoculation of 1×10^9 CFU of an exponential phase, rifampicin resistant APEC O78:H9 strain, while controls received saline. Clinical signs, mortality, lesion scores, and ileal and cecal bacterial loads were assessed. Mortality increased with stress duration, ranging from 16.6% without stress to 33.3% after 6 hours and 50.0% after 12 hours. Challenged hens exhibited significantly higher lesion scores at 24, 48, and 72 hours, with differences among stressed groups observed at 48 hours. Generic *E. coli* loads remained unchanged, suggesting IP inoculation didn't induce intestinal dysbiosis. Overall, IP inoculation with exponential phase APEC O78:H9 reliably induced typical colibacillosis lesions in hens at peak lay. A 6-hour light stress period best simulated field conditions while limiting mortality, yielding a practical model for evaluating antimicrobial and non-antimicrobial control strategies for colibacillosis.

C1 Metal-based nanomaterials: innovative antimicrobial strategies against enterotoxigenic *Escherichia coli* F4 in swine production systems

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Post-weaning diarrhea caused by enterotoxigenic *Escherichia coli* F4 (ETEC) remains a major challenge in swine production and drives the search for alternatives to conventional antibiotics. Hypothesis - Metallo-glycodendrimers and silver (AgNPs) and copper (CuNPs) nanoparticles supported by carboxymethylcellulose (CMC) are metal-based nanomaterials that may exert antibacterial and anti-adhesive activities against ETEC, thereby reducing its intestinal infectivity in swine. Objectives - (i) To evaluate in vitro the antimicrobial activity of these metal nanomaterials; (ii) to determine their efficacy in inhibiting ETEC adhesion and proliferation; and (iii) to analyze their effects using porcine intestinal IPEC-J2 cell models. Experimental approach - Nanomaterials were synthesized and characterized using biophysical techniques. Cell viability and ETEC adhesion to porcine intestinal epithelial cells (IPEC-J2) were assessed in vitro using colorimetric assays. In parallel, their capacity to mitigate infection and cellular alterations was investigated. Results - Metal-based nanomaterials significantly inhibited ETEC growth, with bacterial reductions reaching 70–80% depending on concentration. ETEC Adhesion to IPEC-J2 cells decreased by 60–75%. At active concentrations (5–20 µg/mL), cell viability remained above 80–85%, indicating limited cytotoxicity. Conclusion - Metallo-glycodendrimers and CMC-supported nanoparticles reduced ETEC infection and associated intestinal cytotoxicity. These findings highlight their potential as promising alternatives to conventional antibiotics for preventing ETEC infections in swine production.

C2 Starch derivatives as excipients and prebiotics for oral probiotic formulations: an alternative to fecal transplantation in swine

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Post-weaning diarrhea is a major risk factor in swine production systems. The conventional approach relies on antibiotic administration; however, fecal microbiota transplantation is not logistically feasible due to the large number of animals involved. We therefore propose an oral formulation of healthy porcine fecal microbiota in the context of enterotoxigenic *Escherichia coli* (ETEC) infection. According to the specific objectives, the experimental approach included: (i) evaluating bacterial growth and the prebiotic effect of starch derivatives using spectrophotometric measurements at 600 nm and the MTT assay [3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide]; (ii) characterizing resistance profiles through antibiograms on Luria-Bertani (LB) agar plates; and (iii) assessing formulations containing starch derivatives (carboxymethyl starch) using dissolution tests. In parallel, a pharmaceutical bacterial cocktail (Visbiome®), commonly administered under inflammatory enteritis conditions, was used for comparison to evaluate microbial robustness and growth dynamics. Bacterial viability and antibiogram assays showed that penicillin, phosphomycin, geneticin, and kanamycin (5 µg/mL) exerted no toxic effects on the beneficial microbial cocktail. Similar findings were observed with metal derivatives (AgNO₃, AgNP, CuSO₄, CuNP). The porcine-derived microbiota exhibited 20% lower resistance compared to the pharmaceutical formulation. Excipients promoted bacterial growth by 3–36%, suggesting a potential prebiotic effect. Future perspectives focusing on oral formulations derived from pooled healthy donors may represent a promising therapeutic alternative for controlling ETEC infections in swine production.

C3 Starch-derived gastro-resistant coatings for targeted probiotic delivery against post-weaning diarrhea caused by enterotoxigenic *E. coli* in swine

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Post-weaning diarrhea (PWD) in pigs, primarily caused by enterotoxigenic *Escherichia coli* (ETEC), remains a major health and economic challenge in modern swine production. Coated probiotics have been increasingly investigated as antibiotic alternatives, particularly when matrices have gastro-resistant and intestine delivery properties. However, the literature is characterized by variability in terminology, study design, and publication types. This study aimed to (1) systematically identify and compare primary experimental research on coated probiotics targeting PWD caused by enterotoxigenic *E. coli* in swine; (2) apply rigorous inclusion criteria to exclude reviews, theses, non-peer-reviewed publications, and duplicate datasets in order to ensure methodological consistency; and (3) evaluate heterogeneity in terminology, study design, and reporting quality prior to quantitative synthesis. A systematic search was conducted in PubMed, Web of Science, Scopus, CAB Abstracts, and ScienceDirect using the keywords coated probiotics, post-weaning diarrhea, starch-carboxylic, and enterotoxigenic *E. coli*. A total of 1,284 records were identified, with 312 duplicates removed. After screening 972 titles and abstracts, 146 full-text documents were assessed. Reviews (n = 34), theses/dissertations (n = 19), and non-peer-reviewed articles (n = 11) were excluded. Twenty-eight peer-reviewed experimental studies met inclusion criteria. Random-effects modeling indicated moderate heterogeneity ($I^2 = 47%$). Overall, while pooled data support the potential of starch-derived gastro-resistant coatings, substantial variability in reporting and terminology highlights the need for standardized methodological frameworks to strengthen reproducibility and future comparative analyses.

C4 Nanoliposome Mediated Co-delivery of Amoxicillin and Tazobactam Remediate Intracellular Infection by a Multidrug-Resistant *Salmonella enterica* serovar Typhimurium

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Multidrug-resistant (MDR) *Salmonella enterica* serovar Typhimurium (*S. Typhimurium*) poses a growing threat to food safety and animal health, particularly in the swine industry. In this study, we characterized a highly resistant ST strain isolated from a Quebec swine farm using whole-genome sequencing and phenotypic assays. The isolate harbored two plasmids, one of which encoded resistance to seven major antibiotic classes, including β -lactams, aminoglycosides, and sulfonamides, along with multiple virulence factors. To counteract these resistance mechanisms, we developed a nano-enabled antibacterial combination therapy (NeACT) by co-encapsulating amoxicillin (AMOX) and the β -lactamase inhibitor tazobactam into cyclodextrin encapsulated in liposomes (LP-CAT). Physicochemical analysis confirmed optimal particle size, charge, and stability, while checkerboard assays demonstrated strong drug synergism. The LP-CAT formulation drastically restored antimicrobial efficacy, reducing the AMOX minimum inhibitory concentration (MIC) from $>2000 \mu\text{g/mL}$ to $\sim 60 \mu\text{g/mL}$. Using porcine intestinal epithelial (IPEC-J2) cells as an intracellular infection model, our study showed the potential of LP-CAT to remove $>94%$ of intracellular bacteria with no cytotoxic effect. The ability of LP-CAT to resolve intestinal infection was further verified in *Caenorhabditis elegans* (*C. elegans*) intestinal infection model. These findings establish LP-CAT as a safe and effective strategy to revive antibiotic potency against intracellular MDR pathogens, offering a novel tool for combating antimicrobial resistance in livestock and safeguarding public health.

V1 Multi-omics approach to elucidate deoxynivalenols' antiviral effect against porcine reproductive and respiratory syndrome virus infections in vitro

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Deoxynivalenol (DON) is a mycotoxin produced by *Fusarium* spp, often found in animal feed. Pigs are particularly sensitive to its harmful effects. Our laboratory has demonstrated a significant antiviral effect of DON against porcine reproductive and respiratory syndrome virus (PRRSV) infection in vitro and in vivo, but a cellular and mechanistic explanation for this effect has not been explored. This study aims to elucidate the in vitro antiviral mechanisms of DON against PRRSV using a multi-omic approach. In summary, cells infected with a Quebec strain were treated with DON [280 ng/mL]. Total RNA and proteins were extracted 72 hours after infection and, with the relevant controls, 16 mRNA samples (MiSeq) and 12 protein samples (UHPLC-MS/MS) were sequenced. Transcriptomic results revealed 154 differentially expressed genes (DEGs), while proteomic results revealed 23 DEGs [p-value<0.05; |Log2FC|>1]. Enriched with GSEA, a network of signaling pathways involved in the antiviral effect was created. Its analysis suggests a decrease in the expression of the APOE, NAGA and LAMP1 genes, all of which are important in the viral cycle, and the transcription factor SP1 appears to be activated. Identical results from porcine macrophages are currently being curated to cross-analyze DEGs through this bioinformatic pipeline and more comprehensively select genes from significantly enriched pathways. Multi-omic analysis has thus revealed cellular mechanisms (not mentioned) and genes essential for antiviral activity against PRRSV. DON, which has no realistic direct application against PRRSV, could therefore pave the way for new antiviral targets and strategies against this highly costly swine virus.

V2 MiRNAs involved in Avian Infectious Bronchitis Virus (IBV) during In Ovo Infections

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The research focuses on the avian infectious bronchitis virus (IBV), cases of which have been on the rise in Quebec since 2015. Although the virus mainly attacks broilers, causing increased mortality and secondary infections, it also affects laying hens. This virus leads to a drop in egg production as a result of false layer syndrome, causing heavy losses to the poultry industry, since Quebec supplies around 20% of Canadian production. Combining the nature of the virus, the emergence of new strains between 2015 and 2017 and the difficulty of achieving anything other than local immunity, this research proposes an alternative. The objective of this study was to develop an in ovo IBV infection model and characterize microRNA (miRNA) modulation by high-throughput sequencing following IBV infection in the organs of infected chicken embryos. While in ovo models have been used to study IBV, their application to miRNA profiling during the early stages of infection remains unexplored. MiRNAs are small non-coding RNA sequences whose role is to regulate protein synthesis. It was found that some miRNAs were differentially expressed in the presence of the virus and that they seemed to be involved in various cellular pathways like MAPK, FoxO, and p53 signaling pathways as well as in cellular senescence and cytokine-cytokine interactions. This study proposes an innovative model, a tool for future mechanistic studies, and has identified differentially expressed candidate miRNAs for potential functional studies that could lead to therapeutic targets or biomarkers in the context of IBV infection.

V3 Isolation and molecular characterization of West Nile virus circulating in wild bird populations in Quebec

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West Nile Virus (WNV) is an arbovirus transmitted by mosquitoes and maintained in nature through infected wild birds, which act as reservoirs. It is endemic in several regions worldwide, including Eastern Canada, and infection in humans can cause severe encephalitis and meningitis, leading to fatal outcomes. Despite its global impact, no vaccines or antiviral treatments are currently available. Monitoring the evolution of WNV in wildlife is critical to identify potential changes that could increase risks to human health. This study aims to isolate and characterize WNV strains circulating in wild bird populations in Quebec. WNV-positive tissues collected in 2023–2024 were used to isolate and amplify viruses under biosafety level 3 conditions. Replication kinetics were compared to the NY99 reference strain in mosquito (C6/36), human (Huh7.5 and A549), and avian (DF-1) cell lines to assess viral fitness across vector and vertebrate hosts. Overall, isolates exhibited replication kinetics comparable to NY99. However, C6/36 cells showed delayed replication with higher titers at days 2–3, together with reduced induction of antiviral genes compared to human and avian cells. Viral replication and host innate immune responses were monitored using plaque assays, RT-qPCR, and immunofluorescence. Viral RNA sequencing identified lineage 1a strains containing polymorphisms in non-structural regions of the polyprotein. Selected mutations will be introduced into a lineage 2 WNV GFP-reporter replicon to assess their impact on viral RNA replication and innate immune modulation. Ultimately, this study will determine whether newly acquired polymorphism circulating in Quebec influence viral replication and thus, potentially human health.

V4 Fowl Aviadenvirus (FAdV) Genomic Diversity in Poultry Diagnostic Liver Samples Collected From 2019 to 2024 in Quebec, Canada

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Fowl aviadenoviruses (FAdV) species D and E are the etiological agents of inclusion body hepatitis (IBH) in poultry. No treatment is available to cure infected fowls, but autogenous vaccines are widely used in Quebec, Canada, to prevent IBH. The autogenous vaccine's efficacy, however, depends on its genomic/antigenic similarity to the field-involved virus strain, which is usually identified using partial hexon gene sequencing. This region represents only 1.24% of the whole genome. The hypothesis for this study is that whole-genome sequencing (WGS) will give more information to veterinarians to adjust their vaccination strategies. Liver samples were either directly sent to the Molecular Diagnostic Laboratory of CDVUM for FAdV qPCR analysis by Québec poultry veterinarians, or by the Quebec Ministry of Agriculture, Fishery and Food following the necropsy of dead birds. Positive samples were then selected, and whole-genome sequencing of FAdV was carried out using Illumina's MiSeq platform. Out of 134 qPCR FAdV-positive cases, 106 complete and 5 partial FAdV sequences were obtained. Among those sequences, 73, 24, and 9 sequences were classified as genotypes E/8b, E/7, and D/2, respectively. Only type E strains were found between 2020 and 2023, while type D/2 strains were newly identified in 2024. Interestingly, WGS changed the classification of 31.13% FAdV strains compared to the partial hexon gene sequencing method. This study gives us a better insight into the genomic diversity of FAdV strains present in Quebec poultry flocks. Rapid identification of new strains could help practitioners adapt their autogenous vaccine strategy.

D1 Reference gene validation for RT-qPCR applications in *Gryllobates sigillatus*: implications for insect health and farming

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The tropical house cricket *Gryllobates sigillatus* has attracted increasing interest in insect biology, immunity, and edible insect farming due to its ease of rearing, short life cycle, and growing importance in animal feed. The study of key biological processes in this species increasingly relies on molecular approaches, particularly RT-qPCR-based gene expression analysis, the reliability of which depends on the use of stable reference genes for data normalization. To address the lack of validated reference genes in *G. sigillatus*, we assessed the expression stability of six candidate genes (ACTB, EF1 α , GAPDH, His H3, RPL5, and 18S rRNA) across four tissue types (abdomen, head, legs and whole body) using a combination of complementary statistical approaches, geNorm, NormFinder, BestKeeper, the Δ Ct method, the R statistical software, and RefFinder. The candidate genes were identified and annotated using a recently released *G. sigillatus* genome through sequence comparisons with closely related insect species via BLAST and reciprocal BLAST analyses, multiple sequence alignments, and open reading frame (ORF) prediction. All procedures were conducted in strict compliance with MIQE 2.0 guidelines to ensure methodological rigor and transparency of the results. The results showed that ACTB, EF1 α , RPL5, and 18S rRNA were the most stable reference genes across all analyzed tissues, whereas GAPDH and His H3 exhibited high variability, with the exception of GAPDH in head tissue. This study provides the first validated set of reference genes for *G. sigillatus*, establishing a foundation for reliable and reproducible gene expression analyses and enabling the development of qPCR-based diagnostic tools.

D2 Characterization of IncHI Plasmids in Pathogenic *Escherichia coli* Strains

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Multidrug-resistant *Escherichia coli* represent a major challenge in both public health and animal health. Conjugative plasmids enable bacteria to acquire genetic material, such as resistance genes, through horizontal gene transfer. While conjugative plasmids belonging to the IncHI incompatibility group carry numerous resistance genes, their transfer mechanisms and their role in pathogenic *E. coli* remain poorly documented. The hypothesis of this project is that IncHI plasmids encode systems that enable dissemination across a broad host range, thereby influencing the virulence, metabolism, and resistance profiles of bacterial isolates. To test part of this hypothesis, IncHI plasmids from *E. coli* strains of clinical relevance in animal production were characterized using bioinformatic analyses, and their intra- and inter-species transfer efficiency is currently being evaluated. Preliminary results revealed a high diversity of resistance genes harbored by IncHI plasmids, including resistance to cephalosporins, beta-lactams, streptomycin, spectinomycin, and kanamycin. Multilocus sequence typing (MLST) identified three distinct sequence types (ST): ST2, ST3 and ST4. Pangenome analysis demonstrated substantial diversity in accessory genes, with plasmid sizes ranging from 200 to 300 kb. In vitro conjugative transfer assays are currently underway to assess intra- and interspecies transfer efficiency. These results will contribute to a better understanding of the role of IncHI plasmids in the emergence of multidrug-resistant pathogenic strains.

D3 Identification of Virulence Genes in *Staphylococcus hyicus* Using a Genome Editing Approach

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Exudative epidermitis is a bacterial disease affecting piglets, causing skin lesions, impaired growth, and significant economic losses when outbreaks occur. The causative agent, *Staphylococcus hyicus*, remains poorly studied, and the genetic determinants underlying the high virulence of certain strains are still largely unknown. This knowledge gap complicates accurate diagnosis and limits the development of effective alternatives to antibiotics, which are increasingly needed in the context of antimicrobial resistance. This master's project aims to identify and functionally characterize genes involved in *S. hyicus* virulence. To achieve this, a CRISPR-Cas9 genome-editing system is being adapted for use in *S. hyicus* to selectively inactivate candidate virulence genes. An electroporation protocol has been successfully established and shown to work across multiple *S. hyicus* strains with different plasmids. In parallel, mutagenesis plasmids are currently being constructed for upcoming CRISPR-Cas9 genome-editing assays. The impact of gene disruptions on bacterial pathogenicity will then be evaluated using in vitro cell-based infection models. By combining genome editing and functional assays, this study is expected to establish molecular tools for genetic manipulation and identify novel virulence genes in *S. hyicus*. Ultimately, the identification of these virulence determinants will help distinguish highly virulent strains and improve the prevention and management of exudative epidermitis in swine.

D4 Sequence Type distribution among clinically relevant serotypes of *Streptococcus suis* recovered from diseased pigs in Quebec (Canada), 2020-2024

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Streptococcus suis is a Gram-positive bacterium recognized for its pathogenicity in pigs and its zoonotic potential. Among the 29 described serotypes, some are part of the porcine commensal flora, while others are associated with severe infections, including meningitis, septicemia, and arthritis, conditions that lead to substantial economic losses in the swine industry. In Canada, serotypes 1, 1/2, 2, 9 and 14 are frequently recovered from such cases. This study aimed to characterize recent changes in the distribution of sequence types (STs) within these serotypes among isolates recovered in Quebec, Canada, between 2020 and 2024. A total of 199 isolates were analyzed using the standard multilocus sequence typing (MLST), scheme for *S. suis* targeting the *aroA*, *gki*, *dpr*, *recA*, *mutS*, *thrA*, and *cpn60* genes. The dominant STs were ST1, ST28, ST25, ST94, and ST620. All ST1 isolates, associated with strain high virulence, were restricted to serotypes 1 and 14. Absent in previous reports, we observed the emergence of ST126 and ST156 among serotypes 1 and 14, respectively. Additionally, nine serotype 14 isolates belonged to a novel, previously undescribed ST assigned to MLST clonal complex 1372. For serotype 2, as reported in the past, the main STs were ST28 and ST25; as also reported in the past, highly virulent and zoonotic ST1 genotype, commonly found among serotype 2 isolates from Europe and Asia, were not detected. Our findings provide new insights into the changing population structure of *S. suis* in North America and may inform future surveillance and vaccine development strategies.

D5 Foodborne pathogen detection and microbiota characterization of broiler chicken carcasses and parts.

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Improving the microbiological quality of broiler chicken carcasses and their parts represents a major challenge for the poultry industry. Chicken is not only the most widely consumed meat, whose shelf life is largely influenced by its initial level of contamination, it is also one of the most significant contributors to the prevalence of foodborne illnesses in Canada. The finality of this project consists of improving food safety of chicken meat products. Before this, there is a need to assess the current situation. To this aim, we will evaluate the presence of *Salmonella* spp. and *Campylobacter* spp. on broiler chicken carcasses and in different meat parts. Their microbiota will also be described. The sampling will take place in 3 slaughterhouses that will be visited 5 times each. At each visit, the first five flocks slaughtered will be sampled at five key stages of the slaughter line by thoroughly rinsing one carcass per step. *Salmonella* will be detected and characterized by selective isolation, *invA* PCR-based amplification and CRISPR typing using the Nanopore technology. *Campylobacter* will be identified through rapid 16S rRNA detection, selective isolation, and confirmation by MALDI-TOF mass spectrometry. Simultaneously, different related meat parts will be sampled at different storage times (d0, 10, 13 and 15) at 4°C for the detection of both pathogens and for microbiota analysis that will also be documented on their corresponding carcasses. Ultimately, the findings will contribute to a better understanding of carcass microbiota and contamination by *Salmonella* and *Campylobacter* to improve contamination prevention measures in slaughterhouses.

D6 Impact of *Salmonella* Typhimurium on the gut proteome of newly weaned piglets and the role of dietary supplements.

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The gut proteins were associated with physiological and metabolic functions. The intestinal epithelium is exposed to external stimuli, leading to protein secretion, and previous studies have shown that proteins are altered in the intestines of *S. Typhimurium*-infected pigs. The aim of this to investigate the impact *S. Typhimurium* on gut proteome and the role of dietary supplements on it. This study was conducted on 64 piglets and weaned at 21 days of age and fed commercial diets with or without dietary supplements. After two weeks of treatment, piglets were orally inoculated with *S. Typhimurium* except a negative control. The groups were as followed: (1) non-infected and commercial diet, (2) infected with *S. Typhimurium* and commercial diet (3) infected, commercial diet with bovine colostrum (4) infected, commercial diet with colostrum, MCFA and yeast extract. Half of the piglets were euthanized at 3 days post infection (DPI) and others half at 10 DPI. The colon contents were collected and sent to Allumiqs for proteomic analysis by using LC-MS/MS platform. Results: *S. Typhimurium* and dietary supplementation altered the protein expression in the gut of newly weaned piglets. Gene Ontology (GO) and KEGG pathway analyses were performed for altered proteins at both 3 and 10 DPI. Collectively, the GO terms results of significantly altered proteins were associated with protein degradation, immune cell recruitment, and stress-related defense mechanisms and extracellular signaling. The KEGG pathway analyses results were involved in proteins digestion and absorption, fatty acid biosynthesis, renin-angiotensin system and various other biological pathways.

D7 Characterization of new species from the genus *Streptococcus*

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A proper identification of bacterial infection in swine is essential for a proper diagnosis, especially when it comes to *Streptococcus suis* and other closely related species since they can cause sudden death. Typically, this identification is done using MALDI-TOF MS, followed by a species-specific PCR targeting the *recN* gene. However, in the recent years an increasing amount of strains identified as *S. suis* by MALDI-TOF MS have tested negative in the *recN*-based PCR. After further genomic analysis and the recent description of 11 new species closely related to *S. suis*, we aim to characterize some of those species. To accomplish that, we employed a range of techniques previously used to characterize other new species close to *S. suis*: 16S rRNA, *recN*, average amino acid identity (AAI), average nucleotide identity (ANI), digital DNA-DNA hybridization (dDDH) and other traditional biochemical assays. Preliminary genomic analyses confirmed the strains from the new species were indeed new species. We then characterized them phenotypically through Gram staining, catalase, oxidase, hemolysis, and motility tests. Results for these assays were largely consistent with those typically observed in *S. suis*. Lastly, we did a Rapid ID 32 Strep test. Those results revealed significant differences from *S. suis* and other known related species. Additionally, different results were observed among strains within the same group, suggesting the presence of subgroups and underscoring the high diversity of these novel species. Another evidence of this diversity was found during the analysis of the *cps* locus responsible for the biosynthesis of the polysaccharide capsule. Our results are further supporting the presence of new species close to *S. suis*. Which we will keep on characterizing genomically and biochemically. Their virulence will also be assessed using various experimental infection model.

D8 Host range and zoonotic potential linked to P-like fimbrial adhesin specificity in avian pathogenic *Escherichia coli*

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Fimbrial adhesins are surface-associated bacterial proteins that contribute to colonization, tissue tropism, and biofilm formation. Genomic analysis of the avian pathogenic *Escherichia coli* (APEC) strain QT598 identified a plasmid-localized fimbrial operon, termed *plf* which encodes P-like (PL) fimbriae. Herein, we investigated the role of P-like (PL) fimbriae, encoded on the ColV plasmid of APEC strain QT598, in a natural host turkey respiratory infection model. We determined that deletion of the *plf* genes reduced colonization in the lungs of turkeys. The PlfG class II fimbrial adhesin from APEC strain QT598 demonstrated species- and tissue-specific adherence, as adherence to turkey lung sections in vitro was more pronounced than adherence to chicken lung sections. In vivo, expression of *plf* was also found to be upregulated in the lungs of turkeys during infection, as determined by qRT-PCR. Glycan array analysis showed that the PlfG class II adhesin recognizes Lewis b, Lewis y, and H antigens as potential receptors that are present on human red blood cells and on the surface of turkey respiratory tissues, implicating specific α -1,2-linked glycans as receptors. Structural modelling of Plf adhesin revealed conserved β -sandwich folds with distinct binding pockets that predict receptor specificity differences between Plf adhesin variants and other fimbrial adhesins such as PapG II and the PlfG class I adhesin from UMEA 3703-1. These findings highlight the role of PL fimbriae in APEC virulence and suggest a potential zoonotic and foodborne risk from poultry to humans, demonstrating the common recognition of glycans present on both turkey and mammalian host cells and tissues.

Keywords: Avian pathogenic *E.coli* (APEC), fimbrial adhesins, P-like fimbriae (PL fimbriae), colonization

D9 Unmasking Cryptic Diversity and Diagnostic Obstacles in the Expanding *Streptococcus suis* Complex Through Genomic Approaches

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Accurate species delineation within the *Streptococcus suis* group and its closely related taxa remains problematic, largely due to the limited discriminatory power of routine diagnostic methods and the lack of well-curated, comprehensive reference databases. In this study, we analyzed 64 isolates recovered from diseased pigs that had been identified as *S. suis* by MALDI-TOF MS but yielded negative results in a widely used *recN*-based PCR assay for species confirmation. Whole-genome sequencing demonstrated that only four isolates represented *S. suis sensu stricto*, whereas most belonged to other members of the *S. suis* complex, including *Streptococcus parasuis*, *Streptococcus ruminantium*, and several recently described *Streptococcus* species. Core genome phylogenetic analysis supported the delineation of a monophyletic “*S. suis* complex,” encompassing *S. suis sensu stricto* and multiple closely related, emerging lineages that are frequently misclassified by conventional diagnostics. These taxa formed well-supported, taxonomically coherent clades, in contrast to the *recN* marker, which exhibited limited phylogenetic resolution and evidence of recombination, thereby undermining its reliability for species identification. To facilitate the development of improved molecular tools, we identified 38 genes present in $\geq 95\%$ of *S. suis sensu stricto* genomes that represent promising candidates for future diagnostic assays. Collectively, our results uncover considerable cryptic diversity, demonstrate important shortcomings in current identification strategies, and underscore the clinical significance of several underrecognized taxa within this expanding pathogen complex.

B1 Eastern Canadian hatching egg houses: seasonal variability of air pollutants and animal health and welfare

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Hatching egg production takes place inside confined buildings. Despite air pollutants being exhausted by mechanical fans, workers and birds are still exposed to important concentrations of gases and airborne dust particulates (PM). While higher values than the occupational exposure limits (OEL) for ammonia, carbon dioxide and total dust particulates are considered harmful to workers, for domestic fowls, ammonia concentrations greater than 25 ppm could be responsible for short-term damage to eyes, footpads and respiratory systems. The present project aimed at evaluating the seasonal air quality and breeder bird health and welfare in ten Eastern Canadian hatching egg operations. Twenty-nine visits were conducted during which ammonia and carbon dioxide levels, and PM were measured on both floors of the two-storey buildings. Health (respiratory, eye and foot problems) and welfare were also evaluated in 50 breeder birds, 25 per floor, per visit. On-site visits, during the summer, fall and winter seasons, revealed concentrations of total PM and carbon dioxide mostly lower than 10 mg/m³ (OEL) and 5,000 ppm (OEL), respectively, while, for ammonia, half of the samples were above 25 ppm (OEL). There were significantly more PM and ammonia in autumn than summer in the visited hatching egg productions (no difference between autumn and winter). No eye or respiratory health problems nor behavioral issues were found among the flocks. However, swollen (10% of the birds) or necrotic (30%) feet were observed. These findings underscore the need for the implementation of targeted environmental controls to improve air quality in broiler breeder facilities.

B2 Does the organic status impact air quality, microbial communities, and antimicrobial resistance genes in egg farms?

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By 2036, Canadian egg farmers will replace conventional cages with alternative housing that provides hens with more room and enrichments, improving welfare. Organic egg production is also increasing, limiting antibiotics and providing added enrichments. However, increased movement and added litter in aviary systems generate more bioaerosols and particulate matter (PM) compared to caged housing. Despite this, microbiological risks associated with organic systems remain poorly documented. This study compares PM concentrations, microbial communities, bacterial diversity, and antimicrobial resistance genes (ARG) in organic and free-range farms. Four aviaries (two organic, two free-range) were sampled three times over two years (winter and summer 2024; winter 2025). Air, litter, and egg wash samples were collected and PM concentrations measured. Indicator and pathogenic taxa were assessed with quantitative PCR (qPCR), while high-throughput qPCR assessed ARG profiles. Amplicon sequencing evaluated bacterial diversity. Overall, results do not indicate trends driven by farm status (organic vs. non-organic), but rather by farm-specific factors such as hen age, density, litter presence, and temperature. For example, *Enterococcus* spp. quantified by qPCR was detected at significantly higher levels on egg surfaces in organic farms, while concentrations were higher in free-range farms for air and litter samples. Different patterns emerged in ARG profiles, where certain genes were exclusively found in free-range farms. Patterns also varied across substrate, with several ARG absent in litter samples yet present in air and egg washes. Bacterial diversity analyses are ongoing. Results will help fill critical knowledge gaps in our understanding of microbial communities in organic egg production.

B3 Microorganisms monitoring during manure spreading using various manure types and spreading techniques

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Animal feces contain large quantities of microorganisms, including potential pathogens. Bioaerosols emitted during agricultural activities have long been overlooked. Manure spreading can disperse these bacteria into the environment, including soil, water, crops, and air. Bioaerosols generated during manure spreading could facilitate spread of potentially pathogenic microorganisms. This project aimed to monitor airborne microbial indicators (total bacteria, Enterococcus, and Archaea) during and after manure spreading activities, at three distances, comparing manure types and spreading techniques. Microbial indicators were quantified in air samples, manures, and slurries using high-throughput PCR. Air samples were collected at 6, 18, and 36m downwind from the spreading area before, during, and after standardized manure application. Solid manures (beef, dairy cow, poultry with litter, and poultry without litter) and liquid slurries (pig and dairy cow) were tested 3–4 times using 6 spreading techniques (vertical beaters, horizontal beaters, and incorporator prototype (IP) for solid manures; splash plate, dribble bar, and dribble bar with incorporation for liquid slurries). Concentrations of microbial indicators in the manures and slurries varied from 10⁶ to 10¹¹ per gram. Airborne concentrations generally decreased with distance from the source and within 20 min after spreading. Poultry manure—particularly when applied using IP and vertical beaters—resulted in the highest emissions during spreadings, reaching approximately 10⁵–10⁶ indicators per m³ of air, before rapidly returning to background levels after spreading. Results suggest that manure type and spreading technique influence airborne emissions during spreading. The results may help reduce exposure of agricultural workers and surrounding populations.

B4 Insights from a Canadian multi-center project on antimicrobial resistance genes in bioaerosols

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Les bioaérosols sont des particules d'origine biologique en suspension dans l'air qui peuvent contribuer à la dissémination de microorganismes résistants aux antimicrobiens (MRA). Malgré leur impact potentiel, les bioaérosols demeurent peu étudiés dans la surveillance de la résistance aux antimicrobiens. Ce projet transdisciplinaire visait à caractériser le rôle des bioaérosols dans la dissémination environnementale des gènes de résistance aux antibiotiques (GRA) au Canada. La modélisation de la dispersion, l'évaluation intégrée des risques, les modèles animaux et les analyses du génome entier ont également été inclus. Des échantillons d'air ont été prélevés dans divers environnements, notamment des milieux agricoles et lors d'épandages de fumier. Différentes stratégies d'échantillonnage de l'air ont été évaluées, dont: l'échantillonnage actif, les filtres d'habitacle de voiture et les branches d'arbres situés à proximité de sites agricoles. Un panel de 40 GRA a été quantifié par PCR à haut débit dans les 2 600 échantillons collectés. Notre étude a permis de quantifier les taux d'émission de GRA par des activités agricoles et de proposer des stratégies d'atténuation lors de l'épandage de fumier. La modélisation de la dispersion a permis d'estimer l'exposition de la population aux GRA d'origine agricole. Les résultats ont été incorporés au modèle canadien intégré d'évaluation du risque de la résistance aux antimicrobiens (iAM.AMR). Cette étude démontre la faisabilité de l'intégration de l'air dans la surveillance de la résistance aux antimicrobiens grâce à des méthodes abordables et souligne que la résistance aux antimicrobiens est un défi mondial et intersectoriel qui exige des solutions intégrées.

B5 Seasonal assessment of Clostridium perfringens contamination in feed ingredients and production environments of Quebec feed mills

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Clostridium perfringens is a major pathogen in animal production, particularly responsible for necrotic enteritis in poultry, causing substantial economic losses worldwide. Certain feed ingredients, including meat-and-bone meal and plant-based meals, may serve as contamination sources and contribute to the spread of *C. perfringens* into finished feed. In Quebec, approximately 5.3 million tonnes of livestock feed are produced annually by commercial feed mills. Despite the importance of this industry, no previous study has evaluated the dynamics of *C. perfringens* contamination within Quebec feed mills. The objective of this study was to assess the presence of *C. perfringens* in major feed ingredients, finished feed, and production environments in three commercial feed mills, while also examining seasonal variation during spring, summer, and autumn. Samples of key ingredients (e.g., corn, wheat), finished feed, and environmental sites (e.g., mixer, pelletizer) were collected during each season. Samples were cultured anaerobically on TSC agar, and presumptive isolates were confirmed by PCR targeting the *cpa* gene, followed by detection of the *netB* toxin gene. Preliminary culture findings showed that the majority of feed ingredients (e.g., corn, soybean meal, lamb meal), multiple environmental sites (e.g., mixer and pelletizer), and even post-cooking finished feed were positive for *C. perfringens*. Seasonal trends indicated that contamination levels were highest in summer, intermediate in autumn, and lowest in spring. These findings highlight the need for improved operational environmental hygiene in feed mills and stricter control of processing parameters (e.g., cooking temperature and duration), particularly during high-risk seasons.

B6 Study of contamination of Quebec's broiler chicken supply chain, from farm to slaughterhouse

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The Canadian broiler poultry production chain faces significant food safety challenges, particularly due to *Salmonella* spp., a persistent zoonotic pathogen. Total bacterial load (TBL) is commonly used as an indicator to identify critical control points of contamination. This study aimed to characterize the presence of *Salmonella* spp. and TBL throughout the broiler chicken supply chain in Québec in order to better understand contamination dynamics, from farm to slaughterhouse. Eighty-seven broiler breeder flocks were surveyed through litter sampling, and 25 broiler chicken farms were visited twice: prior to chick placement and before bird catching. Environmental samples included feed, litter, walls, fans, feeders, chick boxes and transport crates. At the slaughterhouse, 11 carcasses were sampled for each broiler chicken farm. *Salmonella* isolation was performed using standard bacteriological methods, and total bacterial load was quantified using 16S rRNA gene qPCR. Several stages of the supply chain were identified as critical points, combining high TBL and *Salmonella* positivity: the hatchery, represented by chick boxes (TBL: 1.32×10^8 copies/ng; *Salmonella*: 20%); broiler breeder flocks (TBL: 1.14×10^8 copies/ng; *Salmonella*: 44%); transport, represented by transport crates (TBL: 1.06×10^8 copies/ng; *Salmonella*: 64%); and the bleeding step at the slaughterhouse (TBL: 8.36×10^7 copies/ng; *Salmonella*: 96%). Overall, these results highlight key contamination hotspots along the broiler production chain and emphasize the need for targeted hygiene and biosecurity interventions to reduce bacterial contamination and improve food safety.

B7 Small RNA RyfA and TimR Coordinate Stress Resistance and Virulence in Avian Pathogenic E. coli

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Introduction. Avian pathogenic *Escherichia coli* (APEC) are a major cause of economic losses in the poultry industry. These bacteria share several similarities with uropathogenic *E. coli* (UPEC). Work on the UPEC CFT073 model identified a small regulatory RNA, RyfA, involved in stress resistance and virulence. More recently, a study conducted on *Salmonella* revealed the existence of a second RNA, TimR, in the same region as RyfA. **Materials and Methods.** In the APEC CH138 strain, we studied the impact of these two small RNAs using mutagenesis and phenotypic approaches. The production of type 1 fimbriae, involved in bacterial adhesion, was assessed by yeast agglutination. Motility was characterized by using in vitro assays. Resistance to oxidative stress was measured in the presence of H₂O₂, and macrophage infection allowed bacterial survival to be studied. Finally, an avian infection model was used to assess virulence. **Results and Discussion.** Inactivation of TimR alone had no effect, while deletion of RyfA resulted in decreased fimbriae production, increased sensitivity to oxidative stress, and hypermotility. Loss of RyfA attenuated virulence in vivo. However, the combined deletion of RyfA and TimR showed no additional effect. **Conclusion.** These observations suggest that, in an APEC context, RyfA also plays a key role in stress adaptation and survival. However, the interactions between RyfA and TimR remain to be elucidated.