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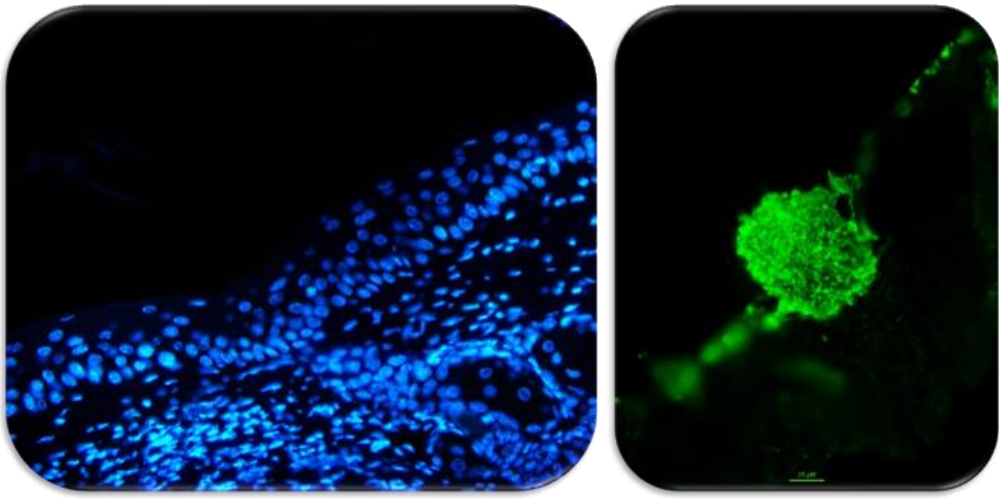
Proceedings of the 12th FARAH-Day

Faculty of Veterinary Medicine
(University of Liège - Belgium)

December 18, 2025

One Health
L'Animal et l'Homme, une même santé



Proceedings of the 12th FARAH-Day

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December 18, 2025

Edited by C. Cesarini Latorre, C. Delguste,
C. Douny, J. Eppe, L. Fiévez, T. Franck, V. Frisée, T. Jauniaux, J. Ledeck, M. Levoz, W. Poirier,
I. Tosi, D.M. Votion, S. Vroomen, A.S. Van Laere, B. Vandenhove, C. Wielick.

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" Murmure des constellations nucléaires" & " Emeraude fongique au coeur de l'épiderme "
@Wilfried Poirier, 2025

Welcome to the 12 th FARAH Day

In 2011, the Scientific Staff of the Faculty of veterinary Medicine organised its first annual meeting. Each annual meeting has been a great success with an average of 100 abstracts submitted, among which about twenty were selected for an oral presentation by an independent scientific committee.

In 2013, an interdisciplinary structural research centre was created at the University of Liège. It has been named FARAH for "Fundamental and Applied Research for Animals & Health".

The founding principles of the FARAH incorporate the notion of interaction between scientists of the Centre and, as such, the annual meeting of the scientific staff gives us the opportunity to share our knowledge. Also, it is now under the auspices of the FARAH that the annual meeting will be held with the same organizers (i.e. members of the Scientific Staff). This edition gathers about 60 abstracts dedicated to fundamental, clinical and or applied researches.

Marie-Louise Scippo, **Jean-Luc Hornick & Dominique Votion**.

Bienvenue à la 12ème journée du FARAH

En 2011, le Personnel Scientifique de la Faculté de Médecine vétérinaire organisait sa première journée scientifique annuelle. Chaque réunion annuelle a été un grand succès avec, en moyenne, une centaine de résumés de recherche soumis dont une vingtaine était sélectionnés pour une présentation orale par un comité scientifique indépendant.

En 2013, un centre structurel interdisciplinaire de recherche a été créé au sein de l'Université de Liège. Ce centre est désigné par l'acronyme FARAH pour « Fundamental and Applied Research for Animals & Health ».

Les principes fondateurs du FARAH intègrent la notion d'interaction entre les Scientifiques du Centre et à ce titre, la réunion annuelle du personnel scientifique nous donne l'opportunité de partager nos connaissances. Aussi, c'est dorénavant sous l'égide du FARAH que s'organise, avec les mêmes forces vives (i.e. les membres du Personnel scientifique), la réunion annuelle des scientifiques. Cette édition inclut une soixantaine de travaux ayant trait à la recherche fondamentale, clinique et/ou appliquée.

Marie-Louise Scippo, **Jean-Luc Hornick & Dominique Votion**.

Organisers of the meeting

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Program

08:30 - Registration (lecture hall C, building B45)

09:00 - Opening and Welcome Speech

Prof. Antoine Clinquart, Dean of veterinary faculty &
Prof. Marie-Louise Scippo, President of Farah

09:15 Invited speaker

Etienne Baise Award

09:35 - Oral session 1: Short talks (lecture hall C, building B45)

Chair: Marie-Louise SCIPPO & Vinciane TOPPETS

09:35 Gauthier RAWAY – *The use of mosquito bloodmeals to monitor wildlife infections: Orthoflavivirus IgG detection in wild Balinese macaques.*

09:45 Kristi LEKA - *Exploring the Antiviral Activity of a Plant-Derived Compound Against Prominent Viruses.*

09:55 Clara ALAMAR MALVOISIN - *Comparative efficacy of omeprazole-sucralfate versus misoprostol in the treatment of equine glandular gastric ulcers: a retrospective study (2016–2022).*

10:05 Salem DJEBALA - *Identified bacteria in the surgical site during the realisation of elective caesarean section in Belgian blue cows.*

10:15 Pham Tran Thuy HUONG - *Variation in ODAP content among modern grass pea species: A comparison with an archaeological specimen.*

10:25 Constance WIELICK - *Dynamics of hepatitis E virus infection in Belgian pig farms: longitudinal study from birth to slaughter, modelling and evaluation of some zoonotic risk mitigation measures.*

10:35 - Coffee break and poster session 1 (Room P, building B45)

11:00 Invited speaker

Coraline Radermecker

Neutrophils by billions

11:30 - Oral session 2: Short talks (lecture hall C, building B45)

Chair: Nicolas KORSAK & Irène TOSI

11:30 Corentin ALSTEENS - *Prevalence of tachypnea and/or acute respiratory distress following packed red blood cell transfusion in cats and association with survival.*

11:40 Dorian GRANDJEAN - *Validation of a photoplethysmography sensor for measuring heart rate in dogs during exercise.*

11:50 Lucie GILLARD - *Study of the importance of tegument proteins pORF45 in the biology of gammaherpesvirus infection.*

12:00 Yassine EL MEHDI-LAMGHARI - *Nanopore sequencing of high-risk HPV via amplicon and rolling circle amplification points to HPV integration and new HPV types.*

12:10 Sofia ROBBIANO MUNOZ - *Videotracking identifies acute and chronic neurological and behavioral deficits in murine models of West Nile Virus infection.*

12:20 Annie TAKAM NGOUNO - *Unveiling the Nutritional and Microbiological Changes in Carbap K74 Plantain Hybrid Flours: A Focus on Processing Effects.*

12:30 - Lunch and poster session 2 (Room P, building B45)

14:00 - Oral session 3: Short talks (lecture hall C, building B45)

Chair: Justine EPPE & Calixte BAYROU

14:00 Laurie CONTI - *A journey towards the discovery of Cyvirus cyprinidallo 3 ORF57 functions.*

14:10 Abbas HAMIM - *Forage protein strategies for sustainable organic egg production in Wallonia in relation to the microbiota of hens.*

14:20 Sovannmony LAY - *Effect of deep-frying and air-frying on fatty acid profile and lipid oxidation of common carp (Cyprinus carpio).*

14:30 Lisa CONTI - *Is ORF112 of the Cyvirus cyprinadallo 3 essential or not essential ?*

14:40 Alexis BALTHAZAR - *The role of gammaherpesvirus in shaping IBD-associated immune profiles: insights from advanced immunophenotyping in murine and translational models.*

14:50 Françoise LESSIRE - *Mitigation and adaptation plans : A review of Climate Smart Solutions chosen by Belgian pilot farms taking part in the EU project Climate Farm Demo.*

15:00 Manon Marie JAGER - *Effect of different viral infections on the development of experimental autoimmune encephalomyelitis in mice.*

15:10 Ophélie PIEDFORT - *Modulation of effector memory T lymphocyte responses to vaccination by helminth infections.*

15:20 Margaux LEGRAND - *Evaluation of different right heart echocardiographic parameters for the diagnosis of precapillary pulmonary hypertension in dogs with chronic respiratory disorders: a prospective study.*

15:30 Georgios PETRELLIS - *IL-4 receptor signaling regulates lung macrophages during helminth coinfection resulting in enhanced gammaherpesvirus permissiveness.*

15:40 Didier MARLIER - *The smartest, the fastest, and the highest-flying: a pigeon's (Columba livia) perspective on La Fontaine's 'The Hare and the Tortoise' fable.*

15:50 Invited speaker

Elodie Roels
Overview of the current research initiatives at the small animal teaching hospital (DCC)

16:10 - Coffee break and poster session 3 (Room P, building B45)

16:40 - Oral session 4: Awardee from FSR (lecture hall C, building B45)
Chair: Bénédicte MACHIELS & Bernard TAMINIAU

16:40 Valeria BUSONI - *Microvascular flow imaging of the equine forelimb tendons in race horses in training (EQ-MVFI).*

16:45 François FOCROULLE - *Defining the role of endothelium in orchestrating the cytokine storm during severe viral respiratory disease (ORCHESTORM).*

16:50 Etienne ESCANDE – *CANDAR-Coagulation Abnormalities in Dogs undergoing Adrenal Resection.*

17:00 Gaëlle SCHILS - *Chimeric Antigen Receptor (CAR) T cells targeting the Fibroblast Activation Protein (FAP): perspectives in dogs.*

17:05 Rafael BERNARDES - *Characterization of urinary and gut microbiota in dogs with urothelial bladder carcinoma and their association with response to adjuvant therapies (UROGENmicrobiotalIV).*

17:10 Etienne ESCANDE - *LYSICAN – LYSis timer in CANine: Evaluation of the use of the Lysis Timer to measure fibrinolysis in dogs.*

17:20 Questions

17:25 Picture contest: preview

17:30 – Invited speaker (Room C, building B45)

Alain Vanderplasschen
Unveiling of the memorial stone in honor of Professor Paul-Pierre Pastoret

17:45 – Closing session

Prof. Michel Moutschen, Vice-Rector for Research of ULiège University &

Prof. Marie Mutien Garigliany, Vice-Dean for Research of veterinarian faculty

18:00 – FarahDay awards (Room P, building B45)

18:30 – Live music, drinks and appetizers

Starting at 19:30 – Food and Fun (Games, Blind Test, Music, …)

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Short talks

The use of mosquito bloodmeals to monitor wildlife infections: Orthoflavivirus IgG detection in wild Balinese macaques

Raway G.[1], Subrata S.-A.[2], Nicaise H.[1], Brotcorne F.[1,±], Garigliany M.-M.[3,±]

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Tropical regions with dense mosquito populations are hotspot for vector-borne diseases such as Dengue, Japanese Encephalitis, etc. These infections also occur in non-human primates, warranting close attention for their global health relevance. Despite high zoonotic risk, mosquito-borne infection dynamics at the human-primate interface in Bali (Indonesia) remain poorly documented. Wildlife infections surveillance is often constrained by logistical and ethical considerations associated with biological sampling. To address this, mosquito bloodmeal analysis ("xenosurveillance") offers a powerful non-invasive tool to monitor pathogen circulation in wild vertebrates. This preliminary study aimed to optimize this approach to screen free-ranging Balinese macaque (*Macaca fascicularis*) for Orthoflavivirus infections. Blood-fed mosquitoes were collected daily for 4 months using a handheld aspirator in macaque occupied areas. Vertebrate hosts of the bloodmeals were identified via DNA barcoding. Primate samples underwent serological screening with a commercial ELISA kit for Orthoflavivirus IgG, adapted for bloodmeal-sized volumes. In total, 89 blood-fed mosquitoes were captured, revealing diverse vertebrate hosts. Macaque samples (N=7) were solely obtained during the last month in a densely populated macaque area. Seven human-derived bloodmeals from the same site were screened in parallel. All macaque and five human samples tested positive for Orthoflavivirus IgG. Although preliminary, these results suggest high Orthoflavivirus infection rates at the human-primate interface in Bali, underscoring xenosurveillance's potential for monitoring protected species at the population scale.

Exploring the Antiviral Activity of a Plant-Derived Compound Against Prominent Viruses

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Coronaviruses have circulated in animal reservoirs for decades, but in the past twenty years, several highly pathogenic strains have made the jump to humans with devastating consequences. *SARS-CoV-1* emerged in 2002, followed by *MERS-CoV* in 2012, and most recently *SARS-CoV-2* in 2019, which sparked a global pandemic. These zoonotic spillovers exposed a critical gap: the lack of effective antiviral options, with overwhelmed hospitals and more than seven million lives lost worldwide. To address this challenge, we screened a complex molecule obtained from a *Strychnos* genus against a panel of relevant circulating viruses. The compound showed broad-spectrum antiviral activity against multiple coronaviruses, with no detectable effects on unrelated viral families. We also explored its mechanism of action to better understand its antiviral potential. This unique activity profile opens the door to the development of novel antiviral candidates. Plant-derived compounds remain a largely untapped source of antiviral agents, and this work highlights their promise within a One Health framework, emphasizing strategies that bridge animal and human health to confront future zoonotic threats more effectively.

Comparative efficacy of omeprazole-sucralfate versus misoprostol in the treatment of equine glandular gastric ulcers: a retrospective study (2016–2022)

Alamar Malvoisin C., Amory H., Cesarini C., Poliakoff C., Storm M., Lecoq L.

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Current treatment recommendations for equine squamous gastric ulcers (SU) consider omeprazole (OME) as the drug of choice. In contrast, the approach to glandular gastric ulcers (GU) remains more controversial, as their pathogenesis is still not fully understood. Treatment options include a combination of omeprazole and sucralfate (OMESUCR) or misoprostol (MISO), but to date, only one study has compared their efficacy. This retrospective study aimed to compare the effect of OMESUCR and MISO on GU taking into account their effect on SU in horses. Horses were included if they were diagnosed with GU during the initial gastroscopy and underwent a control gastroscopy 3-6 weeks after initiating one of the treatments. Outcome was categorized as stable, improved, healed, or deteriorated GU and developed or deteriorated SU. Treatment effect was assessed using univariate and multivariate regression analyses, with the horse's breed, age, sex, and treatment duration included as covariates. A total of 139 horses met the inclusion criteria, 38 were treated with MISO and 101 with OMESUCR. No statistically significant difference ($p = 0.78$) in improvement or healing rates of the GU was observed between OMESUCR or MISO treated horses. However, development or deterioration of SU was significantly ($p = 0.025$, OR = 4.55) more frequent in horses treated with MISO (6/38 or 15.8 %) than in horses treated with OMESUCR (4/101 or 4.0%). In conclusion, OMESUCR and MISO appear to have comparable efficacy in the treatment of GU, although MISO may be associated with an increased risk of secondary SU development.

Identified bacteria in the surgical site during the realisation of elective caesarean section in Belgian blue cows

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This study aimed to identify the bacteria contaminating the surgical site (SS) during the realisation of elective caesarean section (ECS).
The first part of the study was conducted on 76 Belgian Blue cows (BBC). Bacteriology was performed on cotton swab sampled from the visceral and parietal peritoneum of each cow during the realisation of ECS. Most of samples showed a negative culture (55/76), 19/76 were positive ($p < 0.0001$) and two were contaminated. In total, 32 isolates belonging to 18 species were identified. Most of them are aerobic (17/18) and half of them were gram-negative (G-). The most encountered bacteria were *Acinetobacter* sp.(6/32), *Pseudomonas* sp.(4/32), *Aerococcus viridans* (4/32), *Psychrobacter* sp. (3/32), and *Escherichia coli* (2/32). Among the identified isolates, 31/32 were aerobic and 1/32 was anaerobic ($p = 0.0001$). Furthermore, 20/32 strains were G- while 12/32 were gram-positive (G+) ($p = 0.012$). Most of cultured strains were aerobic G- (20/32), 11/32 were aerobic G+ and 1/32 was anaerobic G+ ($p < 0.0001$).
In the second part, swabs were taken from the abdominal incision (muscular layers) of 23 BBC during the realisation of ECS. Bacteriology was positive in 6/22 samples, negative in 16/22 ($p = 0.03$) and one was contaminated. All identified bacteria were aerobic and 8/14 isolates were G+ while 6/14 were G- ($p = 0.7$). The most encountered bacteria were *Acinetobacter sp.* (2/14), *Aerococcus viridans (2/14)*, *Neisseria sp.* (2/14). and *Streptococcus sp.* (2/14); other species were isolated only once. The SS of ECS is contaminated by ubiquitous aerobic G+ and G- bacteria coming from the environment while the risk of endogenous contamination is low.

Variation in ODAP content among modern grass pea species: A comparison with an archaeological specimen

Huong T. T. Pham[1], Amira Ali[1], Samiha Boutaleb[1], Annette M. Hansen[2], Frits Heinrich[2,3], Marie-Louise Scippo[1], Caroline Douny[1]

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Grass pea is a nutritious legume known for its resilience to drought, waterlogging, and soil salinity. However, its consumption is restricted in some countries due to the presence of the neurotoxin β-N-oxalyl-L-α,β-diaminopropionic acid (β-ODAP), which can cause lathyrism in humans and animals with prolonged intake. This study examined β-ODAP and α-ODAP content in 161 germplasm accessions from four *Lathyrus* species, namely *L. sativus*, *L. cicera, L. ochrus* and *L. clymenum* originating from over 22 countries, along with one archaeological *L. sativus* specimen from Greco-Roman Egypt. A liquid chromatography–tandem mass spectrometry (LC-MS/MS) method was modified and validated before being applied to quantify β-ODAP and α-ODAP. The results showed that *L. clymenum* had the highest average β-ODAP content (10502 mg/kg), followed by *L. ochrus* (8833 mg/kg), while *L. sativus* and *L. cicera* had lower levels, at 2975 mg/kg and 1366 mg/kg, respectively. α-ODAP levels ranged from 159 to 1397 mg/kg, about 3 to 24 times lower than the β-ODAP content, with no significant variation among the four species. The ancient grass pea had a remarkably low β-ODAP content (112 mg/kg), and its α-ODAP level was below the quantification limit. These findings point to variability in toxin content among modern *Lathyrus* species and suggest that historical accessions may have contained lower levels of these compounds.

Dynamics of hepatitis E virus infection in Belgian pig farms: longitudinal study from birth to slaughter, modelling and evaluation of some zoonotic risk mitigation measures

Wielick C.[1,2], Ludwig-Begall L.F.[2], Dams L.[2], Vandersmissen T.[3], Ribbens S.[3], Faes C[4], Salines M.[5], Andraud M.[5], Thiry E.[2,*], Durand B.[6,*], Saegerman C.[1,*]

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Hepatitis E viruses (HEV) are responsible for hepatitis E in humans. In developed countries, sporadic infections, typically associated with HEV genotypes 3 or 4, are generally asymptomatic. However, the infection can become chronic and may lead to liver cirrhosis in immunocompromised individuals. Pigs serve as asymptomatic carriers of these same HEV genotypes, making them a key animal reservoir for zoonotic transmission. The presence of HEV particles in pigs at the time of slaughter suggests that raw or undercooked pork products could pose a risk of infection to humans. To improve the current understanding of HEV spread within the Belgian pig population, an in-depth and systematic virological screening was conducted as part of a comparative, longitudinal study involving one batch from thirteen pig farms. Based on these data, two epidemiological MSEIR models (Maternally immune-Susceptible-Exposed-Infected-Recovered) representing conventional and unconventional farm systems were developed to describe HEV within-farm dynamics using the R package SimInf (for stochastic infection simulation). The models included farm demography, animal movements and changes in infection status over time. Both direct contact and environmental transmission routes were considered, as well as potential co-infection with immunomodulating viruses (IMVs) known to influence HEV infection dynamics. Different scenarios were tested to evaluate possible mitigation measures aimed at reducing the risk of sending HEV-positive pigs to slaughter. These outcomes could help design HEV control strategies at the farm level and prevent its zoonotic transmission, either through occupational exposure of slaughterhouse workers or consumption of contaminated pork products.

Prevalence of tachypnea and/or acute respiratory distress following packed red blood cell transfusion in cats and association with survival.

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Respiratory complications are the leading cause of mortality in human transfusion medicine. Acute respiratory distress (ARD) and transfusion-associated volume overload (TAVO) have been reported in cats, but risk factors and predisposing conditions are poorly defined. The study aimed to determine the prevalence, risk factors, and 24-hour survival impact of ARD and TAVO in transfused cats.
This cross-sectional retrospective study included cats that received a packed red blood cell (pRBC) transfusion between January 2020 and February 2025. ARD was defined as the development of tachypnoea and/or dyspnea within 24-hours after transfusion. Cats were subsequently subdivided into TAVO, transfusion related acute lung injury (TRALI) or undetermined origin.
Comparison and association between groups were tested using Mann-Withney U test and chi-square test, respectively, significance was set at $p<0.05$.
A total of 352 transfusions on 264 cats were included. ARD occurred in 15% of transfusions, with TAVO accounting for 10.8%, TRALI for 0.3%, and undetermined ARD for 4%. Older cats were significantly more likely to develop TAVO ($p<0,023$). ARD cats had lower heart rate and body temperature before transfusion ($p<0,013$). Gallop rhythm, enlarged left atrium and furosemide administration prior to transfusion were more frequent in ARD cats ($p<0,003$). Twenty-four hours survival was negatively impacted by ARD ($p<0.001$), whereas TAVO did not affect 24-hour survival.
ARD and TAVO occurred relatively frequently in cats receiving pRBC-transfusions. Lower heart rate, temperature and increased LA/Ao ratio were risk factors for ARD. ARD, but not TAVO was negatively associated with 24-hour survival.

Validation of a photoplethysmography sensor for measuring heart rate in dogs during exercise.

Grandjean D.[1], Art T.[1], Tosi I.[1]

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Heart rate (HR) is an essential indicator of exercise intensity, training efficiency and physical condition in any athlete, human or animal. Electrocardiography (ECG) remains the gold standard to assess HR, but it is expensive, requires extensive clipping and electrodes may come off during exercise. Moreover, obtaining an ECG in dogs is challenging, due to their smaller body size, skin movement and panting. Photoplethysmographic sensors detect HR via variations in blood perfusion through light reflection. They are cost-effective, easy to install and to use, reusable and require minimal clipping. We compared data obtained by a photoplethysmographic sensor (DECATHLON® HRM band) to those obtained by a gold-standard telemetric device (TELEVET) on 8 healthy and fit dogs (3.4 ± 1.5 y.o.) using Pearson's correlation, Bland-Altman and t-tests as statistical analyses. Dogs performed a graded exercise test of 28 minutes on a treadmill, followed by a recovery period. The photoplethysmographic sensor was placed on the ventral aspect of the tail and the ECG on the thorax (base-apex configuration). We observed a significant correlation ($r=0.844$; $p<0.001$) between the two systems. The t-test revealed no significant differences between the two data sets. Bland-Altman analysis indicated that the photoplethysmographic sensor slighty underestimates HR compared to ECG, particularly during exercise. All dogs tolerated sensors, with only minor skin irritation due to clipping and ECG electrodes. In conclusion, the photoplethysmographic sensor is a practical, reliable, and well-tolerated tool for assessing HR in dogs during exercise, an alternative to ECG that may be used in field trials.

Study of the importance of tegument proteins pORF45 in the biology of gammaherpesvirus infection.

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Gammaherpesviruses (γHVs) are widespread pathogens that establish lifelong infections in a wide range of mammalian hosts, often associated with significant disease burdens. In humans, Kaposi's sarcoma-associated herpesvirus (KSHV) is linked to several malignancies, making it an important subject of study. Tegument proteins are key regulators of the γHV lifecycle. In particular, the KSHV tegument protein pORF45 has been implicated in immune evasion through interactions with innate immune signaling components, including ERK and RSK kinases pathways commonly exploited by many pathogens. However, KSHV research is hindered by its restricted replication *in vitro* and the lack of a suitable animal model. To address these limitations, we used Murid herpesvirus 4 (MuHV-4), a close relative of KSHV, as a model to investigate ORF45 function in the γHV lifecycle. Using co-immunoprecipitation assays, we identified the specific domains mediating interactions between pORF45 and the RSK and ERK proteins. To assess the biological relevance of these interactions, we generated MuHV-4 mutant strains bearing targeted disruptions in these domains and evaluated their effects on viral replication both *in vitro* and *in vivo*. Collectively, our findings provide new insights into the molecular mechanisms by which ORF45 contributes to γHV biology and may help clarify its role in the pathogenesis of KSHV and related viruses.

Nanopore sequencing of high-risk HPV via amplicon and rolling circle amplification points to HPV integration and new HPV types

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Human papillomavirus (HPV), the most widespread sexually transmitted infection worldwide, causing a number of cancers, including cervical cancer, the fourth leading cause of cancer-related death in women. Despite the role out of the effective vaccines against some high-risk HPVs and screening efforts in high income countries, access remains limited in low-resource countries, where the majority of deaths due to this oncogenic virus occur. Building on our genomic surveillance work during the SARS-CoV-2 pandemic, we developed two complementary, low-cost, nanopore-based approaches (amplicon and rolling circle amplification) to amplify and sequence HPV genomes. Both approaches were applied to 191 HPV-positive leftover cervical smear samples collected in the DRC and Liège, generating 232 complete and 117 partial HPV genomes. We developed a bioinformatics tool capable of classifying HPV variants down to the sublineage level to facilitate the identification of higher-risk sublineages and to improve HPV genomic surveillance. In addition to known HPV types, we identified eight novel HPVs (>10% divergence in L1) and explored their oncogenic potential via AlphaFold modelling of key viral oncogenic proteins. Finally, by comparing results from both sequencing approaches, we identified five cases where HPV had integrated into host genomes. In one case, integration occurred in a known cancer driver gene. As HPV integration is found in the vast majority of cervical cancers, early identification of such integrations could serve as a useful biomarker.

Videotracking identifies acute and chronic neurological and behavioral deficits in murine models of West Nile Virus infection.

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In 2025, over 650 human cases of West Nile virus (WNV) infection have been reported in Europe. Primarily transmitted by mosquitoes, WNV is the most widely distributed Orthoflavivirus worldwide and is capable of causing severe neuroinvasive disease. Beyond this acute, potentially fatal presentation, WNV infection has been associated with long-term neurological sequelae, including motor impairments and cognitive deficits persisting months to years after infection. To investigate neurological and behavioral alterations during both the acute and chronic phases of infection, we established a murine model of WNV disease using cutaneous inoculation in C57Bl/6 mice, thereby mimicking natural transmission by mosquito bite. Animals were monitored daily post-infection through visual neurological scoring and unsupervised videotracking for 15 consecutive days. Preliminary analyses revealed a strong correlation between the two approaches, with infected mice exhibiting ataxia, reduced locomotor activity, decreased velocity, and impaired social, feeding, and drinking behaviors. Mice surviving the acute phase were reassessed at 30 days post-infection by 24-hour videotracking. Notably, despite the absence of overt clinical signs, recovered animals consistently displayed marked reductions in locomotor parameters and characteristic behavioral abnormalities. These findings identify key neurological and behavioral manifestations of WNV infection during both acute illness and recovery. Moreover, the application of unsupervised videotracking provides a robust and sensitive tool for the clinical assessment of experimental models of viral encephalitis. Future studies are warranted to elucidate the relationship between WNV tropism within the central nervous system and the observed phenotypes, as well as to clarify the pathogenic mechanisms underlying long-term sequelae, whether attributable to acute-phase tissue damage or to persistent neuroinflammation with or without viral persistence.

Unveiling the Nutritional Changes in Carbap K74 Plantain Hybrid Flours: A Focus on Processing Effects

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This study evaluated the effects of blanching (85 °C, 5 min) and precooking (100 °C, 15 min) on antioxidant, nutritional (polyphenols, flavonoids, minerals), and microbiological properties of pulp and whole fruit flours from the Carbap k74 plantain hybrid at three ripening stages, including commercial flours. Polyphenol (0.17–4.2 mg GAE/g), flavonoid (0.04–1.6 mg QE/g) contents, and antioxidant activities (DPPH EC_{50}: 27.8–1682.7 µg/ml; FRAP 98.8-128 mmol $FeSO4/g$) varied significantly by treatment, matrix, and maturity. In general, whole fruit flours showed higher levels of minerals such as K, Mg, Ca, and Zn, whereas Fe and Cu were more concentrated in pulp-based flours. Microbial loads were highest in unwashed whole fruits (up to 4.41 log CFU/g) but significantly reduced after washing and thermal processing. Commercial flours generally exhibit higher levels of total aerobic mesophilic flora (up to 4.33 log CFU/g), fungal flora (up to 4.42 log CFU/g) and Staphylococci (4,40 log CFU/g). Enterobacteria are markedly reduced by thermal treatments, as is E. coli, and sulfite-reducing bacteria are generally absent except in one commercial sample. PCA and HCA showed that advanced ripening and whole fruit use improved nutritional quality. Whole fruit flours and ripening stages 3 and 5 enhance the nutritional value of Carbap K74 plantain flours, while strict drying and hygiene are key to ensuring microbial safety.

A journey towards the discovery of Cyvirus cyprinidallo 3 ORF57 functions

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Cyvirus cyprinidallo 3 (CyHV-3) is a major viral pathogen of common and koi carp. The host laboratory previously developed a live attenuated recombinant vaccine based on the deletion of CyHV-3 ORF56 and ORF57. While this double-deleted strain exhibited strong attenuation *in vivo*, it also displayed a reduced production of infectious virions in cell culture. Recent analyses revealed that this phenotype originates primarily from ORF57 deletion. Despite similar quantities of virus particles released by ORF57-deleted and wild-type viruses, the former exhibited lower infectivity, indicating that ORF57 is required for producing fully infectious virions. Proteomic analysis of purified particles confirmed that ORF57 is a major tegument component and highlighted the concomitant loss of ORF34 in ORF57-deficient virions, suggesting a potential interaction between these proteins. Electron microscopy showed no ultrastructural differences between ORF57 deleted and wild-type particles, implying that infectivity loss is not due to gross morphological defects. Together, these data indicated that ORF57, directly or through ORF34, likely contributes to viral entry or early post-entry events. To address this hypothesis, we initiated two complementary approaches: (1) generation of polyclonal sera against purified CyHV-3 capsids to visualize virion entry, and (2) construction of recombinant CyHV-3 strains expressing EGFP-tagged capsid proteins to study early infection steps. This work provides the basis for a deeper understanding of CyHV-3 entry mechanisms and the contribution of tegument proteins to the early stages of infection.

Forage protein strategies for sustainable organic egg production in Wallonia in relation to the microbiota of hens

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Organic poultry farming in Belgium faces significant challenges, particularly a strong dependence on imported soybean byproducts. These constraints increase production costs and reduce farm autonomy. The F2P project, funded by the Fédération Wallonie-Bruxelles, explores locally produced forages as a nutrients source for laying hens. The research focuses on legumes, such as alfalfa and red clover, for their high protein content as well as their potential role in supplying vitamins and dietary fiber. The trial was conducted with 100 Novogen Brown hens allocated to two groups of 50. One group received a standard industrial control diet, while the other was fed with a test diet in which 20% of the ration was replaced with ensiled clover. Both diets were designed to be iso-nitrogenous and iso-energetic. The experiment followed a two-period cross-over design (two months per period), separated by a 10-day transition phase, to assess zootechnical performances, egg quality and microbiota modulation. The test diet improved yolk pigmentation and the Haugh index, traits valued by consumers, without affecting laying rate or egg quality parameters. However, hens receiving clover showed reduced body weight. Microbiota analyses revealed a higher abundance of *Lactobacillus* - a genus associated with improved gut health - in clover-fed hens and a greater presence of *Saccharomyces*, a yeast genus known for its positive role in digestion and intestinal balance. Overall, the results highlight the potential of clover-based diets for sustainable organic egg production.

Effect of deep-frying and air-frying on fatty acid profile and lipid oxidation of common carp (*Cyprinus carpio*)

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Freshwater fish and marine fish are considered healthy food in the human diet due to their high protein content, micronutrients, and essential fatty acids, particularly high concentrations of n-3 long-chain polyunsaturated fatty acids (LC-PUFAs), such as eicosapentaenoic acid (EPA, 20:5n-3), and docosahexaenoic acids (DHA, 22:6n-3). However, the LC-PUFAs in fish are the most sensitive to oxidation and can be subjected to degradation during cooking, notably during deep-frying. Nowadays, air-frying is more and more used as an alternative frying technique, which provides the same characteristics of a fried product. Frying is performed without the incorporation of oil, by forced convection of heated air. However, it is known how this cooking process will affect the fatty acid profiles and oxidation products formation. Therefore, this research aimed to compare fatty acid content and fatty acid oxidation products, including peroxide value (PV), p-Anisidine (p-AnV), and thiobarbituric acid reactive substances (TBARS), in deep-fried and air-fried common carp (*Cyprinus carpio*). The fatty acid profile (expressed in percentage of total fatty acids) in raw fish showed SFA, MUFA, and PUFA proportions of 32.2, 35.6, and 32.3%, respectively, while in deep-fried fish, it was 19.7 % SFA, 26.9 % MUFA, and 53.4 % PUFA. In air-fried fish, these percentages were 25.1 %, 37.4% and 37.5 %, respectively. About fatty acids oxidation products, deep-frying showed PV, p-AnV, and TBARS values of 5.86 $\pm$0.16 milliEq.O_2/Kg fat, 1.25 $\pm$0.32, and 2.64$\pm$0.32 μmol/g, respectively, while air-fried fish displayed PV, p-AnV, and TBARS values of 2.80 $\pm$0.0 milliEq.O_2/Kg fat, 0.42 $\pm$0.13, and 6.44 $\pm$0.46 μmol/g, respectively. So, in deep-fried, PV and p-AnV are higher than in air-fried, but TBARS is higher in air-fried. According to TBARS results, which are significantly lower in deep-fried fish than in air-fried fish, it seems that fat was protected from oxidation when the fish was cooked in frying oil. This could be due to the presence of antioxidants in oil during the frying process prevents fish fat from directly oxidizing. Furthermore, PUFAs increased, maybe due to the penetration of soybean oil into fried fish. This aspect will be investigated further in future experiments.

Is ORF112 of the *Cyvirus cyprinadallo* 3 essential or not essential ?

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Zα domains are helix–turn–helix motifs capable of specifically binding to DNA and RNA in the Z conformation. They are found in certain innate immune proteins as well as in three large double-stranded DNA viruses, where they participate in immune evasion mechanisms. Among these viral proteins, CyHV-3 ORF112 (encoded by *Cyvirus cyprinidallo* 3) has recently been identified as possessing three major properties: Z-binding ability, conversion of B-DNA to Z-DNA, and induction of liquid–liquid phase separation (LLPS). Unlike its homologs in vaccinia virus and African swine fever virus, ORF112 is essential for viral replication in cell culture. However, this conclusion was based on a limited number of observations of cells showing abortive infection in the absence of ORF112. The objective of this study was therefore to develop experimental models enabling the generation of a large number of such cells, in order to better understand ORF112 functions. Two complementary strategies were implemented. The first consisted of producing a recombinant CyHV-3 strain expressing a EGFP reporter cassette and a mCherry-ORF112 gene flanked by LoxP sites. Notably, infection of CCB cells previously transfected with mRNA encoding Cre recombinase resulted in the early death of infected cells positive only for green fluorescence. The second approach relied on generating stable CCB cell lines using a transposon–recombinase system. Two cells line was produced, expressing either Cre recombinase or mCherry–ORF112. Selection of the Cre line is ongoing and will enable the specific deletion of ORF112 in the recombinant virus encoding a mCherry-ORF112 gene flanked by LoxP sites, whereas the mCherry–ORF112 line will be used to propagate a CyHV-3 ΔORF112 virus. The virions produced in this trans-complementation system will be used to inoculate wild-type CCB cells. Together, these tools pave the way for an in-depth investigation of ORF112 functions in the biology of CyHV-3.

The role of gammaherpesvirus in shaping IBD-associated immune profiles: insights from advanced immunophenotyping in murine and translational models

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Inflammatory bowel diseases (IBDs) are chronic inflammatory disorders with rising global incidence. Beyond genetics and microbiota changes, persistent viral infections, especially Epstein-Barr virus (EBV), are emerging as potential risk factors. Studies increasingly associate EBV with IBD onset or severity, though mechanistic proof remains limited due to its ubiquity and confounding variables. Using *Murid gammaherpesvirus* 4 (MuHV-4) as an EBV-relevant model, we show that infection induces long-lasting systemic expansion of effector-memory $CD8^+$ T cells with enhanced cytotoxicity. These cells infiltrate the colonic lamina propria independently of major microbiota changes. In experimental colitis models, MuHV-4–infected mice accumulate large numbers of activated, proliferative, cytotoxic $CD8^+$ T cells (Sca-1, Ly6C, KLRG1, CD11c, Ki-67, IFNγ, T-bet, granzyme B), alongside CXCL9-producing monocytes that likely drive recruitment and polarization. While this signature does not worsen symptoms in wild-type mice, it causes severe inflammation in IL-10–deficient mice, indicating that, without key regulatory pathways, gammaherpesvirus infection promotes T-cell–driven intestinal pathology. EBV-infected humanized mice and immunophenotyping of an IBD patient cohort similarly reveal expanded, activated, tissue-infiltrating $CD8^+$ T cells linked to disease severity. Overall, persistent γHV infection drives systemic and mucosal immune remodeling by pre-arming cytotoxic $CD8^+$ T cells, offering mechanistic insight into IBD heterogeneity and potential personalized therapeutic targets.

Mitigation and adaptation plans : A review of Climate Smart Solutions chosen by Belgian pilot farms taking part in the EU project Climate Farm Demo

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The European Climate Farm Demo project aims to build a network of 1,500 pilot farms (PDFs) across 28 EU countries, committed to climate transition and adopting more sustainable practices. An initial environmental audit helps define an Adaptation and Mitigation Plan (AMP) with the farmer to reduce climate impact. In Belgium, 56 farms were recruited (28 in Wallonia, 28 in Flanders). Only livestock farms were included in this study: dairy (60%), beef (26%), small ruminants (12%) and pigs (2%). Farmers choose from 276 practices grouped into seven categories: herd management, feeding management, energy, soil management, grazing management, and agroforestry to build their AMP. The goal of this study is to list existing practices (set_1) and those planned in the AMP (set_2), to identify key areas of interest, improve monitoring, and expand AMP actions. Two hypotheses were tested: (1) the same categories are selected in set_1 and set_2; (2) some categories are more frequently chosen in set_2. The χ^2 test yielded a p-value of 0.08, indicating a trend toward significance. This tendency is mainly driven by the overrepresentation of the category "soil management" lever in set_2 (30 choices vs 10 in set_1). Fisher's exact test performed on set_2 confirmed this interest ($p < 0.01$). Some farms selected similar practices in both sets, especially for the category "energy". Production type (dairy or beef) had no influence. The most popular measures were installing solar panels from the category "energy" ($n = 11$) and reducing mineral fertilisers ($n = 8$) from the category "soil management".

Effect of different viral infections on the development of experimental autoimmune encephalomyelytis in mice

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Multiple sclerosis (MS) is a complex autoimmune disease affecting over 2.8 million people worldwide, with onset predominantly in young adult women. Its multifactorial etiology involves both genetic predisposition and environmental factors. Epstein–Barr virus (EBV), one of the most prevalent human pathogens (>90% seropositivity), has emerged as a strong candidate risk factor. A recent 20-year longitudinal study of 10 million U.S. army personnel reported a 32-fold increased risk of developing MS in EBV-seroconverted individuals. Experimentally, infection with Murid Herpesvirus-4 (MuHV-4, the murine EBV homolog) exacerbates experimental autoimmune encephalomyelitis (EAE), a mouse model of MS. Whether this effect is specific to MuHV-4 or shared with other viral infections remains unclear. C57BL/6 mice were infected with MuHV-4, Influenza A/Puerto Rico/8/1934 (H1N1, PR8), murine cytomegalovirus (MCMV), or left uninfected (mock). Neuroinflammation and circulating leukocyte profiles were then characterized by spectral flow cytometry after EAE induction. Then, to assess whether infection-specific neuroinflammation also translated into behavioral changes, EAE was induced in MuHV-4-infected or mock-treated mice, and behavior was continuously monitored using the Noldus EthoVision Phenotyper over a period two weeks. MuHV-4-infected EAE mice displayed distinct immunological alterations compared to all other groups, characterized by increased activation of T lymphocytes and myeloid cells, together with reduced frequencies of regulatory T cells. These changes were not detected following PR8 or MCMV infection, underscoring the specificity of the MuHV-4-driven effect on neuroinflammation. Then, behavioral monitoring revealed significant alterations in feeding and drinking patterns in MuHV-4-infected EAE mice compared to mock-infected controls although most other parameters were similar. MuHV-4 infection uniquely aggravates neuroinflammation and alters immune cell dynamics in EAE, reinforcing the link between EBV and MS risk. In addition, automated behavioral tracking uncovered previously unrecognized phenotypic differences, highlighting the importance of infection history in shaping both immune and behavioral outcomes of CNS autoimmunity.

Modulation of effector memory T lymphocyte responses to vaccination by helminth infections

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Gastrointestinal helminth infections are a recurring issue in our pets and livestock, impacting viral coinfection and vaccination responses. Whereas most vaccines against viral diseases are designed to induce neutralizing antibodies, the humoral response is in general not sufficient to provide long term protection. However, eliciting an appropriate T cell-mediated response is important for long-lasting immunity. Modulation of the T cell mediated immune response could explain a lower efficacy of vaccination during parasitic worm infection.
We used *Heligmosomoides polygyrus* (Hp) and a recombinant Vesicular Stomatitis virus (rVSV) vector as experimental mouse models to investigate how persistent helminth infection affects the establishment of effective memory T responses to vaccination. Mice were infected with Hp before intramuscular vaccination with rVSV-GP-OVA expressing the glycoprotein GP1 of LCMV and chicken ovalbumin. In addition, to investigate the antigen-specific response to vaccination, a recombinant strain of the murid gammaherpesvirus 4 expressing the ovalbumin antigenic peptide (MuHV-4-OVA) was used to recall the OVA-specific memory $CD8^+$ T cells.
A significant systemic reduction in the number of total $CD8^+$ T cells and antigen-specific $CD8^+$ T cells was observed after helminth infection. In addition, a respiratory challenge of vaccinated mice with a Murid gammaherpesvirus 4 (MuHV-4) strain expressing the same antigenic ovalbumin peptide revealed a less effective recall of specific memory $CD8^+$ T lymphocytes in mice infected with Hp. The mechanisms remain to be investigated to understand how parasitic infection modulate the efficacy of vaccination.

Evaluation of different right heart echocardiographic parameters for the diagnosis of precapillary pulmonary hypertension in dogs with chronic respiratory disorders: a prospective study.

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Pulmonary hypertension is a frequent complication of canine respiratory diseases, worsening clinical signs and prognosis. Echocardiography is the preferred non-invasive method for estimating the probability of pulmonary hypertension, as described in the American College of Veterinary Internal Medicine consensus statement. This prospective, cross-sectional, double-blind study evaluated the diagnostic performance of previously published cut-off values for single echocardiographic parameters in identifying an intermediate-to-high probability of pulmonary hypertension in at-risk dogs. Client-owned dogs with chronic lower respiratory diseases underwent complete Doppler echocardiography. The probability of pulmonary hypertension was classified as low (unaffected) or intermediate/high (affected). Dogs with left atrial enlargement were excluded. Echocardiographic measurements, performed by a blinded operator, included: right ventricular size and function, septal geometry, pulmonary artery morphology and flow, and right atrial size. Receiver operating characteristic curve analysis was used to evaluate diagnostic performance. In this population, four parameters showed acceptable diagnostic ability for the detection of pulmonary hypertension: right ventricular wall hypertrophy, pulmonary vein-to-artery ratio, pulmonary flow acceleration time, and the ratio of pulmonary flow acceleration time to ejection time. No parameter demonstrated excellent discriminative ability. Combining several echocardiographic variables may improve the accuracy of pulmonary hypertension diagnosis in dogs with chronic respiratory disease.

IL-4 receptor signaling regulates lung macrophages during helminth coinfection resulting in enhanced gammaherpesvirus permissiveness

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Viral infections are often studied in pathogen-free settings, yet in regions where helminth infections are endemic, host susceptibility and viral control can be can profoundly altered. To investigate this interaction, we examined murid gammaherpesvirus 4 (MuHV-4) infection in helminth-coinfected C57BL/6 mice, where viral replication in the lungs was markedly enhanced. MuHV-4 has a natural tropism for alveolar macrophages (AlvMs) in vivo, and we observed an increased permissiveness restricted to AlvMs and monocyte-derived macrophages after helminth infection. Phenotypic changes in lung macrophages, after helminth exposure, consisted of an Il4ra signalling dependent disappearance of SiglecF+ macrophages and concomitant enrichment of CD11b+ macrophages of monocytic origin, in the lung. Using single-cell RNA sequencing and flow cytometry, we demonstrated that after helminth infection, lung macrophages upregulated proteoglycans known to be decorated with heparan sulfates, potentially improving virion attachment. We further observed a dampened type-I interferon stimulated gene signature in mice coinfected with helminths and MuHV-4. Finally, we found that airway macrophages isolated from helminth-infected C57BL/6 mice were more permissive to low doses of MuHV-4 infection ex vivo and that IL-4 and IL-13 could potentiate macrophages susceptibility to MuHV-4 infection. In conclusion, we propose that helminth infection causes phenotypical and functional IL-4Rα-dependent restructuration of the airway and lung macrophages, significantly increasing their permissiveness to gammaherpesvirus coinfection.

The smartest, the fastest, and the highest-flying: a pigeon's (*Columba livia*) perspective on La Fontaine's 'The Hare and the Tortoise' fable.

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Pigeon racing applies selective breeding to favor athletic performance and navigational ability in pigeons (*Columba livia*). Although orientation performance long fascinated breeders and researchers, its estimation remained limited. In the 1980s–1990s, it relied on visual observation at release sites, with orientation inferred from the angle between disappearance and the loft, providing no information between departure and arrival. Miniaturized GPS loggers now allow precise monitoring of speed, altitude, and route efficiency. Three releases of ten pigeons were analyzed using Spearman's rank correlation (ρ) to assess links between arrival order, distance ratio (straight-line vs actual distance), real flight speed, and altitude. In Release 1, arrival order correlated with ratio (ρ=0.96, $p<0.001$), and speed with altitude (ρ=0.82, p=0.004). In Release 2, arrival order was linked to ratio (ρ=0.90, $p<0.001$) and speed (ρ=−0.93, $p<0.001$), while ratio correlated negatively with speed (ρ=−0.76, p=0.011). In Release 3, arrival order and ratio were perfectly correlated (ρ=1.00, $p<0.001$); other links were not significant. Wilcoxon tests comparing Releases 1 and 3 from the same site showed lower ratios (p=0.016) and higher speeds (p=0.047) in Release 3, with no altitude difference (p=0.078), indicating improved athletic and navigational performances. Arrival ranks were poorly conserved across races. Route efficiency consistently emerged as the strongest predictor, suggesting that navigational efficiency is the main determinant of arrival order and highlighting the value of GPS-based monitoring for avian navigation research.

Posters

Sustainable livestock production

1. Rosemary Essential Oil as a Natural Eggshell Disinfectant: Effects on Bacterial Load, Hatchability, and Oxidative Stress in Japanese Quail (*Coturnix Coturnix Japonica*).

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Microbial contamination of hatching eggs remains a major challenge in poultry production. Bacterial and fungal infections reduce embryonic and hatching performance, and impair chick survival mainly through septicemia and oxidative imbalance. Egg disinfection before incubation has attracted global interest, particularly as natural alternatives to conventional disinfectants are increasingly investigated. Conventional agents often show embryo toxicity and increase oxidative stress by generating excess reactive oxygen species in vital organs. Therefore, this study evaluated the potential of rosemary essential oil (REO) as a natural disinfectant for eggshells and its impact on hatching success. A total of 225 Japanese quail eggs were divided into four groups: a negative control (non-disinfected), two positive controls (alcohol or 10% quaternary ammonium), and a group disinfected with REO at concentration of 10 µL/mL. Eggshell surfaces were swabbed, and bacterial load (cfu/mL) was quantified by agar plate counting, while hatchability, chick weight, and oxidative stress markers were assessed. Lipid peroxidation and antioxidant capacity were determined by TBARS, and ABTS assays, respectively, in liver and intestine samples. Results showed that REO significantly reduced bacterial loads (p=0.0001) and improved hatchability. Chicks from this group exhibited higher body weights and stronger antioxidant defenses, with lower TBARS and higher ABTS values. In conclusion, REO at 10 µL/mL represents a promising, safe, and natural eggshell disinfectant. Its application not only improved hatchability and chick growth but also preserved oxidative balance, supporting its potential use in commercial poultry production.

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2. Effects of Probiotic, Prebiotic, and Synbiotic Supplementation during the Transition Period on Milk Quality in Montbeliarde Dairy Cows

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Dairy farming plays a key role in Algerian agriculture, contributing to food security. Its success relies on proper management and the optimization of dairy cow health and productivity, particularly during the transition period. Feed additives such as probiotics and prebiotics are increasingly recognized for improving animal performance and milk composition. In this study, forty Montbeliarde cows (5 primiparous, 35 multiparous) were assigned from 30 days prepartum to 60 days postpartum into four groups (n = 10): a control group (CNT) without supplementation, a probiotic group (SC) receiving 5 g/day/cow of *Saccharomyces cerevisiae*, a prebiotic group (PL) receiving 5 g/day/cow of yeast cell wall fractions, and a synbiotic group (MIX) receiving both. Milk yield and composition were measured on days 15, 45, and 60 postpartum and analyzed using IBM SPSS v22.Significant differences were observed between the control and SC groups in milk fat at day 15 (p = 0.035) and day 45 (p = 0.01), and similar results appeared for the PL group. No difference was detected between the control and MIX groups. For milk proteins and lactose, highly significant differences occurred between the control and MIX groups at all sampling points (proteins: day 15 p = 0.002, day 45 p = 0.000, day 60 p = 0.000; lactose: day 15 p = 0.043, day 45 p = 0.01, day 60 p = 0.003). Overall, supplementation influenced milk composition differently. SC and PL improved fat content, while MIX showed stronger effects on protein and lactose. These results suggest that combined probiotic–prebiotic supplementation enhances milk's nutritional quality, particularly its protein and carbohydrate fractions.

3. Influence of Breeding and Selection Practices on the Performance of Working Dogs: A Preliminary Study in Algeria

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Working dogs play a crucial role in various fields, including security, public health, and animal production, particularly in detection, search and rescue, and protection tasks. In Algeria, the growing demand for high-performing working dogs highlights the need to better understand the impact of breeding and selection practices on their functional abilities.

This preliminary study aims to analyze the relationships between breeding methods, selection criteria, and the behavioral and physical performance of working dogs from different institutions (security forces, civil protection, private breeders). Collected data include zootechnical parameters, pedigree information, and performance results from work aptitude tests (obedience, endurance, olfaction, reactivity).

A descriptive and analytical approach will be used to identify the breeding factors influencing training success and behavioral stability. Initial results are expected to reveal significant variability associated with the choice of breeders, rearing environment, and socialization practices.

This study paves the way for the development of a national evidence-based selection program, integrating both genetic and behavioral criteria, with the aim of sustainably improving the performance and utilization of working dogs in Algeria.

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4. Comparative analysis of prolactin levels and their influence on milk production in local and improved dairy cow breeds

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The present study aims to examine prolactin levels in dairy cows, focusing on both improved and local breeds. More specifically, it seeks to evaluate how serum prolactin concentration influences milk production in terms of both quantity and quality. Additionally, the analysis of blood biochemical parameters was conducted to assess the overall health status of the animals. Prolactin is a multifunctional hormone that affects various physiological aspects in ruminants, including lactation, reproduction, metabolism, and thermoregulation. To investigate its impact on milk production, blood samples were collected and analyzed for serum prolactin levels. The study involved cows from the Prim'Holstein breed and local Algerian breeds. Physicochemical parameters of milk were also assessed to determine its quality. The results revealed that improved breeds exhibited higher prolactin levels compared to local breeds, with respective values of 49 ng/ml (early lactation), 61 ng/ml (mid-lactation), and 55 ng/ml (late lactation), versus 46 ng/ml, 52 ng/ml, and 44 ng/ml for local breeds. Biochemical analyses indicated that both groups were in good health. However, milk quality was superior in local breeds, while improved breeds produced a greater volume of milk. In conclusion, prolactin (PRL) levels appear to have a modest influence on milk yield, but not significantly on milk quality.

5. Impact of Partial Substitution of Prickly Pear *(Opuntia ficus-indica L.)* Seed Meal on Blood Biochemical Profile and Intestinal Microbiota of Arbor Acres Plus Broiler Chickens

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The objective of this study was to evaluate the effect of partially substituting commercial broiler feed with defatted prickly pear (*Opuntia ficus-indica L.*) seed cake (PPO), obtained after 81% oil extraction. A total of 150 one-day-old Arbor Acres broiler chicks were randomly assigned to five dietary groups, each with three replicates of 10 birds. The experimental groups received diets containing PPO at 0% (control), 10%, 20%, 30%, and 40% inclusion levels for a period of six weeks, divided into four feeding phases corresponding to four diet formulations. At the end of the trial, five birds from each replicate were randomly selected and slaughtered following a 12-hour feed withdrawal. The aim was to assess the impact of PPO seed cake inclusion on serum biochemical parameters and intestinal microbiota composition. Serum and cecal samples were collected for biochemical analysis and PCR-based microbial profiling. Results indicated that PPO dietary treatments significantly ($P<0.05$) reduced serum concentrations of glucose, total protein, total cholesterol, and overall lipid levels compared to the control group. A significant decrease ($P<0.05$) in hepatic enzymatic activity was also observed in PPO-treated groups. Furthermore, electrolyte analysis revealed a significant reduction ($P<0.05$) in serum levels of magnesium (Mg), phosphorus (P), and calcium (Ca) in PPO-fed birds relative to controls. Microbiota analysis at the phylum level showed that Firmicutes and Bacteroidetes were the dominant microbial groups in the intestines of broilers fed PPO-based diets. In conclusion, the inclusion of defatted prickly pear seed cake may exert protective effects on renal and hepatic functions in broiler chickens. Additionally, PPO supplementation was associated with increased diversity in both phylum and genus composition of the intestinal Microbiota.

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6. Cross-sectional and histopathological study of Eimeriosis in camels (Camelus dromedarius), Algeria

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Coccidiosis in dromedaries is an intestinal protozoan infection caused by apicomplexan parasites belonging to the genus *Eimeria*. A prospective examination was conducted at two slaughterhouses in southern Algeria. The primary objective of this investigation was to ascertain the prevalence of intestinal parasites in camels, elucidate the associated microscopic lesions, and identify the risk factors contributing to this infestation. In pursuit of this, we procured four segments of the intestines from 31 dromedarieas that appeared healthy and displayed no symptoms. Subsequently, these samples were collected, preserved, subjected to routine processing, and subsequently stained with haematoxylin and eosin (H&E). Intestinal parasitic infection showed an incidence rate of 45.16% (14 out of 31). Specifcally, two types of parasites were discerned in the intestinal specimens through microscopic examination, namely *Eimeria* (41.93%; 13 out of 31) (p-value = 0.046) and Taenia (3.22%; 1 out of 31) (p = 0.001). Eimeria cameli was observed in the ceacum (41.93%; 13 out of 31), jejunum (12.90%; 4 out of 31), and in one instance in the duodenum (3.22%; 1 out of 31). Furthermore, numerous development stages of coccidia were identifed, including gamonts, schizonts and oocysts. Deep microscopic lesions attributed to *Eimeria cameli* were detected, such as enteritis, eosinophilic infltration and inflammation. In addition, associated risk factors were identifed. Tis study has furnished valuable insights into parasitic infestations aﬀecting dromedaries, particularly *Eimeria cameli*. The molecular studies are needed to delineate the diverse variations within Eimeria strains. Eﬀective parasite control strategies specifc to dromedary camels need to be developed.

Posters

7. Sustainable Sheep Production in Algeria: Mapping Challenges and Opportunities Across the Value Chain

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Sheep farming plays a vital role in Algerian rural life and contributes significantly to national food systems. However, the sector faces numerous challenges that hinder its sustainability and overall performance. This study adopts a value chain approach to better understand structural weaknesses, missed opportunities, and possible pathways for transformation. Drawing on field surveys, stakeholder interviews, and multi-criteria modeling, the research analyzes each stage of the chain, from production to consumption, across three key regions that reflect the country's diversity of farming systems.

Three development scenarios are explored. The first focuses on incremental technical improvements. The second emphasizes cooperative organization and stronger coordination among value chain actors. The third scenario involves the integration of traceability tools and smart technologies to enhance quality, efficiency, and market access. While the first scenario may be easier to implement in the short term, the cooperative and smart farming models demonstrate greater potential for long-term sustainability, innovation, and social inclusion.

The findings highlight the need for targeted public support adapted to the realities of smallholders, improved veterinary services, easier access to financing, and more structured market channels. Particular attention is also given to the valorization of by-products, local meat processing, and environmentally responsible practices.

Rather than promoting a one-size-fits-all solution, this research advocates for a phased, integrated strategy that builds on existing strengths while fostering practical innovation. Supporting the development of Algeria's sheep sector is not only an economic imperative but also a key lever for empowering rural communities and advancing national food security.

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8. Diagnosis and management of a lungworm outbreak in an Irish grass-based dairy farm following the introduction of new animals to the herd

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A growing cough unresponsive to antibiotics, along with reduced milk production and body condition was reported since late August 2024 on a pasture-based herd of 79 cows of which 34 were bought in November 2023. The herd produces an average of 6000 L of milk/cow/year, managed on a 44-hectare grazing platform. The vet practitioners suspected lungworm infestation, but the faecal egg count was negative at this time.

On October 15th (2024), a farm visit was organised (University College Dublin) and a bronchoalveolar lavage (BAL) revealed adult *Dictyocaulus viviparus* worms in three cows, histology of BAL fluid showed an eosinophilia and larvae were found in dung sample of two out of three cows with positive BAL.

We believe the newly purchased cows, previously unexposed to lungworms, became infested after grazing on contaminated pasture. Lacking immunity, they shed large numbers of larvae, heavily contaminating the pasture and causing reinfestation in the resident herd.

The farmer was advised to treat all the cows urgently with a single injection of 0.2 mg/kg, of eprinomectin subcutaneously (Eprecis 20 mg/ml®, CEVA, Ireland). A repeat injection after four weeks was recommended for relapsing cows. Moreover, a two-dose lungworm vaccine (Bovilis Huskvac®, MSD, Ireland) administered with a one-month interval, is recommended for youngstock at least four weeks before the start of the next grazing season.

In Ireland, introducing new cattle is a high risk of lungworm infestation. To confirm the diagnosis, BAL followed by branchial fluids histology is recommended over the Baermann test in symptomatic cows.

9. In vitro digestibility and feed unit evaluation of sugar crop by-products in Northern Morocco

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The production of sugar crops (sugar cane and beet) in Northern Morocco generates substantial amounts of by-products, including cane pulp and beet residues, which represent valuable resources for animal feeding. This study evaluates the in vitro true digestibility (IVTD) and feed unit values (UFL and UFV) of sugar crop by-products from Northern Morocco, providing insights into their potential as alternative feed resources for ruminants. Digestibility was assessed using the DAISY II system and the pepsin–cellulase enzymatic method, while feed values were estimated as net energy for lactation (UFL) and net energy for meat production (UFV). Preliminary analyses indicate that sugar crop by-products exhibit high digestibility and energy values comparable to conventional feed resources, suggesting they can effectively complement ruminant diets. This approach provides a comprehensive assessment of the nutritional value of cane and beet by-products, supporting their use in sustainable livestock feeding strategies. By promoting the valorization of locally available feed resources, these by-products contribute to enhanced feed efficiency, reduced feed costs, and sustainable livestock production systems in Northern Morocco.

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10. Rapeseed by-products as feed resources for ruminants: Digestibility and forage unit

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In Northern Morocco, goat is the most dominant herd among ruminants. Their diet relies mainly on forest rangelands characterized by seasonal and annual variabilities. Thus, it is necessary to diversify goat diet to meet their nutritional requirements and improve productivity. Rapeseed (*Brassica napus*) crop generates by-products that could be used as alternative feed resources for ruminants. This study aims to evaluate the digestibility and nutritive values (forage units "UF") of rapeseed by-products. Samples of leaves and pods were collected from local farms and analyzed to determine *in vitro* true digestibility (IVTD, DAISY II system) and enzymatic digestibility (pepsin–cellulase method) of dry matter (dCs) and organic matter (dCo). Forage units were also calculated as UFL (net energy for lactation) and UFV (net energy for meat production). According to the results, rapeseed leaves showed an IVTD of 59.1%, dCs of 57.2% and dCo of 52.5%, with estimated forage units of 0.68 UFL/kg DM and 0.60 UFV/kg DM. Rapeseed pods presented similar values with an IVTD of 61,1%, dCs of 58.9% and dCo of 53.8%, and forage units of 0.69 UFL/kg DM and 0.63 UFV/kg DM. These findings highlight that rapeseed by-products present high digestibility and acceptable energy values, which support their potential incorporation in ruminant feeding strategies as sustainable alternatives to conventional feed resources.

11. Ethnoveterinary study of medicinal plants used against gastrointestinal parasites of cattle and chicken, evaluation of their anthelmintic potential and of parasites load in northern Benin (CoSAP)

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Livestock productivity in West Africa is hampered by gastrointestinal parasites, which reduce growth, cause economic losses, and present zoonotic threats. In northern Benin, Fulani herders widely rely on ethnoveterinary medicine, a practice that represents a key, yet underexplored and poorly assessed, resource for livestock health. This study combined ethnobotanical surveys, parasitological analyses, and laboratory assays to evaluate medicinal plants used in traditional parasite control. A total of 144 surveys were conducted in the municipalities of Tchaourou and Gogounou, recording 91 medicinal plants, of which 65 were cited for cattle and 39 for chickens. *Khaya senegalensis* was most frequently mentioned. Bark was the predominant plant part used, administered as decoctions, macerations, or feed additives. Coproscopy of cattle and poultry showed low infestation levels during the dry season, while helminthological autopsies in poultry confirmed moderate parasite presence without site-related differences. In vitro assays against adult *Haemonchus* spp. revealed that extracts from *Azadirachta indica*, *Khaya senegalensis*, *Bridelia ferruginea*, and *Detarium microcarpum* significantly reduced worm motility in a dose-dependent manner. Phytochemical screening of selected plants identified active compounds consistent with anthelmintic activity. The results confirm that ethnoveterinary practices might play a vital role in maintaining livestock health in smallholder systems and identify candidate plants for further validation. Integrating traditional knowledge with modern approaches offers a sustainable strategy to improve animal health and reduce reliance on synthetic drugs.

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12. Effect of incorporating olive leaf powder on animal performance, carcass yield, and antioxidant status of Japanese quail (*Coturnix coturnix japonica*)

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The effects of olive leaf powder (OLP) on biological parameters of Japanese quail (*Coturnix coturnix japonica*) remain poorly understood. This study evaluated the impact of dietary OLP on growth, carcass traits, and antioxidant status. A total of 480 one-day-old quails were randomly assigned to four groups (120 birds each) and fed diets containing 0 (control), 1, 2, or 3 % OLP for 42 days. Quails receiving 2 % OLP showed the highest final body weight (225.2 g vs. 210.4 g in controls; $p < 0.01$) and the most efficient feed conversion ratio (2.14 vs. 2.27, respectively), corresponding to a 7 % increase in weight gain, while mortality remained low (<3 %).

Carcass analysis revealed that 2 % OLP increased breast muscle yield by 12 % and reduced abdominal fat by 25 % compared to controls ($p = 0.01$). Dietary OLP also improved biochemical and antioxidant markers ($p < 0.05$), including a 13 % reduction in total cholesterol, a 30 % decrease in muscle malondialdehyde (MDA), and a 33 % increase in total antioxidant capacity (TAC). These effects are likely associated with the high polyphenol content of OLP, particularly oleuropein, which exerts antioxidant and digestive-stimulant activities.

Overall, moderate inclusion of OLP (~2 %) enhances growth performance, feed efficiency, carcass quality, and antioxidant status, highlighting its potential as a natural and effective feed additive for Japanese quail.

13. Genetic Valorization of the Hamra Ewe: An Integrated Approach for Resilient and Sustainable Sheep Farming Systems

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In a context of agroecological and economic transitions, sheep farming systems must evolve towards greater sustainability. The Hamra sheep breed, deeply rooted in the pastoral traditions of western Algeria, represents a valuable genetic resource, particularly due to its hardiness, adaptability to semi-arid environments, and high-quality meat. However, the valorization of this local heritage remains hindered by heterogeneous productive performance and the lack of a structured breeding program. This work proposes an integrated genetic improvement approach for the Hamra breed, based on in-depth characterization of key zootechnical traits (growth, reproduction, morphology) and the active involvement of stakeholders in co-developing selection tools. The dual objective is to optimize both individual and collective flock performance while preserving the breed's local adaptive traits. The study also highlights the need to establish a reliable techno-genetic database, which is a critical prerequisite for implementing participatory breeding schemes. Strengthening the technical capacities of farmers and aligning the strategy with the socio-economic realities of the territory are identified as key levers to anchor the breed in a sustainable development process. Ultimately, this project aims to reposition the Hamra breed as a cornerstone of localized, competitive, and resilient sheep production systems, by enhancing its integration into high-value, traceable, and environmentally responsible value chains.

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14. Reducing stress in pigs in the slaughterhouse resting area by playing music

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Before slaughtering pigs are subjected to multiple stresses, increasing the risk of PSE (pale, soft, exudative) meat. Reducing stress in pigs during the waiting period and during transport to the stunning area is one of the ways to improve their welfare while reducing this risk. The objective of this study was to test the influence of playing music in the slaughterhouse on pig behaviour and carcass pH. The study involved 24 batches of pigs from six farms: for each farm, two control batches (C) were compared with two batches exposed to music (M). The 12 C batches (n=588) and 12 M batches (n=580) were slaughtered on different days. The time between unloading and lying down (D, in minutes), facility of movement to the stunning area (F, score 1=difficult, 2=intermediate, and 3=fluid), and final pH (pH24) were measured/scored and compared using the Kruskal-Wallis test. During the resting period, a 40-minute playlist of country music (to mask the noise of the slaughterhouse) was played, followed by a lullaby for 1h50 (to relax the animals) and 30-minutes of reggae (to reactivate and facilitate their movement to the stunning area). Pigs C and M layed down after 69 ± 28 minutes vs. 59 ± 20 minutes, respectively, and obtained a score of 2.7 ± 0.5 vs. 3.0 ± 0.0 ($p < 0.05$). Playing music had no significant influence on carcass pH (C: 5.60 ± 0.13 vs. M: 5.59 ± 0.12; P=0.22). In conclusion, playing music in the resting area was not associated with a difference in final pH, but was associated to a shorter time to lie down after unloading and seemed to facilitate movement to the stunning area, thereby reducing pig stress during the waiting period.

15. Analysis of the effects of nutritional intakes (ufl/pdi) on dairy performance: phenotypic approach and modelling in cattle farms of eastern algeria.

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This study investigated the influence of feeding practices on dairy production performance across six cattle farms in Eastern Algeria. Ration analysis indicated that diets predominantly composed of dry forages, silages (sorghum, alfalfa, maize), and concentrates provided year-round. Wheat straw was generally offered ad libitum, with one exception. Concentrates were either commercially sourced or locally formulated (e.g., mash). Grazing was still practiced on five of the six farms and played a significant supplementary role. Chemical analyses of the feed revealed substantial variation in dry matter content, UFL (feed unit for lactation), and PDI (protein digestible in the intestine), depending on feed type and farm. Forages from Farms 01 and 05 exhibited the highest energy values (>1.8 UFL/kg DM), while the concentrates frequently exceeded INRA standards for PDI, suggesting instances of protein oversupply. Average dry matter intake was 18.94 ± 1.38 kg/cow/day. Milk yield was significantly correlated with concentrate intake. Theoretical milk yield, calculated based on energy (UFL) and protein (PDI) values, closely matched the actual yield (21.33 vs. 22.46 kg/cow/day), indicating that nutrition may be a limiting factor in production. The linear model explained 44.5 % of the variation in milk yield, 35.1 % of fat content, and 23.1 % of protein content, showing moderate predictive power. Nutrient coverage varied among farms, with some over- and others under-supplying nutrients, mainly due to ration quality and grazing management. Balanced feeding strategies combining forages, concentrates, and pasture are essential to optimize milk production.

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16. Responses of dairy cows to supplemental rumen-protected form of lysine

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The living conditions and environmental factors of farm animals played a crucial role in determining their welfare, health, and productive performance, thereby representing a major concern for livestock production systems. Animal welfare was considered satisfactory when several criteria were met, including adequate comfort, proper management practices, good health status, and, most importantly, an optimal nutritional balance. In dairy cows, particularly those with high milk yield potential and during early lactation an appropriate and balanced diet was essential to sustain performance and maintain metabolic health. Numerous scientific studies had highlighted the significance of supplementing ruminant diets with essential amino acids, particularly lysine, which was recognized as one of the primary limiting amino acids for milk protein synthesis. The objective of this study (Setif) was to evaluate the effect of lysine supplementation, provided in a rumen-protected form (Lys, n=45), on milk production and composition. Compared with a non-supplemented control group (T, n=35), several trials assessing the post-ruminal supply of lysine were reviewed to determine its impact on dairy performance. The results indicated that supplementation with rumen-protected lysine (RP) could lead to a significant increase in milk yield ($p<0.0001$, d15 and d30), as well as improvements in milk protein ($p= 0.003$, d7 and $p=0.0005$, d35) and fat contents ($p= 0.0003$, d7 and d35). These effects were further supported by statistical modeling, which allowed for the simultaneous assessment of the impact of supplementation and time on production parameters while accounting for individual animal variability.

17. Is microphthalmia in pigs a congenital anomaly of genetic origin or part of an oculo-auriculo-vertebral syndrome?

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In native pig breeds at risk of extinction, the birth of a piglet affected by hereditary congenital abnormality raises questions: should all the other piglets in the litter, one or both parents also be excluded from breeding? In small size herds, to take the right decision matters. A male piglet (C) born from a primiparous sow (A) and an unrelated boar kept in a boar stud caught our attention because of severe bilateral microphthalmia. The litter consisted of four piglets, three of which were weaned. One male (C) and two females (D and E). A thorough clinical examination of the sow (A) and boar (B) revealed a slight similar defect of the left ear and suspected unilateral left vertical strabismus (or hypertropia). The significance of these abnormalities had gone unnoticed until then. The question was then: is piglet C an isolated case of bilateral microphthalmia or is it an oculoauricular syndrome, as described in human medicine? With the approval of the Animal Ethics Committee, the three pigs were raised and bred, giving birth to piglets presenting eye, ear, and/or spinal lesions, suggesting an oculo-auriculo-vertebral syndrome (OAVS). In humane, autosomal dominant as well as autosomal recessive types of inheritance have been described. In pigs, the inheritance of the defect is unknown. So, facing with a case of bilateral microphthalmia in a piglet, a prudent genetic advice should be to exclude all piglets from the litter and both parents from breeding.

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18. Integrated management of a Psocid infestation in a SPF animal facility: Response strategy and preservation of health status

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On September 20, 2024, an infestation of psocids (*Psocoptera* sp.) was detected by animal care staff in several bags of feed stored within a Specific Pathogen Free (SPF) animal facility and an adjacent laboratory. Although psocids are not pathogenic to rodents, their presence in an SPF environment poses a critical risk of cross-contamination, particularly in animal housing areas.

An immediate, coordinated response was initiated. The entomology department at the University of Liège confirmed the identification of the specimens through microscopic examination and on-site photographic documentation. An emergency meeting involving entomology experts, feed manufacturers, and animal facility personnel was held to develop a strategy aligned with the stringent SPF requirements.

The action plan comprised multiple complementary measures: immediate destruction of contaminated feed batches by the manufacturer; targeted insecticide treatment of peripheral zones (storage rooms, corridors) using deltamethrin-based products (Deltasect®) by a professional pest control company; and thorough cleaning and decontamination of premises and equipment, including removal of non-essential materials.

New feed batches received between September 23 and October 24 were frozen for 48 hours before use to prevent reinfestation. Two suspect animal rooms were quarantined and monitored using entomological sticky traps, which were regularly replaced. A biweekly enhanced cleaning protocol was established, combining chemical disinfection (Umonium®), application of 7° vinegar (potentially repellent), and diatomaceous earth (a natural insecticide). All cages and housing materials were replaced completely every week for eight weeks.

By week six, no psocids were detected. The protocol was maintained for three months as a precaution. The use of ventilated cages on racks effectively minimized the risk of insect spread to animals.

This rapid, multidisciplinary approach preserved the SPF status, highlighting the importance of proactive bio-contamination management in highly controlled environments.

19. Modulation of hatchability and embryo survival by *in ovo* delivery of rosemary essential oil in Japanese Quail *(Coturnix coturnix japonica)*

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Heat stress during incubation can adversely affect embryo development, hatchability, and post-hatch performance in poultry. The use of natural antioxidants such as essential oils is gaining interest as a potential strategy to mitigate these effects. The objective of this study was to investigate the effects of air sac injection of rosemary essential oil at different *in ovo* concentrations in quail eggs on hatching rate, relative chick weight at hatching, and embryonic mortality rate. A total of 288 fertilized eggs were injected on day 13 of incubation and allocated into four groups: negative control (non-injected), positive control (30 µL sterile distilled water/egg), and two treatments groups receiving 0.1 µL and 0.5 µL/egg. The hatching rate was higher with 0.5 µL (61.36%) and 0.1 µL (56.41%) compared to the negative and positive controls with 48.83% and 44.19%, respectively. At hatch, there was no significant difference in relative weight between treated groups (67.67% for 0.5 µL and 65.26% for 0.1 µL) compared to the negative control (71.60%). Embryonic mortality was reduced in treated groups 0.5 µL (38.63%) and 0.1 µL (43.58%) groups compared to the negative and positive control groups with 51.16% and 55.81%, respectively. Our observations support an important role of rosemary essential oil in both hatchability and embryonic survival.

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20. Phytogenic resources as feed additives for ruminants: Evaluation of phenolic composition

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Ruminant production plays an essential role in ensuring food security worldwide. Growing pressure for higher productivity and environmental sustainability highlights the need for natural and efficient feed alternatives. Among these, phytogenic additives, derived from aromatic and medicinal plants, are gaining attention for their potential to improve digestion and animal performance. The present work focused on comparing the phenolic composition and secondary metabolites of two promising plants, fenugreek (*Trigonella foenum-graecum*) and rosemary (*Rosmarinus officinalis*). Several parameters were analyzed, including total phenols, total tannins, condensed tannins, and hydrolysable tannins, to assess their potential use in ruminant feeding. The analysis revealed that rosemary exhibited higher total phenolic content (6.5%), with a predominance of non-tannic phenols (5.8%) and hydrolysable tannins (0.61%), with 0.09% condensed tannins, while fenugreek showed lower levels (1.8% total phenols, 0.66% total tannins, and 0.14% condensed tannins). These differences suggest a stronger antioxidant and antimicrobial activity for rosemary, which could enhance rumen fermentation, nutrient absorption, and the quality of animal products. Fenugreek, despite its lower phenolic content, may contribute other beneficial bioactive compounds. Further chemical characterization is ongoing to explore additional secondary metabolites before conducting vivo evaluation in ruminants.

21. Innovative Use of Phytogenic Additives to Optimize Ruminant Growth and Milk Production: A Review

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Enhancing ruminant productivity while maintaining environmental sustainability is a major challenge in animal nutrition. In many developing regions, feed resources are often low in protein and energy, leading to reduced growth and product quality. Phytogenic additives, derived from plants such as garlic, rosemary, and nigella, have gained increasing attention as natural alternatives to synthetic growth promoters. Supplementation of rams' diets with garlic (*Allium sativum* L.) powder at 40 g per head per day significantly improves meat production, increasing average daily gain to 184 g and highlighting its potential as a natural growth enhancer. In dairy animals, rosemary (*Rosmarinus officinalis*) supplementation at 10 g per head per day enhanced milk quality, notably by increasing monounsaturated fatty acids (MUFA), polyunsaturated fatty acids (PUFA), and conjugated linoleic acid (CLA) by 15%, 11%, and 15%, respectively. Likewise, the inclusion of nigella (*Nigella sativa* L.) seed at 10 g per day improved both milk yield and composition, resulting in a 37% increase in milk production. Overall, phytogenic feed additives could enhance ruminant performance by improving meat growth and milk quality, offering an efficient and sustainable approach to livestock production.

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22. Intestinal parasites of dogs in urban Algiers

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Canine intestinal parasitoses are a veterinary and public-health concern. Objective: to estimate the prevalence of digestive parasites in dogs seen in clinics and a shelter in two urban municipalities of Algiers (Chéraga, Staouéli) and to explore associated factors. Methods: cross-sectional study of 62 fresh fecal samples (≥5 g) stored at 4 °C; coprological flotation (saturated NaCl, density 1.20; sucrose, density 1.27) and microscopic examination. Results: overall prevalence 58% (36/62). Detected parasites: Strongyloides stercoralis (53% of infestations), Toxocara canis (11%), Toxascaris spp (8%), Ancylostoma spp (8%), Taenia spp (6%), Isospora spp (1%). Polyparasitism (35.4%) exceeded monoparasitism (22.5%). Risk Factors: higher prevalence in males (71% vs 54% in females) and in dogs >6 years (73% vs 59.5% at 1–6 years and 54.5% <1 year). Conclusion: The parasitic burden remains significant and potentially zoonotic; strengthened preventive measures (deworming, vector control, and waste hygiene) are recommended.

23. Stakeholder Knowledge and Parasitological Evidence: A Mixed-Methods Approach to Tilapia Health in Kenya

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Nile tilapia (*Oreochromis niloticus*), a key farmed fish globally, faces under-reported parasitological challenges. In Kenya's Upper Tana River region, we conducted a mixed-methods study combining biological health assessments with a qualitative survey on fish health management. From mid-January to mid-February 2024, we examined 157 Nile tilapia for parasite diversity and tissue-level impacts. Parasites from external and internal organs were identified using light microscopy, molecular barcoding, and scanning electron microscopy. We documented a diverse parasite assemblage, including members of *Clinostomum*, *Euclinostomum*, *Cichlidogyrus*, *Scutogyrus*, and *Acanthogyrus,* with variable prevalence and intensity among hosts. Histopathological examination of gill, intestine and liver tissues was performed and the gill tissues revealed notable changes typical of infections including epithelial hypertrophy and hyperplasia, lamellar fusion, vascular congestion of secondary lamellae, and associated inflammation. In parallel, we engaged 48 stakeholders (36 fish farmers, 11 fisheries and extension officers, and one veterinarian) to understand local knowledge and practices. Findings showed persistent neglect of parasites in farm decision-making a “don’t know, don’t care” dynamic. This is driven by low awareness, weak diagnostic capacity, and limited institutional feedback. Farmers rarely linked disease signs to parasitism, and training gaps among extension officers eroded trust, encouraging improvised treatments. Framed as “undone science”, this local neglect is structural rather than individual. We propose a Challenge and Reconstruct Learning (ChaRL) approach. This method uses parasitological evidence to prompt collective reflection and coordinated action. By making biologically confirmed infections visible, this study bridges pathology and practice, offering a practical way to improve tilapia health management in the region.

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24. A high percentage of folded tails in boar semen consecutive to zinc excess in feed

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The semen of three 18- (A), 15- (B) and 9- (C) month-old Piétrain boars kept in an educational herd presented the same morphological abnormality. Sampled once a week since mid-September, boars A and B showed an increasing rate of flagellar abnormalities: tails bent between the mid- and the main piece or even coiled tails. Boar C, which was first trained for semen production at the end of November, immediately presented abnormal semen. The normal spermatozoa rate of boar A fell from 84% to 16% between 30/09/2024 and 3/12/2024. At that moment, the normal spermatozoa rate, semen mobility and motility were respectively 16%, 30% and 2 (boar A), 0%, 10% and 1 (boar B) and 0%, 5% - 2 (C). On 3/12/2024, boar C's ejaculate was hemorrhagic, suggesting urolithiasis. On that day, the boars' feed was modified, and blood samples were taken to measure zinc levels (boars A-B). A feed analysis was also carried out. The blood zinc concentration of boars A and B was 148 and 194 µg/dL (normal range: 65-131 µg/dL). The feed analysis has shown that zinc, manganese, copper, iodine, cobalt and selenium concentrations were respectively 4,201; 226; 670; 1,400; 55 and 1,788 mg/kg of dry matter. So, the toxicity threshold was exceeded for zinc (>2000 mg/kg), copper (>250 mg/kg), selenium (>5 mg/kg) and iodine (>800 mg/kg). In boar, an excess of zinc in the seminal fluid is known to cause folded tails. In pig farms, an abnormal sperm motility/morphology is primarily associated to iatrogenic (hyperthermia consecutive to vaccination), infectious, environmental (heat stress), traumatic or genetic causes. Nutritional imbalances should also be included in the differential diagnosis as zinc excess in feed is associated to a high percentage of folded tails.

25. Development of a model to stratify the degree of organ failure and prognostic value in calves under 6 months of age

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Sepsis is defined as an excessive host response to infection, which can lead to severe organ failure. Definition of sepsis has evolved over time both in human and in veterinary medicine, but this concept still needs to be studied in calves because of practical specificities and drug restrictions. This study aims to develop a model for diagnosing sepsis and organ failure in calves. All calves under six months of age referred in emergency at the Clinic of the University of Liège were included. Clinical parameters, biochemistry, hematology and hemoculture were performed to evaluate several scores to aid in the diagnosis of sepsis, systemic inflammation, and organ failure. Twenty calves were enrolled in our study, mainly males Belgian-blue, with a median age of 20 days and a median weight of 70,65 kg. Significant correlations were found between the SIRS score and age, blood proteins and chloremia and also between the qSOFA score and age, weight, heart rate, leukocytes and platelets. Mean arterial pressure and hematocrit were associated with survival as lower values were associated with a better prognosis. However, no significant link was found between scores and blood culture results or survival, although a qSOFA score greater than or equal to two was associated with an increased risk of mortality. These parameters could be useful, either alone or in a score adapted to calves under 6 months of age, for diagnosing organ failure. Future studies on a larger cohort of calves could confirm these results, enabling faster treatment and improving their survival rates.

Comparative veterinary medicine

Posters

26. Single-cell spatial transcriptomic analyses of severe Covid-19 lungs identifies disease-associated spatial niches

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Severe COVID-19 lung pathology is thought to be highly heterogenous, encompassing areas of immune cell infiltration and inflammation, diffuse alveolar damage, and fibrotic remodeling. Yet, the single cell spatial organization associated to these processes remains poorly understood. Here, we applied imaging-based single-cell spatial transcriptomics using the CosMx Spatial Molecular Imager to human lung tissue samples from patients who died of COVID-19 and of unrelated causes. We identified and spatially mapped distinct cell subpopulations, including macrophages, fibroblast subsets, and epithelial cells, using a combined approach of manual marker annotation from filtered samples and reference-based classification. Notably, we identified, in COVID-19 lungs, pathological cell types such as COL1A1^{+} fibroblasts, CHI3L1/MMP9hi macrophages and KRT17^{+} basal epithelial cells that were associated with fibrotic niches in the lung. Spatial niche analysis revealed distinct microenvironments, highlighting both pro-fibrotic and regenerative architectures. Ligand-receptor inference suggested that TGF-β and galectin-3 secreted by CHI3L1/MMP9hi macrophages may drive fibroblast reprogramming, while AT2-derived CSF2 may promote the resolution of fibrosis by rewiring monocyte-derived macrophages toward a homeostatic phenotype. This study provides a proof-of-concept that single cell spatial transcriptomics are useful to elucidate the immunopathology of human lung disorders.

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27. Gentle and innovative approach to transfect primary human muscle-derived stem (hmdMSCs) using photoporation technics

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Our research focuses on developing a gentle and efficient transfection method to modify primary human muscle-derived stem cells (hmdMSCs). Photoporation represents a promising and innovative strategy for these notoriously difficult-to-transfect cells. This laser-based technology relies on the excitation of nanoparticles to induce brief yet controlled membrane perturbation, allowing the entry of molecules of interest while maintaining high cell viability. Unlike traditional methods such as viral transfection, photoporation eliminates major safety, cost, and scalability issues. Encouraging initial results have been obtained using FITC-Dextran molecules of various sizes (up to 2000 kDa), with 35–70% of cells showing successful uptake. This technique also allows the delivery of pDNA up to 6 kb into the cytoplasm of hmdMSCs, maintaining over 90% viability and more than 10% GFP expression up to 168 hours post-treatment. Each photoporation run can process approximately 2×10^{6} cells and can be easily scaled up through multiple consecutive runs. We have therefore developed a robust Proof-of-Concept protocol combining high yield, safety, efficiency, and affordability. Together with our patented non-invasive muscle sampling method, this approach paves the way for applying photoporation to cells from patients affected by age-related myopathies. Delivering pDNA encoding Sirt6 could restore mitochondrial function in diseased cells before their reimplantation.

28. Transcriptionally distinct airway neutrophils distinguish severe from moderate asthma phenotype in horses

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Equine asthma is a prevalent chronic respiratory disease characterized by airway hyperreactivity, bronchospasm and severe neutrophilic inflammation. It can be classified in two phenotypes, i.e., moderate and severe asthma, which are differentiated by various criteria such as clinical signs, endoscopic examination and bronchoalveolar lavage cytology. The immunological mechanisms leading to asthma disease phenotypes are still poorly understood and could improve disease diagnosis, management and treatment. We recently found that neutrophil extracellular traps (NETs) were uniquely found in severe asthma. To further investigate the immunological mechanisms involved in disease severity, we performed bulk RNA sequencing of equine neutrophils isolated from the blood and bronchoalveolar lavage fluid (BALF) of 5 healthy horses, 3 horses suffering from severe asthma and 5 horses suffering from moderate asthma. First, we identified marked differences in gene expression between blood neutrophils and airway neutrophils in healthy horses, highlighting the influence of the microenvironment in shaping neutrophil identity. Second, we found a distinct genetic signature of airway neutrophils from horses with severe asthma compared with those from horses with moderate asthma or with healthy horses. Such signature suggested a profound dysregulation of the IL-6/IL-27 balance and could be associated with the pathogenesis of equine asthma and its severity. Our results and ongoing analyses will provide novel insights into equine asthma pathogenesis and could also be leveraged to better understand human neutrophilic asthma.

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29. Magnetic Resonance Imaging diagnosis and surgical outcome of non-keratoma benign hoof masses in four horses

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Keratoma-like lesions are the most common benign hoof space-occupying lesions (SOL) in horses, causing typical pressure lysis of the distal phalanx, recognizable on radiographs [1]. However, they have variable signal intensity at magnetic resonance (MR) imaging [2, 3], that may hinder the diagnosis. This short case series describes the MR appearance of benign hoof SOL other than keratomas. Horses with a standing low-field MR diagnosis of SOL confirmed at surgery were included. On MR, SOL were defined as well-delineated lesions of the stratum medium, impinging on the dermal tissue and causing pressure lysis of the distal phalanx. Their signal pattern was described in T1/T2* 3D and T2W/STIR FSE-weighted sequences. Horses with penetrating injuries and surgically confirmed keratoma-like lesions were excluded. Four horses were included: one with a chronic crack, two with abscesses, and one with a haematoma. The SOL were conical or tubular along the proximodistal hoof axis, with variable height and cross-section. All but one were T2W and STIR FSE non-intense. They had variable signal intensity on GRE-weighted sequences, associated with the presence of magnetic susceptibility artefacts. Occasionnally, SOL other than keratomas occur in the equine hoof, including abscesses and haematomas. Their signal pattern is comparable to keratomas signal, namely non-intense in T2W and STIR FSE images, and inconsistent T1/T2* GRE signal due to magnetic susceptibility artefacts. In some instances when these artefacts occur, a definite MR diagnosis of keratoma may therefore be challenging.

Posters

30. Canine Specific Network for Investigations of Flavour/Scents-searching Faculties (CANI-SNIFF): development and preliminary results of a standardized olfactory testing protocol

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Olfaction is crucial for working dogs' efficiency and can be affected by breed, exercise, diet and medical treatments. This preliminary study aims to evaluate the technical feasibility of 2 different standardized olfactory testing protocols. Two groups of dogs were recruited: drug and explosives detection dogs from the Belgian Federal Police (DACH) and Search & Rescue dogs (SAR) from the Belgian Civilian Security. Both groups underwent different olfactory tests after clinical examination and nasal mucus sampling. DACH dogs (7 males, 5 females; aged 65 ± 34 months – mean ± standard deviation) were tested using a detection track with a concrete block wall, detection cones, scent boxes, and a scent wheel under controlled conditions (relative humidity (RH) 43.75 ± 3.16%, temperature (T) 20.72 ± 1.40 °C). SAR dogs (3 females, 2 males; aged 74 ± 40 months) performed under outside conditions standardized rubble searches (RH 52.20 ± 5.26%, T 18.28 ± 1.71 °C). Mean search duration was 284.6 ± 49.9 seconds for DACH and 579.7 ± 230.7 seconds for SAR dogs. Coefficients of variation for T and RH were respectively 6.76% and 7.23% for DACH dogs and 9.35% and 10.05% for the SAR dogs. These preliminary tests show that the dogs quickly adapted to detection cones, even when unfamiliar, and tolerated nasal mucus sampling well. These preliminary results support the need for further olfactory tests to obtain more baseline olfactory reference values and to determine test accuracy, the influence of environmental parameters, nasal mucus quality, medications effects and nasal protection devices on olfactory performance of working dogs.

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31. The secretome of muscle-derived stem cells inhibits the oxidative response of neutrophils

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Recent data have shown that the secretome of mesenchymal stem cells including soluble factors and extracellular vesicles (EVs) elicit immunomodulatory effects that control inflammation in several diseases. The aim of this work was to determine the effect of the secretome released by equine muscle-derived mesenchymal stem cells (mdMSCs) obtained via muscle microbiopsy on the oxidative response of neutrophils.

MdMSCs-derived secretomes (n=5) were collected and their immunomodulatory properties were assessed on stimulated neutrophils by measuring ROS production-dependent chemiluminescence and active MPO release. The activity of NET-bound MPO was measured after NET capture by an anti-citrullinated histone 3 antibody and the activity of total free MPO was measured after its capture by an anti-equine MPO antibody. The particle size and concentration were analyzed by Nanoparticle Tracking Analysis (NTA) using Nanosight NS300.

NTA analysis of the secretome equivalent to 100,000 mdMSCs per ml showed a mean particle concentration/ml of $4.42x10^{8}$ ± 2.02 x 10^{7} with a mean particle size of 207.03 ± 4.30 nm. The secretome showed a strong dose dependent inhibitory effect on MPO activity. At 125,000 equivalent cells/ml it induced a significant inhibition of the NET-bound MPO activity (54 ± 18 %) and on the total free MPO activity (68 ± 14 %). A significant ROS inhibition (> 30 %) was only observed from secretome equivalent to 500.000 cells/ml.

This study underlines the interest of a cell free therapeutic approach from MSCs to modulate neutrophil inflammation and mostly the activity of MPO, a key factor in numerous chronic and acute inflammatory pathologies.

32. Prevalence and characteristics of bladder wall thickening in dogs without lower urinary tract disease: an ultrasonographic study

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Ultrasound assessment of bladder wall thickness is influenced by bladder distension and body weight, complicating interpretation. Localization of bladder thickening remains poorly documented in healthy dogs. Based on the author's experience, cranial or cranio-ventral wall thickening is commonly observed in dogs without lower urinary tract disease (LUTD). This study aimed to determine the prevalence and characteristics of bladder wall thickening in dogs without LUTD. Medical records of 136 dogs without LUTD signs, undergoing abdominal ultrasound and urinalysis, were retrospectively reviewed. Ultrasound data included presence and localization of thickening, luminal surface, urine aspect, and bladder distension. A wall thickness ratio (maximum/minimum) was calculated in cases of asymmetry. Multivariate logistic regression ($p<0.05$) assessed associations between thickening and medical or ultrasound variables. Bladder wall thickening was detected in 42.6% of cases, mainly in the cranio-ventral area (22.1%), and was more frequent in mildly (29.4%) and moderately (10.3%) distended bladders. Significant associations were found with age (OR=1.16), gastrointestinal (OR=5.49), and renal disease (OR=5.57). Neutered dogs were less likely to show cranio-ventral thickening (OR=0.36). The median thickness ratio was consistent across bladder sizes: 2.0 for mildly, 1.95 for moderately, and 1.9 for severely distended bladders. These results indicate that mild cranio-ventral bladder thickening (ratio ≤2.0) is common in dogs without LUTD and should not be mistaken for cystitis.

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33. Case report: imaging findings and follow up after chemotherapy of a metastatic seminoma in a cryptorchid dog

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A 10-year-old intact cryptorchid Border Collie was referred for abdominal distension and a suspected neoplastic intra-abdominal mass. The dog was in good general condition.

On admission, clinical examination revealed a firm, distended abdomen with a large central mass, and only the left testicle was palpable in the scrotum. Bloodwork was unremarkable. Ultrasonography and computed tomography (CT) identified severe jejunal, lumbar aortic and splenic lymphadenopathy, mild peripheric peritoneal effusion, steatitis and a well-defined ovoid mass adjacent to the prostate, consistent with a cryptorchid testicle. A mediastinum testis-like structure supported this identification. The lumbar aortic lymphadenopathy compressed the right renal vein, leading to infarction of the right kidney. Ultrasound-guided fine-needle aspiration confirmed a malignant seminoma with metastatic lymphadenopathy.

Carboplatin chemotherapy was initiated and administrated every three weeks. Clinical improvement and reduced abdominal distension were noted. A follow-up CT scan at seven weeks demonstrated a significant decrease in the size of the metastatic lymph nodes, while the seminoma mildly reduced in size. The right kidney appeared normal as the renal vein wasn't compressed anymore.

Metastasis of canine seminoma are rare, occurring in less than 10% of cases, and to the author's knowledge, this is the first published report describing detailed imaging findings and follow up after chemotherapy of a metastatic seminoma in a cryptorchid dog.

34. Neutrophil Extracellular Traps Infiltrate The Nasal Mucosa of Dogs with Sino-Nasal Aspergillosis

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Sino-nasal aspergillosis (SNA) is a prevalent cause of chronic nasal discharge in dogs and is predominantly caused by *Aspergillus fumigatus*. The infection is typically localized to the nasal cavity and/or frontal sinus and is characterized by the formation of superficial mucosal fungal plaques, accompanied by severe lymphoplasmocytic and neutrophilic inflammation of the mucosa. While neutrophil extracellular traps (NETs) have been shown to restrict fungal hyphal proliferation in animal models, their presence and putative role in canine SNA remain unexplored. In this study, we investigated NETs in nasal lavage fluid (NALF) or nasal mucosal biopsy from healthy dogs and dogs diagnosed with SNA. In NALF, levels of cell-free DNA and of myeloperoxidase (MPO)-DNA complexes were measured using the PicoGreen assay and by ELISA, respectively. NETs were also visualized directly in nasal biopsies by confocal microscopy. In parallel, we characterized histopathological lesions associated to NETs-enriched areas in adjacent hematoxylin & eosin-stained tissue sections. Interestingly, we found that levels of cell-free DNA and MPO-DNA complexes were significantly higher in NALF of SNA dogs compared to controls. Moreover, we found that NETs often associated with cellular infiltrates in areas around the fungi-rich areas, rather than trapped with fungi. Our results so far suggest that NETs may be involved in the potentially deleterious inflammatory response occurring during SNA, and may therefore contribute to disease pathogenesis. Whether they also positively contribute to host defense against the fungus remains an open question and should be determined before assessing their therapeutic potential.

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35. Abdominal ultrasonographic findings in dogs with a diagnosis of tick-borne disease

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Data on abdominal ultrasonographic changes in dogs diagnosed with tick-borne diseases are limited. This retrospective study aimed to describe the abdominal ultrasonographic findings in dogs diagnosed with anaplasmosis, babesiosis and ehrlichiosis. Medical records from two university teaching hospitals were searched from 2005 to 2024 for dogs diagnosed by cytology and/or PCR with anaplasmosis, babesiosis or ehrlichiosis, that underwent abdominal ultrasonographic examination at the time of the diagnosis. Dogs with long-standing corticotherapy or concurrent diseases affecting abdominal organs were excluded. Fifty-two dogs were included: 42 with babesiosis, 6 with anaplasmosis, 3 with ehrlichiosis and 1 with both babesiosis and anaplasmosis. Forty-nine dogs (95%) had abnormalities on ultrasonographic examination. Splenic and hepatic nodules, mainly hypoechoic, were observed in respectively 27/51 (52.9%) and 17/52 (32.7%) cases. Splenomegaly and hepatomegaly were found in respectively 13/51 (25.5%) and 21/52 (40.4%) cases. Lymphadenomegaly was described in 16 dogs (30.8%) affecting all lymph nodes (2/16, 12.5%) or specific lymph nodes (14/16, 87.5%), hepatic lymph nodes being affected in 6/16 cases (37.5%). Nineteen dogs (36.5%) had peritoneal effusion, mostly in mild amount (13/19, 68%). Biliary sludge was found in 31/48 cases (64%), associated with thickening (4/31, 12.9%) and/or a double-rim appearance (7/31, 22.6%) of the gallbladder wall. Abdominal ultrasonographic findings observed in dogs diagnosed with tick-borne diseases include splenomegaly and hepatomegaly with parenchymal nodules, biliary sludge, lymphadenomegaly, mild peritoneal effusion and steatitis.

36. The extensor fossa sign: a novel radiographic finding in abnormal equine stifles

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In horses, the extensor fossa is a depression on the distal femur serving as the attachment for the long digital extensor and peroneus tertius muscles. On lateromedial (LM) radiographs, it appears as a shallow radiolucency outlined by a radiopaque line. In some horses, the fossa is more visible and better outlined. This study aimed to determine the prevalence of extensor fossa remodeling on LM stifle radiographs and its association with other radiographic abnormalities. Two hundred and six stifle radiographs from 154 horses were evaluated (146 with abnormalities, 60 from sound horses). The extensor fossa was scored from 0 to 2 (0: normal; 1: prominent with proximal sclerotic rim; 2: prominent with proximal and cranial sclerotic rim). A Chi-Square test compared the prevalence between groups. Forty-six of 206 radiographs showed a prominent fossa (27 grade 1, 19 grade 2), 43 of which were from abnormal stifles. The only three prominent fossae in normal horses were grade 1. The prevalence differed significantly between groups ($p < 0.05$). Among affected horses, 26/43 had osteochondrosis, 14/43 medial femoral condyle flattening with degenerative joint disease. A prominent extensor fossa was most frequent with osteochondrosis of the lateral femoral trochlear ridge and may result from mechanical stress on the enthesis linked to altered stifle biomechanics.

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37. Identification of factors affecting the risk of hypotension in anaesthetized dogs

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Perianaesthetic hypotension (PH) is a complication that is related to several adverse post operative outcomes in human and veterinary medicine, so careful monitoring of arterial blood pressure during anaesthesia is crucial. The objective of this study was to identify risk factors for PH in canine patients. For this single centre, retrospective, observational cohort study, 409 dogs undergoing general anaesthesia were studied. Anaesthetic records from dogs in a veterinary teaching hospital between October 2023 and April 2024 were reviewed. Data regarding patient signalment, ASA status, type and emergency of procedure, drugs used in premedication, induction and maintenance of general anaesthesia, use of mechanical ventilation and locoregional anaesthesia, fluid therapy, duration of anaesthetic and procedures were gathered. Primary outcome was the development of PH. Data were analyzed with descriptive statistics and a multivariable logistic regression model. Model fit was assessed with determination of the Akaike Information Criterion. Odds ratios (OR) and 95% confidence intervals (CI) were calculated. Statistical significance was set at $p<0.05$.

PH was present in 77/409 cases (18.8%). An increased OR for PH was found with age <1 year, abdominal surgery, longer anaesthetic duration, while OR for PH decreased with higher body weight and use of locoregional anaesthesia.

This is the first study to analyze a large array of risk factors for PH in dogs. Identification of risk factors for this complication is crucial to develop prevention and treatment strategies to improve patient outcome and safety.

38. Study on neurodegenerative lesions in cetaceans and demonstration of amyloid deposits in the brain in the species Phocoena phocoena: analogies with Alzheimer's disease

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This project has several objectives. First, we review current knowledge of Alzheimer's disease in human medicine to assess whether cetaceans might also develop this pathology and could serve as research models. We then consider how new insights may affect the management and conservation of these species. Finally, we conduct an observational study of histological sections from five harbor porpoise brains (Phocoena phocoena), investigating neuropathological lesions and β-amyloid plaques. Alzheimer's disease is a neurodegenerative disorder characterized by 2 pathological hallmarks: extracellular β-amyloid plaques and neurofibrillary tangles composed of hyperphosphorylated tau protein. Clinical symptoms, such as cognitive decline, typically emerge decades after the onset of the underlying pathological processes. Multiple hypotheses have been proposed to explain the disease mechanisms, most of which converge on synaptic toxicity as a key factor. Rodent models are predominantly used for research, but these animals do not spontaneously develop the disease, which limits the translatability of findings to humans. In light of this limitation, recent studies have reported spontaneous lesions like those seen in human Alzheimer's disease in 6 cetacean species. In this study, we examined brain sections (cortex, cerebellum, and brainstem) from five harbor porpoises (3 adults, 2 juveniles). While no amyloid plaques were detected, intracellular neuronal deposits suggestive of amyloid accumulation were observed in 4 individuals (2 adults, 2 juveniles), along with vascular wall deposits present in all cases. These findings are consistent with previous reports in the literature.

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39. STIR Hyperintensity at the Flexor Surface of the Distal Phalanx – Prevalence and Association with Infrasesamoidean DDFT Lesions and osseous resorption

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High signal in Short Tau Inversion Recovery (STIR) weighted sequences is a common finding in the distal phalanx of horses undergoing Magnetic Resonance Imaging (MRI) for foot lameness. The aim of this study was to assess the prevalence of a STIR hyperintensity at the flexor surface of the distal phalanx (P3FF) and its association to deep digital flexor tendon (DDFT) lesion and podotrochlear bursitis. Feet MRI acquired between 2023 and 2024 were retrospectively reviewed for the presence or absence of P3FF STIR hyperintensity. The association between presence/absence of P3FF STIR hyperintensity and P3FF bone resorption, podotrochlear bursitis and DDFT lesions was calculated using a Chi-square test. A total of 130 MRI exams from 107 horses were reviewed with 16 that didn't make the inclusion criteria. Horses were mainly warmblood, aged 4 to 28 years. Forty-four/114 feet showed P3FF STIR hypersignal. Concurrent MRI lesions found in the 44 feet with P3FF hypersignal were DDFT tendinopathy (35 horses), podotrochlear bursitis (32 horses), navicular bone lesions (33 horses) and FF bone resoprtion (11 horses). All horses with P3FF bone resorption had also a hypersignal. There was the strongest significant association between P3FF hypersignal and infrasesamoïdean DDFT tendinopathy ($p < 0.001$). Results show an association between STIR hyperintensity and bone resorption at the P3FF with adjacent insertional tendinopathy and suggest that this area may function as an anatomical unit similar to synovioentheseal complexes in humans, where enthesis and synovium are functionally integrated.

40. Psychological stress impedes type 2 immunity and Ly6G+ pro-repair macrophages after influenza virus infection

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Infectious and zoonotic diseases, such as Influenza A virus (IAV) infections, represent a constant threat to human and animal health. In a world where global anxiety is increasing, the effect of psychological stress on host homeostasis and disease susceptibility remains unclear, even though stress is increasingly recognized to profoundly influence immune responses. Our laboratory recently identified a novel population of Ly6G+ macrophages dependent on type 2 immunity and contributing to host recovery and euplastic alveolar repair after influenza infection. In this study, we investigated the impact of psychological stress on host immune response after IAV infection. C57BL/6 wild-type mice were subjected to a three-day stress regimen consisting of Water Avoidance Stress (day 1), Light/inclined slope (day 2), and Water Avoidance Stress (day 3), in parallel with Influenza A virus infection, and pulmonary immune responses were assessed. Stressed animals displayed a marked reduction in Ly6G$^+$ macrophages, associated with an impaired type 2 immune response, while type 1 immunity remained unaffected. Stress also altered the post-infection cytokine profile, reducing both pro-repair and adaptive immunity-related mediators. Our findings suggest that psychological stress does not impact viral control but can alter type 2 immunity and lung recovery after viral infection.

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41. Development of a cell therapy product based on mesenchymal stem cells loaded with doxorubicin to treat human gliomas

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In neuro-oncology, MSCs have attracted attention for their ability to home to tumor sites, cross the blood–brain barrier (BBB), and serve as drug delivery vehicles. These capabilities could help overcome one of the major obstacles in treating brain tumors, as most anticancer drugs, such as doxorubicin (DOXO), fail to penetrate the BBB despite their strong in vitro and in vivo efficacy when administered intracerebrally. In this context, we aim to exploit MSCs as drug carriers to deliver DOXO to brain tumors. This study was based on human muscle-derived MSCs (mdMSCs), a patented technology developed in our lab. To load mdMSCs with DOXO, we relied on the photoporation, a gentle physicochemical approach. Our preliminary findings demonstrate that photoporation is an effective and non-disruptive method to load MSCs with doxorubicin while preserving their cellular properties. Indeed, 100% of the mdMSCs from two independent donors were successfully loaded with DOXO following photoporation. However, the gradual decrease of intracellular DOXO highlights the need for optimization strategies to improve drug retention within MSCs. Ongoing experiments focusing on DOXO transfer to tumor cells will help evaluate the therapeutic potential of this cell-based delivery system for brain tumors and provide valuable insights into its applicability in neuro-oncology.

42. Study of fibroblast activation protein expression in canine gastric carcinoma

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Fibroblast Activation Protein (FAP), a type-II transmembrane serine protease, is upregulated in various cancers, while its expression in normal tissues is either low or undetectable. In human gastric carcinoma (GC), high FAP expression has been associated with poor prognosis, drug resistance, and the promotion of an immunosuppressive tumor microenvironment favoring tumor progression. Therefore, FAP represents an attractive therapeutic target in human GC. Many similarities exist between human and canine GC. Canine GC is typically diagnosed at an advanced stage, with limited treatment options and poor prognosis. Presently, there is no data available about FAP expression in canine GC. Accordingly, the aim of the present retrospective case-control descriptive study was to qualitatively assess FAP expression by immunohistochemistry on formalin-fixed, paraffin-embedded gastric tissue samples previously collected and banked from canine cases with GC (n = 8) and controls (n = 6; late-senior and geriatric dogs euthanized for reasons unrelated to gastrointestinal disease). Stromal FAP immunostaining was observed in all tumors. FAP-positive stromal cells primarily colocalized with the tumoral cells in 6 out of 8 cases (75%), often surrounding clusters of neoplastic cells. Neoplastic epithelial cells were predominantly FAP-negative with only a few ambiguous areas showing faint, sporadic positivity in some cases. Small amounts of FAP-positive stromal cells were also detected in all healthy stomachs, except one. In the control group, FAP-positive cells were predominantly found in the submucosa, at the interface between the submucosa and mucosa, and sometimes in the mucosa. Results of this study confirmed FAP expression in canine GC, paralleling observations made in human GC. The spatial organization of the FAP-positive stromal cells surrounding neoplastic cells suggests a role in shaping the tumor microenvironment. Surprisingly, FAP-positive stromal cells were also found in canine control samples. This could represent a physiological specificity of dogs compared with humans, potentially associated with dietary, behavioral and/or age-related factors. In conclusion, this study highlights the relevance of dogs as a spontaneous model for exploring the role of FAP in gastric cancer pathogenesis, providing a foundation for the development of anti-FAP therapies for both canine and human patients.

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43. Autologous Muscle-Derived Mesenchymal Stem Cells for Equine Tendon Repair — A Randomized Controlled Clinical Trial

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Tendon and ligament injuries represent a major cause of morbidity in sport horses. This autologous therapy based on muscle-derived mesenchymal stem cells (mdMSCs), offers a novel approach by combining anti-inflammatory, paracrine, and regenerative properties.

A prospective, randomized, double-blinded, placebo-controlled clinical trial was conducted to assess its efficacy and safety. Client-owned sport horses were enrolled (20 treated, 10 placebo). All 30 horses received an intralesional injection of autologous PRP (platelet rich plasma). After the period of mdMSCs production and qualification, treated horses received 10^7 autologous mdMSCs in Cryostor CS5® and placebo horses received 1 mL of Cryostor CS5® without cells, injected under ultrasound guidance. Assessments included clinical (TCS – Total clinical score) and ultrasonographic (fiber alignment score (FAS), echogenicity, lesion size) parameters.

Significant improvements were observed in all main variables from baseline to week 6 post injection. The median TCS decreased from 6.5 to 2.0 ($p<0.001$), with 56.7% of horses achieving complete or near-complete recovery. If we exclude horses almost healed after PRP injection, treated horses showed significant gains versus placebo after the first injection ($p=0.01–0.04$ for the different parameters). A second injection administered to partial responders resulted in significant additional improvements ($p=0.001–0.013$ for the different clinical and ultrasonographic parameters). Only echogenicity showed a positive but non-significant trend ($p=0.059$). No systemic adverse effects occurred; extremely rare local reactions were mild and transient.

These results confirm the safety and robust efficacy of autologous mdMSCs in equine tendinopathies. The therapy demonstrated significant clinical and ultrasonographic improvement supporting its value in regenerative equine sports medicine.

44. Autologous muscle-derived mesenchymal stem cells improve lameness and clinical scores in horses with chronic osteoarthritis: results of a prospective, open-label clinical trial.

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Intra-articular administration of mesenchymal stromal cells (MSCs) has emerged as a promising therapy for equine osteoarthritis (OA). However, most controlled studies have evaluated allogeneic products, often combined with plasma components, and data on autologous MSCs used as a pure product remain scarce. The objective of this prospective clinical trial was to assess the efficacy and safety of a single intra-articular injection of autologous muscle-derived MSCs (RVT-CELL-J) in horses with chronic OA of more than three months' duration. Thirteen horses with radiographically and clinically confirmed OA received one intra-articular injection of 1×10^7 autologous mdMSCs, and lameness (AAEP), joint inflammation/swelling (IS), and the Total Clinical Score (TCS = AAEP + IS, range 0–8) were evaluated at baseline (T0), 6 weeks (T1), and 12 weeks (T2). Horses were considered responders if they achieved a ≥2-point reduction in AAEP at T1 or T2 or an AAEP score of 0 at T2. Seven of the thirteen horses (53.8%) met this composite responder criterion. Median AAEP decreased from 3.0 at baseline to 2.0 at T1 and 1.0 at T2, IS decreased from 2.0 to 1.0 at both follow-ups, and TCS decreased from 5.0 to 3.0 at T1 and T2, with all improvements reaching statistical significance ($p<0.01$). No major adverse events were observed. These findings demonstrate that intra-articular injection of $1x10^7$ autologous mdMSCs is safe and associated with significant improvement of lameness grade improvement in horses with chronic OA, thereby complementing existing evidence on MSC therapy and providing direct proof of efficacy for autologous MSCs intra-articular administration as a stand-alone treatment.

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45. Analysis of exhaled breath of horses with non-septic inflammatory airway conditions using selected-ion flow-tube mass spectrometry (SIFT-MS).

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Exhaled breath analysis is a promising tool for the early detection of various airway conditions in humans and animals. Selected Ion Flow Tube Mass Spectrometry (SIFT-MS) is a highly sensitive analytical technique quantifying volatile organic compounds (VOCs) in matrices such as exhaled breath. Equine asthma (EA) and exercise-induced pulmonary hemorrhage (EIPH) are common inflammatory conditions of the lower respiratory tract (LRT) limiting performance in equine athletes; their diagnosis relies on endoscopic examination; however, assessing their severity and extent is not straightforward. Our aim was to assess the feasibility of SIFT-MS for equine breath analysis and to screen the profile of VOCs in breath of horses suffering from non-septic inflammatory airway conditions compared to healthy ones. A total of 7 healthy horses and 31 pathological horses were recruited. Pathological horses were divided into 3 groups: 11 horses with EA or other LRT inflammatory conditions; 7 horses with EIPH and 13 horses with both EIPH and LRT inflammatory conditions. Exhaled air was collected in Tedlar® bags via the endoscopic or Bivona® channel. Exhaled air was analyzed by SIFT-MS using a Syft Tracer i8 with H_3O^+, NO^+, and O_2^+ as precursor ions. Statistical analyses consisted in a one-way ANOVA and non-parametric Kruskal–Wallis test for multiple comparisons. Sampling of equine exhaled breath was easy to perform in conjunction with endoscopic examination. The number of horses, particularly healthy ones, was too small to detect significant differences between groups. However, some VOCs stood out in the untargeted screening, such as 2-propanol and ethanol (both alcohols), which have also been reported in human COPD and cystic fibrosis. Collection and analysis of VOCs is a promising technique that may enable the identification of biomarkers for different airway pathologies and to better quantify the extent and severity of these disorders, particularly of multifocal diseases such as EIPH.

46. Microct characterization of subchondral bone lesions in 5 isolated equine proximal phalanges

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Subchondral bone (SCB) lesions in the proximal phalanx (P1) are a common cause of lameness in horses. This study aims to assess the micro-computed tomography (µCT) appearance of the SCB in isolated P1 specimen with Magnetic Resonance Imaging (MRI) changes.
Five P1 proximal epiphyses, with MRI evidence of SCB thickening and/or resorption, were scanned using µCT. µCT changes and objective trabecular bone analysis parameters were assessed in the glenoid and sagittal groove, including degree of anisotropy, trabecular thickness and spacing, and bone volume fraction (BV/TV). These findings were compared between different anatomical locations (medial glenoid, lateral glenoid, sagittal groove), and between areas with and without MRI changes.
µCT revealed loss of SCB plate integrity, coalescing microcracks, collapse of the chondro-osseous interface and articular cartilage defects in areas of resorption identified on MRI. Areas of µCT hypoattenuation were also observed in regions where MRI showed only SCB thickening. Mean values for the degree of anisotropy, trabecular thickness and BV/TV were highest in the medial glenoid and lowest in the sagittal groove. Trabecular spacing was greatest in the sagittal groove. The degree of anisotropy was significantly higher adjacent to SCB abnormalities ($p<0.05$) compared to normal SCB plate.
Early signs of resorption were detected on µCT in SCB plates with only thickening at MRI, and the highest degree of anisotropy was found medially and adjacent to SCB changes. These results suggest that SCB lesions could develop secondary to repetitive biomechanical stimulation in horses, supporting the hypothesis of overload arthropathy.

Veterinary Public Health

47. Genomic and virulence insights of Western European *Aeromonas salmonicida* subsp. *salmonicida* and development of *Galleria mellonella* infection assay

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Aeromonas salmonicida subsp. *salmonicida* is the etiological agent of furunculosis, a fish disease highly aggressive for salmonids and responsible for significant economic losses in aquaculture worldwide. This study aimed to explore genomic and antimicrobial resistance traits of Western European *A. salmonicida* subsp. *salmonicida* strains and to develop an adapted *Galleria mellonella* infection model to assess the pathogenic potential of this psychrophilic subspecies. Three strains isolated from salmonids displaying symptoms of furunculosis were tested against a panel of antibiotics and sequenced to characterize their genome. Virulence was evaluated in *G. mellonella* larvae using bacterial doses ranging from 10^1 to 10^6 CFU/larva. Two isolates exhibited multidrug resistance to antibiotics commonly used against furunculosis. Although closely related to the reference strain A449, genomic analyses revealed multiple plasmids known to encode antibiotic resistance genes. Virulence assays demonstrated that this subspecies is lethal at doses as low as 10^1 CFU/larva, and that a fully functional Type III Secretion System (T3SS) is not essential for the infection of *G. mellonella*, likely due to the presence of other virulence factors in T3SS-deficient strains. These findings enhance the genomic characterization of European *A. salmonicida* subsp. *salmonicida* and validate the use of *Galleria mellonella* larvae as a relevant alternative infection model for studying this psychrophilic subspecies.

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48. Characterization of bacterial resistance to bacteriophages targeting *Escherichia coli* strains causing bovine mastitis

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Bacteriophage resistance is a major challenge in phage therapy because it impairs the treatment efficacy and alters the bacterial fitness. A recent study highlighted that bacteria isolated from bovine mastitis became resistant to bacteriophages after 5 h of incubation in raw milk. The aims of this study were to evaluate the in vitro onset of resistance in raw milk and to characterize these bacterial mutants. Mutants were isolated in raw milk inoculated with bacteriophages and a wild-type (wt) strain after 5 and 12 h of incubation, which was associated to bacterial regrowth. Characterization studies involved stability of the resistance after 10 passages, capsule visualization using the Maneval staining, evaluation of the adsorption time and antimicrobial susceptibility. Finally, the Appelman method was applied to try to restore phage efficacy. A total of seven mutants were isolated, two of them lost their resistance after 10 passages. All mutants presented a thinner capsule compared to the wt strain. Phages could not adsorb to the resistant bacteria, suggesting a modification of the bacterial receptors. One mutant showed an increased antimicrobial susceptibility. After 40 passages, an adapted phage was isolated, which showed a better lysis against 3 strains, including one resistant strain. Genomic analysis of the adapted phage revealed a deletion of 3 genes encoding hypothetical proteins. In conclusion, the resistance mechanism could involve modifications in phage receptors, which will be confirmed by genome sequencing. Further in vivo experiments in Galleria mellonella model will compare the virulence of mutants and assess the efficacy of both wt and adapted phages on larvae survival.

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49. Tick-Borne Diseases in Sub-Saharan Africa: A Systematic Review of Pathogens, Research Focus, and Implications for Public Health

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Sub-Saharan Africa (SSA), is a conducive zone for tick proliferation. These vectors pose a major challenge to both animal and human health in the region. Despite evidence of tick-borne disease emergence, very few studies have been dedicated to investigating zoonotic pathogens transmitted by ticks in this area. This systematic review considers the trends of research on tick-borne bacteria, parasites, and viruses from 2012 to 2023, to raise awareness of the risks of tick-borne zoonotic diseases in SSA, and to define a direction for future research, focusing on the circulation of these pathogens in ticks, cattle, sheep, goats, and humans. A total of 159 papers fitting designed inclusion criteria were used for qualitative analyses. Substantial diversity of tick-borne pathogens in SSA were revealed, including 37 bacterial species, 27 parasite species, and 14 viruses. Among these pathogens, 27% were zoonotic. However, only 11 studies investigated their presence in humans. Interest in investigation of bacteria and parasites in ticks and ruminants has increase. However, research into viruses is limited and has only received notable interest from 2021 onwards. While studies on the detection of bacteria, including those of medical interest, have focused on ticks, little consideration has been given to tick in studies of spirochete circulation. Given the limited focus on zoonotic pathogens transmitted by ticks, in humans, and the need of an understanding of associated drivers and public perceptions, future research should adopt a One Health approach to comprehensively address the impacts on human and animal health and uncover emerging threats.

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50. The development of Usutu virus-mediated fatal neuroinvasive disease in WT 129/Sv mice is determined in the earliest stages following peripheral infection

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Mosquito-borne *Orthoflaviviruses* like Dengue, Zika, West Nile (WNV) and Usutu (USUV) viruses are massively circulating worldwide. While some are causing seasonal episodes of mass mortalities in reservoir bird species (USUV, WNV), all are responsible for sporadic neurological diseases in both healthy and immunocompromised mammals. The host-pathogen factors involved in these occurrences haven't been described yet, and the increasing number of cases diagnosed recently undoubtedly represent a serious threat for public health. Thus, the need to develop a relevant model of infection in mammals has become crucial. Considering their occasional susceptibility, the mammalian models used to study the pathogenicity of *Orthoflaviviruses* are most commonly immunocompromised mice. We started by developing our own wild type model of neurotropic Orthoflaviviral disease based on the age-dependent susceptibility of 129/Sv pups to USUV (a biosafety level 2-pathogen), which showed a drastic drop in a very short age gap. We then compared the viral dissemination between our susceptible and resistant groups over time, to identify the main host-pathogen interfaces involved in these contrasting outcomes. Interestingly, major dissimilarities in viral propagation and immune response were observed as soon as 24h post injection, suggesting a very early determination of the phenotype and a significant role of the skin in the control of the infection. The later combination of cellular, transcriptomic and proteomic approaches to describe the earliest stages of the pathogenesis as decisive to prevent neuroinvasion represents the first skin-focused strategy to study *Orthoflaviviruses* infections in mammals.

51. Evaluating the impact of polysorbate 80 on the gut microbiota of healthy individuals

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Consumers generally trust the safety of foods available on the market. Manufacturers ensure this by implementing strict control measures, including raw material selection, hygiene procedures, temperature management, and, when needed, the addition of food additives. These additives serve functions such as preservation, coloring, or texturing and become part of the final product. The European Food Safety Authority (EFSA) has re-evaluated all additives approved before 2009. In parallel, concerns have arisen about the safety of emulsifiers, particularly polysorbate 80 (P80), which is commonly used in dairy products, ice cream, confectionery, and baked goods. P80 has been associated with intestinal inflammation and colon carcinogenesis. Although in 2015, EFSA concluded that P80 posed no safety concerns, it recommended further studies. This work assessed the impact of P80 on the gut microbiota of three healthy donors using the L-SHIME® gastrointestinal model. After a two-week stabilization period, 4.5 g/day of P80—corresponding to EFSA's maximum estimated consumer exposure—were administered for two weeks. Microbial changes and metabolite production were measured using qPCR and chromatographic methods. P80 increased the relative abundance of *Bacillota* and reduced *Bacteroidota*. Higher levels of *Enterococcus, Bifidobacterium, Lactobacillus*, and *Megasphaera* were also detected, some of which have been linked to intestinal inflammation. In addition, acetate, butyrate, and branched-chain fatty acids increased in the presence of P80. A direct relationship between P80 exposure and the promotion of intestinal inflammation or fibrosis could not be established.

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52. Lasting viral-induced reprogramming of lung immunity shapes a pro-tumoral microenvironment

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Respiratory viruses can induce substantial immune alterations. *Respiratory Syncytial Virus* (RSV), a major cause of severe respiratory illness in infants and the elderly, shows low antigenic variability. Yet, reinfections occur throughout life, suggesting defective establishment or maintenance of immune memory. The mechanisms behind these defects remain unclear and may involve lasting alterations in immune or structural lung cells, affecting both anti-RSV and heterologous immunity. Using *Pneumonia Virus of Mice* (PVM) as an RSV-like model and Lewis Lung Carcinoma (LLC) cells, we examined whether prior pneumovirus infection modulates immune surveillance and lung cancer development. Mice infected with PVM one or two months before LLC cell injection displayed enhanced tumor establishment and growth. This correlated with sustained accumulation of immunosuppressive cells, including monocyte-derived cells, neutrophils, and eosinophils, indicating durable myeloid reprogramming that fosters a tumor-permissive microenvironment. Similar effects were observed with other lung cancer cell lines and *KRAS*-driven models. Mechanistically, bone marrow chimera experiments revealed that long-term reprogramming of hematopoietic progenitors from PVM-preinfected mice contributes to tumor promotion. Preliminary analyses also identified pre-fibrotic lesions in PVM-preinfected lungs, suggesting cooperation between tissue remodeling and myeloid alterations. Overall, these findings show that transient viral infections can durably reprogram the lung microenvironment, thereby promoting cancer development.

53. Study of the influence of a prior gammaherpesvirus infection on SARS-CoV-2 long-term sequelae

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Over the past five years, SARS-CoV-2 infection has affected a substantial portion of the global population. While acute and sometimes fatal outcomes have been extensively studied, increasing attention is being directed toward long-term sequelae affecting 5-10% of infected patients, collectively referred to as long COVID. This condition is characterized by persistent systemic inflammation and immune dysregulation, often accompanied by cognitive impairment or "brain fog". The factors contributing to the development of long COVID remain poorly understood, but research has linked this condition to the reactivation of persistent viruses, particularly the Epstein-Barr Virus (EBV). To investigate this association, we used a preclinical mouse model combining Murid Herpesvirus 4 (MuHV-4) mimicking EBV and a mouse-adapted SARS-CoV-2 strain (MA30). Young C57BL/6 females were infected intraperitoneally with MuHV-4. After latency establishment, they were superinfected intratracheally with MA30. Prior MuHV-4 infection offered moderate protection against acute SARS-CoV-2 symptoms but induced significant systemic immune alterations, including changes in circulating T cells and monocytes. Notably, we observed remodeling of microglial cells and CD8 T cell infiltration in the brains of MuHV-4 pre-infected mice following SARS-CoV-2 superinfection. These findings suggest that prior gammaherpesvirus infection may alter the pathogenesis of SARS-CoV-2 on the long term and underscore the importance of considering the history of infection in order to better decipher long COVID.

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54. From Fish to Human: A Conserved p38–VCP Pathway Regulating Stress Granule Disassembly by Viruses

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Stress granules (SGs) are dynamic cytoplasmic membraneless organelles that form under environmental or pathogenic stresses. During viral infection, SGs can restrict viral protein synthesis and support innate immune responses. Many viruses inhibit SG formation to maintain a pro-replicative environment. Here, we show that Cyvirus cyprinidallo 3 (CyHV-3) markedly suppresses arsenite-induced SG formation in infected cells. CyHV-3 infection triggers robust p38 MAPK activation at 12h post infection, coinciding with SG inhibition and suggesting a functional link between p38 activation and SG suppression. Chemical inhibition of p38 with SB203580 or BiRB796 restores SG formation upon arsenite treatment. Together with previous evidence linking p38 to ULK1 and ULK1 to VCP, our results suggested a p38–ULK1–VCP signaling axis that coordinates SG disassembly. Supporting this hypothesis, we observed that the inhibition of ULK1 (SBI0206965) or VCP (DBeQ, MDBN) compromised the ability of CyHV-3 to inhibit SG formation induced by arsenite treatment. VCP inhibition by higher doses of inhibitors induced spontaneous SGs in CyHV-3 infected cells without exogenous stress. Inhibitor treatments at different infection stages revealed that VCP activity is continuously required to suppress SG formation. In CCB cells, VCP colocalized with the SG core protein G3BP1, and its blockade delays SG disassembly, underscoring its key role. Notably, this regulation is not restricted to CyHV-3: in SARS-CoV-2–infected cells, inhibition of p38 or VCP also induced spontaneous SG formation, revealing a convergent mechanism of SG inhibition acquired by unrelated viruses. Despite the evolutionary distance between fish and human viruses, both appear to rely on the p38–VCP axis to suppress SGs. These findings highlight a conserved stress-response pathway that viruses can exploit from fish to human.

55. Residues and risk assessment of antibiotics in commercial white leg shrimp (*Litopenaeus vannamei*) in Can Tho City, Vietnam

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Shrimp farming plays an important role in the global seafood supply, however the use of antibiotics in farming raises concerns about dietary exposure and food safety, leading to potential risks to consumer health. The aim of this study was to evaluate the antibiotic residues in commercial white leg shrimp (*Litopenaeus vannamei*) collected from markets in Can Tho City, Vietnam and to perform a survey of food consumption to assess the risk exposure of local consumer to antibiotics through shrimp consumption. Thirty white leg shrimp samples were sampled from local markets and supermarkets for screening by some test kits i.e. Premi test, Beta star. The quantification of antibiotic residues in shrimp muscle was assessed using two analytical methods: ELISA on 30 samples for group-specific screening and Liquid Chromatography-Mass Spectrometry (LC-MS/MS) on 10 representative samples for specific compound identification and quantification. The concentrations determined by LC-MS/MS were used to calculate estimated daily intake (EDI; µg/kg body weight/day) of antibiotics based on local shrimp consumption data. The calculated EDI values were compared with the accepted daily intake (ADI) values to assess exposure levels. Analytical results from LC-MS/MS showed that antibiotic residues of 5/10 samples were lower than LOD for all 5 antibiotics. Doxycycline (DOX) was the most prevalent compound, reaching 52.87 µg/kg, followed by oxytetracycline (OTC, 31.5 µg/kg), enrofloxacin (ENR, 8.02 µg/kg), ciprofloxacin (CIP, 1.47 µg/kg), and sulfamethazine (SMZ, 1.04 µg/kg). OTC was notably detected at a high concentration of 31.50 µg/kg in a sample collected from supermarket, another supermarket sample presented a significant profile of multiple residues, including DOX, ENR, CIP and SMZ. Regarding the exposure assessment study, the survey results showed that 88% of interviewees stated that they like to eat shrimp. The average amount of shrimp consumption was 116 g per person per day. Based on the antibiotic residue concentration in shrimp and mean of body weight of interviewed people, the EDI values of the analyzed antibiotics ranged from 0.001 to 0.12 µg/kg bw/day, and these EDI values were much lower than their respective ADIs, suggesting negligible health risks for consumers. The findings suggest that, under current consumption and residue levels, health risk from antibiotic exposure through these shrimp products is low. Nevertheless, continued monitoring and prudent antibiotic use in shrimp culture are essential to ensure long-term food safety and maintain consumer confidence.

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56. Effect of different viral infections on the development of experimental autoimmune encephalomyelytis in mice

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Multiple sclerosis (MS) is an autoimmune disease affecting over 2.8 million people worldwide. Its multifactorial etiology involves genetic predisposition and environmental factors. Epstein–Barr virus (EBV) (more than 90% seropositivity globally) is as a strong risk factor. A recent 20-year longitudinal study of 10 million U.S. army personnel reported a 32-fold increased risk of developing MS in seroconverted individuals. Experimentally, infection with Murid Herpesvirus-4 (MuHV-4, murine EBV homolog) worsens experimental autoimmune encephalomyelitis (EAE), an MS mouse model. Whether this effect is specific to MuHV-4 or shared with other viral infections remains unclear. C57BL/6 mice were infected with MuHV-4, Influenza A/Puerto Rico/8/1934 (H1N1, PR8), murine cytomegalovirus (MCMV), or left uninfected (mock). Neuroinflammation and circulating leukocyte profiles were characterized by spectral flow cytometry after EAE induction. To assess whether this also translated into behavioral changes, EAE was induced in MuHV-4-infected or mock mice and behavior was monitored using Noldus EthoVision Phenotyper for two weeks. MuHV-4-infected EAE mice displayed distinct immunological alterations compared to other groups, characterized by increased activation of T lymphocytes and myeloid cells, together with reduced frequencies of regulatory T cells. These changes were not present after PR8 or MCMV infection. Behavioral monitoring revealed alterations in feeding and drinking patterns in MuHV-4-infected EAE mice compared to mock controls, most other parameters were similar. These results highlight the importance of infection in shaping immune and behavioral outcomes of CNS autoimmunity.

57. Potential role of nematode larvae for vectorial transmission of brucellosis

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Since their discovery in 1994, marine Brucella spp. have been isolated from various marine mammals, B. ceti infecting cetaceans. The transmission pathways of marine Brucella spp. remain unclear, but there is evidence that marine mammals can contract brucellosis by vertical and horizontal transmission. Vectorial transmission via lungworm carrying the bacteria is suspected. This study aims to confirm the presence of Brucella ceti and the potential transmission by lungworm larvae. First-stage larvae were isolated and by sequencing, B. ceti was identified in larvae from airways of a common dolphin. These results support the hypothesis of a potential vectorial transmission of Brucella spp. by lungworms larvae in marine mammals.

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58. Athletes and Probiotics: A case for precision bioengineering?

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The complex interaction between the gut microbiome and the host is significant to gut health research. The gut microbiome is not only demonstrated to play a big role in modulating gut health but is also indicated pivotal to systemic conditions that include dermatitis, vaginosis, mental health and respiratory conditions. A better understanding of how the gut microbiome directly, or indirectly, impacts different conditions is of major interest to parties from different aspects of research. Equally important is elucidating how internal and external factors shape the microbiome itself, knowledge that could ultimately enable the manipulation of the gut microbiome for therapeutic or preventive purposes.

Although studies demonstrate significant differences in the gut microbiome of individuals clustering along lifestyle, diets, genetic background, health conditions and extent of physical activity, studies into how these different clusters respond to an identical microbial modulating treatment are becoming of great interest in the microbiome field. Through use of a human gut simulation model, we recently demonstrated a differential response to a probiotic, *Lactiplantibacillus plantarum,* from 3 donors meeting a 'healthy' donor criterion. Donor 2 presented with a significantly different microbial profile compared to Donor 1 and Donor 3 at baseline. Furthermore, samples from Donor 2, who comes from an athletic background, clustered separately from the other 2 donors after probiotic treatment. The same donor exhibited increased propionic and lactic acid production before and after probiotic treatment, with a significantly truncated butyrate acid signature. Interestingly, fermentation of Donor 2 fecal material after probiotic treatment in the SHIME system resulted in statistically reduced colony forming units on MRS agar, suggesting that the metabolic profile of Donor 2 resident microbes did not support the growth and colonization of *Lactiplantibacillus plantarum*, as well as other microbes capable of growing on MRS agar. In conclusion, although probiotics are designed and optimized to effect a standard beneficial impact on a wide range of individuals and gut microbiomes, certain specific clusters that include high intensity athletes will benefit from precisely designed probiotics, given their highly modified gut microbiome that has evolved to support intense physical activity.

59. Aeromonas spp. as candidate indicator for antimicrobial resistance surveillance in Belgian aquaculture.

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In Belgium, aquaculture is primarily semi-intensive, with salmonids raised in river-fed ponds. The absence of authorized fish-specific vaccines or antibiotics leads to the use of antimicrobials approved for other animal species. Unlike other food-producing animals, aquaculture lacks systematic monitoring of antimicrobial resistance (AMR). This study aimed to evaluate *Aeromonas* spp. as a potential AMR surveillance indicator by isolating them from water, and sediment across 22 Belgian fish farms during winter. Water samples (n = 88), and sediment (n = 29) were cultured on Glutamate Starch Phenol-red (GSP) Agar and Columbia Blood Agar at 18°C and 30°C. Yellow GSP colonies were subcultured and stored. One colony per sample type per farm from GSP at 18°C was selected for identification using API® 20 NE. Among 22 isolates identified to date: *Aeromonas hydrophila/caviae* (n = 13), *Aeromonas sobria* (n = 2), *Vibrio alginolyticus* (n = 1), *Mannheimia haemolytica* (n = 2), *Burkholderia* cepacia (n = 1), Pseudomonas putida (n = 1), Pseudomonas *fluorescens* (n = 1), and *Ralstonia pickettii* (n = 1) were found. Further identification using MALDI-TOF MS was performed on isolates from the sampling campaign. Comparison of the results for 15 *Aeromonas* spp. and one *Vibrio* isolate identified by API® 20 NE showed full agreement for all *Aeromonas* spp. The isolate initially identified as *Vibrio* by API® 20 NE was reclassified as *Aeromonas* spp. by MALDI-TOF. Confirmed *Aeromonas* isolates will undergo antimicrobial susceptibility testing and whole-genome sequencing to assess their AMR profiles.

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60. Interest of a diet enriched with organic Selenium during finishing period for BBB beef production

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Selenium (Se) is an essential trace element involved in antioxidant status, immune function, and selenoprotein synthesis. Organic Se (SeOrg), such as selenomethionine (SeMet), is more bioavailable and less toxic than inorganic forms. We compared 0.5 ppm Se supplementation as SeMet or sodium selenite (inorganic form, SeI) in 12 Belgian Blue cows over a 90-day finishing period. Blood Se, glutathione peroxidase activity, blood vitamin E, and meat quality including total Se content and Se speciation were assessed. Baseline plasma Se was similar in both groups. Plasma Se increased in both (SeOrg +20.1 µg/L; SeI +15.0 µg/L), and glutathione peroxidase tended to be slightly higher in SeOrg, but neither difference was statistically significant. Blood vitamin E was significantly higher in SeOrg (17.1 vs. 9.8 µg/mL), indicating improved antioxidant status. Meat from SeOrg cows contained higher total Se (*Rectus femoris* 0.682 vs. 0.493 mg/kg DM; *Longissimus thoracis* 0.642 vs. 0.498 mg/kg DM) and SeMet (2.1-fold increase), while fatty acid composition and most technological parameters were not affected by any Se forms. Color stability was improved in SeOrg meat. These findings demonstrate that SeMet supplementation efficiently increases muscle Se, enhances antioxidant activity during finishing, and produces nutritionally enriched meat capable of meeting daily human Se requirements with 100 g serving without exceeding safe intake. Belgian Blue cattle show remarkable Se storage capacity, highlighting their potential for high quality meat production.

61. Isolation and characterization of bacteriophages targeting carbapenem-resistant *Klebsiella pneumoniae* from Tunisian hospital.

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The global burden of antimicrobial-resistant *Klebsiella pneumoniae*, especially the increase of carbapenemase-producing strains (CRKP), presents a rising challenge to public health. These bacteria commonly harbored the carbapenemase-encoding genes on mobile genetic elements, thereby promoting further resistance dissemination and severely subsequently limiting treatment options. From March to September 2024, a total of 58 CRKP was recovered from a hospital in Sousse, Tunisia and investigated using PCR, antimicrobial susceptibility (CLSI), whole genome sequencing (Illumina technology). Resistance genes (*blaNDM-5, blaOXA-48, blaCTX-M-15*) and plasmids (IncF, IncL) were detected as well as the major capsular types KL51 and KL64 associated with the high-risk ST147 clone. Eight wastewater samples were screened for phages targeting the dominant capsular types. Thirteen phages were isolated with the enrichment method, and amplified by double layer agar technique with titers between 2.3×10^{6} PFU/ml to 2.8×10^{9} PFU/ml. Preliminary genomic analysis have indicated that nine of these phages were obligately lytic. Most of the phages had a high efficiency of plating (≥ 0.5) and also a rapid adsorption ($\leq$10 min for 90% of particles, $k = 1.5\times10^{-8}$ mL/min). These results highlight the importance of combining bacterial molecular epidemiology to phage isolation to counteract multidrug-resistant *K. pneumoniae*, paving the way for personalized phage cocktail design.

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62. Study of *Staphylococcus aureus* behaviour and enterotoxin production in a model of Belgian smear-ripened cheese

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Staphylococcal food poisoning (SFP) is caused by the ingestion of food contaminated with staphylococcal enterotoxins (SEs), particularly in dairy products. While classical SEs are typically implicated, recent studies have identified *S. aureus* strains involved in SFP that lack classical SE genes but carry genes encoding new SEs. This study replicated the production of smear-ripened cheese under Biosafety Level 2 conditions, evaluating two contamination routes: inoculation of milk after pasteurization and contamination during the rind-washing process. In trial 1, milk was inoculated with a *S. aureus* strain harboring the sec, sei, and seg genes. In trial 2, cheese was inoculated during the washing step. Bacterial growth was monitored using culture-based methods, qPCR and metagenetic analysis. Toxin production was assessed via immunological assays. Results showed that *S. aureus* growth during the acidification phase and declined during ripening and storage. SEI was detected at low concentrations, while SEC was not detected despite the presence of its gene. Discrepancies between culture, qPCR, and metagenomic data suggest that *S. aureus* may have entered a viable but non-culturable state. In the second trial, the strain was not recovered by culture, and qPCR indicated a slight decline. Metagenomics failed to detect *S. aureus*, likely due to its low abundance and limited sequencing depth. In conclusion, the findings suggest a higher risk when contamination occurs early in the production process. Future research will focus on the effects of inoculum size, strain variability, and cheese-making parameters to better understand the dynamics of new SE production and enhance food safety strategies.

63. CRISPR/Cas9-Mediated Deletion of the mCherry Reporter from an ORF35-Deleted *Anguillid herpesvirus 1* Vaccine Strain

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Cyvirus anguillidallo 1 (AngHV-1) is a major pathogen of several eel species, causing substantial economic losses in eel aquaculture. In this study, we aimed to modify a previously developed attenuated *ORF35*-deleted AngHV-1 vaccine strain carrying dual fluorescent markers, a mCherry expression cassette replacing ORF35 and an EGFP expression cassette inserted in a non-coding region between ORF32 and ORF33. The red (mCherry) and green (EGFP) signals allow direct visualization of viral replication and discrimination between recombinant populations. We employed CRISPR/Cas9-mediated genome editing to remove the mCherry reporter and generate a recombinant strain expressing only EGFP, this approach could be used to apply marker free vaccine candidate. Four single-guide RNAs (sgRNAs) targeting distinct sites within the mCherry open reading frame were designed to ensure efficient cleavage. Viral DNA extracted from the dual-fluorescent AngHV-1 strain was incubated *in vitro* with CRISPR Cas9 RNP complex to achieve targeted double-strand breaks. The CRISPR-cleaved DNA was subsequently separated using phenol-chloroform method and transfected into EK-1 cells along with desired plasmid to allow rescue of recombinant viral progeny by homologous directed recombination. The resulting virus exhibited exclusive green fluorescence, confirming successful deletion of the mCherry cassette. This work demonstrates, for the first time, the feasibility of CRISPR/Cas9-mediated *in vitro* for editing of AngHV-1 genomic DNA and establishes a versatile approach to generate high successive rate of genetically defined attenuated vaccine strains for further functional and immunogenicity studies.

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64. Development and Validation of a High-Dimensional Spectral Flow Cytometry Panel for Immune Phenotyping of Canine Whole Blood

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Flow cytometry is an immunophenotyping tool of choice in the context of clinical, translational and systems immunology studies. Although dogs are increasingly recognized as valuable translational clinical models, progress in canine immunology is constrained by the limited development of such technique and availability of validated reagents. New generation of flow cytometers with spectral technology enable high-dimensional immune cell characterization.

The objective of this study was (1) to develop and validate a spectral flow cytometry panel for immune phenotyping of canine whole blood, and (2) to perform in-depth characterization of immune cell subsets isolated by fluorescence-activated cell sorting, using single-cell RNA sequencing.

In the first phase of this study, we developed a high-dimensional flow cytometry panel comprising 19 fluorescent markers, optimized for cryopreserved whole blood samples from dogs, using a spectral flow cytometer. As a starting point for analysis, we used unsupervised clustering and visualization techniques unveiling unexpected immune cell populations. From these, we established a supervised gating strategy to define 35 immune cell phenotypes. Then, we selected 13 subpopulations of interest, sorted them using a spectral cell sorter and performed single-cell RNA sequencing. This approach enabled the validation of the immunophenotypic profiles and revealed the transcriptional heterogeneity within our marker-defined immune cell subsets.

The development and validation of this spectral flow cytometry panel not only provide a valuable tool for canine immunology but also holds great potential to bridge existing gaps in comparative immunology.

65. Evolutionary adaptation of *Cyvirus cyprinidallo* 3 (CyHV-3) ORF131 by lateral gene transfer from carp

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Cyvirus cyprinidallo 3 (CyHV-3) is a major pathogen of common carp (*Cyprinus carpio*), and its genome evolution offers valuable insights into host–virus interactions. This study focused on CyHV-3 ORF131, a gene assumed to have originated in part from the genome its host. Comparative genomic analyses suggested that CyHV-3 ORF131 underwent several evolutionary events, including non-homologous recombination with a host locus, shortening of non-coding regions, homologous directed recombination and accumulation of point mutations, ultimately giving rise to the current version of the gene. To evaluate the functional consequences of these molecular events, recombinant strains representing hypothesized evolutionary intermediates were generated and analyzed both *in vitro* and *in vivo*. The strains represented: (i) what is thought to be the ancestral strain before lateral gene transfer from the host genome (ancestral strain); (ii) what is thought to be the strain after acquisition of a sequence derived from the C locus of the host genome (C strain), (iii) what is thought to be a recombinant strain between the C strain and the B locus of host genome (C+B strain). These strains were compared to actual (OTU) CyHV-3 strain representing the C+B strain with mutations acquired by the virus. Replication kinetics revealed that all the recombinant strains replicated efficiently, although the C strain grew slower and the ancestral variant formed smaller plaques. Infection trials in common carp revealed that the ancestral strain and the C strain had no negative impact on fish health, whereas the C+B strain induced a milder disease than the OTU strain. Six weeks post-infection with the different strains, fish were challenged with the OTU CyHV-3 Luc strain. These experiments revealed that the protective immune response induced by the recombinants was inversely related to their virulence, with the ancestral strain providing the lower immune protection. Together, these data demonstrate that the evolution of the CyHV-3 ORF131 gene through lateral gene transfer from the host genome contributed to the adaptation of this virus to carp.

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66. In vivo modeling of dermatophytosis reveals infection dynamics influenced by the ecological niche of the fungus but a conserved host immune response

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Dermatophytoses are superficial skin infections caused by keratinophilic filamentous fungi known as dermatophytes and represent the most common fungal infections worldwide. Dermatophyte species are classified by their ecological niches - anthropophilic (human-associated), zoophilic (animal-associated) or geophilic (soil-dwelling) - which affects their mode of transmission, host specificity and pathogenicity. To characterize the infection mechanisms, we used a murine infection model and three dermatophyte species: Trichophyton rubrum (anthropophilic), Microsporum canis (zoophilic) and Nannizzia gypsea (geophilic). Clinical scoring and histopathological analyses were performed to assess the severity of infection and tissue damage. Relative RNA expression levels of fungal proteases (deuterolysin, subtilisins 6 and 10) and host cytokines (interleukins 1β, 17A and 22) were determined to characterize the host-pathogen interaction. Infection dynamics varied between species: T. rubrum caused moderate lesions, M. canis caused a more persistent infection with delayed healing, while N. gypsea caused acute and severe inflammation. All species overexpressed the three fungal proteases studied, and host responses were dominated by a Th17 profile with an upregulation of three interleukins during infection. The results obtained from our murine model revealed a coordinated and conserved expression level of fungal proteases and host cytokines, demonstrating dynamic host-pathogen interactions. We also highlighted the variability of infection depending on the ecological niche of the dermatophyte, in terms of lesion severity and tissue invasion.

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67. Monitoring of *Orthoflavivirus usutuense* circulation in wild bird populations in Wallonia (2023–2024)

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The *Orthoflavivirus usutuense* (USUV) and *Orthoflavivirus nilense* (WNV), both belonging to the *Orthoflavivirus* genus, are emerging arboviruses in Europe.

The objectives of this study were to investigate the presence and circulation of USUV, and to monitor the potential emergence of WNV in wild bird populations across Wallonia during the 2023–2024 period.

A passive surveillance program was conducted and a total of 1,274 bird carcasses, collected from nine wildlife rehabilitation centers, were examined. After necropsy, various tissue samples were analyzed using RT-qPCR, and USUV-positive samples were subsequently subjected to Sanger sequencing.

No WNV cases were identified in Wallonia during the 2023-2024 period. In contrast, 180 USUV cases were confirmed, corresponding to an overall prevalence of 14.61% in 2023 and 13.69% in 2024. The virus was detected in 11 avian orders and 33 different species, confirming its broad host range. The Eurasian blackbird (*Turdus merula*) was the most affected species, followed by the Eurasian jay (*Garrulus glandarius*). The Eurasian sparrowhawk (*Accipiter nisus*) and the European green woodpecker (*Picus viridis*) were identified as USUV-positive for the first time in Europe.

The high prevalence (44%) observed in blackbirds during 2023–2024 indicates a resurgence of USUV and suggests a cyclical pattern of viral activity. The increase in juvenile cases in 2024 may reflect the development of herd immunity within avian populations.