7th International Conference of the European College of Veterinary Microbiology (ECVM)

Wednesday 10 September 2025 - Friday 12 September 2025

Kaiserin-Friedrich-Stiftung, Berlin

Programme

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Wednesday 10 September 2025

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Welcome Talk and Soft Opening (18:00 - 20:00)

Thursday 11 September 2025

Check-in - Foyer (ground floor) (08:30 - 09:00)

Introduction and Welcome - Lecture Hall (09:00 - 09:30)

Keynote Lecture: Martin Beer - Lecture Hall (09:30 - 10:15)

-Conveners: Fulde, Marcus (Freie Universität Berlin)

[157] Viral Zoonoses in Germany: What Lurks in the Reservoirs? (09:30)

Presenter: BEER, Martin (Institut für Virusdiagnostik, Friedrich-Loeffler-Institut, Suedufer 10, 17493 Greifsald-Insel Riems)

Viral zoonoses pose a persistent and evolving threat to public health in Germany, where various animal reservoirs harbor significant pathogens. Wild birds play a central role in the ecology of highly pathogenic avian influenza viruses, such as H5N1. Recurrent outbreaks affect wild birds and domestic poultry, and spillover infections in different mammalian species occur. Swine are important reservoirs for swine influenza viruses, which have the potential to reassort and transmit across species. Birds and mosquitoes maintain the circulation of the West Nile virus, a pathogen that has become established in parts of Germany in recent years. Additionally, shrews are recognized as natural hosts of Borna disease virus 1, a rare but severe zoonotic pathogen. Ticks and small mammals sustain the transmission cycle of the tick-borne encephalitis virus, an endemic flavivirus with an increasing incidence in humans in Germany. Beyond these established risks, novel threats may emerge. For instance, biting midges (Culicoides spp.) and ruminants could transmit exotic arboviruses, such as the Oropouche and Shuni viruses. These potential incursions raise concerns under changing climatic, ecological, and globalization conditions. In this context, we will discuss the various zoonotic risks, emphasizing the indispensable role of the One Health approach in surveillance, prevention, and research efforts.

Coffee (10:15 - 10:45)

Keynote Lecture: Ilse Jacobsen - Lecture Hall (10:45 - 11:15)

-Conveners: La Ragione, Roberto (University of Surrey); Ghazisaeedi, Fereshteh (Freie Universität Berlin)

[162] The commensal to pathogen transition of Candida albicans (10:45)

Presenter: JACOBSEN, Ilse D. (Leibniz Institute for Natural Product Research and Infection Biology)

Candida albicans is a pathobiont in warm-blooded animals that can cause various mucosal infections as well as life-threatening disseminated disease. Diagnosis of systemic candidiasis is challenging due to unspecific symptoms, low sensitivity of blood culture, and lack of standardized biomarkers differentiating colonization and infection. Delayed diagnosis and limited treatment options result in high mortality rates, which led to C. albicans being assigned to the Critical Priority Group of fungal pathogens by the WHO. Although case reports suggest that mucosal and systemic candidiasis occur in different animal species, resembling infections in humans, lack of awareness in veterinary medicine likely results in underdiagnosis. Here, I will summarize the current knowledge on why and how C. albicans shifts from a commensal lifestyle to invasive growth, and highlight how tissue-specific difference shape host-pathogen interactions on different mucosal sites. By investigating different C. albicans strains, we found that strain heterogeneity impacts adaptation to and survival on different mucosal surfaces, with consequences for virulence but also immunological responses to colonization. The later in turn affects host immunity to systemic candidiasis caused by colonizing C. albicans strains. Furthermore, it can reduce susceptibility to bacterial infections, raising the question whether eradicating C. albicans colonization is a desirable goal.

Keynote Lecture: Kristin Heenemann - Seminar Room (10:45 - 11:15)

-Conveners: Friese, Anika (Freie Universität Berlin); Papageorgiou, Konstantinos (Aristotle University of Thessaloniki)

[163] Paramyxovirus infections in small animals and rodents: an update (10:45)

Presenter: HEENEMANN, Kristin (University of Leipzig, Faculty of Veterinary Medicine, Institute of Virology)

Paramyxoviruses have significant impact on veterinary medicine and global public health. The family Paramyxoviridae includes significant pathogens such as the Measles virus (the causative agent of measles) and Rinderpest virus, which has now been eradicated worldwide. The relevance of these enveloped, single-stranded RNA viruses is further highlighted by the global impact of Canine Distemper Virus (CDV) on carnivores. The epidemiological and clinical implications of these viruses are far-reaching, affecting a wide range of host species, including companion animals (such as ferrets), rodents (mice), poultry, and marine mammals. The zoonotic potential of selected paramyxoviruses like Hendra virus (HeV) and Nipah virus (NiV), which can be transmitted to humans from intermediate animal hosts like horses and pigs, emphasizes the "One Health" paradigm and the interconnectedness of animal, human, and environmental health. Understanding infection dynamics requires elucidating their complex transmission routes, including direct contact, aerosol transmission, and indirect environmental pathways. Prominent paramyxoviruses in veterinary practice include the Feline Morbillivirus (FeMV), which is frequently associated with renal pathologies in cats, and the Canine Parainfluenzavirus (CaPIV), a key etiological agent in canine respiratory disease complexes. Other examples, like the Sendai virus in mice, highlight the phylogenetic diversity that continues to gain relevance with the discovery of new viruses like the Jeilongvirus, an emerging virus with implications for research integrity and animal welfare. This overview aims to deepen the scientific and clinical understanding of paramyxovirus infections in small animals and rodents. It seeks to foster improved veterinary surveillance, effective disease control, and enhanced public health preparedness.

Bacterial Pathogenicity - Lecture Hall (11:15 - 12:45)

-Conveners: La Ragione, Roberto (University of Surrey); Ghazisaeedi, Fereshteh (Freie Universität Berlin)

[24] Highly variable Receptor Binding Proteins in Tequatrovirus phages targeting Escherichia coli contribute to their host specificity (11:15)

Presenter: DIDERICH, Jacob (University of Liège)

Bacteriophages, particularly those targeting E. coli, are known for their specificity. The narrow host ranges of four isolated Tevenvirinae phages targeting E. coli prompted us to investigate their Receptor Binding Proteins (RBP), which binds to bacterial receptors during adsorption. A better understanding of the factors determining the host range is crucial to select phages for treatments. The serotypes of 53 strains isolated from bovine mastitis was determined and associated with the host range. To identify RBPs, the phage genomes were annotated and aligned with their 5 closest homologs in databases. Proteins with low nucleotide identities and located in the tail were further analyzed using phageDPO to detect depolymerase activity. Finally, the 3D structure of the selected proteins were predicted and the normalized RMSD scores were calculated. The host range showed limited dependance on the serotype. In all phages, both long and short tail fibers were identified as RBPs and displayed depolymerase activity. Analyze of the 3D structure and the RMSD revealed a highly specific reversible attachment to the distal subunit of the long tail fiber, followed by a less specific irreversible attachment to the short tail fiber. In conclusion, although phages from the same genus have the same located RBP's, mosaïcism drives their specificities. Further investigations should try to identify the bacterial receptors to predict the interaction between the RBP and its receptor.

[103] Capsular polysaccharide promotes a stealth-like immunological state towards Mycoplasma mycoides (11:30)

Presenter: JORES, Joerg (University of Bern)

Mollicutes are minute cell wall less bacteria encompassing important pathogens. We show that pathogenic *Mycoplasma mycoides* can switch expression of capsular polysaccharide (CPS) which creates phenotypic diversity and had dramatic repercussions on immune responses. For characterizing the immune responses, we employed the highly virulent wild-type GM12 as well as its engineered CPS-deficient mutant strain in a set of assays employing primary blood cells from its native ruminant host. Primary blood cells stimulated with GM12 showed only very moderate effects on apoptosis as well as activation marker expression supporting an immunological stealth-like lifestyle. Interestingly, GM12 showed the capacity to survive and replicate inside monocyte-derived macrophages (MDMs), which fosters dissemination and persistence in the host. Stimulation with the CPS-deficient mutant strain, which exposes surface proteins including lipoproteins, increased apoptosis, strongly suppressed expression of major histocompatibility complex on antigen-presenting cells and induced secretion of several pro-inflammatory cytokines/chemokines which is a clinical hallmark in infected animals. Moreover, the CPS-deficient strain elicited apoptosis in MDMs. In conclusion, we showed that M. mycoides can switch the expression of CPS, which leads to different immunological trajectories paving the way for clinical disease, dissemination and persistence in the host.

[76] Mono- and Co-Infections of Primary Porcine Respiratory Cells with Bordetella Bronchiseptica and Streptococcus Suis Are Not Affected by the Dermonecrotic Toxin (11:45)

Presenter: Dr SCHAAF, Désirée (Institute for Microbiology, University of Veterinary Medicine Hannover, Foundation, Hannover, Germany)

Bordetella bronchiseptica is a Gram-negative bacterium that contributes to respiratory infections in many different animal species. In swine, it is involved in the Porcine Respiratory Disease Complex as well as in atrophic rhinitis. One of its virulence factors, the dermonecrotic toxin (DNT), is partly responsible for the destruction of the nasal conchae, by having detrimental effects on osteoblastic cells. Remarkably, only little is known about the interactions between DNT and respiratory epithelial cells. We investigated the role of DNT during mono- and co-infections of porcine respiratory epithelial cells *in vitro* by using porcine precision-cut lung slices (PCLS) and air-liquid interface (ALI) cultures. PCLS and ALI cultures were first infected with a DNT-positive wild-type strain or its isogenic DNT-deficient mutant strain and subsequently infected with *Streptococcus suis* for co-infection experiments. During infection, we determined cytotoxic effects and the colonization capacity of both pathogens as well as cytokine expression and secretion of the host cells. We found no evidence that DNT contributes to colonization or cytotoxic activity of *B. bronchiseptica* neither does it facilitate co-infection with *S. suis* in any way. Pro-inflammatory cytokines were primarily produced upon infection with *B. bronchiseptica*, independent of DNT, but hardly upon infection with *S. suis*, whereas co-infection with both pathogens resulted in higher cytokine levels.

[102] The global epidemiology of Streptococcus canis identifies genomic features of host adaptation, virulence and antimicrobial resistance (12:00)

Presenter: Dr DRESEN, Muriel (Institut für Mikrobiologie und Tierseuchen, Freie Universität Berlin, Berlin, Germany)

Streptococcus canis can cause severe infections mainly in dogs, cats, and cattle with symptoms such as keratitis, dermatitis, endocarditis, sepsis, or mastitis, but also occasionally causes zoonotic disease in humans. Infections of companion animals have dramatically increased in Europe over the last decades leading to increased antibiotic usage due to the lack of alternative

treatment options. To better understand host adaptation, antimicrobial resistance, and evolutionary dynamics, we analysed the genomes of over 800 S. canis isolates from different host species and geographical locations. Lineages tended to be comprised of either one of two S. canis M (SCM) protein types, one of the pathogen's most important virulence factors. In addition, bovine S. canis isolates significantly clustered together on the phylogenetic tree suggesting a degree of host adaptation. The isolates typically had around six antimicrobial resistance genes mostly belonging to the classes tetracyclines, macrolides and aminoglycosides. We did not detect any beta-lactam resistance, but penicillin-binding-protein (pbp) genes exhibited different allele patterns. In conclusion, this work provides fundamental knowledge on the transmission and host adaptation of S. canis for establishing a prediction pipeline to assist diagnostic labs in genomic epidemiology studies. Although no beta-lactam resistance is reported in S. canis, variation in pbp alleles might assist in selection for resistance in the future.

[121] Investigation of the clade-specific pathogenic potential of Campylobacter coli (12:15)

Presenter: BEYER, Sarah (Institute of Food Safety and Food Hygiene, Freie Universität Berlin)

Human campylobacteriosis is a major foodborne disease, with ~11% due to *Campylobacter coli* (*C. coli*) infections. Most *C. coli* strains isolated from human cases belong to clade 1A. In contrast, clade 2 and 3 strains are less frequently identified in human cases, but are widespread in the environment. This study aims to investigate whether *C. coli* strains of clades 2 and 3 exhibit lower pathogenic potential than clade 1A strains. Human colonic cell lines (HT-29/B6, T84) were used for *in vitro* assays to determine the cytotoxicity (WST-1-assay), as well as the adhesion- and invasion-ability of *C. coli* strains belonging to clades 1A, 1C, 2 and 3, respectively. All *C. coli* strains were able to adhere to and invade both cell lines, with strain-dependent variances. The cytotoxic potential of clade 3 strains was exceeding those of the other clades, as they reduced the metabolic activity of HT-29/B6 cells as early as 18h after infection. A similar reduction induced by most strains from other clades was observed only after 48h. However, reduction of the metabolic activity of T84 cells was exclusively measurable after infection by clade 3 strains after 48h. In conclusion, our results indicate a higher cytotoxic potential for *C. coli* clade 3 strains, whereas no apparent difference in the adhesion or invasion ability could be detected. Therefore, the lower prevalence of clade 3 strains in human cases appears to depend on factors other than those investigated in this study.

[25] Efficiency test of a live, attenuated Mycoplasma hyorhinis vaccine candidate strain (12:30)

Presenter: NAGY, Eszter Zsofia (HUN-REN Veterinary Medical Research Institute, Budapest, Hungary)

Background: Mycoplasma (M.) hyorhinis causes significant economic losses in swine. Prevention and treatment rely on antibiotics, as no vaccines are available in Europe. However, antibiotics cannot eliminate the bacteria. Applying an efficient vaccine would provide a long-term control method, reducing the economic losses. Materials and methods: A temperature-sensitive M. hyorhinis strain was developed via 1-methyl-3-nitro-1-nitrosoguanidine treatment. The immunogenicity and efficacy of the adjuvanted, attenuated vaccine candidate were tested. Three-week-old piglets were immunized, and the vaccination site was monitored daily. At six weeks, the pigs were challenged on two subsequent days. Clinical exams were conducted daily, and blood and nasal swabs collected weekly for M. hyorhinis ELISA, real-time PCR, and isolation. Three weeks post-challenge, animals underwent gross and histopathological examinations. Body temperature was recorded daily, and body weight was measured at arrival, six, and nine weeks. Results: Vaccination reduced clinical ($p=0.001$), gross pathological ($p<0.001$), and histopathological ($p<0.001$) lesions. The vaccinated group showed earlier, higher M. hyorhinis-specific antibody levels post-challenge. However, vaccination did not prevent weight gain reduction. Discussion: Overall, the adjuvanted, attenuated strain provided adequate protection. The attenuated strain was patented under number P2500036 at the Hungarian Intellectual Property Office.

Viral Epidemiology and Case Reports - Seminar Room (11:15 - 12:45)

-Conveners: Friese, Anika (Freie Universität Berlin); Papageorgiou, Konstantinos (Aristotle University of Thessaloniki)

[43] A case report of equine infectious anemia in the Netherlands (11:15)

Presenter: GRAHAM, Heather (Wageningen Bioveterinary Research, Wageningen University and Research, Lelystad, The Netherlands)
Equine infectious anemia (EIA) is a notifiable viral disease in equids caused by a vector-borne lentivirus. In March 2025, EIA was diagnosed in a horse in the Netherlands for the first time since 2017. The animal showed no clinical signs of illness and originated from Eastern Europe, where EIA is endemically present. The infection came to light when the horse was tested for antibodies against EIAV as part of an export screening. Official samples were collected and tested positive according to the ELISA and Coggins test. Consequently, necropsy was performed and tissue samples were sent to the European Reference Laboratory for EIA (ANSES, France). EIAV genomic DNA was detected in samples from the liver, spleen and mesenteric lymph nodes by realtime-PCR, while RNA detection was unsuccessful. Molecular characterization of the isolated strain is ongoing. The horse had been residing in the Netherlands for three years and following an investigation by the authorities, 40 horses with an epidemiological link at three different locations were traced and sampled twice for serological screening. The second sampling took place after a period of 90 days, during which the horses were quarantined. In addition, movement of horses and manure was not allowed on these locations. All horses tested negative during the first and second round of sampling. This case highlights the importance of the screening of animals to prevent the introduction of infectious diseases into non-endemic areas.

[44] First outbreak of emerging ha-MYXV-associated myxomatosis in European hare (Lepus europaeus) in Austria (11:30)

Presenter: AUER, Angelika (Department of Biological Sciences and Pathobiology, Infectiology and Virology, University of Veterinary Medicine, Vienna, Austria)
In the spring of 2025, an unusually high number of dead European hares (Lepus europaeus) were found in a region northeast of Vienna, Austria. Pathological and histological examinations revealed typical swellings around the eyes, nose and genital tract with epithelial viral inclusions, consistent with a poxvirus infection. PCR analysis and cytopathic effects on RK13 cells confirmed the presence of the Myxoma virus, and sequencing of the M009L gene region identified the characteristic 2.8 kb insertion associated with the highly pathogenic ha-MYXV strain. Myxomatosis is a severe disease primarily affecting wild and domestic rabbits (Oryctolagus cuniculus). Originally introduced to Europe in the 1950s, the virus has since become endemic in many countries, with variants of differing pathogenicity emerging over time. However, these variants have historically posed little threat to hares. In 2018, the recombinant ha-MYXV strain emerged on the Iberian Peninsula, causing significant declines in Iberian hare (Lepus granatensis) populations. This report marks the first documented outbreak of ha-MYXV-associated myxomatosis in European hares in Austria. Genome sequencing and epidemiological analyses are currently being carried out to better understand the evolution and spread of this emerging pathogen. Given the potential impact of myxomatosis, along with other infectious diseases, continuous monitoring of European hare populations is essential to mitigate future threats.

[54] Discovery of novel hepadnaviruses in passerine birds (11:45)

Presenter: PELLEGRINI, Francesco (University of Bari Aldo Moro)
The Hepadnaviridae family comprises circular DNA viruses with hepatotropism [1]. The genome sequence of a novel avian hepadnavirus was serendipitously generated in a passerine ornamental bird while performing a sequence-independent enrichment protocol for circular DNA, based on rolling cycle amplification (RCA) [2]. An archival collection of samples was screened with a specific qPCR, with an overall prevalence of 7.9% (8/101). The presence of replicative covalently closed circular DNA (cccDNA), indicative of active viral replication, was confirmed in embryonated eggs, feather quills, and liver through RCA enrichment and inverse PCR [3]. By in-depth sequencing on Oxford Nanopore TechnologiesTM (ONT) platform, the whole genome sequence was obtained from 3 strains detected in Gouldian finch (Chloebia gouldiae), Society finch (Lonchura striata domestica) and Long-tailed finch (Poephila acuticauda). On phylogenetic analysis, the viruses were genetically distinct from other known avian hepadnaviruses, thereby forming a novel viral clade. These findings expand the known host range of hepadnaviruses to passerine birds. More importantly, they suggest potential vertical and feather-based transmission routes, as observed for other avian viruses [4,5]. The identification of hepadnavirus DNA in feather quills also represents a valuable, non-invasive method for future epidemiological surveillance in wild and domestic avian populations.

[12] Case report of a cat infected with EBLV-1 in the Netherlands (12:00)

Presenter: EBLÉ, Phaedra (Wageningen Bioveterinary Research (WBVR))
In October 2024 an infection of European bat lyssavirus type 1 (EBLV-1, lyssavirus Hamburg) was confirmed in a domestic cat in the Netherlands. The cat started to show abnormal behavior on October 22nd. Several weeks before, the animal owners had found a dead bat in their home, which was thought to be caught by the cat. At October 25th the cat was euthanized and sent to the national reference laboratory for veterinary rabies of the Netherlands, Wageningen Bioveterinary Research. Brain material of the cat tested positive in the fluorescent antibody test. Subsequently, the genotype specific Realtime-PCR (RT-PCR)test for EBLV-1 tested positive. Additionally, salivatory gland material and swab material from the mouth of the cat tested positive for EBLV-1 in

the RT-PCR, indicating potential infectiousness of the cat. Histopathology of formalin-fixed and paraffin-embedded sections of the brain showed a viral encephalitis with positive immunohistochemical staining against rabies nucleocapsid protein. Using Oxford nanopore technology, the entire genomic sequence could be determined. Persons exposed to the cat received post-exposure prophylaxis and domestic animals from the same household were quarantined. Pet owners in the same (rural) municipality were informed and were requested to report behavioral changes of pets immediately to a veterinarian. This case stresses the need for vigilance of rabies infections of pets in countries where lyssavirus infections in bats are endemic.

[26] Black proventriculus in broiler chicks: recent Italian clinical case and laboratory findings (12:15)

Presenter: GIOVANARDI, Davide

Avian colibacillosis refers to any localised or systemic infection caused entirely or partly by avian pathogenic Escherichia coli (APEC). It includes colisepticemia, air sac disease, peritonitis, salpingitis, synovitis, and, in young birds, yolk sac infection. Over the past decade, a new syndrome known as “Black proventriculus-Bp,” caused by APEC, has been recognised in two different broiler breeding farms (Wang et al., 2015; Talebi et al., 2020). In Italy in 2025, we observed eleven clinical cases of Bp in broiler chicks aged three to six days. One hundred and thirty-three chicks were necropsied and submitted for bacteriology and histological examination. Thirty per cent of chicks displayed the classical Bp lesion, while the remainder exhibited a combination of pericarditis and omphalitis/yolk sac infection. Escherichia coli of different serotypes (O88, O45, O15, O1) was isolated as the sole bacteria from the mucosa of the proventriculus in Bp lesions. The strains isolated were classified as weak biofilm producers. The histological investigation in one clinical case showed catarrhal erosive bacterial proventriculitis with mild ectasia of the submucosal glands, cellular necrotic cells, and bacteria in the lumen. Vascular congestion and bacteria in the lumen of the vessels, as well as fibrinous bacterial serositis with the presence of rare macrophages and heterophils. Etiopathogenetic hypotheses will be speculated and presented at the Scientific Symposium.

[100] Coronavirus detection in British Red Foxes (Vulpes vulpes) (12:30)

Presenter: PARKER, Charlotte (University of Nottingham)

Britain has eight species of carnivorous wild mammal which, in their international populations, are known to be susceptible to a range of Alphacoronaviruses and Betacoronaviruses (CoV’s). Previous work in 2020-2021 to determine if SARS-CoV-2 was present in UK wildlife demonstrated no detection of this pandemic virus. However, a novel mustelid coronavirus, a previously uncharacterised stoat Minacovirus, was discovered. Further to this, in 2022 a highly divergent coronavirus (*MelesCoV*) in Italian badgers (*Meles meles*) was reported, that to date, has not been found in UK animals. Over 500 carnivore samples have been screened, the sample type dependant on the requirements of the sample provider (samples including faecal and tissue (lung and enteric lymph node) samples, as well as oronasal and rectal swabs). Samples were preserved with RNAlater. RNA was extracted using ThermoFisher’s Kingfisher Apex and screened for CoV’s using pan-coronavirus primers. PCR positive results have been found in a Red Fox (*Vulpes vulpes*) rectal swab. Sanger and Illumina sequencing were conducted, and downstream bioinformatic pipelines identified the sequence as a coronavirus similar to other canid and canine viruses. Britain’s wild carnivores play an important role in ecosystems, with red foxes inhabiting both wild and urban habitats. Determining the presence of coronaviruses within these animals is critical to our preparedness for the emergence and detection of novel viruses.

Lunch & Poster (12:45 - 14:15)

Keynote Lecture: Asisa Volz - Seminar Room (14:15 - 14:45)

-Conveners: Salvaggiulo, Anna (University of Bari "Aldo Moro"); Ludlow, Martin (University of Veterinary Medicine Hannover)

[158] New vaccines against emerging zoonotic infections: From animal models to clinical evaluation (14:15)

Presenter: VOLZ, Asisa (Stiftung Tierärztliche Hochschule Hannover, Bünteweg 2, 30559 Hannover)

Modified Vaccinia virus Ankara (MVA) is a licensed third-generation smallpox vaccine and a potent vector platform for developing vaccines against infectious diseases and cancer. Developed by serial passage in chicken cells, MVA lost replication ability in mammalian hosts and many orthopoxvirus virulence genes, enhancing its safety profile. MVA-based vaccines have demonstrated safety, immunogenicity, and protective efficacy in animal models, including an MVA-MERS-S candidate tested successfully in dromedary camels—the primary MERS-CoV reservoir—supporting its use as a One Health strategy to prevent zoonotic transmission. Clinical safety and immunogenicity of MVA-MERS-S were confirmed in a phase I human trial, with phase II studies underway in Europe. Recent preclinical work on MVA-based COVID-19 vaccines showed that a recombinant MVA expressing stabilized SARS-CoV-2 spike protein (MVA-SARS-2-ST) elicited superior S1 surface expression and stronger neutralizing antibody responses across variants compared to the native S protein. Intramuscular vaccination with MVA-SARS-2-ST protected mice and hamsters from disease and lung pathology upon challenge. These results support MVA-SARS-2-ST as an improved clinical vaccine candidate, highlighting the importance of membrane-bound S1 for protective immunity.

Keynote Lecture: Elke Genersch - Lecture Hall (14:15 - 14:45)

-Conveners: Zendri, Flavia (University of Liverpool); Scarpellini, Raffaele (University of Bolgona)

[156] Pathogenesis of P. larvae - 20 years of research on an important but understudied bacterial pathogen (14:15)

Presenter: GENERSCH, Elke (Institute for Bee Research, Dept. f. Molecular Microbiology & Bee Diseases, Friedrich-Engels-Str. 32, 16540 Hohen Neuendorf)

American foulbrood (AFB) is one of the most important and devastating infectious diseases of the Western honey bee Apis mellifera. It is caused by the gram-positive, spore-forming bacterium Paenibacillus larvae, which not only kills the brood of a colony but also the entire colony as the disease progresses. Since P. larvae is highly infectious and contagious, the disease spreads very easily within a colony and between colonies. Therefore, AFB is listed as a notifiable animal disease in many countries. The species P. larvae is divided into several, so-called ERIC-genotypes, which also differ phenotypically. Only two of these genotypes, ERIC I and ERIC II, are currently driving the global AFB-outbreak situation. P. larvae ERIC I and ERIC II differ in their suite of expressed virulence factors resulting in variations in pathogenesis and virulence differences. Over the past two decades, we have intensively studied the species- and genotype-specific virulence factors of P. larvae, thereby deepening our understanding of the molecular pathogenesis of AFB. We have identified a chitin-degrading protein as key virulence factor of the species P. larvae, toxins and an S-layer protein as genotype-specific virulence factors, and unravelled the role of secondary metabolites during biotrophic and necrotrophic growth of P. larvae in the host. One practical result of this basic research is the recently completed development of a highly specific point-of-care immunoassay for P. larvae diagnosis.

AMR & Evolution - ES - Lecture Hall (14:45 - 15:30)

-Conveners: Scarpellini, Raffaele (University of Bolgona); Zendri, Flavia (University of Liverpool)

[151] Chromosomal ampR Regulates Plasmid-Mediated Antibiotic Resistance and Gene Duplication Amplification in Enterobacter cloacae (14:45)

Presenter: FANG, Yuwen (Institute of Microbiology and Epizootics, Centre for Infection Medicine, School of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany)

Background and Objectives: Gene duplication and amplification (GDA) is crucial for bacterial adaptation to antibiotic pressure [1]. In Enterobacter cloacae strain IMT49658-1, ceftazidime induces GDA of a genomic region containing blaDHA and adjacent ampR(DHA) [2]. The strain also carries plasmid-borne blaTEM and blaCTX, and chromosomal blaACT with ampR(ACT). Given the regulatory role of ampR in β-lactamase expression, we aimed to investigate whether ampR(ACT) influences GDA and the expression of plasmid-borne resistance genes, thereby modulating antibiotic susceptibility and bacterial fitness. **Methods:** ampR(ACT) was deleted via λ Red recombineering, confirmed by PCR and sequencing. Antibiotic susceptibility was tested by agar disc diffusion assay. GDA copy number was quantified by qPCR of genomic. Meanwhile, Expression of blaDHA and ampR(DHA) was measured by RT-qPCR. ScanLag was used to assess colony appearance and growth times. **Results:** Deleting ampR(ACT) unexpectedly increased ceftazidime resistance, despite reduced GDA. RT-qPCR showed blaDHA upregulation and ampR(DHA) downregulation, suggesting altered regulation. ScanLag revealed delayed growth, indicating a fitness cost. **Conclusions:** These findings indicate that ampR(ACT) functions as a key regulatory element, influencing both chromosomal and plasmid-borne resistance genes. This study provides new insights into the genetic and regulatory mechanisms shaping antibiotic resistance evolution in E. cloacae.

[20] Within-host evolution of Staphylococcus pseudintermedius in dogs with skin disease (15:00)

Presenter: WORTHING, Kate (The University of Sydney)

This study assessed within-host phenotypic and genotypic evolution amongst methicillin-resistant Staphylococcus pseudintermedius (MRSP) isolates from two dogs with chronic skin disease and recurrent pyoderma. Phenotypic antimicrobial susceptibility was determined by broth microdilution. Isolates underwent genome sequencing using both short read and long read platforms. Genome short reads were assessed for the accumulation of core genome single nucleotide polymorphisms (SNPs). Assembled genomes were interrogated for variations in accessory genome content. Phylogenetic, phenotypic and genotypic variation in antimicrobial resistance was evident in longitudinally isolated S. pseudintermedius from both dogs. Dog 1 had three infections with the same MRSP clone (ST316) and one infection with an unrelated methicillin-susceptible (MSSP) clone. Dog 2 had three different clones over five infection episodes: two infections were due to ST64 MRSP, two ST257 MSSP and one ST2814 MSSP. Non-synonymous SNPs accumulated in genes relating biofilm formation, rifampicin resistance, metabolism and cell wall synthesis. Sequential ST316 MRSP isolates from Dog 1 developed a mutated rpoB gene which conferred phenotypic rifampicin resistance, making the isolate extensively drug resistant. Within clonal types, plasmid content was stable while prophage content was variable. These findings provide evidence for the emergence of extensive drug resistance during recurrent S. pseudintermedius infection.

[150] Investigating the Role of the DUF445-Containing Putative Membrane Protein in Albicidin Resistance in Acinetobacter baumannii IMT51508 (15:15)

Presenter: KHAN, Sana (Institute of Microbiology and Epizootics, Freie Universität Berlin, Berlin, Germany)

Albicidin, a promising antibacterial peptide, functions by inhibiting the activity of bacterial DNA gyrase. This study aims to elucidate the mechanisms underlying albicidin resistance in ESKAPE pathogens, which are leading contributors to nosocomial infections. Specifically, we focus on investigating the resistance mechanisms in *Acinetobacter baumannii* (IMT51508), a clinically significant multidrug-resistant pathogen. The MIC of albicidin was determined, followed by laboratory evolution, where the albicidin concentration was increased by two-fold. The evolution of bacterial strains was confirmed by MIC assays of all independently evolved replicates. Subsequently, genomic DNA was extracted from the wild-type strain and eight evolved strains, and WGS was performed. Genome analysis revealed a consistent mutation in an uncharacterized protein, containing a DUF445 domain, YjiN, in 7 out of the 8 evolved strains. Bioinformatics analysis was employed to analyze YjiN protein, suggesting its role as a 2-3 transmembrane domain containing protein. To further elucidate the operon structure of gene cluster, RT-PCR was conducted. In addition, mutations in YjiN and MATE in *Acinetobacter baumannii* were performed, and their effects were measured through MIC assays. The involvement of the YjiN protein in *Acinetobacter baumannii* will provide valuable insights into the role of this putative membrane protein in the bacterial resilience to albicidin.

Innovative Techniques - Seminar Room (14:45 - 15:30)

-Conveners: Ludlow, Martin (University of Veterinary Medicine Hannover); Salvaggiulo, Anna (University of Bari "Aldo Moro")

[65] Application of Machine Learning to Predict Antigenic Distance Between Newcastle Disease Virus Strains from Sequence Data (14:45)

Presenter: Prof. FRANZO, Giovanni (Padua University)

Newcastle disease virus (NDV) remains a major vaccination challenge due to its rapid evolution and the emergence of new variants.. Although molecular and sequence data are now quickly and inexpensively produced, genetic distance rarely are a good proxy for cross-protection, while experimental studies to assess antigenic differences are time-consuming and resource-intensive. In the present study several machine learning (ML) methods were developed and compared to predict the antigenic distance between NDV strains as determined by haemagglutination-inhibition (HI) assays based on F and HN gene sequences -and corresponding amino acid features - analysis. Among the models evaluated, the random forest (RF) approach outperformed traditional linear models, achieving a predictive accuracy with an R^2 value of 0.723 compared to only 0.051 for linear models based on genetic distance alone. This significant improvement demonstrates the usefulness of applying flexible ML approaches as a rapid and reliable tool for vaccine selection, minimizing the need for labour-intensive experimental trials. Moreover, the flexibility of this ML framework allows the application of comparable approaches to other infectious diseases in both animals and humans, particularly in scenarios where prompt response and ethical constraints limit conventional experimental approaches.

[56] Virome Diversity in Ticks Associated with Wild Boars: A Metagenomic Approach (15:00)

Presenter: LANAVE, Gianvito (Univesity of Bari Department of Veterinary Medicine)

Tick-borne viruses (TBVs) include several emerging zoonotic agents with variable pathogenic potential ranging from asymptomatic to mild to severe symptoms, such as encephalitis, or meningitis. As part of the project “Ricerca Corrente 2022 – IZS ME 02/22 RC,” we investigated the virome of ticks collected from wild boars in Southern Italy, a species with potential epidemiological relevance for both domestic pigs and humans. A total of 36 *Dermacentor spp*. ticks were pooled (6 pools of 6 individuals) and analyzed using a metagenomic approach based on SISPA enrichment and Oxford Nanopore Technology sequencing. Viral reads corresponding to segments L and S of Tacheng tick virus 2 (TTV-2; Uukuvirus tachengense, family *Phenuiviridae*) were detected in 3 out of 6 pools. Nearly complete genomes of Tacheng tick virus 3 (*Rhabdoviridae*), Tacheng tick virus 5 (*Chuviridae*), Orthonairovirus sulainense, and Norwavirus grotenhoutense (*Nairoviridae*) were also recovered in other pools. TTV has been detected in human patients with TBV-like febrile disease in China, and it has since been detected in several tick genera/species across Asia and Europe. Its wide vector range suggests potential for ecological adaptation and cross-species transmission. These findings highlight the diversity of tick-associated virome in wildlife and the importance of surveillance.

[37] NOVEL STRATEGY FOR THE SEQUENCING AND DISCOVERY OF CIRCULAR DNA VIRUSES (15:15)

Presenter: DIAKOUDI, Georgia (Department of Veterinary Medicine, University of Bari Aldo Moro, Bari, Italy)

The emergence of COVID-19 and recent zoonotic outbreaks highlight the need of early pathogen detection, thus the development of quick and reliable diagnostic strategies. In this study, we developed an agnostic and cost-effective unbiased sequence-independent enrichment (USIE) protocol for the complete genome sequencing of circular DNA viruses. DNA extracts from different hosts and biological samples are enriched by multiply primed rolling circle amplification (RCA). RCA products are debranched using T7 endonuclease and used as input for libraries and sequencing by Oxford Nanopore Technology™. The generated reads are analyzed using different metaviromic tools and customized pipelines. Thus far, this diagnostic strategy has been successfully used for the complete genome sequencing and discovery of the following viruses; hepadnaviruses in domestic dogs (Diakoudi et al, 2022), Iberian lynxes (Diakoudi et al., 2025), and passerine birds (unpublished data), emerging papillomaviruses in horses (unpublished data), several CRESS DNA viruses in cats (Vasinioti et al., 2023), squamates (Capozza et al, 2022), Iberian lynxes (Castro-Scholten et al., 2024), and wolves (unpublished data), and avian polyomaviruses (unpublished data). Overall, the USIE protocol is a host- and tissue-independent strategy that can be used to sequence circular DNA viruses. Updating and implementing the diagnostic algorithms is crucial for the effective prevention and control of emerging and re-emerging viruses.

Coffee (15:30 - 16:00)

AMR - genetic basis - Lecture Hall (16:00 - 17:00)

-Conveners: Van der Most, Marleen (Wageningen University & Research); Schwarz, Stefan (Freie Universität Berlin)

[23] A novel macrolide-lincosamide resistance gene in Actinomyces bowdenii isolated from an abscess in a dog (16:00)

Presenter: KITTL, Sonja (Institute of Veterinary Bacteriology, University of Bern, Switzerland)

Acquired resistance in actinomycetes infecting companion animals is rare. Usually β-lactams, tetracyclines and clindamycin are considered for treatment. There are however studies about human isolates reporting acquired resistance, especially against clindamycin. Over the last five years three out of 98 actinomycetes isolated from dogs and cats in our diagnostic laboratory were resistant to clindamycin. One *Actinomyces bowdenii* strain (21MD1404) isolated from a dog abscess was subjected to whole genome sequencing to determine the genetic basis of resistance. Analysis with ResFinder-4.7.2 revealed no known resistance genes. However, a genome alignment with clindamycin susceptible strain 07KM1036 using mauve 1.1.3 led to the discovery of a potential rRNA-methylase gene. The gene was related to known *erm* genes which usually confer macrolide, lincosamide and streptogramin B resistance. The most closely related showed 40% amino acid identity, clearly below the threshold of 79% for designating new genes. To test the functionality of the new gene, plasmid pacti_erm3 was constructed consisting of partial vector pJRD215 and the resistance gene including the promoter region. The plasmid was transferred into the susceptible strain 07KM1036 where it led to a clindamycin MIC increase from 0.12 mg/L to 32 mg/L and an erythromycin MIC increase from 0.03 mg/L to 1 mg/L. These results indicate that the discovered gene is indeed responsible for the clindamycin resistance of strain 21MD1404.

[96] Genetic basis of antimicrobial resistance in Pasteurellaceae of diseased cattle and pigs from Germany (16:15)

Presenter: KRÜGER-HAKER, Henrike (Institute of Microbiology and Epizootics, School of Veterinary Medicine, Freie Universität Berlin, Germany)

This study investigated the genetic basis of macrolide resistance and further antimicrobial resistance (AMR) properties in *Mannheimia haemolytica* and *Pasteurella multocida* from diseased cattle and pigs. Seventeen macrolide-resistant isolates from respiratory diseases included in GERM-Vet (*M. haemolytica*, cattle, 2008-2020, n=13/780; *P. multocida*, pigs, 2008-2021, n=4/1115) and eight bovine *P. multocida* from sporadic cases of mastitis (2021-2023) were investigated. Antimicrobial susceptibility testing was done according to CLSI recommendations. Closed whole genome sequences were generated via hybrid assembly of Illumina MiSeq and Oxford Nanopore MinION reads. Among the 25 isolates tested, resistance to several of the antimicrobial agents, including aminoglycosides, phenicols, penicillins, tetracyclines, macrolides and sulfonamides, was detected. In 19 isolates (respiratory disease n=12, mastitis n=7), integrative and conjugative elements (ICEs) were identified that conferred multidrug resistance. These ICEs, some of them novel, harbored the AMR genes *erm*(T), *lnu*(H), *estT*, *mef*(C), *mph*(G), *floR*, *catA3*, *aadA31*, *aad(3")(9)*, *aph(3')-Ia*, *aac(3)-IIa*, *strA*, *strB*, *tet*(H), *tet*(Y), and *sul2* in varying combinations. Four *M. haemolytica* also carried a 4,613-bp plasmid with the β-lactamase gene *blaROB-1*. Resistance-mediating ICEs or plasmids, as found here, can promote the rapid spread of AMR via horizontal gene transfer and co-selection events.

[111] Antimicrobial resistance profile and mobilome of *Klebsiella pneumoniae* isolates from the reproductive tract of mares and stallions (16:30)

Presenter: Dr KAWARIZADEH, Amin (The Centre for Equine Infectious Disease, Melbourne Veterinary School, Faculty of Science, University of Melbourne)

Klebsiella pneumoniae is associated with reproductive infections in both mares and stallions, and has great potential for acquiring antimicrobial resistance genes. Reproductive samples collected from thoroughbred horses in Australia were cultured (2020 and 2022 [inclusive]). Conventional laboratory methods (colony morphology, biochemical, motility tests) were used to presumptively identify *K. pneumoniae*. Antimicrobial susceptibility testing and whole genome sequencing were performed. Genetic diversity and phylogeny were evaluated by MLST and alignments/comparisons of complete sequences. Further analysis was performed to detect resistance genes and mobile genetic elements. Of 91 *K. pneumoniae* isolates (mare: 76, stallion:15), multidrug-resistance (MDR) was identified in 59% and 33% of isolates from mares and stallions respectively. Thirty-one sequence types were identified, and phylogenetic analysis suggested a significant level of genetic diversity, with isolates grouped into 31 distinct subclades. A high frequency of IncFIB(K) plasmids and integrons was detected among MDR isolates and several novel configurations of resistance genes were identified. This study revealed a concerning level of antimicrobial resistance and a diverse population of *K. pneumoniae* in the equine reproductive tract. These findings highlight the crucial need for ongoing monitoring and characterization of *K. pneumoniae* for effective disease control and management.

Viral Pathogenicity I - Seminar Room (16:00 - 17:00)

-Conveners: Tarlinton, Rachael (University of Nottingham); Facile, Veronica (University of Bologna)

[4] Superinfection exclusion and enhancement of infection in pestiviruses (16:00)

Presenter: LAMP, Benjamin (JLU Gießen)

Some viruses can suppress superinfections of their host cells by related or different virus species. The phenomenon of superinfection exclusion can be caused by inhibiting virus attachment, receptor binding and entry, by replication interference, or competition for host cell resources. Blocking attachment and entry not only prevents unproductive double infections but also stops newly produced virions from re-entering the cell post-exocytosis. In this study, we investigated the exclusion of superinfections between the different pestivirus species. Bovine and porcine cells pre-infected with non-cytopathogenic pestivirus strains were evaluated for susceptibility to subsequent superinfection using comparative titrations. Our findings revealed significant variation in exclusion potency depending on the virus species as well as the host cells. Despite this variability, all tested classical pestivirus species reduced host cell susceptibility to subsequent infections, indicating a conserved entry mechanism. Unexpectedly, pre-infection with atypical porcine pestivirus (APPV) increased host cell susceptibility to classical pestiviruses. These results indicate that APPV uses different binding and entry mechanisms than the other pestiviruses. The observed increase in susceptibility of cells post-APPV infection warrants further investigation and could aid challenging isolations from diagnostic samples.

[55] Feline Bocaparvovirus in domestic cats with gastrointestinal disease (16:15)

Presenter: Dr SALVAGGIULO, Anna (Department of Veterinary Medicine, University of Bari, Valenzano (Bari), Italy)

Bocaparvoviruses (BoVs) are non-enveloped viruses with linear single-stranded DNA genome and are classified in the genus Bocaparvovirus (subfamily Parvovirinae, family Parvoviridae). BoVs infect the respiratory and gastrointestinal tracts of young animals and humans and have been detected in a wide range of mammalian hosts (i.e. primates, carnivores, ungulates and rodents). In cats, feline BoV (FBoV) has been identified in three genetic types, namely FBoV-1, -2, and -3 (Bocaparvovirus carnivoran 3, 4 and 5, respectively), which have been described in cats with gastrointestinal symptoms. We investigated the prevalence of FBoV in 126 feline rectal swab samples of cats with gastroenteritis from two different regions, Apulia (collection A, 101 samples) and Abruzzi and Molise (collection C, 25 samples) between 2023 and 2025. We used a pan-bocavirus PCR assay with broadly reactive primers able to identify all human and animal BoVs. Overall, 16.7% (21/126) stool samples tested positive for BoVs. Partial NS1 sequences were generated for 9 strains, with nucleotide identities ranging from 95.0 to 100% to FBoV-1 strains. A quantitative PCR assay specific for FBoV-1 was designed and used to re-screen the sample collections, with an infection rate of 19.0% (24/126). Gathering epidemiological data is necessary to improve our understanding of the enteric virome of companion animals.

[99] A defective canine distemper virus strain responsible for CNS disease in a Eurasian Lynx shares key phenotypic traits with measles virus strains associated with SSPE in humans (16:30)

Presenter: LUDLOW, Martin (University of Veterinary Medicine Hannover)

Canine distemper virus (CDV) can cause chronic central nervous system (CNS) infections such as old dog encephalitis with parallels to subacute sclerosing panencephalitis (SSPE) in humans. However, it has not been possible to correlate such clinical manifestations to viral molecular determinants. The complete genome sequence of a CDV strain (CDV-lynx) previously identified in the brain of a Eurasian lynx was obtained by next generation sequencing. Sequence analysis showed unique amino acid (aa) changes in all viral proteins, including a premature stop codon in the matrix protein, four aa changes in the F protein and several additional changes in other proteins. A recombinant (r) CDV-lynx-EGFP was rescued, and several gene-swap constructs were generated with a closely related rCDV-Raccoon-EGFP with the resulting recombinant viruses used to study virus infection of immune cells and organotypic ferret brain slices. The CDV-lynx F protein was hyperfusogenic in cell fusion assays as fusion was observed in receptor negative Vero cells. A single aa change (P479A) could abrogate cell fusion in Vero cells. Furthermore, a significant reduction in the entry of VSV pseudotyped with CDV-lynx glycoproteins into Vero-Dog-SLAM cells was observed. Our data show an animal morbillivirus acquired a hyper-fusogenic phenotype and defective matrix protein expression following long-term CNS infection, findings that are strikingly homologous to the phenotype of SSPE strains of measles virus.

[116] Pseudorabies virus-associated encephalitis in hunting dogs in Greece: The role of wild boars as a persistent reservoir in Greece (16:45)

Presenter: PAPAGEORGIOU, Konstantinos (School of Veterinary Medicine, Faculty of Health Sciences, Aristotle University of Thessaloniki, Greece)

Introduction: Pseudorabies, caused by Suid herpesvirus 1 (SuHV-1), primarily affects swine and accidentally other mammals. Although eradicated from domestic pigs in many European countries, SuHV-1 persists in wild boar populations. Hunting dogs are at particular risk due to direct exposure during wild boar hunts. Methods: Between 2022–2024, seven cases of neurological disease and death in hunting dogs were investigated in the regions of Epirus and Thessaly, Greece. Postmortem brain tissues were tested by PCR targeting a part of the glycoprotein D gene of SuHV-1. Positive samples were subjected to sequencing and

phylogenetic analysis. Results: All seven cases tested PCR-positive for SuHV-1. Phylogenetic analysis of the gD gene sequences revealed genetic divergence among the isolates. The Epirus strains formed a separate clade, suggesting localized viral evolution. The Thessaly isolate showed greater divergence, clustering independently and indicating a potentially unique lineage within the Greek wild boar reservoir. Conclusion: Our findings confirm the ongoing circulation of SuHV-1 strains in wild boar populations in Greece and demonstrate the fatal risk posed to hunting dogs. These data highlight the need to raise awareness among veterinary practitioners to include pseudorabies in the differential diagnosis of encephalitis in dogs.

Guided Tour (Berlin Museum of Medical History) - Berliner Medizinhistorisches Museum der Charité (17:15 - 18:45)

Conference Dinner (Reinhard Bär Restaurant) - Reinhard Bär Restaurant (19:30 - 23:59)

Friday 12 September 2025

Check-in - Foyer (ground floor) (08:30 - 09:00)

Keynote Lecture: Martin Wagner - Lecture Hall (09:00 - 09:45)

-Conveners: Alter, Thomas (Freie Universität Berlin)

[155] Listeria monocytogenes: Survival strategies in food processing environments (09:00)

Presenter: WAGNER, Martin (Center for Food Safety and VPH, Department for Farm Animals and Food Systems Science, University of Veterinary Medicine, Veterinärplatz 1, 1210 Vienna; Austrian Competence Center for Feed and Food Quality, Safety and Innovation, 3430 Tulln)

Listeria monocytogenes poses a significant risk, especially in ready-to-eat (RTE) foods, as it can grow at refrigeration temperatures, unlike many other pathogens. This species survives in a variety of harsh environments, including the food processing environment. Long-term survival of Listeria is usually addressed as persistence and the mechanisms are still unelucidated. One trigger of *Listeria* survival is seen in biofilm formation that consists of microbial communities attached to surfaces, embedded in a protective matrix. In food processing facilities, these biofilms can form on equipment, conveyor belts, storage bins, and drains. We found 9-12% of sampling sites carrying a true biofilm in food operations. We have studied the biofilm forming capacity of *L. monocytogenes* in various environments and found *Listeria* being a weak biofilm former. Once in a biofilm, *Listeria* is less susceptible to cleaning agents, disinfectants, and even physical removal, making it extremely difficult to eradicate from the environment. An intriguing question is how Listeria co-colonize biofilms. Data show that other species such as Pseudomonas are drivers of biofilm formation, obviously scarcely in interaction with *Listeria* residing in the same biofilm. We further looked into the genome of persisting clones of *L. monocytogenes* by browsing a database storing more than 17000 *L. monocytogenes* genomes. A thorough bioinformatic analysis revealed that single genetic markers explaining persistence do not exist. Conclusively, survival of *Listeria* in food processing environments is more likely explainable due to failures of hygiene practices than by particular genetic features allowing some clones to persist.

AMR: Transmission - Spread - Envirnoment - Lecture Hall (09:45 - 10:15)

-Conveners: Alter, Thomas (Freie Universität Berlin); Robé, Caroline (Freie Universität Berlin)

[48] Wild coypu (Myocastor coypus) as sentinel of antimicrobial resistance in water ecosystems: preliminary insights using Aeromonas spp. as bioindicator (09:45)

Presenter: MASSELLA, Elisa (IZSLER, Brescia, Italy)

This study investigates the potential role of wild coypu (*Myocastor coypus*) as a sentinel of antimicrobial resistance (AMR) in freshwater ecosystems, using *Aeromonas* spp. as bioindicator. Between December 2024 and May 2025, 51 coypu carcasses and 13 water samples were collected along the Reno River and its tributaries in Italy. *Aeromonas* spp. were isolated and identified by MALDI-TOF. Their AMR profiles were determined using the broth microdilution method. A total of 74 *Aeromonas* strains isolated from animals (57) and water (17) were detected, belonging to 7 different species. The most common were *A. veronii* (21/74) and *A. media* (19/74). About 17.54% (10/57) of *Aeromonas* isolates from animal sources were resistant to at least one antimicrobial, most commonly sulphamethoxazole (8/57) and tetracycline (4/57). Only one *A. veronii* strain was multidrug-resistant (MDR) to sulphamethoxazole, tetracycline and gentamicin. The number of resistant and MDR isolates, as well as the AMR profiles of *Aeromonas* strains of aquatic origin, were comparable to those of animal origin. The ecological traits of wild coypu (semi-aquatic habits, wide distribution, sedentary behaviour and long lifespan), along with the strong similarity between AMR profiles of *Aeromonas* from animal and aquatic sources, suggest this species as an effective sentinel for AMR monitoring in aquatic environments and its potential use in future surveillance programs targeting freshwater ecosystems.

[146] EVIDENCE AND SPREAD OF MULTIDRUG-RESISTANT ACINETOBACTER SPP. IN FARM ANIMALS AND ENVIRONMENT UNDER A ONE HEALTH PERSPECTIVE (10:00)

Presenter: MELIGRANA, Marina C T (University of Camerino)

This study aimed to address the knowledge gap on *Acinetobacter calcoaceticus–baumannii* (ACB) and non-ACB complex species in farm animals by: -investigating the occurrence of multidrug-resistant (MDR) strains in animals, operators, and the farm environment; -assessing their potential role in transmission within a One Health framework. From cattle, horses, sheep, goats, pigs, poultry, human hands, and farm environment, samples were collected. Isolates were identified via culture and MALDI-ToF MS. Antibiotic susceptibility was assessed using E-test and Kirby-Bauer methods. From 840 samples, 128 *Acinetobacter* strains (ACB: 10.2%, 13/128; and 18 different non-ACB complex: 89.8%, 115/128) were isolated in farm animals (83.6%), humans (13.3%), and environment (3.1%). ACB strains were more frequent in diseased animals (*P*=0.0028), particularly cattle (*P*=0.0002), where a high proportion of *A. baumannii* (81.8%, 9/11) was significantly identified. Both ACB (92.3%) and non-ACB strains (46.1%, *P*=0.0016) showed MDR profile that was significantly associated to carbapenem resistance (3.9%; *P*=0.029, Cramer's V=0.235, Lambda=0.095±SE 0.074). Non-ACB strains showed polymyxin (1.7%) and aminoglycoside resistance (11.3%). Isolates from animals, humans, and the environment shared identical MDR profiles. Farm animals and their environments may act as reservoirs for MDR *Acinetobacter* spp., supporting the need for further research on transmission dynamics in a One Health context.

Viral Pathogenicity II - Seminar Room (09:45 - 10:15)

-Conveners: Schulz, Claudia (University of Veterinary Medicine, Vienna); Osterrieder, Klaus (University of Veterinary Medicine Hannover)

[21] Communicating emerging diseases to animal owners (09:45)

Presenter: TARLINTON, Rachael (School of Veterinary Medicine and Science, University of Nottingham)

Europe has seen continual outbreaks of emerging diseases in both its human and animal populations in recent years. Part of effective response to these disease outbreaks is maintaining public confidence in control measures and the communication of risk, yet many scientists struggle with public communication of specialist knowledge. Veterinarians are trusted figures in animal health and have a key role in communication with animal owners in these outbreaks. This talk will draw on social sciences research that the author has participated in, into owner attitudes, knowledge, impacts (financial and emotional) and compliance and provide recommendations for communication of disease risk and control options using examples from recent UK Avian Influenza, Schmallenberg and Bluetongue communication campaigns.

[69] The Hunt for Maedi Visna Resistance: Understanding the Current TMEM154 Genetic Situation within the UK National Flock (10:00)

Presenter: JONES, Scott (University of Nottingham)

MV is a chronic viral disease affecting nearly 10% of the UK national flock. Its long latency period which ultimately ends in fatality in conjunction with the lack of treatment or vaccination options make control efforts difficult. Current strategies rely on voluntary testing and culling, which are costly and not widely effective. Selective breeding for genetic resistance therefore offers an alternative. Studies have identified a mutation in Transmembrane protein 154 (TMEM154) to be strongly associated with decreased risk of MV. Prior to implementing a selective breeding programme, there are several questions requiring answers such as do the resistant genetics have adverse effects on animal welfare and what resistant genetics are currently present within the UK flock. The latter of these is addressed in the current work. Animals from major UK sheep breeds were genotyped to assess allele frequency and determine the prevalence of MV resistance. A minimum of 20 animals per breed from diverse bloodlines were tested to ensure accurate breed representation at a national level. Data from 35 UK sheep breeds showed a wide range (3-90%) of animals homozygous for MV resistance. No breed lacked resistance, supporting selective breeding for this trait in UK breeds. The variation in prevalence suggests breed-specific approaches would be necessary to avoid genetic bottlenecks and loss of valuable genetics.

Coffee (10:15 - 10:45)

Keynote Lecture: Dennis Rubbenstroth - Seminar Room (10:45 - 11:15)

-Conveners: Lübke-Becker, Antina (Freie Universität Berlin); Pellegrini, Francesco (University of Bari Aldo Moro)

[160] Rustrela virus (RusV; species Rubivirus strelense) (10:45)

Presenter: RUBBENSTROHT, Dennis (Friedrich-Loeffler Insitute, Germany)

Rustrela virus (RusV; species Rubivirus strelense) is a recently discovered relative of the human rubella virus and causes usually fatal non-suppurative meningoencephalomyelitis in a broad range of mammals, including felids, canids, mustelids, rodents and even marsupials. The virus was first identified in zoo animals from northeastern Germany, in 2019. Meanwhile, it has been found also in domestic, wild and zoo animals in Germany, Austria, Sweden and the USA. Meanwhile, RusV has been demonstrated to be the causative agent of ‘staggering disease’ in domestic cats as well as ‘lion encephalitis’ in lions, two neurological disorder that had remained of unknown aetiology for almost five decades. The clinical course is characterized by a broad range of neurological signs, with hind leg ataxia being the most prominent. Based on its broad range of susceptible hosts, a zoonotic potential of RusV cannot be excluded. While encephalitic individuals appear to act as dead ends and do not spread the virus after spill-over transmission, apparently healthy yellow-necked field mice (Apodemus flavicollis) and wood mice (Apodemus sylvaticus) were identified as potential wild reservoir hosts of RusV. Experimental studies have confirmed the susceptibility of wood mice to RusV infection via intracerebral and oculonasal inoculation, but not via subcutaneous and intramuscular route and demonstrated shedding of viral RNA. The phylogeographic pattern of RusV sequences, with different sequence clusters occurring in separated, non-overlapping parts of the known dispersal areas, further suggests the virus to be bound to a rather non-mobile reservoir host, such as small mammals. However, many questions regarding the biology and epidemiology of RusV in reservoir and spill-over hosts remain elusive, such as course of infection, pathogenesis, and transmission routes.

Keynote Lecture: Jennie Fischer - Lecture Hall (10:45 - 11:15)

-Conveners: Broens, Els (Utrecht University); Marques, Cátia (Universidade Lusófona)

[159] WGS challenges and opportunities in bacteriological diagnostics (10:45)

Presenter: FISCHER, Jennie (German Federal Institute for Risk Assessment)

Whole-genome sequencing (WGS) has attracted the attention of experts in various fields for decades. Due to the development of new and highly efficient sequencing technologies, sequencing costs per genome have drastically decreased in the last decade, making WGS a powerful and widely used application for diverse scientific questions. In modern bacterial diagnostics there is also a methodological shift from classical detection and typing techniques towards WGS-based approaches, utilizing different Next Generation Sequencing (NGS) technologies. WGS allows for comprehensive analysis and possesses high discriminatory power for bacterial characterization, thus enabling a wide range of applications in routine diagnostics and fundamental research. Whereas some promising approaches using NGS to facilitate bacterial detection and characterization from complex samples are still primarily applied and optimized in research projects, WGS-based bacterial isolate characterization has already replaced traditional standard methods in microbiological laboratories worldwide. Also, at the NRL for Salmonella in Germany, WGS is now used on a routine basis and is the gold standard approach for Salmonella characterization. However, new developments are accompanied by new challenges that affect decision making, risk management strategies and even national or international regulations.

AMR - Epidemiology & Surveillance: "ESGVM Session" - Lecture Hall (11:15 - 12:45)

-Conveners: Marques, Cátia (Universidade Lusófona); Broens, Els (Utrecht University)

[144] Towards harmonised methods for surveillance of antimicrobial resistance in clinical infections from companion animals in the UK (VetCLIN AMR) (11:15)

Presenter: Prof. TIMOFTE, Dorina (University of Liverpool)

Introduction: Understanding antimicrobial resistance (AMR) transmission between different sectors requires robust surveillance systems aligned with One Health principles. However, the lack of consensus for performing and interpreting antimicrobial susceptibility testing (AST) on veterinary clinical isolates, is hampering the usefulness of these data. Aim: to evaluate the current methodological approaches used by veterinary diagnostic laboratories in the UK, for AST and clinically relevant AMR phenotypes in companion animals bacterial isolates. Methods: New minimum inhibitory concentration (MIC) plates were designed. Target bacterial isolates (Staphylococcus aureus, n=189; S. pseudintermedius n=641; Escherichia coli, n=669) were collected from collaborating laboratories and tested with a standardised AST method. Results were interpreted according to CLSI VET01 7th Ed. and compared with results generated by laboratories. A free proficiency testing (PT) assay was established to identify variability in AST methodology. Results: Initial AST data comparison showed important discrepancies in the clinical interpretation of AST for some bacterial pathogen/antibiotic combinations. PT assays revealed that 92% and 85% of laboratories correctly detected methicillin resistance in S. aureus and ESBL-production in E. coli, respectively. Conclusions: Further training and guidance for AST methodology must be addressed to harmonise methods and improve data comparability for AMR surveillance.

[51] First Epidemiological Surveillance of Methicillin-Resistant Staphylococci in a Veterinary Teaching Hospital Using IR Biotyper® (11:30)

Presenter: Dr SCARPELLINI, Raffaele (Department of Veterinary Medical Sciences, Alma Mater Studiorum—University of Bologna)

In a global view on Antimicrobial Resistance (AMR), Methicillin-resistant Staphylococci (MRS) are one of the most threatening pathogens in both human and veterinary medicine. The aim of this work was to assess the impact of MRS within a Small Animal Veterinary Teaching Hospital (VTH) in Italy, through a multilevel data collection on clinical, commensal and environmental isolates and a subsequent analysis through Fourier-transform infrared (FTIR) spectroscopy by IR Biotyper®. From May 2021 to May 2023, a total of 81 MRS clinical isolates was recorded, mainly MR *S. pseudintermedius* (MRSP, 81.1%). High resistance rates towards most of the antimicrobials tested were recorded, such as 87.8% for tetracycline and 85.6% for enrofloxacin. MRS prevalence in hospitalized patients' oral flora was 22% (33/150) at admission, while in-hospital acquisition was 19.7% (23/117). The environmental analysis showed a high frequency of MRS detection in the Intensive Care Unit area (29.4%), and in the personnel' shoe soles (85.7%) and the floor (71.4%). Strains typing using IR Biotyper® on 96 selected MRSP isolated showed the presence of three main clusters, one of them detected at all levels, suggesting its endemic presence within the hospital. These findings confirm the importance of MRS in small animal practice, highlighting as a multilevel surveillance program can consent to achieve an exhaustive overview that could lead to tailored measures of infection control.

[59] Methicillin-resistant Staphylococcus pseudintermedius and Staphylococcus aureus in dogs and cats: isolation rates from different clinical conditions (11:45)

Presenter: Dr RATTI, Gabriele (I-Vet s.r.l.)

Methicillin-resistant Staphylococcus pseudintermedius (MRSP) and Staphylococcus aureus (MRSA) are important pathogens in companion animals with implications for both animal and human health due to their zoonotic potential. This retrospective study evaluated MRSP and MRSA presence in samples from animals with various clinical conditions. Bacterial identification was performed by MALDI-TOF, and antimicrobial resistance was assessed via MICs and PCR targeting the mecA gene. Clinical conditions were classified using anamnestic data, cytology, or histopathology. Methicillin resistance was detected in 48/128 (37%) S. pseudintermedius and 2/9 (22%) S. aureus, corresponding to 50/137 (36%) of the total isolates. Particularly, MRS was found in 26/69 (38%) of suspected urinary infections, 8/34 (23%) otitis externa, 8/18 (44%) pyodermitis, and 8/16 (50%) surgical site infections. No statistical association was found between clinical condition and MRS presence. The highest resistance rates were against penicillin (84%), erythromycin (55%), clindamycin (46%), enrofloxacin (37%), marbofloxacin (37%), doxycycline (37%), pradofloxacin (36%), oxacillin (36%), trimethoprim/sulfamethoxazole (34%), chloramphenicol (31%), gentamicin (25%), and 1% for amikacin, nitrofurantoin, and florfenicol. Our findings indicate a high prevalence of MRS across clinical conditions, suggesting that methicillin resistance should always be suspected in clinical practice.

[130] The burden and drivers of antimicrobial resistance in commensal E.coli from shelter dogs in North Macedonia (12:00)

Presenter: CVETKOVIKJ, Iskra (Faculty of Veterinary Medicine - Skopje, Ss. Cyril and Methodius University in Skopje, Skopje, North Macedonia)

Dog shelters, with their dynamic populations from varied backgrounds, serve as critical environments for antimicrobial resistance (AMR). This study aimed to determine the prevalence of AMR in commensal E. coli in shelter dogs in North Macedonia and

pinpoint contributing factors within shelter management. A total of 112 E. coli isolates were recovered from 119 fecal samples across six shelters. Antimicrobial susceptibility profiles were established via broth microdilution and resistance genes were identified by PCR. Shelter practices were assessed through a questionnaire. High resistance rates were observed for sulfamethoxazole (68.8%) and ampicillin (52.7%). Multidrug resistance (MDR) was detected in 50% of isolates. Notably, 15.1% of isolates were confirmed as ESBL producers, carrying the blaCTX-M and blaTEM genes. The plasmid-mediated AmpC gene blaCMY-2 was detected in 14.3% of all isolates, indicating potential for horizontal gene transfer. A strong statistical association was found between intensive antimicrobial use (AMU) and ESBL prevalence. All ESBL-producing isolates came from shelters with high AMU. Longer shelter stays also correlated significantly with increased AMR. Shelter dogs in North Macedonia are reservoirs of MDR and ESBL-producing E. coli. The study highlights that specific shelter practices, especially intensive AMU, are critical drivers of AMR. These findings underscore the urgent need for antimicrobial stewardship programs in shelters.

[62] Detection of Antimicrobial Resistance and ESBL-Producing E. coli from Mammals at UK Petting Zoos (12:15)

Presenter: Ms NISHIGAKI, Alice (Royal Veterinary College)

The role of petting zoos in bi-directional zoonotic disease transmission is well documented, however their potential role as reservoirs of antimicrobial resistance (AMR) is un-explored within the United Kingdom (UK). This study investigated AMR in *Escherichia coli* and coagulase-positive staphylococci (CoPS) isolated from mammals at eight UK centres. Faecal and skin samples were collected from 166 animals to recover *E. coli* and CoPS. Samples underwent enrichment culture, followed by plating on non-AMR-selective media (tryptone bile-x agar, mannitol salt agar) and selective media (ESBL ChromID, mannitol salt agar with 6 mg/L oxacillin). Susceptibility to eight antimicrobial classes was assessed using Kirby-Bauer disc diffusion. Antimicrobial usage data from the last 12 months were obtained from 7/8 centres. A total of 145/166 faecal samples yielded *E. coli*, with an overall AMR prevalence of 42.4%, and 8.5% classified as multidrug-resistant. ESBL-producing *E. coli* were detected in five animals. CoPS were recovered from 54 skin swabs: *Staphylococcus aureus* (n=70), *Staphylococcus intermedius* group (SIG) (n=13), *S. hyicus* (n=1), with an AMR prevalence of 25.3% and a single MDR-SIG. No MRSA/MRSP were identified. Antimicrobial usage was positively correlated with AMR for *E. coli* (r=0.81, P=0.03) and CoPS (r=0.87, P=0.05). This study demonstrates for the first time the presence of AMR within bacteria isolated from UK petting zoo animals.

[78] Abortion caused by Coxiella burnetii in captive Finnish Forrest reindeer in a zoo in the Netherlands (12:30)

Presenter: KANNEKENS-JAGER, Marleen (WBVR)

Coxiella burnetii (Cb) is a Gram-negative intracellular bacterium causing coxiellosis in animals and Q fever in humans. Cb causes reproductive disorders in ruminants. Abortions are observed mainly in goats, sheep and less in cattle. The largest Q-fever outbreak was reported in 2007-2010 in the Netherlands caused by Cb shedding dairy goats. Since, there is a mandatory vaccination and monitoring program in the Netherlands for dairy goat and sheep. In a zoo in the Netherlands, four Finnish forest reindeer (Rangifer tarandus fennicus) in a herd of 13, of which six were pregnant, suffered from abortions in April and May 2025. Diagnostic sampling showed positive antigen detection with qPCR from vaginal swabs and positive serology (ELISA) in all cases of abortion (4/4) and in one animal after normal parturition. Placental tissue (n=2) and fetal liver tissue (n=1) retrieved after two abortions indicated positive for Cb infection by qPCR. Necropsy of one female showed positive Cb qPCR results for spleen, liver and vaginal swab. Direct sequencing from placental tissue resulted in a full genome and plasmid sequence. Initial strain typing with in silico Multi Locus Variable Analysis (MLVA) resulted in a Cb strain predominantly associated with cattle. This is the first case of coxiellosis reported in Finnish forest reindeer. Due to the public function of the zoo, immediate preventive measures were taken for animal care takers and visitors according to the Dutch One Health approach.

Diagnostics - Seminar Room (11:15 - 12:45)

-Conveners: Lübke-Becker, Antina (Freie Universität Berlin); Pellegrini, Francesco (University of Bari Aldo Moro)

[80] Comparison of conventional urine culture and BACT/ALERT® PF PLUS bottles for monitoring urinary tract infections in companion animals under different clinical and therapeutic conditions (11:15)

Presenter: Dr RADU, Ioanna Lucia (San Marco Veterinary Clinic and Laboratory, Padua, Italy.)

Urinary tract infections (UTIs) are common in companion animals. According to current guidelines, sporadic UTIs can typically be managed with a short course of antibiotics. However, recurrent UTIs are common and warrants closer follow-up. Assessing treatment efficacy typically requires a temporary suspension for culture to prevent false negative results, which may pose risks of infection worsening or recurrence. This study compares conventional urine culture with BACT/ALERT® PF PLUS bottles, which neutralize antimicrobials and may allow accurate microbiological monitoring during treatment. A total of 814 urine samples, mostly from animals under antibiotic therapy, were collected via cystocentesis. Each sample was tested with both conventional culture on CHROMID® CPS® ELITE and BACT/ALERT® PF PLUS and incubated with the BACT/ALERT® 3D system. Positive samples were plated for identification via MALDI-TOF MS and underwent antibiotic susceptibility testing. Results were evaluated considering clinical history and urinalysis. BACT/ALERT® PF PLUS demonstrated greater sensitivity, detecting pathogens in samples negative by conventional culture and identifying additional bacterial species. This method was especially useful in follow-up of recurrent or complicated UTIs. It supports informed decision-making on antimicrobial therapy discontinuation, thereby promoting targeted treatment and contributing to antimicrobial resistance prevention.

[127] Culture or PCR? Benchmarking Brucellosis Diagnosis Without a Gold Standard (11:30)

Presenter: BELLATO, Alessandro (University of Turin, Italy)

Brucellosis is a zoonosis of major public health concern. However, its near-eradication in high-income countries has limited recent research, and the performance of diagnostic tests in livestock remains unclear due to the lack of a gold-standard. This study evaluated the performance of bacteriological culture and qPCR for diagnosing brucellosis in buffaloes and cattle. A total of 5,149 animals, slaughtered in 2022 from confirmed or suspect infected herds in Campania (Italy), were tested according to the protocols provided by the European Union Reference Laboratory. Tissue samples from both seropositive and seronegative animals underwent culture and qPCR. Results were analysed using Bayesian latent class analysis, which estimates test performance without prior knowledge of true infection status. Overall, 35.9% of animals tested positive to at least one method. Culture sensitivity ranged from 43.9% to 59.2% (median = 51.7%), and qPCR from 65.8% to 82.2% (median = 74.4%). Culture specificity ranged from 89.8% to 99.4% (median = 94.3%), and qPCR from 84.2% to 94.0% (median = 89.3%). Despite qPCR showing higher sensitivity overall, culture yielded better positive predictive values in seronegative animals. These large-scale results provide robust benchmarking of brucellosis diagnostic and confirm that qPCR cannot fully replace culture, especially in low-prevalence settings. Moreover, the enhanced culture protocol adopted here showed promising results warranting further evaluation.

[39] Serovar detector: a bioinformatic tool for serotyping Actinobacillus pleuropneumoniae (11:45)

Presenter: ANGEN, Øystein (Statens Serum Institut)

Serovar detector is a new bioinformatic tool for determining the serovar of *Actinobacillus pleuropneumoniae* using whole genome sequencing. The composition of capsular polysaccharide (*cps*) genes of isolates is compared to those of the serovar reference strains and the serovar is determined both by the number of common genes as well as the similarities between the homologous genes. A validation of the bioinformatic tool was performed using 732 genomes representing all described serovars. The isolates included had been characterized by conventional serotyping and PCR tests. Out of the 732 isolates included in the investigation, only 36 isolates (4.9%) could not be allocated into the 19 recognized serovars. The method could discriminate between most serovars, except for serovar 9 and 11. Phylogenetic analyses showed that although most serovars are genetically homogeneous, there is a degree of genetic variation that cannot be explained by the *cps* genes alone. This indicates that SNP-based phylogeny or wgMLST might be valuable supplements for assessing the variation of *A. pleuropneumoniae* in a given region. Serovar detector is a robust method for determining the serovar of isolates and a valuable tool for further characterization of the genetic heterogeneity within *A. pleuropneumoniae*

[49] Development and evaluation of a Pan-Borrelia TaqMan qPCR for detection of Borrelia spp. in ticks collected from cattle in Tanzania (12:00)

Presenter: Mrs FACILE, Veronica (Department of Veterinary Medical Science, Alma Mater Studiorum - University of Bologna)

Bacteria of the genus Borrelia are tick-borne pathogens divided into two groups: Lyme disease (LD) group and Relapsing Fever (RF) group. Both include numerous species and new ones are still being identified. Recent studies have also reported the presence of Borrelia spp. in different hosts and across different geographical areas, highlighting the existing gaps in knowledge regarding the epidemiology of this pathogen. Continued surveys are needed to understand the prevalence and the host range of each species in order to safeguard the health of wildlife, domestic animals and humans. For this purpose, ticks collected from cattle in Tanzania in 2023, were tested for the presence of Borrelia spp. DNA. Molecular screening was performed using a new

validated TaqMan real-time qPCR targeting the 16S rRNA gene able to detect all Borrelia species. A fragment of the 16SrRNA gene of the identified pathogens was sequenced and analysed for typing. One tick of 62 (1.6%) tested positive for bacteria belonging to the RF group, potentially Borrelia theileri, the main causative agent of bovine borreliosis. This species was already reported in cows in Africa, but never in Tanzania. This result confirms the importance of monitoring the spread of this pathogen in order to control the disease. Supported by EU funding within the NextGenerationEU-MUR PNRR Extended Partnership initiative on Emerging Infectious Diseases (Project no. PE00000007, INF-ACT).

[84] Accelerating blood culture diagnostics in veterinary medicine: pathogen identification and antimicrobial susceptibility testing (12:15)

Presenter: ROBÉ, Caroline (Institute of Animal Hygiene and Environmental Health, School of Veterinary Medicine, Freie Universität Berlin, Berlin, Germany)

Background and objectives: Blood cultures (BCs) are the gold standard for the diagnosis of sepsis, with rapid diagnostics being crucial for treatment. The current standard in veterinary medicine includes pathogen identification (ID) and antimicrobial susceptibility testing (AST). We aimed to accelerate BC diagnostics and compare its performance to the currently applied methodologies. **Methods:** A manual BC system (Oxoid) was inoculated with frequently detected clinical pathogens. ID and AST were determined before positive signal of the BC system without cultivation steps or after short-term incubation of five hours on agar plates. ID was performed using matrix assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-ToF MS). AST was performed by broth microdilution according to the Clinical and Laboratory Standards Institute (CLSI) standards. **Results:** Short-term incubation allows determination of ID and preparation of the inoculum for AST of relevant clinical pathogens. The ID- and AST inoculum preparation of negative BCs without a cultivation step yielded less reliable results. Gram-positive species such as staphylococci posed limitations. **Conclusions:** Shortening BC diagnostic steps in the microbiological laboratory is possible, but limitations exist presumably due to the species-specific growth rates. Together with improved management, short-term incubation of negative BCs can reduce the time to ID and AST communication to the clinician.

[70] Oxytetracycline 30µg agar disk diffusion results for four QC strains (12:30)

Presenter: FESSLER, Andrea

Antimicrobial susceptibility testing is important to predict the outcome of antimicrobial therapy. Therefore, the aim was to compare oxytetracycline 30µg disk and media lots for four reference strains as a pre-requisite to establish QC ranges. Eight laboratories tested *Escherichia coli* ATCC® 25922, *Staphylococcus aureus* ATCC® 25923, *S. aureus* ATCC® 29213, and *Streptococcus pneumoniae* ATCC® 49619 with 2 lots oxytetracycline 30µg disks 10 times on 3 lots agar according to CLSI and EUCAST. As quality control, one lot tetracycline 30µg disks was tested on one medium lot. The data was analyzed using the RangeFinder software. All tetracycline values were in range. For *S. aureus* ATCC® 25923 a range of 21-35mm (98.96% values included), mean values were 25.74mm, 30.63mm and 26.53mm for media und 28.12.mm and 27.15mm for disks. For *S. aureus* ATCC® 29213 the calculated. range was 20-33mm (96.88%; mean 24.45/28.22/25.54mm [media], 26.68/25.46mm [disks]). The *E. coli* ATCC® 25922 range is 17-29mm (99.79%; mean 21.47/25.76/21.78mm [media], 23.85/22.16mm [disks]). For *S. pneumoniae* ATCC® 49619 (CLSI) a range of 24-35mm (98.96 %; mean 28.57/30.49/28.87mm [media], 29.90/28.72mm [disks]) was determined. EUCAST method revealed a range of 24-37mm (100%; mean 29.19/31.60/29.85mm [media], 30.74/29.69mm [disks]). In conclusion, for media lot B the zone diameters seemed larger. When quality control data is out of range, the use of an alternative medium/disks lots might be an option.

Lunch & Poster (12:45 - 14:15)

Keynote Lecture: Marta Kuźmińska-Bajor - Seminar Room (14:15 - 14:45)

-Conveners: Wenderlein, Jasmin (Bundesinstitut für Risikobewertung); Szabo, Istvan (Bundesinstitut für Risikobewertung)

[164] Harnessing phages to combat bacterial pathogens in animal production: From research to application (14:15)

Presenter: KUŹMIŃSKA-BAJOR, Marta (Department of Biotechnology and Food Microbiology, Wroclaw University of Environmental and Life Sciences, 37 Chełmońskiego St., 51-630 Wroclaw, Poland)

The accelerating emergence of antimicrobial resistance in animal production poses a growing threat to both veterinary medicine and public health worldwide, demanding innovative and sustainable alternatives to antibiotics. Bacteriophages are viruses that specifically infect and lyse bacteria and are increasingly recognized as a natural and highly promising solution against pathogenic bacteria. Their unique biological features make them particularly well-suited for veterinary applications: they precisely target pathogenic bacteria, self-amplify at the site of infection, and spare the beneficial microbiota. Phages can be applied in multiple complementary ways: therapeutically to treat infections where antibiotics fail; preventively through biocontrol strategies that reduce bacterial load in herds and flocks; for biosanitation of farm environments and processing facilities; and in biopreservation to enhance the microbial safety and shelf life of animal-derived products. Research and experimental studies have demonstrated phage efficacy against key bacterial pathogens in veterinary microbiology, including Escherichia coli, Salmonella enterica, Campylobacter spp., Clostridium perfringens, Pseudomonas aeruginosa, and Staphylococcus aureus, in both livestock and companion animals. Phage-based approaches therefore represent a versatile, environmentally friendly alternative to antibiotics, with the potential to improve animal health, enhance food safety, and mitigate the public health risks associated with antimicrobial resistance.

Keynote Lecture: Ralph Goethe - Lecture Hall (14:15 - 14:45)

-Conveners: Bellato, Alessandro (Università di Torino); Rösler, Uwe (Freie Universtität Berlin)

[161] Diversity of Mycobacterium avium virulence illustrated by mouse infection models (14:15)

Presenter: GOETHE, Ralph (Institute for Microbiology, University of Veterinary Medicine, Hannover)

Mycobacterium avium is the most important mycobacterial species with medical relevance besides M. tuberculosis and M. bovis. It is a slow-growing non-tuberculous mycobacterium divided into four subspecies (ssp.): M. avium ssp. avium (MAA), M. avium ssp. silvaticum (MAS), M. avium ssp. paratuberculosis (MAP) and M. avium ssp. hominissuis (MAH). Despite high genetic identity, they differ in growth, genome structure, pathogenicity and host preference. MAA, MAS and MAP are obligate animal pathogens. MAA causes avian tuberculosis, mainly in poultry under extensive husbandry or in zoo enclosures. After oral infection, the disease manifests systemically, especially in liver, spleen and intestine. Rare infections occur in cattle, pigs and humans. MAS has been isolated from avian tuberculosis-like lesions in wild pigeons. MAP causes paratuberculosis, a fatal chronic enteritis of ruminants, typically in the distal ileum and ileocecal valve. It can also infect other species and humans, often subclinically. Its potential role in Crohn's disease remains debated. MAH, in contrast, is an opportunistic pathogen occurring in the environment with a broad host range. Rising incidence in pigs and humans suggests certain host preference. In pigs, oral infection leads mainly to regional lymphadenitis affecting intestinal, head and cervical lymph nodes. Infections in cattle, poultry and other animals are usually subclinical. In humans, MAH causes local to systemic infections, primarily in immunocompromised but occasionally also in immunocompetent individuals. Relatively little is known about the pathogenicity and host preference of the subspecies. Despite many studies in mice, immunopathology remains insufficiently investigated. Examining immunopathology of M. avium subspecies in mice will provide insights into pathogenicity and contribute to understanding virulence in natural hosts.

Epidemiology - Lecture Hall (14:45 - 16:00)

-Conveners: Bellato, Alessandro (Università di Torino); Rösler, Uwe (Freie Universtität Berlin)

[73] Characterization of Enterococcal Groups Present in Hospital Environments (14:45)

Presenter: GERALDES, Catarina (CIISA - Centre for Interdisciplinary Research in Animal Health, Faculty of Veterinary Medicine, University of Lisbon, Lisbon, Portugal; Associate Laboratory for Animal and Veterinary Sciences (AL4AnimalS))

Enterococci are one of the most frequent bacteria associated to hospital-acquired infections, so their antibiotic resistance and virulence characterization is important to prevent and treat these infections. This study focusses on bacteria from four different sources: 34 environmental enterococci from the surfaces of a veterinary Biological Isolation and Containment Unit, 10 clinical enterococci from urinary tract infections of dogs, 10 commensal enterococci from the oral cavity of dogs and 10 clinical enterococci from human diabetic foot ulcers. Susceptibility testing by disk diffusion for thirteen antibiotics and phenotypic virulence factor production using six selective mediums were performed. Multiple Antibiotic Resistance (MAR) and Virulence (VIR) Indexes were calculated by dividing the number of resistances or positive expression of virulence factors, by the total number tested. The group that presented the highest MAR index was the environmental enterococci, mainly composed of Enterococcus faecium, known for its high antibiotic resistance. The commensal isolates presented the highest VIR index, probably because 5 of the 10 representative isolates were identified as Enterococcus faecalis, known for their high virulence. When comparing both indexes, human clinical isolates were the ones with the highest pathogenic potential. This study is important in showing that different environments may compile bacteria with different characteristics, even within a single genus.

[114] Identification and phylogenetic analysis of Mycobacterium avium subsp. avium strains isolated from three Abyssinian cats from Northern Italy with disseminated mycobacteriosis (15:00)

Presenter: Prof. LAUZI, Stefania (Università degli Studi di Milano Dipartimento di Medicina Veterinaria e Scienze Animali, Lodi)

Nontuberculous mycobacteria, including those in the *Mycobacterium avium* complex (MAC), are emerging pathogens of humans and animals. An outbreak of fatal disseminated mycobacteriosis caused by MAC was observed in eight Abyssinian cats in Italy in autumn 2024 and isolation of MAC strains was successful in three cats. This study focused on the genomic characterization of these strains. Whole-genome sequencing was obtained with Miniseq Illumina platform. PanX and MTBseq tools were used to characterize the strains. Phylogenetic analysis was performed both on core genome using PanX and whole genome with maximum likelihood method, implemented in iqtree2. All three samples were identified as *Mycobacterium avium* (MA) and were further phylogenetically identified as *Mycobacterium avium* subsp. *avium* (MAA) showing 100% genome sequence identity. Their genome size was 4,855,006 - 4,860,371 bp with a GC content of 69.33-69.34%. Phylogeny showed that the three strains clustered with a MAA strain from Germany (Assembly GCF_020735405). Major virulence factors such as SigE, SigF, and Phop were detected in the three strains, together with antibiotic resistance associated genes. Disseminated mycobacteriosis caused by MAA in Abyssinian cats confirms previous reports showing a breed predisposition to MAC infections, highlighting the need for MAC surveillance and suggesting further studies to define MAA ecology, evolution and pathogenesis.

[81] Tracing the Introduction and Rise of a Single Leptospira Pomona Clone in Animals in Israel (15:15)

Presenter: Dr BLUM, Shlomo (Dept. of Bacteriology, Kimron Veterinary Institute, Rishon Lezion, Israel)

Leptospirosis is a globally important animal infection and zoonosis caused by pathogenic Leptospira species. In Israel, Leptospira serovar Pomona emerged over the past two decades from undetected to endemic status, becoming the dominant cause of bovine leptospirosis. Incidence in cattle culminated in large-scale outbreaks in 2018, coinciding with an exceptional human outbreak. These events prompted enhanced wildlife surveillance. From 2015–2024, >3,400 wildlife sera and ~400 kidney samples were tested by MAT and PCR. PCR-positive samples underwent 7-locus MLST, serovar-specific PCR, and high-resolution AmpSeq (42 genes, ~10,000 bp); isolates from cattle and wild boars were whole-genome sequenced. The highest seroprevalence was found in wild boars (20–43%), with high titers and PCR confirming actual infection with L. interrogans serovar Pomona. MLST identified ST52 in all typed samples from cattle and wildlife. AmpSeq and WGS confirmed complete identity of ST52 profiles across samples from 2011 to 2024. Notably, archival DNA from a 2011 outbreak related to imported cattle—among the first Pomona cases in Israel—matched all later samples, providing genomic evidence of a single introduction event. These findings identify wild boars as key reservoirs and demonstrate the establishment of a single Leptospira Pomona clone in Israel following introduction. Continued surveillance and coordinated response across the wildlife–livestock–human interface are essential.

[19] Mycobacterium bovis infected domestic cats in an officially bovine tuberculosis free country resulting in human infection (15:30)

Presenter: VAN DER MOST, Marleen (Wageningen Bioveterinary Research, Wageningen University & Research, Lelystad, the Netherlands)

Despite the official bovine tuberculosis free status, Mycobacterium bovis sporadically causes tuberculosis (TB) in non-bovine mammals in the Netherlands. In early 2023, two domestic cats from unrelated households were diagnosed with M. bovis following euthanasia due to severe respiratory symptoms. In one household, three additional cats were euthanized, with post-mortem confirmation of M. bovis infection. An epidemiological link was hypothesized but not supported by genetic analysis, as the isolates from the two households differed in spoligotype and by at least 500 single nucleotide polymorphisms (SNPs). Commercial raw pet

food was suspected as the probable source, but this could not be confirmed. Given the zoonotic potential of M. bovis, human contacts were screened using the Tuberculin Skin Test (TST) and Interferon-Gamma Release Assay (IGRA). Lung lesions were detected by computed tomography in a TST-positive, IGRA-negative contact and M. bovis DNA was isolated from a lung biopsy. This DNA contained specific SNPs also identified in the feline M. bovis isolates from the respective household, supporting the hypothesis of intra-species M. bovis transmission. All TST-positive contacts received antibiotic therapy. These cases indicate that TB should be considered in the differential diagnosis of respiratory conditions in companion animals and highlight the need for One Health vigilance to prevent M. bovis transmission among humans, companion animals, wildlife, and livestock.

Omics techniques - Seminar Room (14:45 - 16:00)

-Conveners: Szabo, Istvan (Bundesinstitut für Risikobewertung); Wenderlein, Jasmin (Bundesinstitut für Risikobewertung)

[112] Usefulness of Metagenome-Assembled Genomes (MAGs) for the study of pathogen–microbiota interaction in swine dysetenry model (14:45)

Presenter: GALISTEO, Cristina (UNIVERSIDAD DE LEON)

This study aims to deepen the mapping of bacteria that may participate in infectious processes as pathobionts, using information obtained from short-read sequencing and the subsequent assembly of genomes from these reads, a method known as metagenome-assembled genomes (MAGs) in an experimental infection model of swine dysentery by Brachyspira hyodysenteriae. Shotgun metagenomic sequencing with Illumina NovaSeq technologywas performed in 112 samples which enabled the reconstruction of 3,735 MAGs. These MAGS were filter by quality and GTDB database annotation, identifying 576 MAGs at the species level. We further explored MAGs from species of interest based on metataxonomic analyses Prevotella pectinovora (9 MAGs), Acetivibrio ethanolgingens (7 MAGs), and Campylobacter hyointestinalis (4 MAGs) Roseburia inulinivorans (1 MAG), all exclusively reconstructed from samples of animals affected by the disease, and in all cases, at least one of the sequences was of high quality. No major virulence genes were detected in the MAGs of these species although several minor factors and resisntace genes were identified. In addition, we observed discrepancies in the taxonomic classification of the specie A. ethanolgignens which in the GTDB database is annotated as “Velocimicrobium ethanolgignens” based on gene markers. In conclusion, the study results reveal the usefulness and discriminatory power of metagenomic assemblies to characterise novel species in disease pathogenesis.

[152] Genetic Diversity and Lewis Antigen Status Shape Intestinal Mucus O-Glycome: A Network Perspective in TLR5-Deficient Pig Model (15:00)

Presenter: GHAZISAEEDI, Fereshteh (Institute of Microbiology and Epizootics, School of Veterinary Medicine at the Freie Universität Berlin, Berlin, Germany)

Dissecting intestinal homeostasis requires understanding subtle interactions between host genetics, innate immunity, and the microbiota before overt disease occurs. Using genetically diverse pigs, we mapped O-glycan structures in intestinal mucus under non-induced conditions, integrating these with transcriptomic and microbiota data. Porous graphitized carbon LC-MS/MS identified ~140 distinct O-glycans across gut regions, revealing that Lewis antigen status—particularly Le$^{a/x}$ vs. Le$^{b/y}$—dominates glycan diversity, often outweighing TLR5 deficiency. Transcriptomic data showed Lewis antigen profiles and TLR5 functionality jointly shape glycosylation enzyme expression and immune signatures, indicating a bidirectional interplay between immune sensing and epithelial glycan remodeling. Microbiota changes were subtle but genotype-dependent, with specific taxa enriched in Le$^{a/x}$ animals. Combined analysis of FUT2/3 expression, a MUC13 SNP, and TLR5 deficiency revealed complex, location-specific microbial shifts, especially in the colon. These findings demonstrate that glycomics can be scaled to network-level resolution, underscoring the importance of host genetic variation in maintaining mucus barrier integrity and microbial balance, a key to preventing chronic gut disorders.

[57] Genomic and virulence insights of Western European Aeromonas salmonicida subsp. salmonicida and development of Galleria mellonella infection assay (15:15)

Presenter: Ms DESMECHT, Salomé (Veterinary Bacteriology Laboratory, Department of Infectious and Parasitic Diseases, Fundamental and Applied Research for Animals & Health (FARAH), Faculty of Veterinary Medicine, University of Liège, Liège, Belgium)

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 101 to 106 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 101 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.

[131] PRELIMINARY METABOLOMICS DATA ON VIRUS INFECTION: THE CASE OF BOVINE CORONAVIRUS (BCoV) (15:30)

Presenter: SALVATORE, Maria Michela (University of Naples "Federico II")

Objectives: The mechanisms regulating the interconnections between viruses and cell hosts are not yet fully understood and this is necessary for early diagnosis and an effective operational response to counter infections caused by emerging and/or re-emerging viruses. Metabolomics gives a comprehensive representation of metabolites providing further information on mechanisms involved in cell responses during infectious diseases. This study is focused on bovine coronavirus (BCoV), a betacoronavirus, like SARS-COV-2, causing enteric diarrhea in calves, winter dysentery, as well as Bovine Respiratory Disease. Hence, we developed an in vitro strategy, based on both virology and metabolomics techniques to provide insights into virus-host interactions. In addition, this strategy could be useful in the search for new antiviral compounds. Methods: GC-MS, NMR, cytomorphological analysis, immunofluorescence assay. Results: We developed a full strategy for the evaluation of intracellular metabolites to obtain an insight into the variations caused in bovine cells (MDBK) during BCoV (strain 282/23) infection. The dataset comprises over 50 metabolites belonging to different classes of natural products. Conclusions: In conclusion, in this work we offer a snapshot of the physiological state of the cell before and after BCoV infection. Moreover, the workflow employed by us could be suitable to gather valuable information on the mechanism of action of potential antiviral candidates.

[64] Characterizing the Pathogenic Potential of Vibrio parahaemolyticus: Phenotypic and Genotypic Analysis of Biofilm Formation and Virulence Gene Expression in Clinical and Environmental Strains on Mussel Shells (15:45)

Presenter: HUANG, Xia (Free University of Berlin)

Vibrio parahaemolyticus is a major food-borne pathogen associated with contaminated seafood and capable of causing varying degrees of gastroenteritis in humans. Its pathogenicity is mediated by multiple virulence factors, including flagella and adhesion factors, and is further enhanced by its ability to form biofilms, increasing its resistance to environmental stress. However, the mechanisms underlying its pathogenicity remain incompletely understood. The main objective of this study is to examine the biofilm formation ability and virulence gene profiles of *V. parahaemolyticus* isolates on mussel shells, comparing genotypic and phenotypic traits of clinical reference and environmental strains at 25°C, 30°C and 37°C. A total of 25 strains were examined. Motility was assessed by swimming and swarming assays, while biofilm formation was determined by crystal violet staining. The presence of 32 associated genes was analyzed using real-time qPCR. While the reference strain *V. parahaemolyticus* RIMD 2210633 contained all target genes, some strains lacked key adhesion genes. Swarming motility appeared inversely regulated with biofilm formation. Gene expression analyses following biofilm formation on mussel shells will be conducted to further elucidate regulatory mechanisms.

Summary and Conference close - Lecture Hall (16:00 - 17:00)