One Health Conference Greifswald 2022

Wednesday, April 27, 2022 - Thursday, April 28, 2022

Digital Conference

Program

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Wednesday, April 27, 2022

Early Bird Yoga (7:30 AM - 8:00 AM)

Welcoming remarks (9:00 AM - 9:30 AM)

Session 1a: Pathogen-host-environment interactions (9:30 AM - 10:45 AM)

[100] Beyond Zoonoses: Expanding the Scope of One Health Interactions and Interventions (9:30 AM, 30 minutes)

Presenter: CLEAVELAND, Sarah

Information points as follows: Changes in land-use and agricultural systems underpin many of the intersecting problems around food security, biodiversity loss, climate change and human health. The full potential of One Health for addressing the inter-dependent challenges of the Sustainable Development Goals has yet to be fully realised. Drawing on research in Tanzania, the presentation will illustrate how vulnerability to zoonotic diseases varies widely across agro-ecological systems and will discuss ways in which changes in climate and land-use policies have affected livestock management and disease risk. The presentation will discuss the wide-ranging impacts of transmission and control of diseases at the livestock-wildlife interface in relation to food security livelihoods, ecosystem health, land-use conflict and carbon dynamic One Health needs urgently to move beyond rhetoric towards action to address cross-sectoral problems that can build trust and strengthen the cross-cutting capacities needed to respond effectively to global challenges.

[54] Pathogen traits mediate the effect of biodiversity on rodent-borne pathogen dynamics (10:00 AM, 10 minutes)

Presenter: IMHOLT, Christian

There has been increasing attention to the effect of habitat degradation on the emergence and expansion of infectious diseases in humans and animals. Habitat degradation may alter host abundance, diversity, community composition as well environmental conditions associated with disease transmission. Pathogens with different routes of transmission might respond differently to changes in the environmental conditions. It is important to establish how heterogeneity in life histories among hosts contributes to the persistence/ emergence of different pathogens. Here we present results of a 3-year field study in Central Germany that aimed to compare the dynamics of pathogens differing in transmission traits within the small mammal communities of grassland and forest habitats. For this we considered the Tula orthohantavirus as a species-specific pathogen to the common vole (Microtus arvalis), and Leptospira spp. as ubiquitous within all mammals. Seasonal trapping of small mammals and camera surveillance of larger mammals allowed assessing host features like abundance, diversity and community composition. Network analyses revealed that for both pathogens biodiversity per se was not an overall predictor of pathogen dynamics, but rather trophic interactions within the mammal community that are specific to each pathogen. The results demonstrate that pathogen traits need to be considered to understand the epidemiology of rodent-borne pathogens and help to improve public health responses.

[51] In-depth analysis of potential reservoir species for zoonotic Borna Disease Virus 1 (BoDV-1) (10:10 AM, 10 minutes)

Presenter: HARING, Viola

Lethal non-purulent myeloencephalitis of domestic mammals and humans can be caused by Borna disease virus 1 (BoDV-1, species *Mammalian 1 orthobornavirus*). So far, only the bicoloured white-toothed shrew (*Crocidura leucodon*) has been described as a natural reservoir of BoDV-1. The objective of this study was the characterization of BoDV-1 infections in putative reservoir hosts. Small mammals were collected all over central Europe. Primary screening of brain tissue for bornavirus RNA was performed using a BoDV-1-specific and a broad range panBorna RT-qPCR. Positive results were confirmed by partial or whole genome sequencing. For BoDV-1-positive individuals, viral antigen and RNA tissue distribution was analyzed via immunohistochemistry and RT-qPCR. Screening of about 9000 small mammals resulted in the detection of 28 BoDV-1 RNA-positive shrews (23/95 bicoloured white-toothed shrews [24.2%], 4/38 lesser white-toothed shrews, *Crocidura suaveolens* [10.5%] and 1/243 greater white-toothed shrew, *Crocidura russula* [0.4%]), all originating from known BoDV-1 endemic areas. All three species of shrews show a similarly broad viral RNA and antigen tissue tropism with the highest loads in neuronal tissue and lower amounts in non-neuronal tissue. Phylogenetic analysis of three human-derived BoDV-1 sequences matches sequences from shrews collected nearby residences of human cases, supporting the peridomestic infection risk.

[98] Ecology of African bat-borne hantaviruses and their public health impact in Côte d'Ivoire, West Africa (10:20 AM, 10 minutes)

Presenter: KOUADIO, Léonce
Most hantavirus research has understandably focused on hantaviruses infecting rodents. Recently, bats have been increasingly recognised as additional reservoir hosts. However, so far most viruses were identified in one or few individuals in single studies. We trapped bats in Côte d'Ivoire and screened organs by PCR for the presence of hantaviruses. Additionally, serum samples from humans living in the same regions were collected and tested for IgG antibodies against antigens derived from rodent- and shrew-borne hantavirus. Moreover, using hybrid in-solution capture and next-generation sequencing, we generated the full nucleocapsid sequence of one bat-associated virus from Côte d'Ivoire, which allowed for expression of recombinant protein for use in serological studies. We show that two closely related pipistelle bat species (Neoromicia nanus and N. tenuipinnis) in Côte d'Ivoire were enzootically infected with two distinct hantaviruses (Mouyassue and Ponan virus) and that virus prevalence was stable across four years. All infected animals were captured in vicinity of human settlements and viral sequences were detected in all tested lung organs. While we do not have evidence of spillover events to rodents or shrews in the same areas, human sera showed evidence of hantavirus-specific IgG antibodies. We provide evidence that different bat species adapted to human habitats are natural hosts of hantaviruses and that humans are exposed to these animals and their viruses.

[107] Q & A (10:30 AM, 15 minutes)

Break (10:45 AM - 11:00 AM)

Poster Session 1 (11:00 AM - 12:00 PM)

[99] Ecology and epidemiology of monkeypox virus at human/wildlife interfaces (11:00 AM, 1 hour)

Presenter: SCHLOTTERBECK, Jasmin
Lately the global importance of monkeypox virus (MPXV) as a human pathogen has been highlighted by a rising number of cases in its endemic areas in West and Central Africa, as well as imported cases in Europe, Asia, and the USA. As immunity withers after the eradication of smallpox and the end of the vaccination program, MPXV is considered the most concerning zoonotic agent among orthopoxviruses. Aside from habitat loss and poaching, infectious diseases such as monkeypox may constitute a severe threat to the survival of non-human primates. In this research project we want to investigate the question of its reservoir in wildlife. Samples from sylvatic chimpanzees in Taï National Park, Côte d'Ivoire, where in the past MPX outbreaks have occurred, will be examined. Behavioural data and diet analysis will help identify potential wildlife contacts of the infected chimpanzees and pinpoint possible reservoir species. In a field study performed at the same location, candidate rodent species are being sampled. Present and former infections with MPXV will be identified via PCR and serology. Additionally, to get a better picture of the circulation of MPXV in humans, we aim to identify formerly undiagnosed cases with atypical clinical presentation. Clinical samples from respiratory and fever syndrome patients in endemic areas will be investigated. Altogether, our study will contribute to a better understanding of the ecology and epidemiology of MPXV at human-wildlife interfaces.

[89] Influence of host- and microbiota-derived bile acids on Clostridiodes difficile infections (11:00 AM, 1 hour)

Presenter: SIEVERS, Susanne
The anaerobic bacterium and intestinal pathogen *Clostridiodes difficile* is the main cause of hospital-acquired diarrhea and represents a high economic burden of health care systems world-wide. Although the pathogen is mostly problematic for elderly and people with compromised microbiota, the number of incidences in young patients and community-acquired infections are rising. A high percentage of farm animals are carriers of *C. difficile*, just as people working in medical or care facilities without showing any symptoms of disease, but potentially transmitting highly resistant endospores of the bacterium. Several studies have shown a correlation of *C. difficile* infection (CDI) and the occurrence of specific species in the microbiota and intestinal metabolites. However, why and how these species and metabolites hamper or promote *C. difficile* is only poorly understood. Bile acids and microbial species with the ability to convert bile acids have been shown to be an important determinant for the incidence and course of a CDI. In order to benefit from this knowledge and to apply it in *C. difficile* therapy, the details on the impact of such intestinal species and their metabolic abilities is mandatory. We aim at the elucidation of the molecular action of infection-relevant bile acids on the pathogen *C. difficile* by using a wide spectrum of techniques. This new knowledge will help to prime the individual microbiota of patients to better treat or even prevent an infection.

[87] An epidemiological study of avian influenza viruses in Irish ecosystems (11:00 AM, 1 hour)

Presenter: RUY, Paule-Émilie
Europe is facing unprecedented numbers of outbreaks of avian influenza viruses (AIVs), in wild birds and poultry farms. Worldwide, the cases of human infections by these viruses – including a range of variants – are increasing. The sudden acceleration in outbreaks remains unclear. To preserve animal and human health, it is necessary to better understand the ecology

of AIVs. My PhD research aims to explore the epidemiology of AIVs in Irish ecosystems, improving surveillance and preparedness. For this, we will test for the presence of AIVs at wetland areas. The sediment of several wintering grounds, known to host abundant and diverse populations of migratory waterbirds will be sampled. Viral RNA will be extracted and RT-qPCR will be performed targeting the M gene to detect all subtypes of AIVs. We will analyse positive samples to assess the presence of H and N sequences. Furthermore, we will lead a disease investigation to determine if wild American minks (*Neovison vison*) in Ireland shed AIVs. And, to apprehend if this semiaquatic species can spread AIVs to birds, humans, and other mammals. Blood samples and body fluids from minks' carcasses will be examined for the presence of antibodies against AIVs with a commercial competitive ELISA test kit. Positive sera will be scanned with influenza inhibition assay (HI) using five strains: H5N1, H5N3, H5N8, H7N7, and H10N4. Finally, the work described here will increase our knowledge of reservoirs of AIVs in Ireland.

[75] SORMAS goes One Health: Water-based Outbreak Prediction in Peri-Urban Africa (11:00 AM, 1 hour)

Presenter: KNAUF, Sascha

Surface water can accumulate microbes that circulate at the human-domestic livestock-wildlife interface often before disease outbreaks are reported. Our study aims to generate baseline data and novel insights into the depth of microbial diversity and candidate pathogens for epidemics in peri-urban Africa. In addition, it conceptualises the incorporation of environmental signals into the Surveillance Outbreak Response Management and Analysis System (SORMAS). Ten water sources in the Kumasi area, Ghana, where sampled for seven weeks (1 sample (2L surface water)/site per week). Samples were filtered using a multistep procedure to enrich bacteria and viruses, which are subsequently analysed by cultural, metagenomic and metataxonomic approaches to investigate the microbial diversity and identify candidate pathogens. In addition, pheno- and genotypical analysis, including resistance profiling for enterobacterales is conducted. We present our protocols used to sample the different water sources in Kumasi and provide details about the laboratory downstream processing of water samples including first results on the microbial diversity and antibiotic resistance screening. In addition, we outline the development process of a concept for a digital environmental surveillance component for SORMAS. Our findings have the potential to support the development of strategies for the early detection and management of emerging diseases at the human-wildlife-livestock interface.

[69] BUSHMEAT HUNTING, RISK FACTORS AND ZOONOTIC TRANSMISSION OF SIMIAN T-LYMPHOTROPIC VIRUS 1 IN TROPICAL WEST AND CENTRAL AFRICA (11:00 AM, 1 hour)

Presenter: MOSSOUN, MOSSOUN ARSENE

In West Africa, and Central Africa, tropical forests are subject to intense pressures due to agricultural industries and the uses by local populations for construction, human and animal food needs. These pressures lead to permanent contacts between humans and non-human primates (NHP), which are source of Ebola virus and Simian lymphotropic virus (STLV) transmission. We study transmission of STLV-1 near the Tai National Park and Salonga National Park. NHP carcasses were collected from six species in CIV between 1998 and 2014 and nine species in DRC between 2011 and 2013. Peripheral venous blood was collected from 574 people in CIV and 312 in the DRC among whom, those aged more than twelve years have undergone a questionnaire on contacts with NHP bushmeat. Using ELISA, Western Blot, PCR and phylogeny, we showed that HTLV-1 infection rates are 0.7% in CIV and 1.3% in DRC. At the same time, STLV-1 infected NHP were higher at CIV than at DRC. Two Ivorian human virus sequences were closely related to simian counterparts, indicating ongoing zoonotic transmission. Multivariate analysis of human behavior confirmed participants from CIV to be less often exposed to NHP than those from DRC.We also showed that Young men and mature women were most likely exposed to NHP at both sites. We conclude that a similar ultimate risk of zoonotic STLV-1 transmission. The identification of such high risk groups of NHP exposition may guide future prevention efforts of zoonotic disease spread.

[72] Molecular basis of host adaptation and pathogenicity of zoonotic hantaviruses (11:00 AM, 1 hour)

Presenter: MENKE, Laura

Human pathogenic hantaviruses are rodent-borne pathogens that do not cause obvious pathogenic effects within their natural hosts. Upon transmission to humans, the viruses in Europe can cause hemorrhagic fever with renal syndrome of high severity. Despite the disease burden, our knowledge about the infection mechanism and the influence of adaptive amino acid exchanges within the envelope proteins remains incomplete. Focusing on virus entry, our goal is to investigate hantavirus infection in human and rodent-derived cell models. We use a combination of both single-cell microscopy as well as proteomics to identify receptor candidates and to clarify the signaling pathways that are triggered by viral attachment and entry within the different cell lines. In parallel, we have started to comparatively characterize the different host cell lines with respect to their morphology and physiology, most importantly their endocytic pathways, by applying selected Puumala orthohantavirus strain infections. The overall infectivity of viral strains will be quantified by different microscopy techniques. To increase the validity of our observations, we will complement our imaging results with RT-qPCR and flow cytometry investigations. To correlate cell-type dependent effects with viral adaptation, a further focus of our work is to investigate the spatial and temporal evolution of the hantavirus envelope protein, which is a main determinant in viral tropism.

[71] Gastrointestinal parasites in overlapping populations of mountain gorilla (Gorilla beringei beringei), livestock, and Batwa communities in and around Bwindi Impenetrable National Park, Uganda (11:00 AM, 1 hour)

Presenter: SAMBUCCI, Kelly

Bwindi Impenetrable National Park (BINP), Uganda is home to approximately half of the world's population of endangered mountain gorillas. The area surrounding BINP is densely populated with livestock grazing and a limited buffer zone. The aim of this study was to assess the occurrence of gastrointestinal parasites in overlapping populations of mountain gorilla, livestock and Batwa tribal communities that live in and around BINP. In total 177 faecal samples were analysed, using a combination of microscopy and molecular methods. Protozoans *Entamoeba* spp. were detected in all host groups by diagnostic PCR, with a prevalence of 63.3%, 62.3%, 68.2%, and 70% in gorillas, cattle, goat and humans respectively. Sanger sequencing confirmed *E. bovis* in livestock, *E. hartmanni* in mountain gorilla and *E. coli, E. dispar* and *E. hartmanni* in humans. Phylogenetic analysis identified an *E. hartmanni* haplotype shared between a mountain gorilla and human. Additionally, generic nematode primers were used to screen the gorilla and livestock samples to amplify the nematode of greatest abundance in each sample. *Murshidia* was the most common nematode amplified in the gorilla samples. When comparing to livestock it was found to not be host-specific and demonstrated potential pathogen flow between gorilla and livestock. This study highlights the potential parasite transmission at the human-wildlife-livestock interface in BINP, Uganda.

[70] Overcoming challenges in helminth diagnostics and epidemiology in mountain gorillas (11:00 AM, 1 hour)

Presenter: CERVENA, Barbora

Parasitological studies of endangered wildlife rely heavily on noninvasively collected samples, usually feces. The type of samples (identified/unidentified) and the number of sampling events per individual have a significant impact on the information that can be gained from the sample set. Depending on the taxon, parasite stages shed in feces can be determined to the level varying from the order to the species using optical examination methods. However, interspecies transmission, including zoonotic or wildlife-domestic animal cycles, cannot be evaluated, so DNA barcoding followed by sequence analysis is required. Unfortunately, the utility of molecular taxonomy tools is limited by the pre-existence of reference sequences usually tied to obtaining adult helminth specimens that can be properly morphologically determined and subsequently subjected to DNA sequencing. We used adult specimens collected in necropsies, proglottids extracted from feces and a comprehensive set of both identified and unidentified fecal samples to investigate the epidemiology of anoplocephalid cestode infections in mountain gorillas in Volcanoes National Park, Rwanda. We identified the dominant *Anoplocephala gorillae* and a rarely occurring *Bertiella* sp. Less than 1% of fecal samples contained neither cestode eggs nor DNA. The number of eggs shed by individual gorillas varied widely over time, and some animals even had negative and positive samples recorded within a short period of time.

[67] Distribution borders of Puumala orthohantavirus in its rodent reservoir in Germany (11:00 AM, 1 hour)

Presenter: DREWES, Stephan

Puumala orthohantavirus (PUUV) causes the majority of human hantavirus disease cases in Germany. The frequency of human cases is mainly driven by the abundance and prevalence of PUUV in the natural reservoir, the bank vole (Clethrionomys glareolus). The objective of our study within the research consortium “RoBoPub” (Rodent-Borne-Pathogens-and-Public-Health) is to further characterize the PUUV range in Germany. For that purpose, bank voles were collected along large scale transects in North Rhine-Westphalia/Lower Saxony and within Thuringia and Bavaria. Between 2018-21 2873 bank voles were collected and screened for PUUV-specific RNA and antibodies. In spring, the average PUUV prevalence reached 14% to 16% in non-outbreak years and 17% to 92% in outbreak years (2019 and 2021). The investigation in Lower Saxony confirmed the range border reaching from district Bentheim to district Osnabrück in the northwest of Germany. In Thuringia PUUV occurrence in bank voles was sporadic and geographically restricted to certain forest areas in the northwest and southwest. Preliminary data from Bavaria suggest the absence of PUUV within the central region despite widespread presence of the pathogen in Bavaria’s north and east. Future investigations are needed to identify the reasons for the current PUUV distribution in Thuringia and Bavaria. The identification of PUUV endemic regions based on reservoir screening will help to establish geographically specified risk assessments for the public.

[66] Development of Variegated squirrel bornavirus -1 (VSBV-1) animal models: the tenacious search for the appropriate species (11:00 AM, 1 hour)

Presenter: SCHLOTTAU, Kore

Variegated squirrel bornavirus 1 (VSBV-1) is a zoonotic virus and it is assumed that exotic squirrels represent reservoir hosts. The closest relative, classical Borna disease virus 1 (BoDV-1), is known since a long time and causes fatal Borna disease in horses and sheep in Europe. Today we know that both mammalian bornaviruses can cause severe encephalitis in humans. The aim of this study was to test the susceptibility of different rodent models and non-human primates for VSBV-1, to characterize the course of disease and thereby to establish an infection model which could provide deeper insights into transmissions pathways,

pathogenesis and countermeasure development. VSBV-1 infection studies were done with different rodents (rats, bank voles, mice, gerbils and guinea pigs) in addition to rhesus macaques. Rodents of different ages were infected with VSBV-1 by different infection routes (intracerebral, intranasal or subcutaneous). Rhesus macaques were inoculated either by the intracerebral route or by multiple routes (intranasal, conjunctival, intramuscular and subcutaneously; reflecting possible natural infection routes). All animals were monitored for signs of disease and virus shedding. So far, none of the tested rodents fulfilled all criteria to be used as an infection model for VSBV-1 without virus adaptation whereas macaques intracerebrally infected with mammalian bornaviruses develop a human-like disease and may serve as a surrogate model for human bornavirus infection.

[65] Virome studies of squirrels in Germany (11:00 AM, 1 hour)

Presenter: VESPER, Laura

Rodents in general are reservoir hosts for zoonotic pathogens, and also squirrels in particular have been described as hosts of putative zoonotic viruses (https://doi.org/10.3390/v10070373). In squirrel rescue centres, contact between humans and animals is intense. Selected samples collected in rescue centres were analysed for the presence of viruses. Next-generation sequencing combined with subsequent metagenomics analysis was used to examine samples from animals with pre-reported clinical signs of diarrhoea. Detected viral sequence reads were assembled and genetically and phylogenetically analysed. Subsequently, primers were designed and specific real-time PCR systems were developed and used for a small-scale screening for the detected viruses. More than 500 samples of different tissues from 135 different animals were analysed. Different new viruses of the families *Picornaviridae*, *Astroviridae*, and *Tombusviridae* were detected. According to the results of our sequence analyses, no viruses with suspected or proven zoonotic potential were among the closest relatives. The new viruses were predominantly found in animals belonging to the indigenous species *Sciurus vulgaris* and showed mainly an intestinal tropism. They were also frequently detected in liver, and sporadically in lung and kidney, but never in brain. The association of the occurrence of the viruses with specific clinical signs like diarrhoea and sudden death remains to be confirmed.

[59] Un-mystifying a buzzword: Qualitative analysis of the utilization of the term „human-animal-interface“ in One Health oriented research (11:00 AM, 1 hour)

Presenter: DREYER, Sylvia

Zoonoses are diseases, which readily cross the species barrier. Their effective control is part of the One Health concept with the “human-animal-interface” as one of the key defining features. Although the term is frequently used in describing pathogen transmission, a clear definition is lacking. This study aimed to analyse the use of this term in scientifically identifiable patterns and categories. This study consisted of a systematic literature search of two electronic databases (PubMed, ISI Web of Science) complemented by interviews of health experts in the field of zoonosis/ One Health held from March 2019 to May 2021. From identified publications, keywords and interface descriptions were extracted and categorised. Interviews followed a questioning route, were audio recorded, transcribed and qualitative content was examined. Inductive analysis was applied throughout. Study findings are based on 158 publications supplemented by 27 expert interviews. The results showed consensus in the use of keywords to describe the interface. Seven categories of contact interfaces were derived. Precise descriptions of the interfaces varied greatly depending on the pathogen domain. Specific patterns could be identified that were consistent between the literature and experts. There was a general concordance in using the human-animal-interface term between literature and experts. The results will contribute to a further systematic understanding and definition of the term.

[57] An inventory of zoonotic and food borne disease surveillance systems: Expanding and understanding the One Health knowledge base (11:00 AM, 1 hour)

Presenter: DUPS-BERGMANN, Johanna

Effective disease-management decision making is often underpinned by surveillance data. For zoonotic and food-borne diseases that benefit from a One Health (OH) approach, data from multiple surveillance systems may be required. However, identifying and accessing these data can be difficult. To address this problem, we aimed to develop an accessible inventory of the zoonotic and food-borne disease surveillance systems in existence across Europe. We created spreadsheet-based questionnaires to collect uniform data describing relevant surveillance systems from each of the sectors: animal health, public health, and food safety. The spreadsheets were sent to all European Joint Programme ‘ORION’ and ‘MATRIX’ project partners for data contribution. Currently, the inventory contains 216 entries for public health, 299 for animal health and 204 for food safety. Analysis of the data revealed several instances of pathogens under surveillance across all three sectors within a country, demonstrating scope for cross-sectoral surveillance based on existing systems. However, intersectoral differences were observed in the definitions of common terminologies, and various surveillance elements such as system objectives, sampling context and sampling strategy. In summary, this surveillance inventory both improves cross-sectoral understanding of surveillance approaches, and facilitates information exchange across sectors and countries for improved OH approaches to disease management and prevention.

[49] Oesophagostomum stephanostomum causing parasitic granulomas in wild chimpanzees (Pan troglodytes verus) of Tai National Park, Côte d’Ivoire (11:00 AM, 1 hour)

Presenter: JAFFE, Jenny

Oesophagostomum sp. is a parasitic nematode that frequently infects primates across widely separated field sites in Africa and Asia. In humans, nodular lesions in the abdomen caused by *O. bifurcum* are common in certain areas of Togo and Ghana. Similar granulomas have been observed in chimpanzees, gorillas and baboons post-mortem. At Tai National Park (Côte d'Ivoire), previous research in wild chimpanzees (*Pan troglodytes verus*) has uncovered a variety of *Oesophagostomum* spp. larvae in stool, and nodular lesions associated with unspecified *Oesophagostomum* sp. post-mortem. This study describes three recent cases of parasitic granulomas found post-mortem in the intestinal tract and abdominal wall of chimpanzees at Tai. Descriptions of gross pathology, histopathology and parasitology are complemented by new molecular results obtained by PCR and sequencing of DNA isolated from the parasitic nodules. Histologically, all three animals showed chronic colitis with granulomatous inflammation consisting of macrophages, neutrophils and eosinophils, with an external capsule formed by connective tissue. The larval ITS-2 region (Internal Transcribed Spacer) sequences obtained from the nodules matched (100%) *O. stephanostomum*. Samples from the three Tai chimpanzees were 100% identical to each other and 99-100% similar to *O. stephanostomum* reported from apes and monkeys in Kenya, Uganda, Gabon, Cameroon, Democratic Republic of the Congo, and Tanzania.

[48] Leptospirosis in Germany: The role of bank voles as a reservoir host (11:00 AM, 1 hour)

Presenter: SCHMIDT, Elisabeth

Leptospirosis is a worldwide zoonotic disease with more than 1 million human cases annually. Infections are associated with direct contact to infected animals or indirect contact to contaminated water or soil. In Germany not much is known about the prevalence and species diversity of Leptospira spp. in the reservoir host. The aim of this study was to evaluate Leptospira spp. prevalence and distribution of genomospecies and sequence types (ST) in bank voles (Clethrionomys glareolus). Rodents were collected in the years 2018 to 2020 along a transect from North Rhine-Westphalia to Lower Saxony, Germany. DNA of 1817 kidney samples was analyzed by real-time PCR targeting the lipl32 gene. Positive samples were further analyzed by targeting the secY gene to determine Leptospira genomospecies and multilocus sequence typing (MLST) to determine the ST. The overall prevalence was 7.5% (95% confidence interval: 6.4 – 8.9). Bank voles were significantly more often infected with L. interrogans (83.3%)(ST24) than with L. kirschneri (11.5%)(ST110) and L. borgpetersenii (5.2%)(ST197). This study shows that pathogenic Leptospira spp. are present in bank voles, but at much lower prevalence than in common voles (Microtus arvalis) and field voles (Microtus agrestis). Future One Health studies will be dedicated to find out the reason for the discrepancies between moderate to high Leptospira prevalence in vole hosts and the very low frequency of recorded human disease cases in Germany.

[47] Regulation of host cell signaling molecules in response to arenavirus infection (11:00 AM, 1 hour)

Presenter: HOLZERLAND, Julia

Arenaviruses include important zoonotic pathogens that cause hemorrhagic fever (e.g. Junín virus; JUNV). However, other closely related viruses are often apathogenic in humans (e.g. Tacaribe virus; TCRV). While the basis for this difference remains unclear, we found that TCRV strongly induces apoptosis (i.e. caspase-mediated cell death) in infected cells, while JUNV does not - suggesting a role for this process in pathogenesis. Nonetheless, both viruses trigger similar upstream pro-apoptotic signaling events, including phosphorylation of p53. Further, the pro-apoptotic factor Bad is phosphorylated (leading to inactivation) in TCRV-infected cells. These phosphorylation events clearly implicate upstream kinases in regulating apoptosis. Consistent with this, we show activation of the stress-activated protein kinases p38 and JNK, both of which are known to phosphorylate p53. Further, we observe activation of Akt, which is known to phosphorylate Bad, but surprisingly only in JUNV-infected cells. Importantly, inhibition of these kinases dramatically reduces the growth of both viruses, although inhibition of apoptosis itself does not - indicating that kinase activation is crucial for virus infection, independent of its downstream role in apoptosis regulation. This role of kinase activation, and its relationship to apoptosis regulation as well as virus infection, needs to be further explored as it has the potential to shed further light on the determinants of arenavirus pathogenesis.

[46] Putting theory into practice - One Health Approach to Improve COVID-19 Pandemic Response in Nigeria (11:00 AM, 1 hour)

Presenter: AGUSI, Ebere

Coronavirus disease 2019 (COVID-19)is a zoonotic disease caused by SARS-CoV-2 with increasing rates of human infections and deaths worldwide.Transmission from humans to domestic and wild animals is increasing.To address the threat posed by SARS-CoV-2,a One Health multi-sectoral cooperation is inevitable to contain the spread across human-animal-environment interfaces.In Nigeria,the most populous country in Africa with over 200 million humans and greater number of domestic,farm and wild animals, the visible encroachment and thus the intermingling of wildlife, domestic animals and humans provide favorable conditions for bidirectional transmissions of SARS-CoV-2.Hence,involving inter- and trans-disciplinary actions to reduce disease (re)emergence or to mitigate infections is germane. In a joint endeavor, veterinary, medical and anthropological professionals cooperatively adopt epidemiological, diagnostic and ethnographic methods in investigating and tackling the risks posed by the COVID-19 pandemic. Taking into account the socio-cultural, behavioral and economic conditions, inter-species transmission of SARS-CoV-2 are studied and interpreted. Critical to the success of this mission is the inclusion of the regional key policy makers who are responsible for creating conducive environment and sustainability of actions to improve pandemic response. Here, we would like to introduce the project in general and deliver an example for multi-sectoral transdisciplinary One Health effort.

[42] Characterization of the adaptation of different host-specific cell lines to infection with West Nile virus. (11:00 AM, 1 hour)

Presenter: BRANDT, Janine

West Nile virus (WNV) represents a neurotropic flavivirus that mainly circulates in an enzootic cycle between ornithophilic mosquitoes and wild birds. Nevertheless, WNV can also be transmitted to humans and horses, which occasionally leads to severe infections with deadly outcome. Due to climate change WNV distribution has spread to central Europe leading to autochthonous cases in Germany in the last years, which highlights the importance for better understanding the virus-host interface to improve antiviral treatment. In order to characterize WNV infection of different target species, various host cell lines from bird, horse and human were infected with a recent German WNV mosquito isolate (Berlin 2019) and virus growth kinetic as well as ultrastructural analyses using electron microscopy was performed. Based on these experiments we observed that the used cell lines seem to be highly susceptible for a WNV infection and develop comparable virus titers. Additionally, all cells were infected with WNV in presence and absence of Culex pipiens biotype molestus salivary glands extract (SGE) to analyze the influence of SGE on WNV virus titers. In future, comparative proteome analyses using mass spectrometry will be conducted in order to elucidate potential host specific response patterns to a WNV infection. The better understanding of WNV infection of different host species will contribute to the development of novel therapeutics or suppression strategies in a One-health approach.

[40] Identification of the PepSY domain containing protein Pvr as a novel virulence regulatory protein relevant for SaeRS activation in Staphylococcus aureus (11:00 AM, 1 hour)

Presenter: BOSSELMANN, Julia

Besides a colonization of the human anterior nares, *Staphylococcus aureus* can also cause serious infection, especially in immunocompromised patients. One of the most important virulence gene regulators of *S. aureus* is the two-component system SaeRS. However, regulation of SaeRS activity remains poorly understood. In this study, we were searching for novel virulence associated proteins in *S. aureus* and identified NWMN_0364 as an activator of virulence. NWMN_0364 is a lipoprotein and characterized by two PepSY domains. In a macrophage infection assay, survival of macrophages was induced by a loss of NWMN_0364. Concomitantly, a reduced production of SaeRS dependent virulence factors has been observed using a proteomics approach. In a co-immunoprecipitation assay, we identified SaeP, the negative regulator of SaeRS as interaction partner of NWMN_0364. Cross-linking mass spectrometry (XL-MS) experiments revealed that only the C-terminal PepSY domain of NWMN_0364 interacts with SaeP in a strongly Cu2+ and Zn2+ dependent manner. Based on these XL-MS experiments, we predicted an atomic model of the NWMN_0364-SaeP complex. In summary, we identified NWMN_0364 as an important regulator for SaeRS activity and renamed it as Pvr, PepSY containing, virulence regulatory protein. We demonstrated that PepSY domain proteins, so far mainly known as inhibitors of peptidase activity, can also fulfill regulatory functions in signal transduction pathways in virulence gene expression.

[37] Is Rift Valley fever virus a threat for Germany? Evaluation of the vector competence of German mosquitoes for Rift Valley fever virus (11:00 AM, 1 hour)

Presenter: AL-HOSARY, Amira

Rift Valley fever virus (RVFV; family Phenuiviridae) is transmitted by different mosquito species. The virus is prevalent in Africa and the Middle East. European countries may also be at risk due to passive movement of infected vectors through flights. To investigate the vector competence of German mosquitoes for RVFV, two German lab colonies of Culex pipiens biotype molestus from Hesse (CPM; n=306) and Aedes albopictus from Freiburg (AA; n=207) were offered heparinized bovine blood mixed with 107 TCID50/ml RVFV strain MP-12 using cotton sticks. Blood-fed females were sorted and incubated for 21 days post infection (DPI) at 28°C. Salivation assays and dissection of wings/legs and bodies were performed on 49 females of CPM and 10 AA at 14 DPI and on 38 females of CPM and 3 AA at 21 DPI, followed by qPCR to confirm presence of RVFV RNA in the examined samples. In CPM, infection rates (virus RNA positive bodies) were 26.5 & 34.2%, dissemination rates (positive wings/legs) were 24.5, 15.8% and transmission rates (positive saliva) were 16.3 & 44.7 % at 14 and 21 DPI. In AA infection rates were 30.0 & 33.3%, dissemination rates were 10.0, 0.0% and transmission rates were 20.0 & 33.3% at 14 and 21 DPI. In conclusion, German mosquitoes (CPM-Hesse & AA-Freiburg) are competent vectors for RVFV strain MP12 for a period of 21 DPI. This indicates that Germany may be at risk for the introduction of RVFV and if it is introduced, it might threaten both human and animal health.

[36] Identification of inter-species CD8+ T cell epitopes from zoonotic Influenza A Virus strains (11:00 AM, 1 hour)

Presenters: ALBINUS, Andreas, CAMMANN, Clemens

Natural hosts of Influenza A Virus (IAV) are pigs, poultry and humans. Pigs play a key role in zoonotic IAV-transmission as “mixing vessels” adjusting avian influenza viruses to the human host by re-assortment of viral genes. Virus-specific cytotoxic T lymphocytes (CTLs) are induced by the interaction of MHC class I-epitope and the T cell receptor complex. MHC class I ligands

are produced by proteasome-mediated degradation of intracellular virus proteins. The goal of our project is to determine the IAV-host interaction analyzing the generation of CTL-epitopes by proteasomes obtained from humans, pigs and poultry to assess whether the human host can generate protective CD8+ T lymphocyte (CTL) responses against emerging IAV-reassortants from other species. Based on *in silico* MHC class I-epitope prediction synthetic polypeptide substrates containing several possible MHC class I epitopes were generated. Subsequently, these substrates were processed *in vitro* with proteasomes isolated from humans, pigs and poultry. The resulting peptide products were analyzed by Liquid Chromatography–Mass Spectrometry and identified through bioinformatics. In addition, we compared the activity profile and posttranslational modifications of the proteasomes from different species. The results obtained from these experiments will foster the understanding of the host-pathogen interaction and will also provide a basis for the improvement of vaccination strategies including zoonotic IAV strains.

[31] Ebola virus recruits the nuclear RNA export factor NXF1 for viral mRNA export from inclusion bodies (11:00 AM, 1 hour)

Presenter: WENDT, Lisa

Ebola virus (EBOV) causes severe haemorrhagic fevers in humans with limited treatment options. Virus-host interactions are promising targets for the development of broadly acting antivirals, but knowledge of host factors involved in the EBOV life cycle is very limited. However, recently we identified the nuclear RNA export factor 1 (NXF1) as host cell factor supporting the EBOV life cycle. To better understand its role in this context, we analysed the interaction of NXF1 with viral components, and performed localisation studies and functional analyses using life cycle modelling systems and virus infections. These studies revealed that NXF1 is recruited into EBOV inclusion bodies by the EBOV nucleoprotein. In these structures it binds viral mRNAs, but not viral genomic RNA, and this interaction is required for efficient trafficking of NXF1 out of inclusion bodies. Functional analyses demonstrated that NXF1 is required for a step between viral mRNA transcription and translation. Further studies suggested that this function of NXF1 may be a general feature of several negative-sense RNA viruses replicating in cytoplasmic inclusion bodies. Taken together, our results indicate that NXF1 is recruited into inclusion bodies to promote the export of viral mRNAs from these sites. This mechanism represents a new function for NXF1 in the context of virus infections and may also provide a basis for new therapeutic approaches against EBOV and other emerging viruses.

[30] Development of reverse genetic systems for the novel filovirus Bombali virus for assessment of pathogenicity and possible countermeasures (11:00 AM, 1 hour)

Presenter: BODMER, Bianca S.

Recently, a number of novel filoviruses such as Bombali virus (BOMV) have been discovered in diverse bat species. However, no virus isolates were obtained so far, which hinders an assessment of the pathogenic potential of these viruses, which are related to highly pathogenic filoviruses such as Ebola virus (EBOV). To address this issue, we have developed reverse genetic systems for BOMV, including life cycle modelling systems to analyze the biological activity of proteins encoded by the published BOMV sequences. This also allowed us to test the efficacy of remdesivir, a known inhibitor of the EBOV polymerase L, which showed comparable effectivity against BOMV and EBOV. Testing of the published BOMV glycoprotein sequence suggested a putative sequencing error in a highly conserved region, resulting in a non-functional protein. Combining these results with a BOMV full length clone system we generated allowed us to rescue and characterize recombinant BOMV, and we are now in the process of assessing the pathogenic potential of BOMV in a small animal model that reflects differences in the pathogenic potential of different filovirus species in humans. This study demonstrates the potential of reverse genetics systems to analyze the pathogenic potential of viruses with zoonotic potential in the absence of natural isolates, to quickly test potential antivirals, and to better understand their molecular biology.

[24] Vaccine to Inhibit Autochthonous Transmission of Hepatitis (VaccinATE) (11:00 AM, 1 hour)

Presenter: HRABAL, Isabella

Hepatitis E virus (HEV) infections are a largely underestimated public health problem in Europe affecting an estimated 420,000 humans in Germany every year. HEV infections in central Europe are primarily caused by HEV genotype 3, which is highly prevalent in pigs and wild boar. Infections are mostly attributed to consumption of contaminated meat products or close contact with infected animals. Usually, infected individuals have mild symptoms, but patients with underlying liver diseases or increased alcohol consumption are at risk to develop acute liver injury. Moreover, HEV can cause chronic infections in immunocompromised individuals, with the potential to rapid progress to liver fibrosis and cirrhosis and associated complications. Currently, no approved treatment is available for acute or chronic HEV infection. Approximately 5% of slaughtered pigs have an ongoing HEV infection and up to 20% of tested sausages in German stores are HEV RNA positive and therefore carry the risk to cause infections in humans. The VaccInATE project aims to perform a proof-of-concept study to evaluate different vaccination strategies of pigs for HEV which could consequently prevent the transmission of HEV to humans - supporting the One Health idea of this application. In addition, the anti-HEV IgG seroprevalence and the effect of external factors over time will be determined in human population by using the well-controlled SHIP cohort (population-based project Study of Health in Pomerania).

Session 1b: Pathogen-host-environment interactions (12:00 PM - 1:15 PM)

[120] PROMOTING GORILLA CONSERVATION THROUGH ONE HEALTH (12:00 PM, 30 minutes)

Presenter: KALEMA-ZIKUSOKA , Gladys

Conservation Through Public Health (CTPH) is an NGO and non-profit founded in 2003 that promotes biodiversity conservation by enabling people to co-exist with gorillas and other wildlife through improving animal health, community health and livelihoods in and around Africa's protected areas. Following a fatal scabies outbreak in critically endangered mountain gorillas, CTPH developed three integrated programs: wildlife health and habitat conservation; community health, and alternative livelihoods through group livestock income generating projects and a Gorilla Conservation Coffee social enterprise. CTPH programs began at Bwindi Impenetrable National Park, home to 43% of the world's mountain gorillas. An early warning system to prevent disease outbreaks at the human/gorilla/livestock interface was established through comparative pathogen analysis. Behavior change communication through Village Health and Conservation Teams (VHCTs) led to a significant increase in people referred and tested for infectious diseases, adopting hand washing facilities and modern family planning methods. This One Health model contributed to a reduction in human-related morbidity and mortality in gorillas, reduced human and gorilla conflict, improved community attitudes to conservation and mitigated the impact of the COVID-19 pandemic. CTPH worked with Uganda Wildlife Authority (UWA), NGOs, tour companies and community groups to prevent transmission of COVID-19 among people and from people to gorillas by training park staff and Gorilla Guardians to institute mandatory mask wearing and increased viewing distances. Together with VHCTs and UWA, CTPH established One Health Village COVID-19 taskforces. Through international partnerships, CTPH advocated to governments, donors, tour companies and tourists to strengthen responsible tourism to great apes.

[19] Phylogenetic characterization of multidrug-resistant Escherichia coli from patients, the community, livestock and flies in Rwanda (12:30 PM, 10 minutes)

Presenter: EGER, Elias

The emergence of extended-spectrum β-lactamase-producing *E. coli* (ESBL-EC) is a threat to health across the globe. Only little is known with respect to the characteristics and distribution of ESBL-EC in low and middle income countries like Rwanda. Zoonotic diseases are supposedly more prevalent when people live in close contact to animals. Here, we examined 133 ESBL-EC isolates from patients, caregivers, community members, livestock and flies in a Rwandan hospital and surrounding areas by in-depth bioinformatics analysis. Results revealed the occurrence of 31 different sequence types (STs) dominated by the clonal lineages ST131, ST648 and ST410. Isolates from patients were closely related to the ones from caregivers, community members, livestock and flies, which suggests inter-host transmission. In addition, we found that antibiotic resistance plasmids transferred across various bacterial isolates. All isolates exhibited a multidrug-resistant (MDR) genotype and the majority harbored multiple virulence genes, suggesting their pathogenic character. The accumulation of some particular STs in this area mirrors the global situation regarding the predominance of certain global high-risk clonal ESBL-EC that combine MDR with virulence. The identified missing host adaptation and close phylogenetic relationships indicate rapid transmission of these STs and plasmids in the One Health context, exacerbated by the dissemination through livestock and flies.

[96] Strongylid communities in African great apes are driven by the environmental characteristics (12:40 PM, 10 minutes)

Presenter: PAFČO, Barbora

Strongylid nematodes are highly prevalent across all wild apes' populations, occurring in complex communities and indistinguishable using traditional diagnostic approaches. Thus, only limited information about exact strongylid diversity and epidemiology in great apes have been available. Although strongylids seems not to pose any serious health risk to wild apes, clinical gastrointestinal illnesses linked to helminth infections have been recently recorded in mountain gorilla populations. To increase our knowledge about strongylid infections in great apes, we described and compared the genetic diversity of strongylid communities in gorilla and chimpanzee populations. We used high-throughput sequencing enabling description of the communities and providing sufficient species-specific sequence data. Surprisingly, the composition of strongylid communities were not driven by host phylogeny, but by environmental characteristics. Western lowland gorillas sampled at several localities characterized by similar environments carried similar strongylid communities, which resembled those of sympatric and even allopatric chimpanzees. On the contrary, both populations of mountain gorillas harbored distinct strongylid communities with significant differences across (sub)populations. Geographic differences in strongylid communities in mountain gorillas reflect differences in gorilla ecology and environments across mountain gorilla habitat and subsequent occurrence of gastrointestinal diseases.

[32] An evolutionary anthropology framework to develop phage use in therapy and research (12:50 PM, 10 minutes)

Presenter: GOGARTEN, Jan

Humans harbor diverse communities of microorganisms, the majority of which are bacteria in the gastrointestinal tract. These in turn host diverse phage communities that impact their structure, function, and ultimately human health. The evolutionary and ecological processes shaping human-associated phage communities are poorly understood. A better understanding of these processes could be leveraged to support developing efficient phage therapies and estimating rates of microorganism transmission at human-wildlife interfaces, at the crossroads of evolutionary and precision medicine and One Health. I present an examination of fecal phageomes of wild non-human primates that delineates the evolutionary background of human phageomes, revealing heterogenous long-term dynamics of super host/phage associations, whereby some phages codiverge with their super hosts while others do not. I show that captive primates lose their natural phageomes that are replaced by human phages, highlighting considerable plasticity. This information can help combating antibiotic resistant infections and understanding disease emergence risk. For example, co-diverging phages may be more likely to exhibit a narrow host range and thus less useful for phage therapy and phages may convenient markers of cross-species transmission. These hypotheses could be explored quickly by taking advantage of fast-growing sequencing and computational resources and fostering interdisciplinary and intersectoral initiatives.

[108] Q & A (1:00 PM, 15 minutes)

Lunch break / Networking (1:15 PM - 2:30 PM)

Session 2a: Past, present, and future zoonotic events (2:30 PM - 3:45 PM)

[119] Digital One Health (2:30 PM, 30 minutes)

Presenter: KRAUSE, Gérard

Implementing One Health in daily routine encounters hurdles caused by heterogeneous procedures in separate administrative silos, incompatible data collection systems and different cultures of managing health interventions. The increasing availability of Digital Health tools may help to overcome those hurdles. Clinicians, public health experts and veterinarians jointly developed the open source digital Surveillance Outbreaks Response Management and Analysis System (www.SORMAS.org) with the aim to offer a specialised tool for surveillance and outbreak response of infectious diseases. SORMAS has proven its usefulness in the field with eight countries in four different WHO regions using it and more countries preparing for implementation. A variety of One Health applications are already in use or in development in SORMAS, such as the comprehensive response during a Lassa Fever outbreak in Nigeria by combining public health interventions with a veterinary assessment of rodents in the outbreak area. Another example is the development of integrated drinking water monitoring of pathogens combining human and animal health with environmental aspects. Complementary to most hierarchical and unidirectional information systems, SORMAS also allows for horizontal and multidirectional information exchange and task management, which facilitates engagement by partners from different disciplines and abbreviates information delay. The availability of data in real time allows for data driven decision making for a comprehensive health response among relevant sectors and permits evidence synthesis for future intervention strategies, emphasizing the benefits Digital Health tools offer for One Health.

[55] Connect One Health Data for Integrated Disease Prevention – Challenges in linking data from different sectors (3:00 PM, 10 minutes)

Presenter: HILLE, Katja

Although about 2/3 of infectious diseases in humans are caused by zoonotic agents, the surveillance of infections in humans and animals is still predominantly independent. The "Connect One Health Data" project aims to integrate human and animal health data (www.one-health-hannover.de). The project focuses on the regional level of Lower Saxony. In the first part of the project data sources on zoonotic and antibiotic-resistant pathogens in human and veterinary medicine were identified and described. Currently, the feasibility of an integrated analysis of data is being investigated using Campylobacter spp. as an example. SurvNet (collection of data according to the Infection Protection Act) and the Laboratory Information and Management System (LIMS) of the Lower Saxony State Office for Consumer Protection and Food Safety were identified as the most important data sources on the regional level of Lower Saxony. Data on Campylobacter spp. were provided and analysed. In SurvNet (human data), about 6,000 cases per year were reported, while in LIMS (veterinary data), about 300 detections per year occurred. Seasonal parallels in the number of detections in the two data sources as well as a correlation with temperature could be shown. The presentation will address challenges and opportunities for integrated analysis on data-level (e.g. data structure, spatial and temporal resolution) as well as data privacy aspects.

[93] Striving towards better zoonosis prevention through Responsible Crowdsourcing: SHIP-Next module One Health meets JoinUs4Health (3:10 PM, 10 minutes)

Presenter: DIAZ PEREZ, Andrea Camila

The One Health concept emphasizes the need for transdisciplinary approaches given the intrinsic linkages between human, animal and environmental health. Since mid-2021 animal contacts (dogs, cats and poultry) and study participants of the population-based cohort Study of Health in Pomerania (SHIP) are examined in parallel (One Health Module). Results shall inform risk assessments and the development of husbandry and hygiene recommendations. Different stakeholder groups shall be engaged to gather information needs and feedback on data collection protocols, jointly revise interim results and generate hypotheses. Under the JoinUs4Health project (01/21-12/23), a new method of responsible crowdsourcing is developed and applied to enable different scales of collaboration, i.e. consultive mechanisms typical in crowdsourcing with deeper co-creation processes in smaller groups. We will present the platform developed in JoinUs4Health, summaries of data collections and interim results in citizen-friendly language and input obtained from different stakeholder groups to date. In summary, the engagement of citizens and other stakeholder groups allows incorporating multiple perspectives, which may lead to greater robustness and relevance of research questions, practices and findings. Novel forms of societal engagement could generate tangible benefits for control and prevention of zoonotic diseases and strengthen trust and understanding between stakeholder groups.

[84] Occupational risk factors associated to tick-borne diseases in outdoor workers from Southern Italy (3:20 PM, 10 minutes)

Presenter: LOVREGLIO, Piero

Tick-borne diseases are an emerging issue due to the ticks' geographical expansion. The study aims to define the seroprevalence of selected tick-borne pathogens (TBPs) in different groups of outdoor workers, and the occupational factors that pose a higher risk of TBPs infection. A cross-sectional study was conducted on 170 workers recruited in two different areas of southern Italy, including farmers, forestry workers, veterinarians, geologists/agronomists and administrative employees, determining the presence of IgG antibodies against Bartonella henselae, Borrelia spp, Coxiella burnetii and Ricketsia conorii. Categorical principal component analysis (CATPCA) was applied to investigate the association between general and job characteristics, and the prevalence of each TBP investigated. A high seroprevalence for C.burnetii (30%) and R.conorii (15.3%) was reported, higher in farmers (67.7% and 54.8%, respectively) and forestry workers (29.0% and 16.1%, respectively), while a low prevalence was observed for B.henselae and Borrelia spp (8.8% and 4.1%, respectively). CATPCA showed a significant positive association between C.burnetii and R.conorii prevalence and job, ticks exposure, work area and contact with animals. These findings highlight the need of activating an appropriate occupational health response to minimize the risk in workplaces, also considering specific worker's subgroup vaccination for C.burnetii.

[109] Q & A (3:30 PM, 15 minutes)

Break (3:45 PM - 4:00 PM)

Poster Session 2 (4:00 PM - 5:00 PM)

[23] Increasing preparedness by networking: the network "Rodent-borne pathogens" (4:00 PM, 1 hour)

Presenter: ULRICH, Rainer

Rodents are important as pests in agriculture and forestry, as model organisms for biomedical studies and as pathogen reservoirs. These pathogens may have the potential to cause disease in domestic animals and humans, or might be rodent-specific and have no or yet unknown zoonotic potential. The network "Rodent-borne pathogens" was established as a platform for an interdisciplinary collaboration of scientists working in mammalogy, ecology, genetics, immunology, toxicology, epidemiology, virology, microbiology, parasitology and human and veterinary medicine. The presentation will give an overview on the activities of the network: (i) to identify the diversity of pathogens in rodents and other small mammals, (ii) to estimate the geographical distribution and host specificity of these pathogens, (iii) to understand processes that may lead to outbreaks and to characterize genetic consequences of rodent population dynamics on pathogens, (iv) to evaluate the influence of pest management (and rodenticide resistance) on pathogen occurrence and prevalence in pest species (rats, house mice), (v) to prove the zoonotic potential of novel pathogens, (vi) to develop tools for experimental studies on rodent-borne pathogens, and (vii) to develop tools and workflows for detection of rodent-borne pathogens. In conclusion, the network provides an important infrastructure for interdisciplinary scientific work in a One Health perspective.

[39] Re-emergence of Seoul orthohantavirus in pet rats, Germany, 2021 (4:00 PM, 1 hour)

Presenter: MEHL, Calvin

Seoul orthohantavirus (SEOV, family Hantaviridae), a causative agent of haemorrhagic fever with renal syndrome (HFRS) in humans, is transmitted through contact or inhalation of excreta from infected reservoir rodents (Rattus norvegicus, R. rattus and other Rattus species). SEOV has been found across the globe, in both wild and captive rats. In 2019, the first autochthonous SEOV infection was reported for a HFRS patient in Germany, originating from pet rats. Here, we describe the recent

re-emergence of SEOV in two novel human disease clusters in the same region in Germany in 2021. By means of molecular investigations, we detected SEOV sequences in patient sera from both clusters. SEOV sequences were also detected in tissues of the patients' pet rats. SEOV sequences (partial L segment) from patients and pet rats were (almost) identical to sequences from the first case, suggesting a common origin of the pet rat-associated SEOV strain for all three cases. This hypothesis will be investigated by target enrichment-based high-throughput sequencing of complete coding sequences of the viral S-, M- and L-segments from all three outbreaks. This study highlights the risks of zoonotic infections associated with the pet rat trade and the role pet rats play as reservoir hosts for SEOV. The investigations of these disease clusters fostered interdisciplinary One Health research collaboration between human and veterinary medicine.

[74] The Joint Initiative for Teaching and Learning on Global Health Challenges and One Health experience on implementing an online collaborative course on One Health (4:00 PM, 1 hour)

Presenter: DAU, Paula

In 2021 the Joint Initiative for Teaching and Learning on Global Health Challenges and One Health piloted the online course "Global Health Challenges and One Health" at six universities in Brazil, Germany, Kosovo and Mozambique. We present the pilot's evaluation based on activity data, students' feedback (structured questionnaires and open questions) and course coordinators' evaluation. The course combined synchronous and asynchronous activities accompanied by pre-produced videos and additional material. Thirty participants were initially enrolled, of whom 19 completed the course. Students' challenges included time zone differences and difficulties in communication and coordination of the group work and excessive workload when considering credits awarded. The instruction language (English) posed difficulties for some participants. The joint project, creativity and diversity of videos and activities, especially the synchronous ones, were most appreciated and evaluated positively by students. For the next course in 2022, a FAQ document and a synchronous information session will be prepared to address the issues identified in the pilot phase. Credits will be adjusted to meet the required workload and subtitles will be added to the videos to ease the language barrier for the students. Overall, the course was well-accepted by students and coordinators and can move on to full implementation and later expansion.

[76] Embedding One Health in international development practice: design and initiation of an agile and complex global programme. (4:00 PM, 1 hour)

Presenters: WATT, Nicola, KNOPF, Lea

In the light of the COVID-19 pandemic, political engagement and support for One Health is at an all-time high. A common definition has been put forward by the One Health High Level Expert Panel and tools and systems are increasingly being developed to operationalise the One Health approach. In line with the 2021 Strategy from the Federal Ministry for Economic Cooperation and Development (BMZ), "Initiative area One Health in Development Cooperation", German international development cooperation investments are supporting this shift from theory to practice. This includes joining with other stakeholders to establish a community of practice for learning from international One Health project implementation. BMZ has also commissioned the German Development Corporation, GIZ, to deliver a Global Programme for Pandemic Prevention and Response, One Health, with a budget of nearly €50m to 2024. Its innovative design incorporates organisational development principles, aiming to catalyse change at multiple levels simultaneously, with global level investments to anchor and sustain initiatives at regional and country level. The drive for alignment and harmonisation at all levels results in a complex set of interventions delivered by a team of over 30 employees in four continents. Enhancing scientific cooperation and mutual learning is central to the programme's aims. In this spirit, the authors will showcase progress to date and first conclusions about potential benefits and challenges.

[79] Exceptionally high susceptibility of Golden Syrian hamsters to SARS-CoV-2 infection supports recent findings of zoonotic transmission between pet hamsters and humans (4:00 PM, 1 hour)

Presenter: BALKEMA-BUSCHMANN, Anne

Golden Syrian hamsters (Mesocricetus auratus) have been established as a small animal model for human infections with Severe Acute Coronavirus 2 (SARS-CoV-2) and the associated human disease, Coronavirus Disease 19 (COVID-19), and are widely being used in various fields of research. Millions of Syrian hamsters are being kept as pets in very close contact to humans worldwide. To determine the minimal infectious dose for this species, and to define the optimal infection dose for further studies, we inoculated hamsters with SARS-CoV-2 doses ranging from 1*103 TCID50 to 1*10-5 TCID50, and monitored the body weight, clinical behavior, and virus shedding daily for up to 10 days. We found that an infection dose of 1*10-2 TCID50 was sufficient to induce clinical disease and virus shedding in infected hamsters, while even a dose of 1*10-4 TCID50 (equivalent of 0.7 RNA copies per infection dose) was sufficient to induce a subclinical SARS-CoV-2 infection without detectable shedding. A 2-3 day delay in the onset of virus shedding in the groups infected with doses below 1*10-1 TCID50 occurred, but viral loads detected in the tissue samples reached comparable levels in all infected groups. All uninfected control animals remained negative. This astonishing susceptibility of Golden Syrian hamsters to extremely low infection doses is relevant for the assessment of a transmission risk regarding pet Syrian hamsters.

[58] Discovering the frontline of lung-resident CD8+ T lymphocytes against emerging influenza A virus reassortants (4:00 PM, 1 hour)

Presenter: KRONEMANN, Jenny

As natural hosts and so-called mixing vessels, pigs play a key role in emerging zoonotic influenza A virus (IAV) transmission and the development of IAV reassortants. The aim of the project is to characterize and compare human and porcine immune responses of tissue resident CD8+ cytotoxic T lymphocyte (CTL). We mainly will focus on mucosal-associated invariant T cells (MAITs), a subgroup of CD8+ innate-like T cells, which have a tissue-dependent role in respiratory infections including IAV. More specifically, we will assess whether the human and porcine host generates protective CTL responses against emerging IAV-reassortants and whether a protective memory immune response against CTL-epitopes from new reassortants already exists in subjects with a history of IAV-infection or preceding IAV-vaccination. Here, we will present a workflow to monitor the recruitment of CTLs into lung tissue, which will be established for single cell analysis of tissue-resident MAIT cells. To characterize the immune response at the side of infection, MAITs will be isolated by laser microdissection from paraffin-embedded lung biopsies and investigated in situ using transcriptomics and proteomics. We additionally intend to validate obtained data utilizing well-established IAV mouse infection models. Finally, by applying a pipeline for comparative PlasmaProteomics we expect to identify host-specific biomarkers.

[88] The polymerase segments of zoonotic H7N7 avian influenza virus reduced virulence and transmission in poultry (4:00 PM, 1 hour)

Presenter: PALME, Diana

Avian influenza viruses (AIV) of the subtype H7 can evolve from a low pathogenic (LP) precursor to a high pathogenic (HP) form in chickens, causing severe systemic infections and high mortality rates in infected flocks. A polybasic cleavage site (pCS) in the hemagglutinin surface protein of AIV is one of the main virulence determinants in high pathogenic AIV (HPAIV), whereas less is known about the role of the viral polymerase segments (PB2, PB1 and PA) in the transition of LP to HP AIV. AIV H7N7 are endemic in European wild birds and transmission to land-based poultry has been reported. In 2003, HPAIV H7N7 was isolated from poultry in the Netherlands and further spread to poultry farms in Germany and Belgium resulting in the death and culling of about 31 million birds. Furthermore, the HPAIV H7N7 infected more than 1000 humans. In humans, mutations in the HA and polymerase genes were the main virulence determinants, whereas little is known about the virulence determinants of this virus in poultry. Here, we constructed recombinant LP H7N7 viruses carrying the pCS (designated LP_Poly) with or without PB2, PB1 or PA from HP H7N7. The recombinant H7N7 viruses were characterized in vitro and in vivo in chickens. The pCS increased the virulence of LP H7N7, however, at lower levels compared to HPAIV H7N7. Reassortment of LP_Poly with HPAIV H7N7 PA reduced virus replication in avian cell culture. In chickens, the polymerase segments reduced the virulence of LP_Poly.

[52] PIA@SHIP – Digital One Health Epidemiology (4:00 PM, 1 hour)

Presenters: HEISE, Jana-Kristin, ENZENBACH, Cornelia

One health has attracted increasing attention in epidemiological research in recent years. Population-based research, such as the Study of Health in Pomerania (SHIP), can contribute important insights by linking data from deeply phenotyped individuals with data about transient infections. Technologically, the e-research system “PIA – Prospective Monitoring and Management App” permits real-time monitoring of symptoms and simplifies research on infectious diseases, including zoonoses and antimicrobial resistance. PIA, as a mobile or web app, is easy to use and flexible to adapt to different research areas. It is in use in various epidemiological studies, such as the German National Cohort. In the PIA@SHIP project, we installed an independent PIA instance in Greifswald. For the study, we implemented two-weekly questionnaires to monitor potential symptoms of infections and follow-up questionnaires in case of events in participants or their pets. We also collect data on pre-existing conditions and predictors of infectious diseases, as well as on relevant concomitant factors like the use of antibiotics. A pretest with 14 participants evaluated the feasibility of the PIA module. A PIA based survey is currently ongoing in the SHIP-Trend cohort. The recruitment for SHIP-Next is scheduled to begin soon. By collecting data in the population-based SHIP, PIA@SHIP will enable a deeper understanding of infectious diseases and antibiotic resistance in both humans and pets.

[21] Vector competence of Aedes punctor (Kirby, 1837) for West Nile virus lineages 1 and 2 (4:00 PM, 1 hour)

Presenter: KÖRSTEN, Christin

West Nile virus (WNV) is a zoonotic mosquito-borne flavivirus that occurs globally. WNV circulates in an endemic cycle between birds and mosquitoes, but can also be transmitted to mammals such as humans and horses. Knowledge of the vector competence of mosquito species is crucial for effective WNV surveillance and management. The snow-melt mosquito *Aedes punctor* is common in Europe and could be a potential vector of WNV to humans due to its broad host preference. Since studies on the vector competence of this species are lacking, we conducted an experiment on the vector competence of *Aedes punctor* for WNV. Field collected pupae were reared to adults and infected with WNV via an infectious blood meal. Blood-fed females were sorted and incubated for 14 and 21 days, respectively. Surviving mosquitoes were dissected and forced to salivate. Mosquito

bodies, legs plus wings and saliva were analysed for WNV RNA by RT-qPCR. For WNV lineage 1, two infected mosquito bodies were detected (2/70; 2.86%), one of which had disseminated infection in legs plus wings. In mosquitoes infected with WNV lineage 2, RNA was found in five mosquito bodies (5/85; 5.88%), one of them with a disseminated infection. Viral RNA was not detected in any of the saliva samples. In summary, *Aedes punctor* showed a low susceptibility to WNV infection, and no evidence of possible WNV transmission was observed. Our results suggest that *Aedes punctor* is not a competent vector species for WNV.

[34] #StrongerTogether: Utilizing Health Behavior Change and Technology Acceptance Models to Predict the Adoption of COVID-19 Contact Tracing in the General Population (4:00 PM, 1 hour)

Presenter: TOMCZYK, Samuel

Background. Contact tracing apps (CTA) are promising digital health solutions that can help monitoring infection chains, and provide tailored information to affected individuals. However, studies point to globally low acceptance rates of CTA, therefore theory-based inquiry is needed to examine barriers and facilitators of acceptance and use. This study utilizes established health behavior change and technology acceptance models to predict CTA adoption, and frequency of CTA use. **Methods.** Hierarchical regression models in a German community sample (N=349; mean age 35.62 years; 65.3% female) tested the predictive validity of the theory of planned behavior and the unified theory of acceptance and use of technology as well as additional variables privacy concerns, and personalization regarding CTA acceptance, and use. **Results.** Overall, both theories significantly predicted acceptance (R2=56%-63%), and frequency of app use (R2=33%-37%). An extended model marginally increased the predictive value by about 5%, with lower privacy concerns, and higher threat appraisals (ie, anticipatory anxiety) significantly predicting app use. **Conclusions.** This study confirmed several theory-based predictors of CTA use. The findings suggest that promulgating affirmative social norms and underlining positive emotional effects of app use, while addressing public health concerns, might be promising to foster acceptance and use of CTA in the general population.

[50] Bangladesh: OneHealth Event Based Surveillance and Data visualization (4:00 PM, 1 hour)

Presenter: UZZAMAN, M Salim

The epidemic-pandemic disease impacts on a country's economy through several ways, PH, transportation, livestock, agriculture, tourism many more. Finding outbreaks timely and managing them empirically can reduce illness, death and economic loss. OH approach is an integrated, unifying approach that aims to sustainably balance the PH, AH and ecosystems by timely EIDs events information sharing. The delays are due to 1. Lack to trained workforce, resources and Weakness of inter-sectoral data sharing 2. Lack of OH approach data sharing collaboration through integrated digital-platform for visualization To mitigate the identified difficulties, One Health Secretariat, Bangladesh is developing an electronic, real-time system named ‘One Health event based surveillance and Data visualization dashboard (OHEBS DD). It uses digital monitoring tools to capture “multi sectoral data feeds.” and provides an early signal / warning of potential outbreaks. The dashboard will serve in bidirectional way, it will collect information and data and on the other hand will feed with events of interest to concerned sectors to analyze potential warnings of event of public health concern / threat. Policymakers will also be able to collect information from the ‘OH EBS DD’ to develop OH based multi-sectoral policy and action plans. The Goal is to have to “Strengthen the operational capacity, bridge across local, national, regional, and global areas in order to more efficiently response to future EIDs”

[78] VIRAL ETIOLOGY OF ACUTE RESPIRATORY TRACT INFECTIONS IN CHILDREN AND ADULTS IN MANADO, NORTH SULAWESI, INDONESIA (4:00 PM, 1 hour)

Presenter: PURWANTO, Diana

Background:Epidemiology studies on viral etiology of acute respiratory infections (ARI) patients are limited in Indonesia.Besides,these epidemiology data might be needed by clinicians to consider precise therapy and to avoid unnecessary use of antibiotics on the patients with ARI.Therefore,this study aimed to determine the prevalence of viruses as pathogen causing ARI in Manado,North Sulawesi,Indonesia.MethodsA cross-sectional study was conducted in May 2019–March 2020 in 2 community health centers and 1 public hospital in Manado.A 102 of oropharyngeal swabs were collected from children and adult patients with ARI using flocked swabs,then transferred into 500µL viral transport media.The PCR assays were used for detection of respiratory viruses,followed by sequencing.ResultsThe most common symptom was fever(100%),followed by coughing(95%),runny nose(88%),nasal congestion(66%),malaise(60%),headache(35%),shortness of breath(29%),and sore throat(29%).Majority of the patients were children less than six years old(54%).In total, 41 out of 102 samples(40,2%) were positive for viruses.We detected enteroviruses:Rhino A,Rhino B,Rhino C,and EV-D68(14.7%), influenza A viruses:H1N1 and H3N2(8.8%),respiratory syncytial virus:RSV A and RSV B(6.9%),Herpesviridae:CMV and Epstein-Barr(4.9%),bocavirus(2.9%), and paramyxovirus(2.0%).ConclusionsThis study provides baseline information on the epidemiology of viral etiology in children and adult patients with ARI in Manado,North Sulawesi,Indonesia.

[97] Adaptation of avian influenza H5N1 virus in humans: The role of the neuraminidase (4:00 PM, 1 hour)

Presenter: SCHEIBNER, David

As a member of the family Orthomyxoviridae, the avian influenza viruses (AIV) contain a segmented RNA genome with negative strand orientation. The two surface glycoproteins hemagglutinin (HA) and neuraminidase (NA) enable the differentiation into 16 HA and 9 NA antigenic subtypes. The spread and endemicity of H5Nx Goose/Guangdong AIV pose a continuous zoonotic and pandemic threat. Here, after analysis of the NA sequence of human-origin H5N1 viruses, we studied the role of mutations in residues 46, 204, 219 and 430 for virus fitness. Although H5N1 AIV with avian- or human-like NA had similar replication efficiency in avian cells, human-like NA enhanced replication in human airway epithelia and reduced NA activity conferred by an L204M mutation. This mutation consistently reduced NA activity in nine other influenza viruses, indicating a broad effect. Viruses with reduced NA activity had lower NA expression levels due to reduced viral RNA replication and NA transcription. They demonstrated increased accumulation of NA at the cell membrane and enhanced cell-to-cell spread. Furthermore, NA mutations A46D, S319F and 430G increased virus binding to human-type receptors. While not affecting the high virulence of H5N1 in chickens, NA mutations in human-origin viruses modulated virulence and replication in mice and ferrets. Together, we describe novel mutations in the NA of human-origin H5N1 viruses and studied the underlying mechanism for potential adaptation of H5N1 to mammals.

Goodbye Day 01 (5:00 PM - 5:15 PM)

Thursday, April 28, 2022

Early Bird Yoga (7:30 AM - 8:00 AM)

Good Morning Day 02 (9:15 AM - 9:30 AM)

Session 2b: Past, present, and future zoonotic events (9:30 AM - 10:45 AM)

[114] Pathogen evolutionary genomics for One Health (9:30 AM, 30 minutes)

Presenter: CALVIGNAC-SPENCER, Sébastien

The concept of One Health posits that health is an ecosystem service that results from the complex interactions of humans, animals and their environments. Because these interactions are dynamic and influenced by the shared history of hosts and pathogens, One Health has an explicit evolutionary dimension. In this talk, I will show how evolutionary genomics can capture this dimension and enlighten the trajectories of major human pathogens. For this, I will use the examples of viruses whose association with humans is more or less ancient – from nearly antediluvian herpes simplex viruses with a dsDNA genome to much more recently emerged RNA viruses such as measles and influenza A viruses. It is possible to trace back the evolution of these viruses by identifying viral genomic variation across contemporary host species, for example by determining the existence and genomic make-up of viruses infecting our closest relatives, the African great apes. Another window of opportunity is to directly sample such variation through time, for example by analyzing pathological specimens collected during past pandemics. I will show how both approaches can allow us to trace back viral evolution and how they can help us to better understand pathogen emergence and early spread. I will conclude with a short discussion of recent advances promising massive scale-ups in pathogen genomic data acquiring and analysis, that we can soon leverage to untie and explain the complex evolutionary networks of host/pathogen associations.

[94] Infectious disease surveillance across African great ape sites (10:00 AM, 10 minutes)

Presenter: DÜX, Ariane

African great apes, i.e. chimpanzees, bonobos and gorillas, are our closest living relatives. As such, they are susceptible to many of the same pathogens as humans, and can serve as sentinels for infectious disease emergence. At the same time, pathogens (including those originating in humans) are a major threat to endangered great apes. Monitoring great ape health is therefore relevant for both public health and conservation. Based on our long-term engagement in Taï National Park, Côte d'Ivoire, we established a great ape health surveillance network covering eight field sites and four laboratories in six African countries (Côte d'Ivoire, Central African Republic, Democratic Republic of the Congo, Gabon, Guinea Bissau, and Republic of Congo). Here, we are training veterinary PhD students from the partner countries in non-invasive sampling, biosafety, and wildlife necropsies. Great apes are observed year-round either directly or via camera traps. All signs of disease are recorded and samples are collected non-invasively from sick animals. In addition, necropsies are performed on all carcasses, and flies are collected along transects between human and great ape habitats. Samples are then analyzed in our partner laboratories or by African students in Germany. The project has already contributed to studies on monkeypox and leprosy in chimpanzees. The project as well as its preliminary results will be presented at the One Health Conference Greifswald 2022.

[73] Comprehensive phylogeographic analysis of zoonotic Borna disease virus 1 (BoDV-1) infections in domestic mammals and humans (10:10 AM, 10 minutes)

Presenter: RUBBENSTROTH, Dennis

Borna disease virus 1 (BoDV-1) causes fatal encephalomyelitis in domestic mammals and humans following spill-over transmission from shrews of the genus Crocidura, the known natural reservoir host. The known endemic areas of BoDV-1 are restricted to parts of Germany, Austria, Switzerland and Liechtenstein, whereas specific transmission routes remain obscure. In this study, we performed a comprehensive phylogeographic analysis of BoDV-1 to assess potential sources of human BoDV-1 infections. We collected material and metadata of 182 domestic mammals, 21 human patients, and seven shrews with confirmed BoDV-1 infection from Germany and Switzerland. Complete or partial BoDV-1 genome sequences were generated from 90 domestic mammals, 18 humans and all seven shrews and analysed together with 128 previously published BoDV-1 sequences. Most cases originated from the previously known endemic areas with few exceptions, some of which may indicate previously unknown risk areas for BoDV-1 transmission. In line with the strongly territorial reservoir host, the sequences showed a remarkable geographic association with distinct phylogenetic clades occupying barely overlapping dispersal areas. Our work raised the number of confirmed human BoDV-1 infections to 41. The closest genetic relatives of most available human BoDV-1 sequences were located at distances below 50 km (median 22 km), indicating that the majority of zoonotic spill-over transmissions occurs close to the patient´s residence.

[63] The future of T solium cysticercosis in Africa (10:20 AM, 10 minutes)

Presenter: MWINZI, Pauline

As calls are being made to enhance preparedness for new and emerging zoonotic diseases, we must not lose sight of the burden caused by endemic parasitic zoonoses which continue to affect some of the most vulnerable populations. Amongst them, there is Taenia solium. This parasite has pigs as its intermediate host and can cause two distinct diseases in humans: taeniasis and cysticercosis. People with taeniasis (the adult tapeworm) shed T. solium eggs in their faeces that can infect pigs and humans. The resulting larvae form cysts in the muscles, skin, eyes or central nervous system. Neurocysticercosis (NCC) refers to the development of larval cysts in the central nervous system of humans, causing seizures and epilepsy. NCC is one of the leading causes of preventable epilepsy and in the communities where it is present, it can contribute to up to 70% of the epilepsy cases. Epilepsy in vulnerable populations is difficult to treat and causes stigma affecting people's lives and livelihoods. WHO has launched a new set of tools to assist with the control of this parasite including a mapping tool to assist with the identification of high-risk areas, guidelines for preventive chemotherapy for the control of taeniasis and the guidelines for the clinical management of NCC. WHO is also facilitating the implementation of these tools in several African countries, facilitating the donation of drugs for control of taeniasis, promoting WASH, and supporting One-Health control projects.

[110] Q & A (10:30 AM, 15 minutes)

Break (10:45 AM - 11:00 AM)

Poster Session 3 (11:00 AM - 12:00 PM)

[92] Natural Corona viruses antiseptic in indonesia : An on going research (11:00 AM, 1 hour)

Presenter: SIMANJUNTAK MSI, Tiurma

It has its natural compunds from Camellia Sinensis sp. It has been shown previously that the ethanolic green tea crude extract could not be used for further investigation due to its nature but by using water as a solvent, dry green tea crude extract could be used for research.Unfortunately there is still no information about the activity of green tea crude extract against S. typhi in other solvent. In this thesis i will show that the highest activity of green tea crude extract against S. typhi was in water. This result could be revealed by extraction using water, n-hexane, benzene, dichlorometane and ethyl acetate. This process was followed by antibacterial activity assay using agar diffusion method, and counting plate method. The experiment using agar diffusion method showed an inhibition area of 2 mm, 0 mm, 1 mm, 0 mm and 1 mm for green tea crude extract using water and non water as solvent with concentrations of 54,65 mg/mL, respectively. While the counting plate experiment showed a decrease in the total number of bacteria colonies. There were 1140 colonies in Luria Bertani medium without crude extract and in Luria Bertani with crude extract green tea from fractination using water, n-hexane, benzene, diclorometan, ethyl acetat is 83, 420, 550 320 and 940 colonies, respectively. The advantages of these methods simple, cheaper,easy and could also give other benefits to phytofarmaca science in bulding new Methods against Covid 19 in Indonesia.

[91] Prevalence and multidrug resistant of Gram-negative bacteria in paediatric patients in Duhok Province, Kurdistan-Iraq (11:00 AM, 1 hour)

Presenter: MUHSIN, SALWA

Urinary tract infections (UTIs) are one of the most common bacterial infections in children. The presence of extended–spectrum B-lactamases (ESBLs) producing bacteria among uropathogens is constantly increasing. Thus, this study is undertaken to identify the most common gram-negative bacteria and to detect it is ESBLs production and to determine their antimicrobial susceptibility pattern among children in Duhok-Iraq. A total of 99 Gram-negative bacteria were identified in 260 urine samples of paediatric patients diagnosed with UTIs aged (0-15 years) and collected from Heevi Paediatric Teaching Hospital in Duhok, between August 2021 and the Mid of February 2022. Antibiotic sensitivity pattern and and ESBLs producing were determined by the Kirby Bauer disc diffusion method and the Double Disc Synergy Test, respectively. The proportion of infected females (85%) were significantly higher than male as well as ages (2-5) years were more infected. Escherichia coli was the predominant pathogenic bacteria in these patients (67%) and followed by Klebsiella and Pseudomonas, Acinetobacter and Proteus. The most resistant antibiotics were amoxicillin, ampicillin, tetracycline to E.coli and around 3/4 of E.coli was positive to ESBL phenotypically. These results revealed the emergence of multidrug-resistant E. coli in the treatment of paediatric UTIs in Dohuk, Iraq. Imipenem and Nitrofurantoin were the most effective antibiotic against ESBl-producing E. coli in those paediatric patients.

[85] Vibrio parahaemolyticus from imported seafood in Germany can exhibit toxigenic potential or transmissible plasmids with ESBL and carbapenem resistances (11:00 AM, 1 hour)

Presenter: HAMMERL, Jens

Background As a natural inhabitant of aquatic environments, *V. parahaemolyticus* in fish/seafood poses a public health risk, as they may cause gastrointestinal infections or septicaemia, especially in immunocompromised people. The global commodity flow seems to force the dissemination of MDR isolates, which will limit the therapeutic options for the treatment of *Vibrio* infections. **Materials and Methods** Antimicrobial susceptibility testing (AST) in *V. parahaemolyticus* was conducted in line with principles fixed in CID 2013/652/EU. PFGE, WGS and bioinformatics were performed to characterize the isolates. The transferability of resistance genes was assessed by *in vitro* filter mating. **Results** AST of *V. parahaemolyticus* from imported seafood (n=144) revealed eleven ESBL- and one carbapenemase-producing isolate. WGS showed a broad genetic diversity of the isolates regarding their sequence types and resistance determinants (*bla*CTX/CMY). Carbapenem resistance was caused by a plasmid-associated *bla*NDM-1 gene that could be efficiently transmitted to several clinically relevant *Enterobacteriaceae*. The transmissibility and composition of the individual ESBL-carrying plasmids will be also shown in detail. **Conclusion** As the number of reports on MDR *Vibrio* from imported fish/seafood increases, our findings underline that antibiotic resistance monitoring needs to be extended to food of aquatic origin to protect consumers health.

[82] In vitro and in vivo efficacy of a multi-component drug containing GS-441524 against feline coronavirus and SARS-CoV-2 (11:00 AM, 1 hour)

Presenter: WEBER, Saskia

The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a worldwide public health concern despite available vaccines. In cats another relevant coronavirus the feline Coronavirus (FCoV) causes the deadly disease feline infectious peritonitis (FIP). GS-441524, the metabolite of remdesivir, is effective against SARS-CoV-2 in a mouse model, and has been used successfully to treat cats with FIP. The excellent efficacy of a multi-component drug Xraphconn® containing GS-441524 was demonstrated recently by curing cats with FIP. The aim of this study was to evaluate the antiviral efficacy of Xraphconn® compared to pure GS-441524 in vitro against both FCoV and SARS-CoV-2 as well as in vivo against SARS-CoV-2. Xraphconn® inhibited the viral replication of SARS-CoV-2 and FCoV at non-cytotoxic concentrations. Moreover, even a lower concentration of MTX inhibits the virus growth of SARS-CoV-2 compared to GS-441254. In vivo efficacy of Xraphconn® against SARS-CoV-2 was investigated in orally or intraperitoneally treated K18-hACE-2 mice. Unfortunately, SARS-CoV-2 caused a severe and lethal infection in K18-hACE-2 mice. No in vivo antiviral effects could be demonstrated. Thus, further studies in a SARS-CoV-2 suitable infection model are needed to assess impact of administration route, relationship between efficacy and timing of drug administration and role of additional active ingredients aside from GS-441524 in the multi-component drug Xraphconn®.

[77] Clonality of pneumococcal carriage isolates from children under five years of age, Cape Coast, Ghana (11:00 AM, 1 hour)

Presenter: MILLS, Richael Odarkor

Antibiotics are important in treating pneumococcal infections. However, pneumococcal resistance to commonly used antibiotics is of global concern. This study describes antibiotic resistance patterns, resistance genes, and clonality of pneumococcal isolates from children <5years old in Cape Coast, Ghana. Antibiotic resistance was detected by disk diffusion. Molecular techniques and multilocus sequence typing (MLST) were used to detect resistant genes and the genetic relatedness of pneumococcal isolates. All 151 isolates were susceptible to vancomycin, ceftriaxone, and levofloxacin. Over 50% of the isolates were resistant to cotrimoxazole and tetracycline. Penicillin non-susceptibility and multidrug resistance were 36% and 28.5% respectively. The ermB and mefA genes conferred erythromycin resistance. Penicillin and tetracycline resistance were due to the pbp2b and tetM genes respectively. MLST of 40 isolates revealed 9 known and 10 novel sequence types (STs). Two isolates belonged to pneumococcal molecular epidemiology network (PMEN) clone ST156 (Spain9V-3). Isolates of STs172, 802, and 15461 were closely related to PMEN clones ST338 ST173 and ST273. Carriage isolates were related to internationally disseminated multidrug-resistant pneumococci. The ermB and mefA, tetM, and pbp2b genes were responsible for erythromycin, tetracycline, and penicillin resistance respectively. Continuous monitoring of the pneumococcus through a robust surveillance system is essential in Ghana.

[68] Subclinical bovine mastitis: Significance of the teat canal microbiome and its interrelation with constituents of the human microbiota (11:00 AM, 1 hour)

Presenter: JUNCA, Howard

Dairy products are a key human food source worldwide. Bovine subclinical mastitis, i.e. high somatic cell counts in milk (SSC), is very common in dairy cows posing a negative effect in production, food safety, economy and environment. In healthy cattle, bovine immune system together with commensal bacteria prevent teat canal (TC) damage and intramammary infections. We performed an extensive study of a 250 dairy cow cohort in two farms in Northeastern Germany. Milk samples at different lactation stages revealed a healthy core microbiota of Glutamicibacter, and Romboutsia among others. Microbiota of animals with elevated SSC showed significant differences in diversity and composition being dominated by Streptococcus uberis, Staphylococcus (S.) aureus, S. chromogenes, or Corynebacterium bovis. Several antibiotic-resistant bacterial strains could be isolated. Whole genome sequencing of E. coli isolates detected resistance genes with 1/4 carrying blaCTX-M-1. Experiments with bovine mammary epithelial cells vs. selected phenotypes, phylogenies and interactions of mastitis pathogens isolated within this study are currently being performed. This study on a dairy cow cohort is one of the most extensive and precise to date with respect to the milk

microbiota characterization, representative bacterial genomes sequencing and profiling, identification of dysbiosis and possible etiological agents. Studies of factors promoting resistance to colonization in the TC are currently in process.

[64] The role and function of lipid-reactive guinea pig T cells in mycobacterial granuloma formation and maintenance (11:00 AM, 1 hour)

Presenter: ECKHARDT, Emmelie

The guinea pig is a naturally susceptible host for virulent mycobacteria. After infection granulomas indistinguishable from those in human tuberculosis patients develop. Like humans, guinea pigs express a functional CD1 system and therefore are an ideal animal model to study the lipid-specific immune responses in the host-pathogen interplay. Guinea pigs were either immunized with the vaccine strain Bacille-Calmette-Guérin (BCG) or liposomes containing the lipid mycobacterial antigen Phosphatidyl-Inositol-hexa-Mannoside (PIM6). After twelve weeks they were challenged with Mycobacterium tuberculosis (Mtb). 4 weeks after infection, blood was obtained, the animals were euthanized and dissected. The groups were compared with respect to antigen-specific T-cell-proliferation, pathology and histopathology. Using RT-qPCR expression of cytokines and CD1-molecules was assessed. Vaccinated animals mount a robust CD1b-restricted T-cell response to PIM, and this is accompanied by an elevated CD1b expression in vaccinated animals as shown by RT-qPCR and In-situ-hybridisation. After infection differences are observed in the upregulation of inflammatory cytokines and chemokines between the groups. Infection with Mtb results in local granuloma formation. Despite the absence of clinical symptoms, infected guinea pigs develop systemic infection with granulomas in lung, spleen and liver. Vaccinated animals show reduced granuloma formation and are protected from mycobacterial dissemination.

[61] Multidrug-resistant Enterobacterales in wastewater from German slaughterhouses (11:00 AM, 1 hour)

Presenter: KLEIST, Jette F.

Antibiotic-resistant *Enterobacterales (E.)* are regularly detected in livestock. As pathogens, they cause difficult-to-treat infections in humans and animals and, as commensals, they may serve as a source of resistance features for other bacteria. Slaughterhouses produce significant amounts of wastewater putatively containing antimicrobial-resistant bacteria (AMRB), which are released into wastewater treatment plants and subsequently the environment. Here, we analyzed the wastewater from seven slaughterhouses (pig and poultry) in Germany for the occurrence of extended-spectrum β-lactamase (ESBL)-producing and colistin-resistant *E.* The overall 25 ESBL-producing bacterial strains isolated from poultry slaughterhouses were multidrug-resistant (MDR), which is defined as resistance against a minimum of three different antimicrobial classes. In wastewater from pig slaughterhouses, 64 % were MDR. Regarding the last-resort antibiotic colistin, resistant *E.* were detected in 54 % of poultry and 21 % of pig wastewater samples. Carbapenem resistance was not detected. AMRB were found directly during discharge of wastewater from abattoirs into downstream water bodies (i.e., rivers), which highlights the role of slaughterhouses for environmental surface water contamination and the continuous need of surveillance studies. We prospectively plan to conduct additional investigations addressing the emergence of AMRB in waste- and surface water and associated environmental locations.

[60] One Health resistome analysis in Western-Pomerania (11:00 AM, 1 hour)

Presenter: HOMEIER-BACHMANN, Timo

Infections by multidrug-resistant organisms (MDROs) pose a serious global health threat. Metagenomic analysis provides the possibility to characterize the bacterial resistome in-depth and reveals insights into the abundance and diversity of antimicrobial resistance genes (AMRG). Regional AMR data are often missing, however, they are pivotal for insights in MDRO transmission routes among human and veterinary medicine as well as husbandry, wildlife and the environment. For this project, we initially performed metagenomic profiling of wildlife fecal samples collected from Western Pomerania (wild boar and deer). The results were then compared to samples from dairy farms, which also stem from Western Pomerania. The overall wildlife resistome demonstrated significantly smaller normalized counts for AMRG compared to livestock samples. The AMRG levels were lower in wild ruminants than in wild boar. We observed significant differences between the farms investigated, particularly in the proportions of tetracycline and beta-lactam resistance genes, which seemingly correspond to the antibiotics predominantly used on the respective farm. Our regional analyses helped to eliminate white spots on the Pomeranian AMR map. The results of this pilot study call for future studies with additional wildlife samples from this region (wild boar, deer, gulls) as well as samples from cattle and pig farms. To estimate the anthropogenic influence, additional wastewater samples will also be included.

[56] Identification and characterisation of the novel Macrolide-Lincosamide-Streptogramin B resistance gene erm(54) in LA-MRSA ST398 (11:00 AM, 1 hour)

Presenter: KRÜGER, Henrike

A total of 178 porcine livestock-associated methicillin-resistant *Staphylococcus aureus* (LA-MRSA) isolates collected in Germany from 2007 to 2019 were investigated for novel antimicrobial resistance genes. Whole-genome sequences were obtained via Illumina MiSeq and PacBio Sequel II platforms followed by hybrid assembly. Plasmid pHKS3860 was transferred into *S. aureus* RN4220 by electrotransformation. Antimicrobial susceptibility testing according to CLSI confirmed the functionality of

erm(54). Moreover, a specific *erm*(54)-PCR assay was developed. A new MLSB resistance gene, *erm*(54), was found on a non-conjugative plasmid of 36,929 bp, designated pHKS3860, in a LA-MRSA isolate of sequence type (ST) 398. This gene coded for a 23S rRNA methylase of 245 amino acids (aa) that was next-related to Erm(B) (72%). The transferred *erm*(54) led to distinctly elevated minimal inhibitory concentrations of MLSB antibiotics. The *erm*(54) gene was expressed constitutively. A complex regulatory region comprising a small reading frame for a protein of 30 aa and seven pairs of inverted repeats, which can form different mRNA secondary structures, were detected upstream of *erm*(54). Plasmid pHKS3860 also harboured an *ica* gene cluster and copper, mercury and cadmium resistance genes. In conclusion, the novel *erm*(54) gene was identified in porcine LA-MRSA ST398. Its co-location on a plasmid with heavy metal resistance genes might increase the risk for co-selection.

[45] Current knowledge and education of the general public in Nigeria and Bangladesh on AMR: Why it is important to raise awareness in a One Health approach. (11:00 AM, 1 hour)

Presenter: OJO, Michael Olaoluwa

Antimicrobial Resistance (AMR) remains a threat to human and animal health sectors. Ignorance and misinformation are major barriers to achieving antibiotic stewardship interventions. This study focused on assessing public awareness and knowledge of antibiotic use and AMR in human and animal sectors. This is to identify factors influencing the public's knowledge of antibiotic use and the onset of resistance. Study participants in Nigeria and Bangladesh were invited through networks to fill out the online questionnaire. Convenience and purposive sampling methods were adopted and only persons ≥ 16 years of age participated. Data analysis was carried out with R studio and Microsoft Excel. There were 516 responses, 85.7% in Nigeria and 14.3% in Bangladesh. A majority (75.8%) have heard about antibiotic resistance but the response revealed they misunderstood the proper use of antibiotics. Also, 54.3% are unaware that resistant microbes can spread human to human, while 62.8% do not know that they can be transmitted from animals to humans. The health professionals were more aware than other participants in the survey. Overall, there was a large gap between knowledge and practice among the general public. It shows that the majority of the study population misunderstood the concept of AMR microbes, their spread from animals to humans and from humans to humans, thus, indicating the need for one health awareness on AMR.

[43] Quality control range development for biocide susceptibility testing (11:00 AM, 1 hour)

Presenter: FESSLER, Andrea

Objective Validation of laboratory experiments is a crucial step. So far, neither quality control (QC) strains nor QC ranges for biocide susceptibility testing (BST) had been available. The aim of this study was to fill these gaps. Methodology As QC strains, four well-defined laboratory reference strains (*Staphylococcus aureus* ATCC® 6538, *Enterococcus hirae* ATCC® 10541, *Escherichia coli* ATCC® 10536 and *Pseudomonas aeruginosa* ATCC® 15442), which have been used previously for biocide efficacy testing, were selected for an interlaboratory trial. Eleven laboratories participated in the development of BST QC ranges for four biocides (benzalkonium chloride, chlorhexidine, octenidine and polyhexanide). Performance of three different lots of tryptic soy broth was tested using the broth microdilution method. The data was subsequently evaluated using the RangeFinder software. Results Per reference strain-biocide combination, 330 MIC values were evaluated. All three media lots showed comparable results and QC ranges were developed for all reference strain-biocide combinations, except for *P. aeruginosa* ATCC® 15442 with the two biocides chlorhexidine and polyhexanide. The development of the latter two QC ranges was not possible, due to the limited solubility of the biocides in the test range required for *P. aeruginosa* ATCC® 15442. Conclusion The 14 newly developed QC ranges, comprising three to five dilution steps, will contribute to the BST validation in the future.

[41] Identification of multidrug-resistant Pasteurellaceae carrying novel integrative and conjugative elements (11:00 AM, 1 hour)

Presenter: SCHINK, Anne-Kathrin

Objectives In the pathogenesis of bovine respiratory disease (BRD), Mannheimia haemolytica and Pasteurella multocida play important roles. Therefore, Pasteurellaceae isolates from Germany with rarely occurring phenotypic multidrug-resistance were analysed for the genetic basis. Material and methods Lung samples taken at necropsy from a severe BRD case of a calf were subjected to routine microbiological diagnostics. The antimicrobial susceptibilities of M. haemolytica IMT47952 and P. multocida IMT47951 were determined. Hybrid assembly of MiSeq and MinION reads resulted in closed genomes of both isolates. Results Both isolates were multidrug-resistant. M. haemolytica IMT47952 carried the resistance genes sul2, catA3, floR, tet(Y), strA-strB, mef(C) and mph(G) as part of the novel integrative and conjugative element (ICE) Tn7406. In P. multocida IMT47951, the resistance genes sul2, strA-strB, tet(H) and aph(3')-Ia were located within the novel ICE Tn7407. Chromosomal mutations accounting for macrolide, fluoroquinolone or trimethoprim resistance were also detected. Conclusions The resistance genes tet(Y), mef(C) and mph(G) have not been identified in M. haemolytica before. Moreover, the first occurrence of multidrug-resistance mediating ICEs in respiratory pathogens in Germany is alarming as these elements may diminish treatment options and pose a risk not only for animal, but also for human health, if transferred via the food chain or established in an environmental reservoir.

[35] S. aureus colonization in adult mice induces a Th17-dominated immune response (11:00 AM, 1 hour)

Presenter: HOLTFRETER, Silva

Staphylococcus aureus is a zoonotic pathobiont that colonizes and infects a broad host range. These versatile bacteria persistently colonize their hosts, a feature that could so far not be mirrored in animal models. We have recently established a persistent colonization model in mice using a mouse-adapted *S. aureus* strain. Here, we aimed at unraveling the innate and adaptive immune response to persistent nasal colonization using multi-dimensional flow cytometry. We set-up an *S. aureus*-positive breeding colony of C57BL/6N mice to obtain offspring that are naturally colonized with *S. aureus* after birth (neonatal colonization). In parallel, we colonized 9-week-old mice by intranasal inoculation with *S. aureus* (adult colonization). Both groups were persistently colonized for at least 28 days, reaching comparable bacterial loads in the nose and cecum. Overall, adult colonization seemed to induce a stronger immune response than neonatal colonization, best exemplified by an increased frequency of Th17 cells in lungs and cervical lymph nodes of adult, but not neonatal colonized mice. Moreover, CD8 effector T cells were increased in cervical lymph nodes of adult colonized mice. To conclude, *S. aureus* colonization during adulthood strongly primes the adaptive immune system, while neonatal colonization results in milder responses. Future work will aim at unraveling the impact of pre-existing *S. aureus* colonization on the course of zoonotic viral respiratory infections.

[33] A proteomic approach towards the understanding of african swine fever pathogenicity (11:00 AM, 1 hour)

Presenter: WÖHNKE, Elisabeth

African swine fever, a highly lethal viral disease of swine (*Sus scrofa*), poses a threat to domestic and wild suids world-wide. Currently, neither vaccine nor treatment is available against its causative agent, African swine fever virus (ASFV). For this highly complex dsDNA virus numerous genomic variations affecting its virulence have been identified. However, the molecular basis of the different clinical outcomes is largely unknown. Using quantitative label-free mass spectrometry, we compared the proteomes of monocyte-derived macrophages after in-vitro infection with two closely related ASFV genotype II isolates of different pathogenicity, the highly pathogenic “Armenia 2008” and the moderately pathogenic “Estonia 2014” strains. The expression patterns of the viral proteins were very similar with the exception of the genes not present in ASFV “Estonia 2014” due to deletions within its genome. The observed host proteome response to infection was also very similar irrespective of the ASFV strain used. Pathway analysis showed that both strains impacted on the immune response and mitochondrial processes, and induced ER-stress.

[28] Defective wound healing and antimicrobial drug resistance – a target for gas plasma therapy? (11:00 AM, 1 hour)

Presenter: CLEMEN, Ramona

Novel bacterial strains have developed that are resistant to antibiotics and other drugs. Excessive microbial growth and therapies that fail to reduce wound contamination in hard-to-heal wounds and chronic wounds are challenging for patients and health care systems. Gas plasma technology generates an unmatched variety of long- and short-lived reactive species (ROS/RNS) with immunostimulatory and antimicrobial functions. Gas plasma treatment of chronic injuries and pathogen-related skin diseases showed efficacy in controlling infections, promoting wound healing, and tissue regeneration. Still, direct evidence of gas plasma to control the growth and dissemination of resistant bacteria in wounds is scarce. The BMBF-ANR-funded multicenter-project Plasfect follows an integrative approach from physics to biology and medicine to investigate and optimize the use of plasma to combat Antimicrobial resistance(AMR) in defective wound healing. A newly designed gas plasma multijet is being tested for its antimicrobial effectiveness. For the marketed and certified gas plasma jet kINPen, the ROS/RNS output chemistry will be optimized to find increased anti-infective settings. The proposed superior effect will be tested in infected wounds in vivo. Furthermore, customized NanoString technology is tested to improve the parallel identification of drug-resistance genes in patient chronic wounds. Together, the project’s holistic approach aims to improve clinical wound AMR management in the future.

[27] Recurring Issues in the Development of Vaccines against AMR Infections: Results from the COMBINE Vaccine Expert Workshop (11:00 AM, 1 hour)

Presenter: MARCHIORO, Linda

Only few of the currently marketed vaccines have the potential to limit AMR, and no vaccines against ESCAPE pathogens are licensed. The COMBINE project aims to identify factors associated with late development failures of vaccine candidates against AMR and to improve translation and clinical trial design. In February 2021, the Paul-Ehrlich-Institut, on behalf of COMBINE, organised a Vaccine Expert Workshop to collect typical problems in the development of vaccines against AMR infections. Seventeen project-external chairs and speakers discussed recurring problems in the development of S. aureus, C. difficile, K. pneumoniae, extraintestinal pathogenic E. coli, and aspects of clinical trial design. The experts mentioned the gaps in our understanding of the pathogenesis of the disease, the role of pre-colonisation and the optimal targets as well as the limitations of current animal models in predicting vaccine efficacy as recurring issues in the pre-clinical development. The three most common problems in clinical development were the lack of robust correlates (surrogates) of protection, the uncertainties around risk factors,

and the relatively low incidence of ESCAPE infections, which hinder the feasibility of pivotal clinical trials. We are planning an integrative, data-driven analysis to inspect and validate the hypotheses generated in the workshop. This work has received support from the EU/EFPIA Innovative Medicines Initiative 2 Joint Undertaking (COMBINE grant n° 853967).

[20] Investigation of antimicrobial-resistant E. coli and antibiotic residues from a clinic to the Baltic Sea (11:00 AM, 1 hour)

Presenter: LÜBCKE, Phillip

The emergence of antimicrobial-resistant (AMR) Enterobacteriaceae not only in clinics but also the environment has been previously described. Extended-spectrum beta-lactamase (ESBL)-producing *E. coli* (ESBL-PE) is here a prime example. Over- and misuse of antibiotics mainly drive the emergence of AMR bacteria with not only therapeutic applications resulting in antibiotic selection pressures but also antibiotic residues in sewage and wastewater. Here, we investigate water samples from clinical sewage, a wastewater treatment plant (WWTP) and the Baltic Sea in Western Pomerania. We take samples over a period of one year and screen them for the occurrence of ESBL-PE and antibiotic residues. In addition, we collect clinical ESBL-PE directly from the hospital to tackle the way of this exemplary bacterial pathogen from the clinic to the environment. We characterize the bacterial isolates geno- and phenotypically in-depth including whole-genome sequence and phylogenetic analysis to better understand the exact associations among clinic, WWTP and the environment. Until now, ESBL-PE were mainly found in the clinical sewage and WWTP samples, which suggests that current wastewater treatment is insufficient. More severely, we found ESBL-PE in the Baltic Sea demonstrating the broad occurrence of these potentially pathogenic bacteria. The analysis of connections among isolates from the different locations and the presence of antibiotic residues is currently under investigation.

[11] Dissemination of ESBL-producing Enterobacteriaceae in two Black-Headed Gull colonies in Western Pomerania (11:00 AM, 1 hour)

Presenter: BRENDECKE, Jana

Antimicrobial-resistant (AMR) bacteria incl. extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae do not only occur in medical contexts but also in wildlife. To investigate 1) whether ESBL-*Escherichia (E.) coli* and *Klebsiella (K.)* sp. occur in nature conservation areas, 2) their geno- and phenotypic characteristics, 3) their dissemination over time, and 4) the occurrence of antibiotic residues, fecal samples from Black-Headed Gulls were taken from two islands in Western Pomerania (Riether Werder [RW] and Böhmke [B]). So far, samples include adult birds (n=211) and their nestlings (n=99). In addition, collective fecal samples (n=29) were collected. The latter were screened for ESBL-bacteria, the swab samples also for non-ESBL-isolates on chromogenic plates (+/- cefotaxime). API ID analysis confirmed bacterial species. All isolates are currently investigated for the carriage of additional AMR features and ESBL-producers were subjected to whole-genome sequencing. From RW, only one ESBL-*E. coli* was detected in the collective fecal samples, while none in the swab samples. On B, 2% ESBL-*E. coli* were detected in the adult swabs and 4% in the nestlings. In the collective fecal samples, 28.57 % ESBL-*E. coli* and one ESBL-*K*. sp. were found. Additionally, the samples carried numerous non-ESBL-isolates. We found AMR bacteria in wild birds, which have the potential to infect humans and animals. This highlights the importance of the One Health approach.

[8] Fecal excretion of ESBL-E. coli from calves fed with pooled colostrum (11:00 AM, 1 hour)

Presenter: BACHMANN, Lisa

The prevalence of *E. coli* carrying extended-spectrum beta-lactamase (ESBL) in young calves is higher than in older cattle. As part of another study, calves were fed with pooled colostrum. In this context, the objective of the present study was to determine whether and to what extent the calves show fecal ESBL-*Enterobacterales* carriage. Right after birth, 15 male calves were fed with 3L of pooled colostrum on a dairy farm. Then, they were transported individually to an experimental barn, fed with milk replacer and were separated from each other. On day 1, 5 and 8 of life, fecal swabs were taken and preserved with Amies-medium, followed by an examination for the occurrence of ESBL- *Enterobacterales*. Due the fact that we found high fecal ESBL-*E. coli* loads in the calves, a pooled colostrum sample was also cultivated and similarly processed. All ESBL-*E. coli* were subsequently subjected to whole-genome sequence (WGS) analysis. Already on the first day of life, 14 of 15 calves were tested positive for ESBL-*E. coli*, although they had neither spatial nor temporal contact with each other. In the colostrum sample, ESBL-*E. coli* and ESBL-*Enterococcus cloacae* were found. The results of the WGS analysis suggest a direct transmission of ESBL-*E. coli* via colostrum. ESBL-*E. coli* originating from colostrum might thus be able to colonize the intestine of neonatal calves leading to further release of resistant bacteria into the environment.

Session 3a: AMR, Vaccinology and Prevention (12:00 PM - 1:15 PM)

[122] COVID-19: An urgent call for a new kind of Health Professional (12:00 PM, 30 minutes)

Presenter: AMUASI, John

Humans, animals (including insects), plants, and the abiotic resources of our shared ecosystems are fundamentally interconnected. Though the nature of our interrelation varies over time and space, as well as across species and human cultures, the past century has been one of apparent human dominance over, and undeniable human impact on, the biosphere. This impact takes the form of industrialization, urbanization, and globalization, all of which are developmental trajectories that, by certain standards, have advanced health in unprecedented ways, but have also created multiple new health challenges and operated at the expense of both global health equity and planetary boundaries. Over the past decade, climate change has accelerated, biodiversity has rapidly declined, animal and environmental health are at stake, and humans have become increasingly vulnerable to a range of global health threats spanning infectious diseases, antimicrobial resistance, and non-communicable diseases. Pandemics, resulting from spill-over events and/or accelerated transmission involving infectious pathogens, can culminate in severe global health crises and economic catastrophe as evidenced by the SARS-CoV-2 pandemic which likely began at the human-animal-environment interface - where people and animals interact with each other in their shared environment, but emerged in December 2019 in Wuhan, China. Beyond the transmission of pathogens known to originally affect humans to other animals or vice-versa, is the fact that infectious agents reproduce/replicate and evolve. SARS-CoV-2 is largely thought to be of bat origin but is evolving in the human population with new variants and has already been shown to have been transmitted back to feline, bovidae, cervidae and mustelidae families. The 2014-2016 West African Ebola epidemic and the ongoing COVID-19 pandemic tend to be the focus in building health surveillance, early warning, and emergency response systems at both local and international levels. However infectious processes among non-human species clearly deserve equal attention not only because of their health impact but the implications for biodiversity conservation, the sustainability of future food systems and life on earth. This calls for a sustained One Health approach to addressing the COVID-19 pandemic, as well as other pandemic- and panzootic-prone diseases. Although wild reservoirs of novel pathogens with pandemic and panzootic potential remain poorly understood, they are of high relevance to health, and some research has also highlighted the importance of incorporating wildlife as sentinels into integrated surveillance systems. Four UN bodies known as the quadripartite; the Food and Agriculture Organization (FAO), the World Organization for Animal Health (OIE), the World Health Organization (WHO), and the UN Environment Programme have come together to officially recognize the serious risks to both animal and human health and the far-reaching impacts on economies and livelihoods of pandemic-prone diseases like COVID-19. Interventions such as assembling and analysis of big data for surveillance; building robust human and physical infrastructure for drugs, diagnostics, and vaccines research; infrastructure for cold chain and vaccine delivery; communication on food hygiene and food preparation; waste disposal and waste management; can be efficiently applied to both threats of pandemic- and panzootic-prone diseases. The interconnectedness of lifeforms within our shared environment, the complicated nature of COVID-19 and its drivers i.e. the pivotal role played by the natural and built shared environments, as well as climate, and implications for tailored integrated approaches to mitigation strategies makes COVID-19 the “super wicked” challenge for the decade to which only a concerted, One Health approach spear-headed by a new multidisciplinary army of “One Health Professionals”, could offer insights and solutions.

[12] PreProBiotics – Decolonization of antibiotic-resistant bacteria from the gut environment of animals using combined pre- and probiotic interventions (12:30 PM, 10 minutes)

Presenter: OSBELT, Lisa

Multi-drug resistant (MDR) pathogens, including extended-spectrum β-lactamases-(ESBL)-producing E. coli and carbapenem-resistant K. pneumoniae, have been increasingly reported not only in human and veterinary medicine but also wildlife and the environment. Microbiota-based approaches, such as the use of bacteria or natural compounds to combat the spread of MDR bacteria within and between hosts have demonstrated promising results in preclinical and mouse models. In this study, we investigated 1) the level of natural colonization resistance (CR) against MDR pathogens in fecal samples collected from livestock and wild animals, and 2) the capacity of a recently identified probiotic candidate and selected natural compounds to reduce the colonization potential of MDR bacteria. In brief, CR against MDR bacteria varied between wild animals and corresponding livestock and human samples. Moreover, we identified inhibitory activities of our probiotic candidate against MDR E. coli and K. pneumoniae in samples originating from different hosts. Culture-dependent and independent approaches are used to identify signatures identified with high natural CR and probiotic activity to gain functional insights and select optimal probiotic candidates. We envision that a prophylactic administration of probiotic bacteria could reduce the transmission and spread of MDR pathogen in the One Health context, also in livestock.

[9] Promoting gut decolonization of multi-drug resistant bacteria via the microbiome (12:40 PM, 10 minutes)

Presenter: WENDE, Marie

The fight against multi-drug resistant (MDR) Enterobacteriaceae (MDR-E) has been declared as a high priority by the WHO. Colonization of the gut with MDR-E is associated with an increased risk of bloodstream and systemic infections as well as the dissemination within the community. Due to variable gut colonization potential of individuals towards MDR-E, we hypothesized that the gut microbiota is a great source for probiotics, with the ability to selectively decolonize MDR-E. To identify microbiome and commensal bacteria with protective properties we established an ex vivo assay by spiking human fecal samples or content from mice with MDR E.coli strain and commensal bacteria. As a resource for the identification of potentially probiotic bacteria, a strain collection was generated from 250 donors. Using this assay we were able to identify specific commensal strains that inhibited the growth of MDR E. coli strains after co-cultivation. To further characterize the protective effect, competition experiments in mice were performed. Notably, after administration of a probiotic strain SPF mice were able to promote a complete clearance of a MDR

E. coli strain from the gut. For promising candidates we intend to identify their activity spectrum, their metabolic niche and potential cooperation partners as well as to gain mechanistic insights using loss-of-function genetic screens.

[81] Slaughterhouse wastewater as a reservoir of plasmids harboring blaCTX-M genes in Klebsiella pneumoniae and its impact in a “One Health” perspective (12:50 PM, 10 minutes)

Presenter: GARCÍA-MENIÑO, Isidro

Background Klebsiella pneumoniae (KP) is an opportunistic bacterium of clinical concern that can cause a broad range of infections in hospitalized people. Their occurrence in the gastrointestinal tract of animals/humans may also support their role as distributors of mobile resistance genes (esp. ESBL genes). Currently, comparative data on the diversity of plasmids from the compartments is lacking. Materials and Methods Plasmid of blaCTX-M-positive KP (CTX-M-15; n=42 and CTX-M-1; n=24), from wastewater of two poultry and pig slaughterhouses as well as their receiving municipal wastewater treatment plants (mWWTPs) were characterized (PFGE, WGS), reconstructed and analyzed for their transmissibility. Results blaCTX-M-1 was mainly detected in KP from the slaughterhouse wastewater (63.1% vs. 0% obtained from mWWTPs), while blaCTX-M-15 was broader disseminated in the compartments. Phylogenetic analysis revealed a distinct genetic diversity between the individual *bla*CTX-M plasmid types, which suggests an evolutionary adaption to their sources. Here, the blaCTX-M plasmids were primary assigned to the IncF and IncR groups. Both types seem to play an important role for their spread within Enterobacterales in combination with its transfer systems. Conclusions Slaughterhouse wastewater are hotspots for KP carrying transmissible ESBL plasmids adapted to their specific ecosystems. A further public health risk by their spread and further evolutionary adaption cannot be excluded.

[111] Q & A (1:00 PM, 15 minutes)

Lunch break / Networking (1:15 PM - 2:30 PM)

Session 3b: AMR, Vaccinology and Prevention (2:30 PM - 3:45 PM)

[121] Response to High-Consequence Viral Pathogens (2:30 PM, 30 minutes)

Presenter: FELDMANN, Heinz

Emerging infectious diseases of zoonotic origin are shaping today's infectious disease field more than ever. Despite better knowledge and success in the development of medical countermeasures, worldwide public health remains particularly vulnerable against emerging viruses that cross the species barrier into humans. Animal modeling is a pivotal step in our response to emergence. Those models are instrumental for studying pathogenesis and host responses to establish concepts for countermeasure development. Subsequently, animal disease models are crucial for the licensing pathway as efficacy testing of therapies and vaccines for many of these viral pathogens cannot be achieved in humans. Research strategies will be discussed using relevant examples. Preparedness and response for emerging infectious diseases will remain a top priority for infectious disease research and public/animal health in the future.

[38] Sewage treatment plants as hotspots of critical antibiotic resistances – and how to tackle this health threat (3:00 PM, 10 minutes)

Presenter: HINZKE, Tjorven

Antibiotic resistances spread at alarming pace, being associated with almost 5 million deaths in 2019 alone (The Lancet 2022, 10.1016/S0140-6736(21)02724-0). Sewage treatment plants (STPs) can be a potential source especially for non-naturally occurring antibiotic resistances. To assess whether STPs are indeed a source for antibiotic resistances, we conducted a comprehensive metaproteogenomic survey of two municipal STPs over two years. We show that STPs can be antibiotic resistance hotspots: Proteins for antibiotic resistances, including the critical carbapenemases, are significantly higher abundant in STP effluents as compared to the receiving environment. In addition, STP sludges, which are used as fertilizer, are enriched in antibiotic resistance proteins. Simultaneously, antibiotics themselves are being released by STPs. Thus, STP effluents can potentially increase and alter antimicrobial resistance prevalence in receiving environments. To tackle this highly concerning release of antibiotic resistances, we investigated the effect of physical cold plasma on antibiotic resistance protein abundance in hospital wastewater and STP effluent. Plasma treatment substantially decreases cultivable bacteria counts, and does not enrich resistances of special concern. Taken together, we show that active antibiotic resistances of high concern can reach the environment via STPs, and that physical cold plasma holds promise as additional sewage treatment step to combat this health threat.

[22] Tailored VRPs as the foundation of a zoonotic vaccine concept (ZOO-VAC) (3:10 PM, 10 minutes)

Presenter: DITTRICH, Anne

Vaccine vectors are a promising preventive strategy against zoonotic pathogens, but whether they can be applied in different susceptible species (as a One Health vaccine) to prevent infection or disease is not well understood. VEE replicon particles (VRPs) have been reported to target antigen presenting cells (APCs) in various mammalian species and thereby have the potential to protect against zoonotic pathogens across different hosts. However, the entry mechanism and the heterogeneity of VRP-susceptible APCs across different species remain unclear thereby preventing a deeper understanding of VEE-induced immunity. ZOO-VAC analyzes the heterogeneity of VRP-infected APCs from different species (mouse, bovine human) using single cell RNAseq in combination with bulk-RNAseq with subsequent bioinformatics analysis. In parallel, we setup in vitro cell culture systems to study the interaction with cell membranes and the entry mechanism of VRPs into susceptible cells. Modification of specific cellular factors will then allow us to directly validate our scRNAseq results. Our approach will allow predictions about the success of zoonotic vaccines and immune responses against viral vectors across different species by unravelling new potential regulated biomarkers and entry points in diverse cell types. Bulk-RNAseq of these cell populations will allow deeper insights in the structural adaptation induced by VRP infection and support the development of an optimized synthetic vaccine vector.

[29] From lab to field - Rabies control in Namibia as a One Health intervention (3:20 PM, 10 minutes)

Presenter: FREULING, Conrad

Rabies is a prime example for One Health, and the FAO-OIE-WHO Tripartite Collaboration considers rabies control as an entry point to strengthen and showcase the importance of multi-sectoral collaboration for the control of health risks at the human-animal ecosystems interface. In Namibia, a large but sparsely populated country in southern Africa, rabies is circulating both in domestic dogs as well as in wildlife, causing human cases and losses in livestock and game species. When Namibia implemented a National Dog Rabies Control Program in 2016, this initiative was supported through an OIE-coordinated project involving the OIE/WHO Reference Centre for Rabies at the Friedrich-Loeffler-Institute (FLI). In a cross-sectoral and interinstitutional approach, besides laboratory capacity building, improvement of rabies surveillance and KAP studies, a strong research component allowed to elucidate the ecological and spatiogenetic epidemiology of rabies in the country, the assessment of dog mass vaccination campaigns as well as novel cutting-edge approaches for vaccination of dogs and kudu antelopes with a third-generation oral rabies vaccine, which was studied in detail experimentally at the FLI before. In fact, oral rabies vaccination is promoted by WHO and OIE as important tool to end dog-mediated human rabies by 2030. Altogether, we demonstrate that long-lasting partnerships as opposed to short-lived projects can lead to both sustained improvements and successful research projects.

[112] Q & A (3:30 PM, 15 minutes)

Break (3:45 PM - 4:00 PM)

Final fairwell (4:00 PM - 4:30 PM)

Closing remarks (4:30 PM - 5:00 PM)